



2. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

3. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

4. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring

variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

5 The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

10 The present invention relates to a collection or library of novel nucleic acid sequences assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These sequences of the present invention are designated herein as 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782
15 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. The nucleic acids and polypeptides are provided in the Sequence Listing, wherein for the nucleic acids, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the
20 amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of the aforementioned nucleic acid sequences under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid
25 sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by said nucleic acid sequences, a polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence
30 information from the aforementioned nucleic acid sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID

NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. The sequence information can be a segment of any one of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 that uniquely identifies or represents the sequence information of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID

NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of 748
 5 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or novel
 10 segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath *et al.*, Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782
 15 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; a polynucleotide comprising any of the full length protein coding sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID
 20 NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782
 25 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide
 30 sequences set forth in 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289,

785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides
 5 recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a
 10 polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784
 15 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence
 20 Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

25 The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

30 The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture

medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath *et al.*, Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for

example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to
5 and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a
10 complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of
15 the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides
20 and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of
25 the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is
30 identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology. If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

5. DETAILED DESCRIPTION OF THE INVENTION

5.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded

molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

5 The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from
10 other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult
15 specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the
20 EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or
25 "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G
30 is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil).

Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides; more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et. al., (Walsh, P.S. *et al.*, 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. *et al.*, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. *et al.*, 1989,

Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. The sequence information can be a segment of any one of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 that uniquely identifies or represents the sequence information of that sequence of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position

(3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding
5 for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding
10 sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a
15 number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or
20 "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200
25 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including,
30 but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

5 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during
10 processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes),
15 covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created
20 using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with
25 consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression
30 in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the

polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological

macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source:

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the

recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium

pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences.

Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the

corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially

equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant,

amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65%

identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially

equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop

codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between

sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

5 The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a
10 virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be
15 confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each,
20 unless the context dictates otherwise.

5.2 NUCLEIC ACIDS AND PEPTIDES OF THE INVENTION

Sequences of the nucleic acids and peptides of the present invention are set forth in the Sequence Listing. Table 1 relates the SEQ ID's listed herein to their identification
25 in parent applications from which this application claims priority.

TABLE 1

Gene Family	Serial Number	Date Filed	SEQ ID NO. in Parent Applications	SEQ ID NO: in Current Application	File Name On CD
748	09/205,070	Dec. 3, 1998	SEQ ID NO: 1-45,196	748 SEQ ID NO: 1-45,196	N/A
	09/340,623	Jun. 28, 1999	SEQ ID NO: 1-45,196	748 SEQ ID NO: 1-45,196	

	09/898,888	Jul. 3, 2001	SEQ ID NO: 1-45,196	748 SEQ ID NO: 1-45,196	
752	09/205,155	Dec. 3, 1998	SEQ ID NO: 1-13192	752 SEQ ID NO: 1-13192	N/A
	09/359,922	Jul. 22, 1999	SEQ ID NO: 1-13192	752 SEQ ID NO: 1-13192	
	09/919,002	Jul. 30, 2001	SEQ ID NO: 1-13192	752 SEQ ID NO: 1-13192	
778	09/347,127	Jul. 2, 1999	SEQ ID NO: 1-94	778 SEQ ID NO: 1-94	N/A
	09/905,059	Jul. 12, 2001	SEQ ID NO: 1-94	778 SEQ ID NO: 1-94	
779	09/457,877	Dec. 8, 1999	SEQ ID NO: 1-128	779 SEQ ID NO: 1-128	N/A
	09/952,981	Sep. 14, 2001	SEQ ID NO: 1-128	779 SEQ ID NO: 1-128	
782	09/471,275	Dec. 23, 1999	SEQ ID NO: 1-10,451	782 SEQ ID NO: 1-10,451	Table2(782).doc
784	09/488,725	Jan. 21, 2000	SEQ ID NO: 1-10289	784 SEQ ID NO: 1-10289	Table3(784).doc; Table4(784).doc
	09/552,317	Apr. 25, 2000	SEQ ID NO: 1-10289	784 SEQ ID NO: 1-10289	
785	09/491,404	Jan. 25, 2000	SEQ ID NO: 1-3796	785 SEQ ID NO: 1-3796	(Table 5 and 7 are hard copies)
	09/922,279	Aug. 3, 2001	SEQ ID NO: 1-3796	785 SEQ ID NO: 1-3796	Table6(785).doc
787	09/496,914	Feb. 23, 2000	SEQ ID NO: 1-3960	787 SEQ ID NO: 1-3960	Table8(787).doc; Table9(787).doc; Table10(787).doc
	09/560,875	Apr. 27, 2000	SEQ ID NO: 1-3960	787 SEQ ID NO: 1-3960	
788	09/515,126	Feb. 28, 2000	SEQ ID NO: 1-14074	788 SEQ ID NO: 1-14074	Table11(788).doc; Table12(788).doc Table13(788).doc
	09/577,409	May. 18, 2000	SEQ ID NO: 1-14074	788 SEQ ID NO: 1-14074	
789	09/519,705	Mar. 7, 2000	SEQ ID NO: 1-6391	789 SEQ ID NO: 1-6391	Table14(789).doc; Table15(789).doc Table16(789).doc
	09/574,454	May. 19, 2000	SEQ ID NO: 1-6391	789 SEQ ID NO: 1-6391	
790	09/540,217	Mar. 31, 2000	SEQ ID NO: 1-30533	790 SEQ ID NO: 1-30533	Table17(790).doc; Table18(790).doc Table19(790).doc
	09/649,167	Aug. 23, 2000	SEQ ID NO: 1-30533	790 SEQ ID NO: 1-30533	
791	09/552,929	Apr. 18, 2000	SEQ ID NO: 1-5822	791 SEQ ID NO: 1-5822	Table20(791).doc; Table21(791).doc Table22(791).doc
	09/770,160	Jan. 26, 2001	SEQ ID NO: 1-5822	791 SEQ ID NO: 1-5822	
792	09/577,408	May. 18, 2000	SEQ ID NO: 1-8502	792 SEQ ID NO: 1-8502	(Table 23-25 are hard copies)

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778
5 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; a polynucleotide encoding any one of the peptide

sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides encoded by 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

5 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 15 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 20 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or a portion thereof as a probe. Alternatively, the polynucleotides of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 25 1-8502 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

 The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public 30 databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying

sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO:

1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785
SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID
NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-
8502 with a sequence from another isolate of the same species. Furthermore, to

- 5 accommodate codon variability, the invention includes nucleic acid molecules coding for
the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in
the coding region of an ORF, substitution of one codon for another codon that encodes the
same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present
10 invention, including 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID
NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289,
785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ
ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO:
1-8502, can be obtained by searching a database using an algorithm or a program.

- 15 Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search
for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul
S.F. et. al., J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search
against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are
20 also provided by the present invention. Species homologs may be isolated and identified
by making suitable probes or primers from the sequences provided herein and screening a
suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides
or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide
25 which also encode proteins which are identical, homologous or related to that encoded by
the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences
which encode variants of the described nucleic acids. These amino acid sequence
variants may be prepared by methods known in the art by introducing appropriate
30 nucleotide changes into a native or variant polynucleotide. There are two variables in the
construction of amino acid sequence variants: the location of the mutation and the nature

of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman *et al.*, *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by

the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells *et al.*, *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook *et al.*, *supra*, and *Current Protocols in Molecular Biology*, Ausubel *et. al.*, Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see

Sambrook J et. al., (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3,

pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in
 5 Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an
 10 expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two
 15 appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will
 20 include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat
 25 shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired
 30 characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a

structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan *et al.*, *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

5.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule

comprising the nucleotide sequence of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or antisense nucleic acids complementary to a nucleic acid sequence of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ

ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-

8502, antisense nucleic acids of the invention can be designed according to the rules of

5 Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, 10 for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to 15 increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, 20 hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, n6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, n6-adenine, 7-methylguanine, 25 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-n6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 30 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically

using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, 10 or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, 15 for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular 20 concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms 25 specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.*, (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, (1987) *FEBS Lett* 215: 327-330).

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5.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.*, U.S. Pat. No. 4,987,071; and Cech *et al.*, U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.*, (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the

four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.*, (1996) above; Perry-O'Keefe *et al.*,
5 (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of
10 single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.*, (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance
15 their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA
20 portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.*, (1996) *Nucl Acids Res* 24: 3357-63. For example, a
25 DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.*, (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a
30 5' PNA segment and a 3' DNA segment (Finn *et al.*, (1996) above). Alternatively,

chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.*, (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

5.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which

encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

5 The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). The host
10 cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa
15 cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can
20 also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

25 Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human
30 epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of

primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be

comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by

5 targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing

10 the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader

15 or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome.

20 The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result

25 in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No.

30 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et. al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et. al.; and International

ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and

purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded

5 polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells

10 which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes,

15 *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, *et al.*, in *Molecular Cloning: A Laboratory Manual*; Ausubel *et al.*, *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

20 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models

25 that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds

30 that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for 748 SEQ ID NO: 1-45,196, 752

SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502.

5 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

10 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For
15 example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that
20 are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein
25 that are important for protein function may be determined by the eMATRIX program.

 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

30 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors,

and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ (TOSOH Biosep LLC, Montgomeryville, PA) or Cibacrom blue 3GA Sepharose™ (Pharmacia, Piscataway, NJ); one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

20 **5.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE
IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., *et al.*, Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. *et al.*, J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. *et al.*, Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu *et al.*, J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer *et al.*, Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein

5.7 CHIMERIC AND FUSION PROTEINS

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival.

Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

5 A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends
10 as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can
15 subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et. al., (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the
20 fusion moiety is linked in-frame to the protein of the invention.

5.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to
25 restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (*e.g.*, adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (*e.g.*,
30 liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp. 25-20 (1998). For additional reviews of gene therapy technology

see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient
5 expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human
10 disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their
15 translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative
20 association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be
25 modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650,
30 PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA,

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences.

Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et. al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et. al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi *et al.*, each of which is incorporated by reference herein in its entirety.

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In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination (Capecchi, Science 244:1288-1292 (1989)). Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of

expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination (Capecchi, Science 244:1288-1292 (1989)). Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No.

5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT

Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

5.10 USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or
10 vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including
15 recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs,
20 (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of
25 the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

5.10.1 RESEARCH USES AND UTILITIES

30 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express

recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when
5 labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and
10 making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand
15 interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in
20 assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a
25 particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent
30 grade or kit format for commercialization as research products.

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and CaCo. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai *et al.*, J. Immunol. 137:3494-3500, 1986; Bertagnolli *et al.*, J. Immunol. 145:1706-1712, 1990; Bertagnolli *et al.*, Cellular Immunology 133:327-341, 1991; Bertagnolli, *et al.*, I. Immunol. 149:3778-3783, 1992; Bowman *et al.*, I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries *et al.*, J. Exp. Med. 173:1205-1211, 1991; Moreau *et al.*, Nature 336:690-692, 1988; Greenberger *et al.*, Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith *et al.*, Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring

proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In vitro* assays for Mouse Lymphocyte Function; Chapter 5 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger *et al.*, Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger *et al.*, Eur. J. Immun. 11:405-411, 1981; Takai *et al.*, J. Immunol. 137:3494-3500, 1986; Takai *et al.*, J. Immunol. 140:508-512, 1988.

10 **5.10.4 STEM CELL GROWTH FACTOR ACTIVITY**

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide 15 of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human 20 proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, 25 pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia 30 inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-

CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or *in vivo*. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell

populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more
5 differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus *et al.*, Differentiation, 48: 173-182, (1991);
10 Klug *et al.*, J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza *et al.*, Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an
antagonist of the polypeptide of the invention which would inhibit the effects of
15 endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson *et. al.*, Proc. Natl. Acad. Sci,
20 U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein Blood, 77: 2316-2321 (1991).

25 **5.10.5 HEMATOPOIESIS REGULATING ACTIVITY**

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of
factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in
30 supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating

various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to

5 prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of

10 the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral

15 progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

20 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et. al., Cellular Biology 15:141-151, 1995; Keller et al.. Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al.. Blood 81:2903-2915, 1993.

25 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et. al., eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al.. Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992;

30 Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et. al., eds.

Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al.. Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et. al., eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et. al., eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et. al., eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

10 **5.10.6 TISSUE GROWTH ACTIVITY**

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

15 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an
20 osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative
25 disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide
30 of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally

formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

5 Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention
10 may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or
15 inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);
20 International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J.
25 Invest. Dermatol 71:382-84 (1978).

5.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays
30 are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune

deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*,
in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as
effecting the cytolytic activity of NK cells and other cell populations. These immune
deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or
5 fungal infections, or may result from autoimmune disorders. More specifically, infectious
diseases caused by viral, bacterial, fungal or other infection may be treatable using a
protein of the present invention, including infections by HIV, hepatitis viruses, herpes
viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such
as candidiasis. Of course, in this regard, proteins of the present invention may also be
10 useful where a boost to the immune system generally may be desirable, *i.e.*, in the
treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present
invention include, for example, connective tissue disease, multiple sclerosis, systemic
lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
15 Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus,
myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.
Such a protein (or antagonists thereof, including antibodies) of the present invention may
also be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis,
serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis,
20 allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic
dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome,
allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant
papillary conjunctivitis and contact allergies), such as asthma (particularly allergic
asthma) or other respiratory problems. Other conditions, in which immune suppression is
25 desired (including, for example, organ transplantation), may also be treatable using a
protein (or antagonists thereof) of the present invention. The therapeutic effects of the
polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo*
animals models such as the cumulative contact enhancement test (Lastbom et al.,
Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54,
30 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and
murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful *in situations* of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been

used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow et al.. Science 257:789-792 (1992) and Turka et al.. Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (*e.g.*, a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with

a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells

5 express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected

10 tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta

15 chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated

20 protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing

30 Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al.. Proc.

- Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al.. J. Immunol. 128:1968-1974, 1982; Handa et al.. J. Immunol. 135:1564-1572, 1985; Takai et al.. I. Immunol. 137:3494-3500, 1986; Takai et al.. J. Immunol. 140:508-512, 1988; Bowman et al.. J. Virology 61:1992-1998; Bertagnolli et al.. Cellular Immunology 133:327-341, 1991; 5. Brown et al.. J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al.. J. Immunol. 137:3494-3500, 1986; Takai et al.. J. Immunol. 140:508-512, 1988; Bertagnolli et al.. J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al.. J. Immunol. 134:536-544, 1995; Inaba et al.. Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al.. Journal of Immunology 154:5071-5079, 1995; Porgador et al.. Journal of Experimental Medicine 182:255-260, 1995; Nair et al.. Journal of Virology 67:4062-4069, 1993; Huang et al.. Science 264:961-965, 1994; Macatonia et al.. Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al.. Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al.. Journal of Experimental Medicine 172:631-640, 1990.

- 30 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate

lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al.. Cytometry 13:795-808, 1992; Gorczyca et al.. Leukemia 7:659-670, 1993; Gorczyca et al.. Cancer Research 53:1945-1951, 1993; Itoh et al.. Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al.. Cytometry 14:891-897, 1993; Gorczyca et al.. International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al.. Blood 84:111-117, 1994; Fine et al.. Cellular Immunology 155:111-122, 1994; Galy et al.. Blood 85:2770-2778, 1995; Toki et al.. Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

5.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al.. Endocrinology 91:562-572, 1972; Ling et al.. Nature 321:779-782, 1986; Vale

et al.. Nature 321:776-779, 1986; Mason et al.. Nature 318:659-663, 1985; Forage et al.. Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

5.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

5 A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or
10 attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune
15 responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population
20 of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the
25 migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12,
30 Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et. al., J. Clin. Invest. 95:1370-1376, 1995; Lind et. al., APMIS 103:140-146, 1995; Muller et al Eur. J.

Immunol. 25:1744-1748; Gruber et. al., J. of Immunol. 152:5860-5867, 1994; Johnston et. al., J. of Immunol. 153:1762-1768, 1994.

5.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

5 A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, 10 surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al.. J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al.. Thrombosis Res. 45:413-419, 1987; Humphrey et al.. Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

20 5.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a 25 polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

30 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to

support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be

used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al.. J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al.. Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al.. Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al.. Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

5.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al.. Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al.. J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al.. J. Exp. Med. 169:149-160 1989; Stoltenborg et al.. J. Immunol. Methods 175:59-68, 1994; Stitt et al.. Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being

coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

5.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of

mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

5 Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic
10 collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

15 Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell
20 cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity
25 of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

5.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide
30 *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the

invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

5.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells

involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

5.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

5.10.17 NERVOUS SYSTEM DISORDERS

- Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:
- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
 - (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
 - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
 - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
 - (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

5 (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine
10 myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the
15 invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*,
e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
20 (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et. al., (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et. al., (1980, Exp.
25 Neurol. 70:65-82) or Brown et. al., (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction
30 velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

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5.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an

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immune response against such protein or another material or entity which is cross-reactive with such protein.

5.10.19 IDENTIFICATION OF POLYMORPHISMS

5 The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and
10 this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all
15 generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which
20 appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that
25 provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the
30 present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

5 5.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, 10 Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The 15 control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an 20 overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

5.11 THERAPEUTIC METHODS

25 The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

30

5.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention.

5 While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically,
10 the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water,
15 saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

20 5.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and
25 including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and
30 other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of

administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, 18th edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*,

When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a

therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present

invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

5.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the

compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

5.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95%

protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as sodium chloride injection, Ringer's injection, dextrose injection, dextrose and sodium chloride injection, lactated Ringer's injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral

ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including
5 lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium
10 alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different
15 combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or
20 magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in
25 conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*,
dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon
30 dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges

of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD

co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic

5 compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as 15 dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical 20 nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited 25 to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with 30 inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia,

trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response.

Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should

5 contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant

10 or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active

15 ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of

20 bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular

25 application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure

30 proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass,

aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending

physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

5.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a

circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

5 A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in
10 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of
15 circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount
20 and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine
25 plasma concentrations.

 Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of
30 the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

5.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

5.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein
5 can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence encoded by 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID
10 NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide
15 comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the
20 antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots
25 showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.
30 Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin (BCG) and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide

primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D.

- 5 Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition",
10 as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a
15 particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing
20 antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized *in vitro*. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The
25 lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma
30 cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For

example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

5 Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection,
10 Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be
15 assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal
20 antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for
25 this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown *in vivo* as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel
30 electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv

framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and
 5 typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986;
 10 Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise
 15 from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: *MONOCLONAL ANTIBODIES AND CANCER THERAPY*,
 20 Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, et al., 1985 In: *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96).

25 In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely
 30 inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly,

and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et. al., (Bio/Technology 10, 779-783 (1992)); Lonberg et. al., (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM (Abgenix Inc., Freemont, CA) as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a

rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

5 A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid
10 cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in
15 PCT publication WO 99/53049.

5.13.4 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S.
20 Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the
25 art including, but not limited to: (i) an F(ab')₂ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F(ab')₂ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 BISPECIFIC ANTIBODIES

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second
5 binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have
10 different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed
15 in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain,
20 comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For
25 further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface
30 comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody

molecule are replaced with larger side chains (e.g. tyrosine or tryptophan).

Compensatory “cavities” of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for
 5 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example,
 10 bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to
 15 thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

20 Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific
 25 antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific
 30 antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins

were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcRn, FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16), so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 HETEROCONJUGATE ANTIBODIES

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360;

WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et. al., Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 IMMUNOCONJUGATES

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca

americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, croton, saponaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{125}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al.. Science, 238: 1098 (1987).

Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

5.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily

appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which

allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to
5 identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means,
10 software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for
15 use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present
20 invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means.
25 Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern
30 (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for

conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

5.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al.. Nucl. Acids Res. 6:3073 (1979); Cooney et al.. Science 15241:456 (1988); and Dervan et al.. Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information

contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

5.16 DIAGNOSTIC ASSAYS AND KITS

5 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

10 In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention
15 under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

 In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so
20 that if a complex is detected, a polypeptide of the invention is detected in the sample.

 In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

 Conditions for incubating a nucleic acid probe or antibody with a test sample
25 vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such
30 assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock,

G.R. et al.. Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present

invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to

a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al.. Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al.. Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

5 In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the
10 expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment
15 capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al.. Nucl. Acids Res. 6:3073 (1979); Cooney et al.. Science 241:456 (1988); and Dervan et al.. Science 251:1360 (1991)) or to the mRNA itself (antisense -
20 Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences
25 of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to
30 generate a pharmaceutical composition.

5.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the present invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-14,074, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, *in situ* hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known

genetic and/or chromosomal mapping techniques. These techniques include *in situ* hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent *in situ* hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

5.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared from the sequences disclosed herein by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon® (DuPont). One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.*, (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating

any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups ($>NH$) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.* (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.* (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.* (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.* (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

5.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC

inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCpy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 μ g instead of 2-5 μ g); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed)

5 Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from
10 genomic DNA by methods known in the art.

5.22 PREPARATION OF DNA ARRAYS

The nucleic acid sequences disclose herein can be used to create arrays. Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an
15 array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same
20 genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using
25 a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the
30 membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell

plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

5.23 PREPARATION OF A UNIVERSAL SET OF PROBES

5 The nucleic acid sequences disclosed herein may be used to design universal hybridization probes for detecting genetic markers. Two types of universal sets of probes may be prepared. The first is a complete set (or at least a noncomplementary subset) of relatively short probes, for example all 4096 (or about 2000 non-complementary) 6-mers, or all 16,384 (or about 8,000 non-complementary) 7-mers. Full noncomplementary
10 subsets of 8-mers and longer probes are less convenient inasmuch as they include 32,000 or more probes.

A second type of probe set is selected as a small subset of probes still sufficient for reading every bp in any sequence with at least with one probe. For example, 12 of 16 dimers are sufficient. A small subset for 7-mers, 8-mer and 9-mers for sequencing double stranded DNA may be about 3000, 10,000 and 30,000 probes, respectively.

Probes may be prepared using standard chemistry with one to three non-specified (mixed A,T,C and E) or universal (e.g. M base or inosine) bases at the ends. If radiolabelling is used, probes may have an OH group at the 5' end for kinasing by radiolabelled phosphorous groups. Alternatively, probes labelled with any compatible system, such as fluorescent dyes, may be employed. Other types of probes, such as PNA (Protein Nucleic Acids) or probes containing modified bases which change duplex stability also may be used.

Probes may be stored in bar-coded multiwell plates. For small numbers of probes, 96-well plates may be used; for 10,000 or more probes, storage in 384- or 864-well plates is preferred. Stacks of 5 to 50 plates are enough to store all probes. Approximately 5 pg of a probe may be sufficient for hybridization with one DNA sample. Thus, from a small synthesis of about 50 mg per probe, ten million samples may be analyzed. If each probe is used for every third sample, and if each sample is 1000 bp in length, then over 30 billion bases (10 human genomes) may be sequenced by a set of 5,000 probes.

5.24 PROBES HAVING MODIFIED OLIGONUCLEOTIDES

Modified oligonucleotides may be introduced into hybridization probes described in section 5.23 and used under appropriate conditions therefor. For example, pyrimidines with a halogen at the C5-position may be used to improve duplex stability by influencing base stacking.

2,6-diaminopurine may be used to provide a third hydrogen bond in base pairing with thymine, thereby thermally stabilizing DNA-duplexes. Using 2,5-diaminopurine may increase duplex stability to allow more stringent conditions for annealing, thereby improving the specificity of duplex formation, suppressing background problems and permitting the use of shorter oligomers. The synthesis of the triphosphate versions of these modified nucleotides is disclosed by Hoheisel & Lehrach(1990).

One may also use the non-discriminatory base analogue, or universal base, designed by Nichols *et al.*, (1994). This new analogue, 1-(2'-deoxy-10'-D-ribofuranosyl)-3-nitropyrrole (M), was generated for use in oligonucleotide probes and primers for solving the design problems that arise as a result of the degeneracy of the genetic code, or when only fragmentary peptide sequence data are available. This analogue maximizes stacking while minimizing hydrogen-bonding interactions without sterically disrupting a DNA duplex.

The M nucleoside analogue was designed to maximize stacking interactions using aprotic polar substituents linked to heteroaromatic rings, enhancing intra- and inter-stand stacking interactions to lessen the role of hydrogen bonding in base-pairing specificity. Nichols *et al.*, (1994) favored 3-nitropyrrole-2'-deoxyribonucleoside because of its structural and electronic resemblance to p-nitroaniline, whose derivatives are among the smallest known intercalators of double-stranded DNA.

The dimethoxytrityl-protected phosphoramidite of nucleoside M is also available for incorporation into nucleotides used as primers for sequencing and polymerase chain reaction (PCR). Nichols *et al.*, (1994) showed that a substantial number of nucleotides can be replaced by M without loss of primer specificity.

A unique property of M is its ability to replace long strings of contiguous nucleosides and still yield functional sequencing primers. Sequences with three, six and nine M substitutions have all been reported to give readable sequencing ladders, and PCR

with three different M-containing primers all resulted in amplification of the correct product (Nichols *et al.*, 1994).

Probes may be retrieved one by one and added to subarrays covered by hybridization buffer. It is preferred that retrieved probes be placed in a new plate and labelled or mixed with hybridization buffer. The preferred method of retrieval is by accessing stored plates one by one and pipetting (or transferring by metal pins) a sufficient amount of each selected probe from each plate to specific wells in an intermediary plate. An array of individually addressable pipettes or pins may be used to speed up the retrieval process.

5.25 PREPARATION OF LABELED PROBES

The oligonucleotide probes may be prepared by automated synthesis, which is routine to those of skill in the art, for example, using an Applied Biosystems system. Alternatively, probes may be prepared using Genosys Biotechnologies Inc. Methods using stacks of porous Teflon wafers.

Oligonucleotide probes may be labeled with, for example, radioactive labels (^{35}S , ^{32}P , and preferably, ^{33}P) for arrays with 100-200 μm or 100-400 μm spots; non-radioactive isotopes (Jacobsen *et al.*, 1990); or fluorophores (Brumbaugh *et al.*, 1988). All such labeling methods are routine in the art, as exemplified by the relevant sections in Sambrook *et al.*, (1989) and by further references such as Schubert *et al.*, (1990), Murakami *et al.*, (1991) and Cate *et al.*, (1991), all articles being specifically incorporated herein by reference.

In regard to radiolabelling, the common methods are end-labeling using T4 polynucleotide kinase or high specific activity labeling using Klenow or even T7 polymerase. These are described as follows.

Synthetic oligonucleotides are synthesized without a phosphate group at their 5' termini and are therefore easily labeled by transfer of the ^{32}P or ^{33}P from [^{32}P]ATP or [^{33}P]ATP using the enzyme bacteriophage T4 polynucleotide kinase. If the reaction is carried out efficiently, the specific activity of such probes can be as high as the specific activity of the [^{32}P]ATP or [^{33}P]ATP itself. The reaction described below is designed to label 10 pmoles of an oligonucleotide to high specific activity. Labeling of different

amounts of oligonucleotide can easily be achieved by increasing or decreasing the size of the reaction, keeping the concentrations of all components constant.

A reaction mixture would be created using 1.0 μ l of oligonucleotide (10 pmoles/ μ l); 2.0 μ l of 10 x bacteriophage T4 polynucleotide kinase buffer; 5.0 μ l of [32 P]ATP or [33 P]ATP (sp. act. 5000 Ci/mmol; 10 mCi/ml in aqueous solution) (10 pmoles); and 11.4 μ l of water. Eight (8) units (10u/ μ l) of bacteriophage T4 polynucleotide kinase is added to the reaction mixture, mixed well, and incubated for 45 minutes at 37°C. The reaction is heated for 10 minutes at 68°C to inactivate the bacteriophage T4 polynucleotide kinase.

10 The efficiency of transfer of 32 P or 33 P to the oligonucleotide and its specific activity is then determined. If the specific activity of the probe is acceptable, it is purified. If the specific activity is too low, an additional 8 units of enzyme is added and incubated for a further 30 minutes at 37°C before heating the reaction for 10 minutes at 68°C to inactivate the enzyme.

15 Purification of radiolabeled oligonucleotides can be achieved by precipitation with ethanol; precipitation with cetylpyridinium bromide; by chromatography through Bio-gel P-60; or by chromatography on a Sep-Pak C₁₈ column (Pharmacia).

Probes of higher specific activities can be obtained using the Klenow fragment of *E. coli* DNA polymerase I to synthesize a strand of DNA complementary to the synthetic oligonucleotide. A short primer is hybridized to an oligonucleotide template whose sequence is the complement of the desired radiolabeled probe. The primer is then extended using the Klenow fragment of *E. coli* DNA polymerase I to incorporate [32 P] dNTPs or [33 P] dNTPs in a template-directed manner. After the reaction, the template and product are separated by denaturation followed by electrophoresis through a polyacrylamide gel under denaturing conditions. With this method, it is possible to generate oligonucleotide probes that contain several radioactive atoms per molecule of oligonucleotide if desired.

To use this method, one would mix in a microfuge tube the calculated amounts of [α - 32 P]dNTP's or [α - 33 P]dNTP's necessary to achieve the desired specific activity and sufficient to allow complete synthesis of all template strands. The concentration of dNTPs should not be less than 1 μ M at any stage during the reaction. Then add to the tube

the appropriate amounts of primer and template DNAs, with the primer being in three- to tenfold molar excess over the template.

Klenow buffer is then added and mixed well. 2-4 units of the Klenow fragment of *E. coli* DNA polymerase I would then be added per 5 µl of reaction volume, mixed and
5 incubated for 2-3 hours at 4°C. If desired, the process of the reaction may be monitored by removing small (0.1 µl) aliquots and measuring the proportion of radioactivity that has become precipitable with 10% trichloroacetic acid (TCA).

The reaction would be diluted with an equal volume of gel-loading buffer, heated to 80°C for 3 minutes, and then the entire sample loaded on a denaturing polyacrylamide
10 gel. Following electrophoresis, the gel is autoradiographed, allowing the probe to be localized and removed from the gel. Various methods for fluorophoric labeling are also available, as follows. Brumbaugh *et al.* (1988) describe the synthesis of fluorescently labeled primers. A deoxyuridine analog with a primary amine "linker arm" of 12 atoms attached at C-5 is synthesized. Synthesis of the analog consists of derivatizing 2 -
15 deoxyuridine through organometallic intermediates to give 5 (methyl propenoyl)-2 - deoxyuridine. Reaction dimethoxytrityl-chloride produces the corresponding 5 - dimethoxytrityl adduct. The methyl ester is hydrolyzed, activated, and reacted with an appropriately monoacylated diamine. After purification, the resultant linker arm nucleosides are converted to nucleoside analogs suitable for chemical oligonucleotide
20 synthesis.

Oligonucleotides would then be made that include one or two linker arm bases by using modified phosphoridite chemistry. To a solution of 50 nmol of the linker arm oligonucleotide in 25 µl of 500 mM sodium bicarbonate (pH 9.4) is added 20 µl of 300 mM FITC in dimethyl sulfoxide. The mixture is agitated at room temperature for 6 hrs.
25 The oligonucleotide is separated from free FITC by elution from a 1 x 30 cm Sephadex G-25 column with 20 mM ammonium acetate (pH 6), combining fractions in the first UV-absorbing peak.

In general, fluorescent labeling of an oligonucleotide at its 5'-end initially involved two steps. First, a N-protected aminoalkyl phosphoramidite derivative is added
30 to the 5'-end of an oligonucleotide during automated DNA synthesis. After removal of all protecting groups, the NHS ester of an appropriate fluorescent dye is coupled to the 5

-amino group overnight followed by purification of the labeled oligonucleotide from the excess of dye using reverse phase HPLC or PAGE.

Schubert *et al.* (1990) describes the synthesis of a phosphoramidite that enables oligonucleotides labeled with fluorescent tags to be produced during automated DNA synthesis.

Murakami *et al.* also described the preparation of fluorescein-labeled oligonucleotides.

Cate *et al.* (1991) describes the use of oligonucleotide probes directly conjugated to alkaline phosphatase in combination with a direct chemiluminescent substrate (AMPPD) to allow probe detection.

Labeled probes could readily be purchased from a variety of commercial sources, including GENSET, rather than synthesized.

Other labels include ligands which can serve as specific binding members to a labeled antibody, chemiluminescers, enzymes, antibodies which can serve as a specific binding pair member for a labeled ligand, and the like. A wide variety of labels have been employed in immunoassays which can readily be employed. Still other labels include antigens, groups with specific reactivity, and electrochemically detectable moieties.

In general, labeling of nucleic acids with electrophore mass labels ("EML") is described, for example, in Xu *et al.*, J. Chromatography 764:95-102(1997).

Electrophores are compounds that can be detected with high sensitivity by electron capture mass spectrometry (EC-MS). EMLs can be attached to a probe using chemistry that is well known in the art for reversibly modifying a nucleotide (*e.g.*, well known nucleotide synthesis chemistry teaches a variety of methods for attaching molecules to nucleotides as protecting groups). EMLs are detected using a variety of well known electron capture mass spectrometry devices (*e.g.*, devices sold by Finnigan Corporation). Further, techniques that may be used in the detection of EMLs include, for example, fast atomic bombardment mass spectrometry (see, *e.g.*, Koster *et al.*, Biomedical Environ. Mass Spec. 14:111-116(1987)); plasma desorption mass spectrometry; electrospray/ionspray (see, *e.g.*, Fenn *et al.*, J. Phys. Chem. 88:4451-59(1984), PCI Appln. No. WO 90/14148, Smith *et al.*, Anal. Chem. 62:882-89(1990)); and matrix-

assisted laser desorption/ionization (Hillenkamp, *et al.*, "Matrix Assisted UV-Laser Desorption/Ionization: A New Approach to Mass Spectrometry of Large Biomolecules," Biological Mass Spectrometry (Burlingame and McCloskey, eds.), Elsevier Science Publishers, Amsterdam, pp. 49-60, 1990); Huth-Fehre *et al.*, "Matrix Assisted Laser Desorption Mass Spectrometry of Oligodeoxythymidylic Acids," Rapid Communications in Mass Spectrometry, 6:209-13 (1992)).

In preferred embodiments, the EMLs are attached to a probe by a covalent bond that is light sensitive. The EML is released from the probe after hybridization with a target nucleic acid by a laser or other light source emitting the desired wavelength of light. The EML is then fed into a GC-MS (gas chromatograph-mass spectrometer) or other appropriate device, and identified by its mass.

5.26 PREPARATION OF SEQUENCING CHIPS AND ARRAYS

The nucleic acids of the present invention can be affixed to chips to create arrays. A basic example is using 6-mers attached to 50 micron surfaces to give a chip with dimensions of 3 x 3 mm which can be combined to give an array of 20 x 2020cm. Another example is using 9-mer oligonucleotides attached to 10 x 10 micron surface to create a 9-mer chip, with dimensions of 5 x 5 mm. 4000 units of such chips may be used to create a 30 x 30 cm array. In one embodiment the nucleic acids comprise an oligochip array in which 4,000 to 16,000 oligochips are arranged into a square array. A plate, or collection of tubes, as also depicted, may be packaged with the array as part of the sequencing kit.

The arrays may be separated physically from each other or by hydrophobic surfaces. One possible way to utilize the hydrophobic strip separation is to use technology such as the Iso-Grid Microbiology System produced by QA Laboratories, Toronto, Canada.

Hydrophobic grid membrane filters (HGMP) have been in use in analytical food microbiology for about a decade where they exhibit unique attractions of extended numerical range and automated counting of colonies. One commercially-available grid is Iso-GRID™ from QA Laboratories Ltd. (Toronto, Canada) which consists of a square (60 x 60 cm) of polysulfone polymer (Gelman Tuffryn HT-450, 0.4 micron pore size) on

which is printed a black hydrophobic ink grid consisting of 1600 (40 x 40) square cells. HCMF have previously been inoculated with bacterial suspensions by vacuum filtration and incubated on the differential or selective media of choice.

Because the microbial growth is confined to grid cells of known position and size on the membrane, the HGMF functions more like an MPN apparatus than a conventional plate or membrane filter. Peterkin *et al.* (1987) reported that these HGMFs can be used to propagate and store genomic libraries when used with a HGMF replicator. One such instrument replicates growth from each of the 1600 cells of the ISO-GRID and enables many copies of the master HGMF to be made (Peterkin *et al.*, 1987).

Sharpe *et al.* (1989) also used ISO-GRID HGMF from QA Laboratories and an automated HGMF counter (MI-I 00 Interpreter) and RP- 100 Replicator. They reported a technique for maintaining and screening many microbial cultures.

Peterkin and colleagues later described a method for screening DNA probes using the hydrophobic grid-membrane filter (Peterkin *et al.*, 1989). These authors reported methods for effective colony hybridization directly on HGMFs. Previously, poor results had been obtained due to the low DNA binding capacity of the epoxysulfone polymer on which the HGMFs are printed. However, Peterkin *et al.* (1989) reported that the binding of DNA to the surface of the membrane was improved by treating the replicated and incubated HGMF with polyethyleneimine, a polycation, prior to contact with DNA.

Although this early work uses cellular DNA attachment, and has a different objective to the present invention, the methodology described may be readily adapted for Format 3 SBH.

In order to identify useful sequences rapidly, Peterkin *et al.* (1989) used radiolabeled plasmid DNA from various clones and tested its specificity against the DNA on the prepared HGMFs. In this way, DNA from recombinant plasmids was rapidly screened by colony hybridization against 100 organisms on HGMF replicates which can be easily and reproducibly prepared. Manipulation with small (2-3 mm) chips, and parallel execution of thousands of the reactions. The solution of the invention is to keep the chips and the probes in the corresponding arrays. In one example, chips containing 250,000 9-mers are synthesized on a silicon wafer in the form of 8 x 8 mm plates (15 μ M/oligonucleotide, Pease *et al.*, 1994) arrayed in 8 x 12 format (96 chips) with a 1 mm groove in between. Probes

are added either by multichannel pipette or pin array, one probe on one chip. To score all 4000 6-mers, 42 chip arrays have to be used, either using different ones, or by reusing one set of chip arrays several times. In the above case, using the earlier nomenclature of the application, $F=9$; $P=6$; and $F + P = 15$. Chips may have probes of formula B_xN_n , where x is a number of specified bases B ; and n is a number of non-specified bases, so that $x = 4$ to 10 and $n = 1$ to 4. To achieve more efficient hybridization, and to avoid potential influence of any support oligonucleotides, the specified bases can be surrounded by unspecified bases, thus represented by a formula such as $(N)_nB_x(N)_m$.

10 5.27 HYBRIDIZATION AND SCORING PROCESS

Labeled probes may be mixed with hybridization buffer and pipetted, preferably by multichannel pipettes, to the subarrays. To prevent mixing of the probes between subarrays (if there are no hydrophobic strips or physical barriers imprinted in the membrane), a corresponding plastic, metal or ceramic grid may be firmly pressed to the membrane. Also, the volume of the buffer may be reduced to about 1 μ l or less per mm^2 . The concentration of the probes and hybridization conditions used may be as described previously except that the washing buffer may be quickly poured over the array of subarrays to allow fast dilution of probes and thus prevent significant cross-hybridization. For the same reason, a minimal concentration of the probes may be used and hybridization time extended to the maximal practical level. For DNA detection and sequencing, knowledge of a “normal” sequence allows the use of the continuous stacking interaction phenomenon to increase the signal. In addition to the labelled probe, additional unlabelled probes which hybridize back to back with a labelled one may be added in the hybridization reaction. The amount of the hybrid may be increased several times. The probes may be connected by ligation. This approach may be important for resolving DNA regions forming “compressions”.

In the case of radiolabelled probes, images of the filters may be obtained, preferably by phosphor storage technology. Fluorescent labels may be scored by CCD cameras, confocal microscopy or otherwise. In order to properly scale and integrate data from different hybridization experiments, raw signals are normalized based on the amount of target in each dot. Differences in the amount of target DNA per dot may be corrected for dividing signals of each probe by an average signal for all probes scored on

- one dot. The normalized signals may be scaled, usually from 1-100, to compare data from different experiments. Also, in each subarray, several control DNAs may be used to determine an average background signal in those samples which do not contain a full match target. For samples obtained from diploid (polyploid) scores, homozygotic
- 5 controls may be used to allow recognition of heterozygotes in the samples.

5.28 HYBRIDIZATION WITH OLIGONUCLEOTIDES

Oligonucleotides were either purchased from Genosys Inc., Houston, Texas or made on an Applied Biosystems 381A DNA synthesizer. Most of the probes used were not purified by HPLC or gel electrophoresis. For example, probes were designed to have both a single perfectly complementary target in interferon, a M13 clone containing a 921 bp Eco RI-Bgl II human BI-interferon fragment (Ohno and Tangiuchi, Proc. Natl. Acad. Sci. 74: 4370-4374 (1981)], and at least one target with an end base mismatch in M13 vector itself.

End labelling of oligonucleotides was performed as described (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Cold Spring Harbor, New York (1982)) in 10 μ l containing T4-polynucleotide kinase (5 units Amersham), γ - 32 P-ATP (3.3 pM, 10 mCi Amersham 3000 Ci/mM) and the oligonucleotide (4 pM, 10 ng). Specific activities of the probes were $2.5\text{--}5 \times 10^9$ cpm/nm.

Single stranded DNA (2 to 4 ml in 0.5 NaOH, 1.5 M NaCl) was spotted on a Gene Screen membrane wetted with the same solution, the filters were neutralized in 0.05 M Na_2HPO_4 pH 6.5, baked in an oven at 80°C for 60 min, and UV irradiated for 1 min. Then, the filters were incubated in hybridization solution (0.5 M Na_2HPO_4 pH 7.2, 7% sodium lauroyl sarcosine for 5 min at room temperature and placed on the surface of a plastic Petri dish. A drop of hybridization solution (10 ml, 0.5 M Na_2HPO_4 pH 7.2, 7% sodium lauroyl sarcosine) with a 32p end-labeled oligomer probe at 4 nM concentration was placed over 1-6 dots per filter, overlaid with a square piece of polyethylene (approximately 1 x 1 cm.), and incubated in a moist chamber at the indicated temperatures for 3 hr. Hybridization was stopped by placing the filter in 6X SSC washing solution for 3 to 5 minutes at 0°C to remove unhybridized probe. The filter was either dried, or further washed for the indicated times and temperatures, and autoradiographed. For discrimination measurements, the dots were excised from the dried filters after autoradiography (a phosphorimager (Molecular Dynamics, Sunnyvale, California) may be used) placed in liquid scintillation cocktail and counted. The uncorrected ratio of cpm for IF and M13 dots is given as D.

The conditions reported herein allow hybridization with very short oligonucleotides but ensure discriminations between matched and mismatched

oligonucleotides that are complementary to and therefore bind to a target nucleic acid. Factors which influence the efficient detection of hybridization of specific short sequences based on the degree of discriminations (D) between a perfectly complementary target and an imperfectly complementary target with a single mismatch in the hybrid are defined. In experimental tests, dot blot hybridization of twenty-eight probes that were 6 to 8 nucleotides in length to two M13 clones or to model oligonucleotides bound to membrane filters was accomplished. The principles guiding the experimental procedures are given below.

Oligonucleotide hybridization to filter bound target nucleic acids only a few nucleotides longer than the probe in conditions of probe excess is a pseudo-first order reaction with respect to target concentration. This reaction is defined by:

$$S_t/S_0 = e^{-k_h[OP]t}$$

Wherein S_t and S_0 are target sequence concentrations at time t and t_0 , respectively. (OP) is probe concentration and t is temperature. The rate constant for hybrid formation, k_h , increases only slightly in the 0°C to 30°C range (Porschke and Eigen, *J. Mol. Biol.* 62: 361 (1971); Craig et al., *J. Mol. Biol.* 62: 383 (1971). Hybrid melting is a first order reaction with respect to hybrid concentration (here replaced by mass due to filter bound state) as shown in:

$$H_t/H_0 = e^{-k_m t}$$

In this equation, H_t and H_0 are hybrid concentrations at times t and t_0 , respectively; k_m is a rate constant for hybrid melting which is dependent on temperature and salt concentration (Ikuta et al., *Nucl. Acids Res.* 15: 797 (1987); Porsclike and Eigen, *J. Mol. Biol.* 62: 361 (1971); Craig et al., *J. Mol. Biol.* 62: 303 (1971)). During hybridization, which is a strand association process, the back, melting, or strand dissociation, reaction takes place as well. Thus, the amount of hybrid formed in time is result of forward and back reactions. The equilibrium may be moved towards hybrid formation by increasing probe concentration and/or decreasing temperature. However, during washing cycles in large volumes of buffer, the melting reaction is dominant and the back reaction hybridization is insignificant, since the probe is absent. This analysis indicates workable Short Oligonucleotide Hybridization (SOH) conditions call be varied for probe concentration or temperature.

D or discrimination is defined above:

$$D = H_p(t_w)/H_i(t_w)$$

$H_p(t_w)$ and $H_i(t_w)$ are the amounts hybrids remaining after a washing time, t_w , for the identical amounts of perfectly and imperfectly complementary duplex, respectively.

- 5 For a given temperature, the discrimination D changes with the length of washing time and reaches the maximal value when $H_i = B$ which is equation five.

The background, B, represents the lowest hybridization signal detectable in the system. Since any further decrease of H_i may not be examined, D increases upon continued washing. Washing past t_w just decreases H_p relative to B, and is seen as a
10 decrease in D. The optimal washing time, t_w , for imperfect hybrids, from equation three and equation five is:

$$t_w = \ln(B/H_i(t_0))/k_{m,i}$$

Since H_p is being washed for the same t_w , combining equations, one obtains the optimal discrimination function:

15
$$D = e^{\ln B/H_i(t_0) \cdot k_{m,p}/k_{m,i}}$$

The change of D as a function, of T is important because of the choice of an optimal washing temperature. It is obtained by substituting the Arrhenius equation which is:

$$K = Ae^{-E_a/RT}$$

20 into the previous equation to form the final equation:

$$D = H_p(t_0)/B \times (B/H_i(t_0))^{(A_p/A_i) \cdot e^{(E_{a,i}-E_{a,p})/RT}}$$

Wherein B is less than $H_i(t_0)$.

- Since the activation energy for perfect hybrids, E_{ap} , and the activation energy for imperfect hybrids, E_{ai} , can be either equal, or E_{ai} less than E_{ap} D is temperature
25 independent, or decreases with increasing temperature, respectively. This result implies that the search for stringent temperature conditions for good discrimination in SOH is unjustified. By washing at lower temperatures, one obtains equal or better discrimination, but the time of washing exponentially increases with the decrease of temperature. Discrimination more strongly decreases with T, if $H_i(t_0)$ increases relative
30 to $H_p(t_0)$.

D at lower temperatures depends to a higher degree on the $H_p(t_0)/B$ ratio than on the $H_p(t_0)/H_i(t_0)$ ratio. This result indicates that it is better to obtain a sufficient quantity of H_p in the hybridization regardless of the discrimination that can be achieved in this step. Better discrimination can then be obtained by washing, since the higher
 5 amounts of perfect hybrid allow more time for differential melting to show an effect. Similarly, using larger amounts of target nucleic acid a necessary discrimination can be obtained even with small differences between $K_{m,p}$ and $K_{m,i}$.

Extrapolated to a more complex situation than covered in this simple model, the result is that washing at lower temperatures is even more important for obtaining
 10 discrimination in the case of hybridization of a probe having many end-mismatches within a given nucleic acid target.

Using the described theoretical principles as a guide for experiments, reliable hybridizations have been obtained with probes six to eight nucleotides in length. All experiments were performed with a floating plastic sheet providing a film of
 15 hybridization solution above the filter. This procedure allows maximal reduction in the amount of probe, and thus reduced label costs in dot blot hybridizations. The high concentration of sodium lauroyl sarcosine instead of sodium lauroyl sulfate in the phosphate hybridization buffer allows dropping the reaction from room temperature down to 12°C. Similarly, the 4-6 X SSC, 10% sodium lauroyl sarcosine buffer allows
 20 hybridization at temperatures as low as 2°C. The detergent in these buffers is for obtaining tolerable background with up to 40 nM concentrations of labelled probe. Preliminary characterization of the thermal stability of short oligonucleotide hybrids was determined on a prototype octamer with 50% G+C content, i.e. probe of sequence TGCTCATG. The theoretical expectation is that this probe is among the less stable
 25 octamers. Its transition enthalpy is similar to those of more stable heptamers or, even to probes 6 nucleotides in length (Bresslauer et al., *Proc. Natl. Acad. Sci. U.S.A.* **83**: 3746 (1986)). Parameter T_d , the temperature at which 50% of the hybrid is melted in unit time of a minute is 18°C. The result shows that T_d is 15°C lower for the 8 bp hybrid than for an 11 bp duplex (Wallace et al., *Nucleic Acids Res.* **6**: 3543 (1979)).

30 In addition to experiments with model oligonucleotides, an M13 vector was chosen as a system for a practical demonstration of short oligonucleotide hybridization.

The main aim was to show useful end-mismatch discrimination with a target similar to the ones which will be used in various applications of the method of the invention. Oligonucleotide probes for the M13 model were chosen in such a way that the M13 vector itself contains the end mismatched base. Vector IF, an M13 recombinant containing a 921 bp human interferon gene insert, carries single perfectly matched target. Thus, IF has either the identical or a higher number of mismatched targets in comparison to the M13 vector itself. Using low temperature conditions and dot blots, sufficient differences in hybridization signals were obtained between the dot containing the perfect and the mismatched targets and the dot containing the mismatched targets only. This was true for the 6-mer oligonucleotides and was also true for the 7 and 8-mer oligonucleotides hybridized to the large JF-M13 pair of nucleic acids.

The hybridization signal depends on the amount of target available on the filter for reaction with the probe. A necessary control is to show that the difference in signal intensity is not a reflection of varying amounts of nucleic acid in the two dots.

Hybridization with a probe that has the same number and kind of targets in both IF and M13 shows that there is an equal amount of DNA in the dots. Since the efficiency of hybrid formation increases with hybrid length, the signal for a duplex having six nucleotides was best detected with a high mass of oligonucleotide target bound to the filter. Due to their lower molecular weight, a larger number of oligonucleotide target molecules can be bound to a given surface area when compared to large molecules of nucleic acid that serves as target.

To measure the sensitivity of detection with unpurified DNA, various amounts of phage supernatants were spotted on the filter and hybridized with ^{32}P -labelled octamer. As little as 50 million unpurified phage containing no more than 0.5 ng of DNA gave a detectable signal indicating that sensitivity of the short oligonucleotide hybridization method is sufficient. Reaction time is short, adding to the practicality.

As mentioned in the theoretical section above, the equilibrium yield of hybrid depends on probe concentration and/or temperature of reaction. For instance, the signal level for the same amount of target with 4 nM octamer at 13°C is 3 times lower than with a probe concentration of 40 nM, and is decreased 4 to 5 times by raising the hybridization temperature to 25°C.

The utility of the low temperature wash for achieving maximal discrimination is demonstrated. To make the phenomenon visually obvious, 50 times more DNA was put in the M13 dot than in the IF dot using hybridization with a vector specific probe. In this way, the signal after the hybridization step with the actual probe was made stronger in the mismatched than in the matched case. The H_p/H_i ratio was 1:4. Inversion of signal intensities after prolonged washing at 7°C was achieved without a massive loss of perfect hybrid, resulting in a ratio of 2:1. In contrast, it is impossible to achieve any discrimination at 25°C, since the matched target signal is already brought down to the background level with 2 minute washing; at the same time, the signal from the mismatched hybrid is still detectable. The loss of discrimination at 13°C compared to 7°C is not so great but is clearly visible. If one considers the 90 minute point at 7°C and the 15 minute point at 13°C when, the mismatched hybrid signal is near the background level, which represents optimal washing times for the respective conditions, it is obvious that the amount of several times greater at 7°C than at 13°C. To illustrate this further, the time course of the change discrimination with washing of the same amount of starting hybrid at the two temperatures shows the higher maximal D at the lower temperature. These results confirm the trend in the change of D with temperature and the ratio of amounts of the two types of hybrid at the start of the washing step.

In order to show the general utility of the short oligonucleotide hybridization conditions, we have looked hybridization of 4 heptamers, 10 octamers and an additional 14 probes up to 12 nucleotides in length in our simple M13 system. These include the nonamer GTTTTTTAA and octamer GGCAGGCG representing the two extremes of GC content. Although GC content and sequence are expected to influence the stability of short hybrids (Bresslauer et al., *Proc. Natl. Acad. Sci. U.S.A.* **83**: 3746 (1986)), the low temperature short oligonucleotide conditions were applicable to all tested probes in achieving sufficient discrimination. Since the best discrimination value obtained with probes 13 nucleotides in length was 20, a several fold drop due to sequence variation is easily tolerated.

The M13 system has the advantage of showing the effects of target DNA complexity on the levels of discrimination. For two octamers having either none or five

mismatched targets and differing in only one GC pair the observed discriminations were 18.3 and 1.7, respectively.

In order to show the utility of this method, three probes 8 nucleotides in length were tested on a collection of 51 plasmid DNA dots made from a library in Bluescript vector. One probe was present and specific for Bluescript vector but was absent in M13, while the other two probes had targets that were inserts of known sequence. This system allowed the use of hybridization negative or positive control DNAs with each probe. This probe sequence (CTCCCTTT) also had a complementary target in the interferon insert. Since the M13 dot is negative while the interferon insert in either M13 or Bluescript was positive, hybridization is sequence specific. Similarly, probes that detect the target sequence in only one of 51 inserts, or in none of the examined inserts along with controls that confirm that hybridization would have occurred if the appropriate targets were present in the clones.

Thermal stability curves for very short oligonucleotide hybrids that are 6-8 nucleotides in length are at least 15°C lower than for hybrids 11-12 nucleotides in length (Wallace *et al.*, *Nucleic Acids Res.* 6: 3543-3557 (1979). However, performing the hybridization reaction at a low temperature and with a very practical 0.4-40 nM concentration of oligonucleotide probe allows the detection of complementary sequence in known or unknown nucleic acid target. To determine an unknown nucleic acid sequence completely, an entire set containing 65,535 8-mer probes may be used. Sufficient amounts of nucleic acid for this purpose are present in convenient biological samples such as a few microliters of M13 culture, a plasmid prep from 10 ml of bacterial culture or a single colony of bacteria, or less than 1 ml of a standard PCR reaction.

Short oligonucleotides 6-10 nucleotides long give excellent discrimination. The relative decrease in hybrid stability with a single end mismatch is greater than for longer probes. Results with the octamer TGCTCATG support this conclusion. In the experiments, the target with a G/T end mismatch, hybridization to the target of this type of mismatch is the most stable of all other types of oligonucleotide. This discrimination achieved is the same as or greater than an internal G/T mismatch in a 19 base paired duplex greater than an internal G/T mismatch in a 19 paired duplex *see*, (Ikuta *et al.*, *Nucl. Acids Res.* 15: 797 (1987). Exploiting these discrimination properties using the

described hybridization conditions for short oligonucleotide hybridization allows a very precise determination of oligonucleotide targets. In contrast to the ease of detecting discrimination between perfect and imperfect hybrids, a problem that may exist with using very short oligonucleotides is the preparation of sufficient amounts of hybrids. In practice, the need to discriminate H_p and H_i is aided by increasing the amount of DNA in the dot and/or the probe concentration, or by decreasing the hybridization temperature. However, higher probe concentrations usually increase background. Moreover, there are limits to the amounts of target nucleic acid that are practical to use. This problems was solved by the higher concentration of the detergent Sarcosyl which gave an effective background with 4 nM of probe. Further improvements may be effected either in the use of competitors for unspecific binding of probe to filter, or by changing the hybridization support material. Moreover, for probes having E_a less than 45 Kcal/mol (*eg.*, for many heptamers and a majority of hexamers, modified oligonucleotides give a more stable hybrid (Asseline, et al., *Proc. Nat'l Acad. Sci.* 81: 3297 (1984) than their unmodified counterparts. The hybridization conditions described in this invention for short oligonucleotide hybridization using low temperatures give better discriminating for all sequences and duplex hybrid inputs. The only price paid in achieving uniformity in hybridization conditions for different sequences is an increase in washing time from minutes to up to 24 hours depending on the sequence. Moreover, the washing time can be further reduced by decreasing the salt concentration.

Although there is excellent discrimination of one matched hybrid over a mismatched hybrids, in short oligonucleotide hybridization, signals from mismatched hybrids exist, with the majority of the mismatch hybrids resulting from end mismatch. This may limit insert sizes that may be effectively examined by a probe of a certain length.

The influence of sequence complexity on discrimination cannot be ignored. However, the complexity effects are more significant when defining sequence information by short oligonucleotide hybridization for specific, nonrandom sequences, and can be overcome by using an appropriate probe to target length ratio. The length ratio is chosen to make unlikely, on statistical grounds, the occurrence of specific sequences which have a number of end-mismatches which would be able to eliminate or

falsely invert discrimination. Results suggest the use of oligonucleotides 6, 7, and 8 nucleotides in length on target nucleic acid inserts shorter than 0.6, 2.5, and 10 kb, respectively.

5 5.29 DNA SEQUENCING

An array of subarrays allows for efficient sequencing of a small set of samples arrayed in the form of replicated subarrays; for example, 64 samples may be arrayed on a 8 x 8 mm subarray and 16 x 24 subarrays may be replicated on a 15 x 23 cm membrane with 1 mm wide spacers between the subarrays. Several replica membranes may be made. For example, probes from a universal set of three thousand seventy-two 7-mers may be divided in thirty-two 96-well plates and labelled by kinasing. Four membranes may be processed in parallel during one hybridization cycle. On each membrane, 384 probes may be scored. All probes may be scored in two hybridization cycles. Hybridization intensities may be scored and the sequence assembled as described below.

15 If a single sample subarray or subarrays contains several unknowns, especially when similar samples are used, a smaller number of probes may be sufficient if they are intelligently selected on the basis of results of previously scored probes. For example, if probe AAAAAAA is not positive, there is a small chance that any of 8 overlapping probes are positive. If AAAAAAA is positive, then two probes are usually positive. The
20 sequencing process in this case consists of first hybridizing a subset of minimally overlapped probes to define positive anchors and then to successively select probes which confirms one of the most likely hypotheses about the order of anchors and size and type of gaps between them. In this second phase, pools of 2-10 probes may be used where each probe is selected to be positive in only one DNA sample which is different from the
25 samples expected to be positive with other probes from the pool.

The subarray approach allows efficient implementation of probe competition (overlapped probes) or probe cooperation (continuous stacking of probes) in solving branching problems. After hybridization of a universal set of probes the sequence assembly program determines candidate sequence subfragments (SFs). For the further
30 assembly of SFs, additional information has to be provided (from overlapped sequences of DNA fragments, similar sequences, single pass gel sequences, or from other

hybridization or restriction mapping data). Competitive hybridization and continuous stacking interactions have been proposed for SF assembly. These approaches are of limited practical value for sequencing of large numbers of samples by SBH wherein a labelled probe is applied to a sample affixed to an array if a uniform array is used.

- 5 Fortunately, analysis of small numbers of samples using replica subarrays allows efficient implementation of both approaches. On each of the replica subarrays, one branching point may be tested for one or more DNA samples using pools of probes similarly as in solving mutated sequences in different samples spotted in the same subarray (see above).

- 10 If in each of 64 samples described in this example, there are about 100 branching points, and if 8 samples are analyzed in parallel in each subarray, then at least 800 subarray probings solve all branches. This means that for the 3072 basic probings an additional 800 probings (25%) are employed. More preferably, two probings are used for one branching point. If the subarrays are smaller, less additional probings are used. For example, if subarrays consist of 16 samples, 200 additional probings may be scored (6%).
- 15 By using 7-mer probes ($N_{1-2}B_7N_{1-2}$) and competitive or collaborative branching solving approaches or both, fragments of about 1000 bp fragments may be assembled by about 4000 probings. Furthermore, using 8-mer probes (NB_8N) 4 kb or longer fragments may be assembled with 12,000 probings. Gapped probes, for example, NB_4NB_3N or NB_4NB_4N may be used to reduce the number of branching points.

20

5.30 DNA ANALYSIS BY TRANSIENT ATTACHMENT TO SUBARRAYS OF PROBES AND LIGATION OF LABELLED PROBES

- 25 Oligonucleotide probes having an informative length of four to 40 bases are synthesized by standard chemistry and stored in tubes or in multiwell plates. Specific sets of probes comprising one to 10,000 probes are arrayed by deposition or *in situ* synthesis on separate supports or distinct sections of a larger support. In the last case, sections or subarrays may be separated by physical or hydrophobic barriers. The probe arrays may be prepared by *in situ* synthesis. A sample DNA of appropriate size is hybridized with one or more specific arrays. Many samples may be interrogated as pools
- 30 at the same subarrays or independently with different subarrays within one support. Simultaneously with the sample or subsequently, a single labelled probe or a pool of

labelled probes is added on each of the subarrays. If attached and labelled probes hybridize back to back on the complementary target in the sample DNA they are ligated. Occurrence of ligation will be measured by detecting a label from the probe.

5 This procedure is a variant of the described DNA analysis process in which DNA samples are not permanently attached to the support. Transient attachment is provided by probes fixed to the support. In this case there is no need for a target DNA arraying process. In addition, ligation allows detection of longer oligonucleotide sequences by combining short labelled probes with short fixed probes.

10 The process has several unique features. Basically, the transient attachment of the target allows its reuse. After ligation occur the target may be released and the label will stay covalently attached to the support. This feature allows cycling the target and production of detectable signal with a small quantity of the target. Under optimal conditions, targets do not need to be amplified, e.g. natural sources of the DNA samples may be directly used for diagnostics and sequencing purposes. Targets may be released
15 by cycling the temperature between efficient hybridization and efficient melting of duplexes. More preferably, there is no cycling. The temperature and concentrations of components may be defined to have an equilibrium between free targets and targets entered in hybrids at about 50:50% level. In this case there is a continuous production of ligated products. For different purposes different equilibrium ratios are optimal.

20 An electric field may be used to enhance target use. At the beginning, a horizontal field pulsing within each subarray may be employed to provide for faster target sorting. In this phase, the equilibrium is moved toward hybrid formation, and unlabelled probes may be used. After a target sorting phase, an appropriate washing (which may be helped by a vertical electric field for restricting movement of the samples)
25 may be performed. Several cycles of discriminative hybrid melting, target harvesting by hybridization and ligation and removing of unused targets may be introduced to increase specificity. In the next step, labelled probes are added and vertical electrical pulses may be applied. By increasing temperature, an optimal free and hybridized target ratio may be achieved. The vertical electric field prevents diffusion of the sorted targets.

30 The subarrays of fixed probes and sets of labelled probes (specially designed or selected from a universal probe set) may be arranged in various ways to allow an efficient

and flexible sequencing and diagnostics process. For example, if a short fragment (about 100-500 bp) of a bacterial genome is to be partially or completely sequenced, small arrays of probes (5-30 bases in length) designed on the bases of known sequence may be used. If interrogated with a different pool of 10 labelled probes per subarray, an array of 5 10 subarrays each having 10 probes, allows checking of 200 bases, assuming that only two bases connected by ligation are scored. Under the conditions where mismatches are discriminated throughout the hybrid, probes may be displaced by more than one base to cover the longer target with the same number of probes. By using long probes, the target may be interrogated directly without amplification or isolation from the rest of DNA in 10 the sample. Also, several targets may be analyzed (screened for) in one sample simultaneously. If the obtained results indicate occurrence of a mutation (or a pathogen), additional pools of probes may be used to detect type of the mutation or subtype of pathogen. This is a desirable feature of the process which may be very cost effective in preventive diagnosis where only a small fraction of patients is expected to have an 15 infection or mutation.

In the processes described in the examples, various detection methods may be used, for example, radiolabels, fluorescent labels, enzymes or antibodies (chemiluminescence), large molecules or particles detectable by light scattering or interferometric procedures.

20

5.31 SEQUENCING A TARGET USING OCTAMERS AND NONAMERS

Data resulting from the hybridization of octamer and nonamer oligonucleotides shows that sequencing by hybridization provides an extremely high degree of accuracy. In this experiment, a known sequence was used to predict a series of contiguous 25 overlapping component octamer and nonamer oligonucleotides.

In addition to the perfectly matching oligonucleotides, mismatch oligonucleotides, mismatch oligonucleotides wherein internal or end mismatches occur in the duplex formed by the oligonucleotide and the target were examined. In these analyses, the lowest practical temperature was used to maximize hybridization formation. Washes 30 were accomplished at the same or lower temperatures to ensure maximal discrimination by utilizing the greater dissociation rate of mismatch versus matched

oligonucleotide/target hybridization. These conditions are shown to be applicable to all sequences although the absolute hybridization yield is shown to be sequence dependent.

The least destabilizing mismatch that can be postulated is a simple end mismatch, so that the test of sequencing by hybridization is the ability to discriminate perfectly
5 matched oligonucleotide/targetduplexes from end-mismatched oligonucleotide/targetduplexes.

The discriminative values for 102 of 105 hybridizing oligonucleotides in a dot blot format were greater than 2 allowing a highly accurate generation of the sequence. This system also allowed an analysis of the effect of sequence on hybridization formation
10 and hybridization instability.

One hundred base pairs of a known portion of a human-interferon genes prepared by PCR, i.e. a 100 bp target sequence, was generated with data resulting from the hybridization of 105 oligonucleotides probes of known sequence to the target nucleic acid. The oligonucleotide probes used included 72 octamer and 21 nonamer
15 oligonucleotides whose sequence was perfectly complementary to the target. The set of 93 probes provided consecutive overlapping frames of the target sequence e displaced by one or two bases.

To evaluate the effect of mismatches, hybridization was examined for 12 additional probes that contained at least one end mismatch when hybridized to the 100 bp
20 test target sequence. Also tested was the hybridization of twelve probes with target end-mismatched to four other control nucleic acid sequences chosen so that the 12 oligonucleotides formed perfectly matched duplex hybrids with the four control DNAs. Thus, the hybridization of internal mismatched, end-mismatched and perfectly matched duplex pairs of oligonucleotide and target were evaluated for each oligonucleotide used
25 in the experiment. The effect of absolute DNA target concentration on the hybridization with the test octamer and nonamer oligonucleotides was determined by defining target DNA concentration by detecting hybridization of a different oligonucleotide probe to a single occurrence non-target site within the co-amplified plasmid DNA.

The results of this experiment showed that all oligonucleotides containing perfect
30 matching complementary sequence to the target or control DNA hybridized more strongly than those oligonucleotides having mismatches. To come to this conclusion, we

examined H_p and D values for each probe. H_p defines the amount of hybrid duplex formed between a test target and an oligonucleotide probe. By assigning values of between 0 and 10 to the hybridization obtained for the 105 probes, it was apparent that 68.5% of the 105 probes had an H_p greater than 2.

5 Discrimination (D) values were obtained where D was defined as the ratio of signal intensities between 1) the dot containing a perfect matched duplex formed between test oligonucleotide and target or control nucleic acid and 2) the dot containing a mismatch duplex formed between the same oligonucleotide and a different site within the target or control nucleic acid. Variations in the value of D result from either 1)
10 perturbations in the hybridization efficiency which allows visualization of signal over background, or 2) the type of mismatch found between the test oligonucleotide and the target. The D values obtained in this experiment were between 2 and 40 for 102 of the 105 oligonucleotide probes examined. Calculations of D for the group of 102 oligonucleotides as a whole showed the average D was 10.6.

15 There were 20 cases where oligonucleotide/targetduplexes exhibited an end-mismatch. In five of these, D was greater than 10. The large D value in these cases is most likely due to hybridization destabilization caused by other than the most stable (G/T and G/A) end mismatches. The other possibility is there was an error in the sequence of either the oligonucleotides or the target.

20 Error in the target for probes with low H_p , was excluded as a possibility because such an error would have affected the hybridization of each of the other eight overlapping oligonucleotides. There was no apparent instability due to sequence mismatch for the other overlapping oligonucleotides, indicating the target sequence was correct. Error in the oligonucleotide sequence was excluded as a possibility after the hybridization of
25 seven newly synthesized oligonucleotides was re-examined. Only 1 of the seven oligonucleotides resulted in a better D value. Low hybrid formation values may result from hybrid instability or from an inability to form hybrid duplex. An inability to form hybrid duplexes would result from either 1) self complementarity of the chosen probe or 2) target/target self hybridization. Oligonucleotide/oligonucleotideduplex formation may
30 be favored over oligonucleotide/target hybrid duplex formation if the probe was self-complementary. Similarly, target/target association may be favored if the target was self-

complementary or may form internal palindromes. In evaluating these possibilities, it was apparent from probe analysis that the questionable probes did not form hybrids with themselves. Moreover, in examining the contribution of target/target hybridization, it was determined that one of the questionable oligonucleotide probes hybridized

5 inefficiently with two different DNAs containing the same target. The low probability that two different DNAs have a self-complementary region for the same target sequence leads to the conclusion that target/target hybridization did not contribute to low hybridization formation. Thus, these results indicate that hybrid instability and not the inability to form hybrids was the cause of the low hybrid formation observed for specific

10 oligonucleotides. The results also indicate that low hybrid formation is due to the specific sequences of certain oligonucleotides. Moreover, the results indicate that reliable results may be obtained to generate sequences if octamer and nonamer oligonucleotides are used.

These results show that using the methods described long sequences of any target

15 nucleic acid may be generated by maximal and unique overlap of constituent oligonucleotides. Such sequencing methods are dependent on the content of the individual component oligomers regardless of their frequency and their position.

The sequence which is generated using the algorithm described below is of high fidelity. The algorithm tolerates false positive signals from the hybridization dots as is

20 indicated from the fact the sequence generated from the 105 hybridization values, which included four less reliable values, was correct. This fidelity in sequencing by hybridization is due to the "all or none" kinetics of short oligonucleotide hybridization and the difference in duplex stability that exists between perfectly matched duplexes and mismatched duplexes. The ratio of duplex stability of matched and end-mismatched

25 duplexes increases with decreasing duplex length. Moreover, binding energy decreases with decreasing duplex length resulting in a lower hybridization efficiency. However, the results provided show that octamer hybridization allows the balancing of the factors affecting duplex stability and discrimination to produce a highly accurate method of sequencing by hybridization. Results presented in other examples show that

30 oligonucleotides that are 6, 7, or 8 nucleotides can be effectively used to generate reliable sequence on targets that are 0.5 kb (for hexamers) 2 kb (for septamers) and 6kb (for

octamers). The sequence of long fragments may be overlapped to generate a complete genome sequence.

5.32 ANALYZING THE DATA OBTAINED

5 Image files are analyzed by an image analysis program, like DOTS program (Drmanac *et al.* 1993), and scaled and evaluated by statistical functions included, *e.g.*, in SCORES program (Drmanac *et al.* 1994). From the distribution of the signals an optimal threshold is determined for transforming signal into +/- output. From the position of the label detected, F + P nucleotide sequences from the fragments would be
10 determined by combining the known sequences of the immobilized and labeled probes corresponding to the labeled positions. The complete nucleic acid sequence or sequence subfragments of the original molecule, such as a human chromosome, would then be assembled from the overlapping F + P sequence determined by computational deduction.

One option is to transform hybridization signals *e.g.*, scores, into +/- output
15 during the sequence assembly process. In this case, assembly will start with a F + P sequence with a very high score, for example F + P sequence AAAAAATTTTTT. Scores of all four possible overlapping probes AAAAAATTTTTTA, AAAAAATTTTTT, AAAAAATTTTTTC and AAAAAATTTTTTG and three additional probes that are different at the beginning (TAAAAATTTTTT, CAAAAATTTTTT, GAAAAATTTTTT, are
20 compared and three outcomes defined: (i) only the starting probe and only one of the four overlapping probes have scores that are significantly positive relatively to the other six probes, in this case the AAAAAATTTTTT sequence will be extended for one nucleotide to the right; (ii) no one probe except the starting probe has a significantly positive score, assembly will stop, *e.g.*, the AAAAAATTTTTT sequence is at the end of
25 the DNA molecule that is sequenced; (iii) more than one significantly positive probe among the overlapped and/or other three probes is found; assembly is stopped because of the error or branching (Drmanac *et al.*, 1989).

The processes of computational deduction would employ computer programs using existing algorithms (see, *e.g.*, Pevzner, 1989; Drmanac *et al.*, 1991; Labat and
30 Drmanac, 1993; each incorporated herein by reference).

If, in addition to F + P, F (1)P, F (2)P, F(3)P or F(4)P are determined, algorithms will be used to match all data sets to correct potential errors or to solve the situation where there is a branching problem (see, *e.g.*, Drmanac *et al.*, 1989; Bains *et al.*, 1988; each incorporated herein by reference).

5

5.33 CONDUCTING SEQUENCING BY TWO STEP HYBRIDIZATION

Sequencing is accomplished as described herein. First, the whole chip is hybridized to a mixture of DNA as complex as 100 million of bp (one human chromosome). Guidelines for conducting hybridization can be found in papers such as Drmanac *et al.* (1990); Khrapko *et al.* (1991); and Broude *et al.* (1994). These articles teach the ranges of hybridization temperatures, buffers and washing steps that are appropriate for use in the initial steps of Format 3 SBH.

The present invention particularly contemplates that hybridization is to be carried out for up to several hours in high salt concentrations at a low temperature (-2°C to 5°C) because of a relatively low concentration of target DNA that can be provided. For this purpose, SSC buffer is used instead of sodium phosphate buffer (Drmanac *et al.*, 1990), which precipitates at 10°C. Washing does not have to be extensive (a few minutes) because of the second step, and can be completely eliminated when the hybridization cycling is used for the sequencing of highly complex DNA samples. The same buffer is used for hybridization and washing steps to be able to continue with the second hybridization step with labeled probes.

After proper washing using a simple robotic device on each array, *e.g.*, a 8 x 8 mm array, one labeled, probe, *e.g.*, a 6-mer, would be added. A 96-tip or 96-pin device would be used, performing this in 42 operations. Again, a range of discriminatory conditions could be employed, as previously described in the scientific literature.

The present invention particularly contemplates the use of the following conditions. First, after adding labeled probes and incubating for several minutes only (because of the high concentration of added oligonucleotides) at a low temperature (0-5°C), the temperature is increased to 3-10°C, depending on F + P length, and the washing buffer is added. At this time, the washing buffer used is one compatible with any ligation reaction (*e.g.*, 100 mM salt concentration range). After adding ligase, the temperate is

bound labeled oligonucleotides, detection is simplified (it does not have time and low temperature constraints).

Depending on the label used, imaging of the chips is done with different apparatus. For radioactive labels, phosphor storage screen technology and PhosphorImager as a scanner may be used (Molecular Dynamics, Sunnyvale, CA). Chips are put in a cassette and covered by a phosphorous screen. After 1-4 hours of exposure, the screen is scanned and the image file stored at a computer hard disc. For the detection of fluorescent labels, CCD cameras and epifluorescent or confocal microscopy are used. For the chips generated directly on the pixels of a CCD camera, detection can be performed as described by Eggers *et al.* (1994, incorporated herein by reference).

Charge-coupled device (CCD) detectors serve as active solid supports that quantitatively detect and image the distribution of labeled target molecules in probe-based assays. These devices use the inherent characteristics of microelectronics that accommodate highly parallel assays, ultrasensitive detection, high throughput, integrated data acquisition and computation. Eggers *et al.* (1994) describe CCDs for use with probe-based assays, such as Format 3 SBH of the present invention, that allow quantitative assessment within seconds due to the high sensitivity and direct coupling employed.

The integrated CCD detection approach enables the detection of molecular binding events on chips. The detector rapidly generates a two-dimensional pattern that uniquely characterizes the sample. In the specific operation of the CCD-based molecular detector, distinct biological probes are immobilized directly on the pixels of a CCD or can be attached to a disposable cover slip placed on the CCD surface. The sample molecules can be labeled with radioisotope, chemiluminescent or fluorescent tags.

Upon exposure of the sample to the CCD-based probe array, photons or radioisotope decay products are emitted at the pixel locations where the sample has bound, in the case of Format 3, to two complementary probes. In turn, electron-hole pairs are generated in the silicon when the charged particles, or radiation from the labeled sample, are incident on the CCD gates. Electrons are then collected beneath adjacent CCD gates and sequentially read out on a display module. The number of photoelectrons generated at each pixel is directly proportional to the number of molecular binding events

in such proximity. Consequently, molecular binding can be quantitatively determined (Eggers *et al.*, 1994).

By placing the imaging array in proximity to the sample, the collection efficiency is improved by a factor of at least 10 over lens-based techniques such as those found in conventional CCD cameras. That is, the sample (emitter) is in near contact with the detector (imaging array). and this eliminates conventional imaging optics such as lenses and mirrors.

When radioisotopes are attached as reporter groups to the target molecules, energetic particles are detected. Several reporter groups that emit particles of varying energies have been successfully utilized with the micro-fabricated detectors, including ^{32}P , ^{33}P , ^{35}P , ^{14}C and ^{125}I . The higher energy particles, such as from ^{32}P , provide the highest molecular detection sensitivity, whereas the lower energy particles, such as from ^{35}S , provide better resolution. Hence the choice of the radioisotope reporter can be tailored as required. Once the particular radioisotope label is selected, the detection performance can be predicted by calculating the signal-to-noise ration (SNR), as described by Eggers *et al.*, (1994).

An alternative luminescent detection procedure involves the use of fluorescent or chemiluminescent reporter groups attached to the target molecules. The fluorescent labels can be attached covalently or through interaction. Fluorescent dyes, such as ethidium bromide, with intense absorption bands in the near UV (300-350 nm) range and principal emission bands in the visible (500-650 nm) range, are most suited for the CCD devices employed since the quantum efficiency is several orders of magnitude lower at the excitation wavelength than at the fluorescent signal wavelength.

From the perspective of detecting luminescence, the polysilicon CCD gates have in capacity to filter away the contribution of incident light in the UV range, yet are very sensitive to the visible luminescence generated by the fluorescent reporter groups. Such inherently large discrimination against UV excitation enables large SNRs (greater than 100) to be achieved by the CCDs as formulated in the incorporated paper by Eggers *et al.*, (1994).

For probe immobilization on the detector, hybridization matrices may be produced on inexpensive SiO_2 wafers, which are subsequently placed on the surface of

the CCD following hybridization and drying. This format is economically efficient since the hybridization of the DNA is conducted on inexpensive disposable SiO₂ wafers, thus allowing reuse of the more expensive CCD detector. Alternatively, the probes can be immobilized directly on the CCD to create a dedicated probe matrix.

5 To immobilize probes upon the SiO₂ coating, a uniform epoxide layer is linked to the film surface, employing an epoxy-silane reagent and standard SiO₂ modification chemistry. Amine-modified oligonucleotide probes are then linked to the SiO₂ surface by means of secondary amine formation with the epoxide ring. The resulting linkage provides 17 rotatable bonds of separation between the 3 base of the oligonucleotide and
10 the SiO₂ surface. To ensure complete amine deprotonation and to minimize secondary structure formation during coupling, the reaction is performed in 0.1 M KOH and incubated at 37°C for 6 hours.

In Format 3 SBH in general, signals are scored per each of billion points. It would not be necessary to hybridize all arrays, *e.g.*, 4000 5 x 5 mm, at a time and the
15 successive use of smaller number of arrays is possible.

Cycling hybridizations are one possible method for increasing the hybridization signal. In one cycle, most of the fixed probes will hybridize with DNA fragments with tail sequences non-complementary for labeled probes. By increasing the temperature, those hybrids will be melted. In the next cycle, some of them (~0.1%) will hybridize
20 with an appropriate DNA fragment and additional labeled probes will be ligated. In this case, there occurs a discriminative melting of DNA hybrids with mismatches for both probe sets simultaneously.

In the cycle hybridization, all components are added before the cycling starts, at the T4, or a higher temperature for a thermostable ligase. Then the temperature is
25 decreased to 15-37°C and the chip is incubated for up to 10 minutes, and then the temperature is increased to 37°C or higher for a few minutes and then again reduced. Cycles can be repeated up to 10 times. In one variant, an optimal higher temperature (10-50°C) can be used without cycling and longer ligation reaction can be performed (1-3 hours).

30 The procedure described herein allows complex chip manufacturing using standard synthesis and precise spotting of oligonucleotides because a relatively small

number of oligonucleotides are necessary. For example, if all 7-mer oligos are synthesized (16384 probes), lists of 256 million 14-mers can be determined.

One important variant of the invented method is to use more than one differently labeled probe per base array. This can be executed with two purposes in mind;

- 5 multiplexing to reduce number of separately hybridized arrays; or to determine a list of even longer oligosequences such as 3 x 6 or 3 x 7. In this case, if two labels are used, the specificity of the 3 consecutive oligonucleotides can be almost absolute because positive sites must have enough signals of both labels.

- 10 A further and additional variant is to use chips containing BxNy probes with y being from 1 to 4. Those chips allow sequence reading in different frames. This can also be achieved by using appropriate sets of labeled probes or both F and P probes could have some unspecified end positions (*i.e.*, some element of terminal degeneracy).

- Universal bases may also be employed as part of a linker to join the probes of defined sequence to the solid support. This makes the probe more available to hybridization and makes the construct more stable. If a probe has 5 bases, one may, *e.g.*, use 3 universal bases as a linker.

5.34 DETERMINING SEQUENCE FROM HYBRIDIZATION DATA

- 20 Sequence assembly may be interrupted where ever a given overlapping (N-1) mer is duplicated two or more times. Then either of the two N-mers differing in the last nucleotide may be used in extending the sequence. This branching point limits unambiguous assembly of sequence.

- 25 Reassembling the sequence of known oligonucleotides that hybridize to the target nucleic acid to generate the complete sequence of the target nucleic acid may not be accomplished in some cases. This is because some information may be lost if the target nucleic acid is not in fragments of appropriate size in relation to the size of oligonucleotide that is used for hybridizing. The quantity of information lost is proportional to the length of a target being sequenced. However, if sufficiently short targets are used, their sequence may be unambiguously determined.

- 30 The probable frequency of duplicated sequences that would interfere with sequence y which is distributed along a certain length of DNA may be calculated. This

derivation requires the introduction of the definition of a parameter having to do with sequence organization: the sequence subfragment (SF). A sequence subfragment results if any part of the sequence of a target nucleic acid starts and ends with an (N-1) mer that is repeated two or more times within the target sequence. Thus, subfragments are

5 sequences generated between two points of branching in the process of assembly of the sequences in the method of the invention. The sum of all subfragments is longer than the actual target nucleic acid because of overlapping short ends. Generally, subfragments may not be assembled in a linear order without additional information since they have shared (N-1) mers at their ends and starts. Different numbers of subfragments are

10 obtained for each nucleic acid target depending on the number of its repeated (N-1) mers. The number depends on the value of N-1 and the length of the target.

Probability calculations can estimate the interrelationship of the two factors. If the ordering of positive N-mers is accomplished by using overlapping sequences of length N-1 or at an average distance of A_0 , the N-1 of a fragment L_f bases long is given by

15 equation one:

$$N_{sf} = 1 + A_0 \times KXP(K, L_f)$$

Where K greater than or = 2, and $P(K, L_f)$ represents the probability of an N-mer occurring K-times on a fragment L_f base long. Also, a computer program that is able to form subfragments from the content of N-mers for any given sequence is described

20 below.

The number of subfragments increases with the increase of lengths of fragments for a given length of probe. Obtained subfragments may not be uniquely ordered among themselves. Although not complete, this information is very useful for comparative sequence analysis and the recognition of functional sequence characteristics. This type of

25 information may be called partial sequence. Another way of obtaining partial sequence is the use of only a subset of oligonucleotide probes of a given length.

There may be relatively good agreement between predicted sequence according to theory and a computer simulation for a random DNA sequence. For instance, for N-1 = 7, [using an 8-mer or groups of sixteen 10-mers of type 5' (A,T,C,G) B_8 (A,T,C,G) 3'] a

30 target nucleic acid of 200 bases will have an average of three subfragments. However, because of the dispersion around the mean, a library of target nucleic acid should have

inserts of 500 bp so that less than 1 in 2000 targets have more than three subfragments. Thus, in an ideal case of sequence determination of a long nucleic acid of random sequence, a representative library with sufficiently short inserts of target nucleic acid may be used. For such inserts, it is possible to reconstruct the individual target by the method
 5 of the invention. The entire sequence of a large nucleic acid is then obtained by overlapping of the defined individual insert sequences.

To reduce the need for very short fragments, e.g. 50 bases for 8-mer probes. The information contained in the overlapped fragments present in every random DNA fragmentation process like cloning, or random PCR is used. It is also possible to use
 10 pools of short physical nucleic acid fragments. Using 8-mers or 11-mers like 5' (A, T, C, G) N₈ (A, T, C, G) 3' for sequencing 1 megabase, instead of needing 20,000 50 bp fragments only 2,100 samples are sufficient. This number consists of 700 random 7 kb clones (basic library), 1250 pools of 20 clones of 500 bp (subfragments ordering library) and 150 clones from jumping (or similar) library. The developed algorithm (see Example
 15 1 8) regenerates sequence using hybridization data of these described samples.

5.35 ALGORITHM

This example describes an algorithm for generation of a long sequence written in a four letter alphabet from constituent k-tuple words in a minimal number of separate,
 20 randomly defined fragments of a starting nucleic acid sequence where K is the length of an oligonucleotide probe. The algorithm is primarily intended for use in the sequencing by hybridization (SBH) process. The algorithm is based on subfragments (SF), informative fragments (IF) and the possibility of using pools of physical nucleic sequences for defining informative fragments.

25 As described, subfragments may be caused by branch points in the assembly process resulting from the repetition of a K-1 oligomer sequence in a target nucleic acid. Subfragments are sequence fragments found between any two repetitive words of the length K-1 that occur in a sequence. Multiple occurrences of K-1 words are the cause of interruption of ordering the overlap of K-words in the process of sequence generation.
 30 Interruption leads to a sequence remaining in the form of subfragments. Thus, the

unambiguous segments between branching points whose order is not uniquely determined are called sequence subfragments.

Informative fragments are defined as fragments of a sequence that are determined by the nearest ends of overlapped physical sequence fragments.

5 A certain number of physical fragments may be pooled without losing the possibility of defining informative fragments. The total length of randomly pooled fragments depends on the length of k-tuples that are used in the sequencing process.

10 The algorithm consists of two main units. The first part is used for generation of subfragments from the set of k-tuples contained in a sequence. Subfragments may be generated within the coding region of physical nucleic acid sequence of certain sizes, or within the informative fragments defined within long nucleic acid sequences. Both types of fragments are members of the basic library. This algorithm does not describe the determination of the content of the k-tuples of the informative fragments of the basic library, i.e. the step of preparation of informative fragments to be used in the sequence
15 generation process.

20 The second part of the algorithm determines the linear order of obtained subfragments with the purpose of regenerating the complete sequence of the nucleic acid fragments of the basic library. For this purpose a second, ordering library is used, made of randomly pooled fragments of the starting sequence. The algorithm does not include the step of combining sequences of basic fragments to regenerate an entire, megabase plus sequence. This may be accomplished using the link-up of fragments of the basic library which is a prerequisite for informative fragment generation. Alternatively, it may be accomplished after generation of sequences of fragments of the basic library by this
25 algorithm, using search for their overlap, based on the presence of common end-sequences.

30 The algorithm requires neither knowledge of the number of appearances of a given k-tuple in a nucleic acid sequence of the basic and ordering libraries, nor does it require the information of which k-tuple words are present on the ends of a fragment. The algorithm operates with the mixed content of k-tuples of various length. The concept of the algorithm enables operations with the k-tuple sets that contain false positive and false negative k-tuples. Only in specific cases does the content of the false k-tuples

primarily influence the completeness and correctness of the generated sequence. The algorithm may be used for optimization of parameters in simulation experiments, as well as for sequence generation in the actual SBH experiments e.g., generation of the genomic DNA sequence. In optimization of parameters, the choice of the oligonucleotide probes (k-tuples) for practical and convenient fragments and/or the choice of the optimal lengths and the number of fragments for the defined probes are especially important.

This part of the algorithm has a central role in the process of the generation of the sequence from the content of k-tuples. It is based on the unique ordering of k-tuples by means of maximal overlap. The main obstacles in sequence generation are specific repeated sequences and false positive and/or negative k-tuples. The aim of this part of the algorithm is to obtain the minimal number of the longest possible subfragments, with correct sequence. This part of the algorithm consists of one basic, and several control steps. A two-stage process is necessary since certain information can be used only after generation of all primary subfragments.

The main problem of sequence generation is obtaining a repeated sequence from word contents that by definition do not carry information on the number of occurrences of the particular k-tuples. The concept of the entire algorithm depends on the basis on which this problem is solved. In principle, there are two opposite approaches: 1) repeated sequences may be obtained at the beginning, in the process of generation of pSFs, or 2) repeated sequences can be obtained later, in the process of the final ordering of the subfragments. In the first case, pSFs contain an excess of sequences and in the second case, they contain a deficit of sequences. The first approach requires elimination of the excess sequences generated, and the second requires permitting multiple use of some of the subfragments in the process of the final assembling of the sequence.

The difference in the two approaches in the degree of strictness of the rule of unique overlap of k-tuples. The less severe rule is: k-tuple X is unambiguously maximally overlapped with k-tuple Y if and only if, the rightmost k-1 end of k-tuple X is present only on the leftmost end of k-tuple Y. This rule allows the generation of repetitive sequences and the formation of surplus sequences.

A stricter rule which is used in the second approach has an addition caveat: k-tuple X is unambiguously maximally overlapped with k-tuple Y if and only if, the

rightmost $K-1$ end of k -tuple X is present only on the leftmost end of k -tuple Y and if the leftmost $K-1$ end of k -tuple Y is not present on the rightmost end of any other k -tuple.

The algorithm based on the stricter rule is simpler, and is described herein.

The process of elongation of a given subfragment is stopped when the right $k-1$ end of the last k -tuple included is not present on the left end of any k -tuple or is present on two or more k -tuples. If it is present on only one k -tuple the second part of the rule is tested. If in addition there is a k -tuple which differs from the previously included one, the assembly of the given subfragment is terminated only on the first leftmost position. If this additional k -tuple does not exist, the conditions are met for unique $k-1$ overlap and a given subfragment is extended to the right by one element.

Beside the basic rule, a supplementary one is used to allow the usage of k -tuples of different lengths. The maximal overlap is the length of $k-1$ of the shorter k -tuple of the overlapping pair. Generation of the pSFs is performed starting from the first k -tuple from the file in which k -tuples are displayed randomly and independently from their order in a nucleic acid sequence. Thus, the first k -tuple in the file is not necessarily on the beginning of the sequence, nor on the start of the particular subfragment. The process of subfragment generation is performed by ordering the k -tuples by means of unique overlap, which is defined by the described rule. Each used k -tuple is erased from the file. At the point when there are no further k -tuples unambiguously overlapping with the last one included, the building of subfragment is terminated and the buildup of another pSF is started. Since generation of a majority of subfragments does not begin from their actual starts, the formed pSF are added to the k -tuple file and are considered as a longer k -tuple. Another possibility is to form subfragments going in both directions from the starting k -tuple. The process ends when further overlap, i.e. the extension of any of the subfragments, is not possible.

The pSFs can be divided in three groups: 1) subfragments of the maximal length and correct sequence in cases of exact k -tuple set; 2) short subfragments, formed due to the used of the maximal and unambiguous overlap rule on the incomplete set, and/or the set with some false positive k -tuples; and 3) pSFs of an incorrect sequence. The incompleteness of the set in 2) is caused by false negative results of a hybridization experiment, as well as by using an incorrect set of k -tuples. These are formed due to the

false positive and false negative k-tuples and can be: a) misconnected subfragments; b) subfragments with the wrong end; and c) false positive k-tuples which appears as false minimal subfragments.

Considering false positive k-tuples, there is the possibility for the presence of a k-tuple containing more than one wrong base or containing one wrong base somewhere in the middle, as well as the possibility for a k-tuple with a wrong base on the end.

Generation of short, erroneous or misconnected subfragments is caused by the latter k-tuples. The k-tuples of the former two kinds represent wrong pSFs with length equal to k-tuple length.

In the case of one false negative k-tuple, pSFs are generated because of the impossibility of maximal overlapping. In the case of the presence of one false positive k-tuple with the wrong base on its leftmost or rightmost end, pSFs are generated because of the impossibility of unambiguous overlapping. When both false positive and false negative k-tuples with a common k-1 sequence are present in the file, pSFs are generated, and one of these pSFs contains the wrong k-tuple at the relevant end.

The process of correcting subfragments with errors in sequence and the linking of unambiguously connected pSF is performed after subfragment generation and in the process of subfragment ordering. The first step which consists of cutting the misconnected pSFs and obtaining the final subfragments by unambiguous connection of pSFs is described below.

There are two approaches for the formation of misconnected subfragments. In the first a mistake occurs when an erroneous k-tuple appears on the points of assembly of the repeated sequences of lengths k-1. In the second, the repeated sequences are shorter than k-1. These situations can occur in two variants each. In the first variant, one of the repeated sequences represents the end of a fragment. In the second variant, the repeated sequence occurs at any position within the fragment. For the first possibility, the absence of some k-tuples from the file (false negatives) is required to generate a misconnection. The second possibility requires the presence of both false negative and false positive k-tuples in the file. Considering the repetitions of k-1 sequence, the lack of only one k-tuple is sufficient when either end is repeated internally. The lack of two is needed for strictly internal repetition. The reason is that the end of a sequence can be considered

informatically as an endless linear array of false negative k-tuples. From the “smaller than k-1 case”, only the repeated sequence of the length of k-2, which requires two or three specific erroneous k-tuples, will be considered. It is very likely that these will be the only cases which will be detected in a real experiment, the others being much less frequent.

Recognition of the misconnected subfragments is more strictly defined when a repeated sequence does not appear at the end of the fragment. In this situation, one can detect further two subfragments, one of which contains on its leftmost, and the other on its rightmost end k-2 sequences which are also present in the misconnected subfragment. When the repeated sequence is on the end of the fragment, there is only one subfragment which contains k-2 sequence causing the mistake in subfragment formation on its leftmost or rightmost end.

The removal of misconnected subfragments by their cutting is performed according to the common rule: If the leftmost or rightmost sequence of the length of k-2 of subfragments is present in any other subfragment, the subfragment is to be cut into subfragments, each of them containing k-2 sequence. This rule does not cover rarer situations of a repeated end when there are more than one false negative k-tuple on the point of repeated k-1 sequence. Misconnected subfragments of this kind can be recognized by using the information from the overlapped fragments, or informative fragments of basic and ordering libraries. In addition, the misconnected subfragment will remain when two or more false negative k-tuples occur on both positions which contain the identical k-1 sequence. This is a very rare situation since it requires at least 4 specific false k-tuples. An additional rule can be introduced to cut these subfragments on sequences of length k if the given sequence can be obtained by combination of sequences shorter than k-2 from the end of one subfragment and the start of another.

By strict application of the described rule, some completeness is lost to ensure the accuracy of the output. Some of the subfragments will be cut although they are not misconnected since they fit into the pattern of a misconnected subfragment. There are several situations of this kind. For example, a fragment, beside at least two identical k-1 sequences, contains any k-2 sequence from k-1 or a fragment contains k-2 sequence

repeated at least twice and at least one false negative k-tuple containing given k-2 sequence in the middle, etc.

The aim of this part of the algorithm is to reduce the number of pSFs to a minimal number of longer subfragments with correct sequence. The generation of unique longer subfragments or a complete sequence is possible in two situations. The first situation concerns the specific order of repeated k-1 words. There are cases in which some or all maximally extended pSFs (the first group of pSFs) can be uniquely ordered. For example, in fragment S-R1-a-R2-b-R1-c-R2-E where S and E are the start and end of a fragment, a, b, and c are different sequences specific to respective subfragments and R1 and R2 are two k-1 sequences that are tandemly repeated, five subfragments are generated (S-R1, R1-a-R2, R2-b-R1, R1-c-R2, and R-E). They may be ordered in two ways; the original sequence above or S-R1-c-R-b-R1-a-R-E. In contrast, in a fragment with the same number and types of repeated sequences but ordered differently, i.e. S-R1-a-R1-b-R-c-R-E, there is no other sequence which includes all subfragments. Examples of this type can be recognized only after the process of generation of pSFs. They represent the necessity for two steps in the process of pSF generation. The second situation of generation of false short subfragments on positions of nonrepeated k-1 sequences when the files contain false negative and/or positive k-tuples is more important.

The solution for both pSF groups consists of two parts. First, the false positive k-tuples appearing as the nonexistent minimal subfragments are eliminated. All k-tuple subfragments of length k which do not have an overlap on either end, of the length of longer than k-a on one end and longer than k-b on the other end, are eliminated to enable formation of the maximal number of connections. In our experiments, the values for a and b of 2 and 3, respectively, appeared to be adequate to eliminate a sufficient number of false positive k-tuples.

The merging of subfragments that can be uniquely connected is accomplished in the second step. The rule for connection is: two subfragments may be unambiguously connected if, and only if, the overlapping sequence at the relevant end or start of two subfragments is not present at the start and/or end of any other subfragment.

The exception is if one subfragment from the considered pair has the identical beginning and end. In that case connection is permitted, even if there is another subfragment with the same end present in the file. The main problem here is the precise definition of overlapping sequence. The connection is not permitted if the overlapping sequence unique for only one pair of subfragments is shorter than $k-2$, or it is $k-2$ or longer but an additional subfragment exists with the overlapping sequence of any length longer than $k-4$. Also, both the canonical ends of pSFs and the ends after omitting one (or few) last bases are considered as the overlapping sequences.

After this step some false positive k -tuples (as minimal subfragments) and some subfragments with a wrong end may survive. In addition, in very rare occasions where a certain number of some specific false k -tuples are simultaneously present, an erroneous connection may take place. These cases will be detected and solved in the subfragment ordering process, and in the additional control steps along with the handling of uncut "misconnected" subfragments.

The short subfragments that are obtained are of two kinds. In the common case, these subfragments may be unambiguously connected among themselves because of the distribution of repeated $k-1$ sequences. This may be done after the process of generation of pSFs and is a good example of the necessity for two steps in the process of pSF generation. In the case of using the file containing false positive and/or false negative k -tuples, short pSFs are obtained on the sites of nonrepeated $k-1$ sequences. Considering false positive k -tuples, a k -tuple may contain more than one wrong base (or containing one wrong base somewhere in the middle), as well as k -tuple on the end. Generation of short and erroneous (or misconnected) subfragments is caused by the latter k -tuples. The k -tuples of the former kind represent wrong pSFs with length equal to k -tuple length.

The aim of merging pSF part of the algorithm is the reduction of the number of pSFs to the minimal number of longer subfragments with the correct sequence. All k -tuple subfragments that do not have an overlap on either end, of the length of longer than $k-a$ on one, and longer than $k-b$ on the other end, are eliminated to enable the maximal number of connections. In this way, the majority of false positive k -tuples are discarded. The rule for connection is: two subfragments can be unambiguously connected if, and only if the overlapping sequence of the relevant end or start of two subfragments is not

present on the start and/or end of any other subfragment. The exception is a subfragment with the identical beginning and end. In that case connection is permitted, provided that there is another subfragment with the same end present in the file. The main problem here is of precise definition of overlapping sequence. The presence of at least two specific false negative k-tuples on the points of repetition of k-1 or k-2 sequences, as well as combining of the false positive and false negative k-tuples may destroy or “mask” some overlapping sequences and can produce an unambiguous, but wrong connection of pSFs. To prevent this, completeness must be sacrificed on account of exactness: the connection is not permitted on the end-sequences shorter than k-2, and in the presence of an extra overlapping sequence longer than k-4. The overlapping sequences are defined from the end of the pSFs, or omitting one, or few last bases.

In the very rare situations, with the presence of a certain number of some specific false positive and false negative k-tuples, some subfragments with the wrong end can survive, some false positive k-tuples (as minimal subfragments) can remain, or the erroneous connection can take place. These cases are detected and solved in the subfragments ordering process, and in the additional control steps along with the handling of uncut, misconnected subfragments.

The process of ordering of subfragments is similar to the process of their generation. If one considers subfragments as longer k-tuples, ordering is performed by their unambiguous connection via overlapping ends. The informational basis for unambiguous connection is the division of subfragments generated in fragments of the basic library into groups representing segments of those fragments. The method is analogous to the biochemical solution of this problem based on hybridization with longer oligonucleotides with relevant connecting sequence. The connecting sequences are generated as subfragments using the k-tuple sets of the appropriate segments of basic library fragments. Relevant segments are defined by the fragments of the ordering library that overlap with the respective fragments of the basic library. The shortest segments are informative fragments of the ordering library. The longer ones are several neighboring informative fragments or total overlapping portions of fragments corresponding of the ordering and basic libraries. In order to decrease the number of separate samples,

fragments of the ordering library are randomly pooled, and the unique k-tuple content is determined.

By using the large number of fragments in the ordering library very short segments are generated, thus reducing the chance of the multiple appearance of the k-1 sequences which are the reasons for generation of the subfragments. Furthermore, longer segments, consisting of the various regions of the given fragment of the basic library, do not contain some of the repeated k-1 sequences. In every segment a connecting sequence (a connecting subfragment) is generated for a certain pair of the subfragments from the given fragment. The process of ordering consists of three steps: (1) generation of the k-tuple contents of each segment; (2) generation of subfragments in each segment; and (3) connection of the subfragments of the segments. Primary segments are defined as significant intersections and differences of k-tuple contents of a given fragment of the basic library with the k-tuple contents of the pools of the ordering library. Secondary (shorter) segments are defined as intersections and differences of the k-tuple contents of the primary segments.

There is a problem of accumulating both false positive and negative k-tuples in both the differences and intersections. The false negative k-tuples from starting sequences accumulate in the intersections (overlapping parts), as well as false positive k-tuples occurring randomly in both sequences, but not in the relevant overlapping region. On the other hand, the majority of false positives from either of the starting sequences is not taken up into intersections. This is an example of the reduction of experimental errors from individual fragments by using information from fragments overlapping with them. The false k-tuples accumulate in the differences for another reason. The set of false negatives from the original sequences are enlarged for false positives from intersections and the set of false positives for those k-tuples which are not included in the intersection by error, i.e. are false negative in the intersection. If the starting sequences contain 10% false negative data, the primary and secondary intersections will contain 19% and 28% false negative k-tuples. respectively. On the other hand, a mathematical expectation of 77 false positives may be predicted if the basic fragment and the pools have lengths of 500 bp and 10,000 bp, respectively. However, there is a possibility of

recovering most of the "lost" k-tuples and of eliminating most of the false positive k-tuples.

First, one has to determine a basic content of the k-tuples for a given segment as the intersection of a given pair of the k-tuple contents. This is followed by including all
 5 k-tuples of the starting k-tuple contents in the intersection, which contain at one end k-1 and at the other end k+ sequences which occur at the ends of two k-tuples of the basic set. This is done before generation of the differences thus preventing the accumulation of false positives in that process. Following that, the same type of enlargement of k-tuple set is applied to differences with the distinction that the borrowing is from the
 10 intersections. All borrowed k-tuples are eliminated from the intersection files as false positives.

The intersection, i.e. a set of common k-tuples, is defined for each pair (a basic fragment) x (a pool of ordering library). If the number of k-tuples in the set is significant it is enlarged with the false negatives according to the described rule. The primary
 15 difference set is obtained by subtracting from a given basic fragment the obtained intersection set. The false negative k-tuples are appended to the difference set by borrowing from the intersection set according to the described rule and, at the same time, removed from the intersection set as false positive k-tuples. When the basic fragment is longer than the pooled fragments, this difference can represent the two separate segments
 20 which somewhat reduces its utility in further steps. The primary segments are all generated intersections and differences of pairs (a basic fragment) x (a pool of ordering library) containing the significant number of k-tuples. K-tuple sets of secondary segments are obtained by comparison of k-tuple sets of all possible pairs of primary segments. The two differences are defined from each pair which produces the
 25 intersection with the significant number of k-tuples. The majority of available information from overlapped fragments is recovered in this step so that there is little to be gained from the third round of forming intersections, and differences.

(2) Generation of the subfragments of the segments is performed identically as described for the fragments of the basic library.

30 (3) The method of connection of subfragments consists of sequentially determining the correctly linked pairs of subfragments among the subfragments from a

given basic library fragment which have some overlapped ends. In the case of 4 relevant subfragments, two of which contain the same beginning and two having the same end, there are 4 different pairs of subfragments that can be connected. In general 2 are correct and 2 are wrong. To find correct ones, the presence of the connecting sequences of each pair is tested in the subfragments generated from all primary and secondary segments for a given basic fragment. The length and the position of the connecting sequence are chosen to avoid interference with sequences which occur by chance. They are $k+2$ or longer, and include at least one element beside overlapping sequence in both subfragments of a given pair. The connection is permitted only if the two connecting sequences are found and the remaining two do not exist. The two linked subfragments replace former subfragments in the file and the process is cyclically repeated. Repeated sequences are generated in this step. This means that some subfragments are included in linked subfragments more than once. They will be recognized by finding the relevant connecting sequence which engages one subfragment in connection with two different subfragments.

The recognition of misconnected subfragments generated in the processes of building pSFs and merging pSFs into longer subfragments is based on testing whether the sequences of subfragments from a given basic fragment exist in the sequences of subfragments generated in the segments for the fragment. The sequences from an incorrectly connected position will not be found indicating the misconnected subfragments.

Beside the described three steps in ordering of subfragments some additional control steps or steps applicable to specific sequences will be necessary for the generation of more complete sequence without mistakes.

The determination of which subfragment belongs to which segment is performed by comparison of contents of k -tuples in segments and subfragments. Because of the errors in the k -tuple contents (due to the primary error in pools and statistical errors due to the frequency of occurrences of k -tuples) the exact partitioning of subfragments is impossible. Thus, instead of "all or none" partition, the chance of coming from the given segment ($P(sf,s)$) is determined for each subfragment. This possibility is the function of

the lengths of k-tuples, the lengths of subfragments, the lengths of fragments of ordering library, the size of the pool, and of the percentage of false k-tuples in the file:

$$P(sf,s)=(Ck-F)/Lsf,$$

where Lsf is the length of subfragment, Ck is the number of common k-tuples for a given subfragment/segment pair, and F is the parameter that includes relations between lengths of k-tuples, fragments of basic library, the size of the pool, and the error percentage.

Subfragments attributed to a particular segment are treated as redundant short pSFs and are submitted to a process of unambiguous connection. The definition of unambiguous connection is slightly different in this case, since it is based on a probability that subfragments with overlapping end(s) belong to the segment considered. Besides, the accuracy of unambiguous connection is controlled by following the connection of these subfragments in other segments. After the connection in different segments, all of the obtained subfragments are merged together, shorter subfragments included within longer ones are eliminated, and the remaining ones are submitted to the ordinary connecting process. If the sequence is not regenerated completely, the process of partition and connection of subfragments is repeated with the same or less severe criterions of probability of belonging to the particular segment, followed by unambiguous connection.

Using severe criteria for defining unambiguous overlap, some information is not used. Instead of a complete sequence, several subfragments that define a number of possibilities for a given fragment are obtained. Using less severe criteria an accurate and complete sequence is generated. In a certain number of situations, e.g., an erroneous connection, it is possible to generate a complete, but an incorrect sequence, or to generate “monster” subfragments with no connection among them. Thus, for each fragment of the basic library one obtains: a) several possible solutions where one is correct and b) the most probable correct solution. Also, in a very small number of cases, due to the mistake in the subfragment generation process or due to the specific ratio of the probabilities of belonging, no unambiguous solution is generated or one, the most probable solution. These cases remain as incomplete sequences, or the unambiguous solution is obtained by comparing these data with other, overlapped fragments of basic library.

The described algorithm was tested on a randomly generated, 50 kb sequence, containing 40% GC to simulate the GC content of the human genome. In the middle part of this sequence were inserted various AlI, and some other repetitive sequences, of a total length of about 4 kb. To simulate an *in vitro* SBH experiment, the following operations

5 were performed to prepare appropriate data.

1) Positions of sixty 5 kb overlapping “clones” were randomly defined, to simulate preparation of a basic library:

2) Positions of one thousand 500 bp “clones” were randomly determined to simulate making the ordering library. These fragments were extracted from the sequence.

10 Random pools of 20 fragments were made, and k-tuple sets of pools were determined and stored on the hard disk. These data are used in the subfragment ordering phase: For the same density of clones 4 million clones in basic library and 3 million clones in ordering library are used for the entire human genome. The total number of 7 million clones is several fold smaller than the number of clones a few kb long for random cloning of

15 almost all of genomic DNA and sequencing by a gel-based method.

From the data on the starts and ends of 5 kb fragments, 117 “informative fragments” were determined to be in the sequence. This was followed by determination of sets of overlapping k-tuples of which the single “informative fragment” consist. Only the subset of k-tuples matching a predetermined list were used. The list contained 65% 8-

20 mers, 30% 9-mers, and 5% 10-12-mers. Processes of generation and the ordering of subfragments were performed on these data.

The testing of the algorithm was performed on the simulated data in two experiments. The sequence of 50 informative fragments was regenerated with the 100% correct data set (over 20,000 bp), and 26 informative fragments (about 10,000 bp) with

25 10% false k-tuples (5% positive and 5% negative ones).

In the first experiment, all subfragments were correct and in only one out of 50 informative fragments the sequence was not completely regenerated but remained in the form of 5 subfragments. The analysis of positions of overlapped fragments of ordering library has shown that they lack the information for the unique ordering of the 5

30 subfragments. The subfragments may be connected in two ways based on overlapping ends, 1-2-3-4-5 and 1-4-3-2-5. The only difference is the exchange of positions of

subfragments 2 and 4. Since subfragments 2, 3, and 4 are relatively short (total of about 100 bp), the relatively greater chance existed, and occurred in this case, that none of the fragments of ordering library started or ended in the subfragment 3 region.

To simulate real sequencing, some false (“hybridization”) data was included as input in a number of experiments. In oligomer hybridization experiments, under proposed conditions, the only situation producing unreliable data is the end mismatch versus full match hybridization. Therefore, in simulation only those k-tuples differing in a single element on either end from the real one were considered to be false positives. These “false” sets are made as follows. On the original set of a k-tuples of the informative fragment, a subset of 5% false positive k-tuples are added. False positive k-tuples are made by randomly picking a k-tuple from the set, copying it and altering a nucleotide on its beginning or end. This is followed by subtraction of a subset of 5% randomly chosen k-tuples. In this way the statistically expected number of the most complicated cases is generated in which the correct k-tuple is replaced with a k-tuple with the wrong base on the end.

Production of k-tuple sets as described leads to up to 10% of false data. This value varies from case to case, due to the randomness of choice of k-tuples to be copied, altered, and erased. Nevertheless, this percentage 3-4 times exceeds the amount of unreliable data in real hybridization experiments. The introduced error of 10% leads to the two fold increase in the number of subfragments both in fragments of basic library (basic library informative fragments) and in segments. About 10% of the final subfragments have a wrong base at the end as expected for the k-tuple set which contains false positives (see generation of primary subfragments). Neither the cases of misconnection of subfragments nor subfragments with the wrong sequence were observed. In 4 informative fragments out of 26 examined in the ordering process the complete sequence was not regenerated. In all 4 cases the sequence was obtained in the form of several longer subfragments and several shorter subfragments contained in the same segment. This result shows that the algorithmic principles allow working with a large percentage of false data.

The success of the generation of the sequence from its k-tuple content may be described in terms of completeness and accuracy. In the process of generation, two

particular situations can be defined: 1) Some part of the information is missing in the generated sequence, but one knows where the ambiguities are and to which type they belong, and 2) the regenerated sequence that is obtained does not match the sequence from which the k- tuple content is generated, but the mistake can not be detected.

5 Assuming the algorithm is developed to its theoretical limits, as in the use of the exact k-tuple sets, only the first situation can take place. There the incompleteness results in a certain number of subfragments that may not be ordered unambiguously and the problem of determination of the exact length of monotonous sequences, i.e. the number of perfect tandem repeats.

10 With false k-tuples, incorrect sequences may be generated. The reason for mistakes does not lie in the shortcomings of the algorithm, but in the fact that a given content of k-tuples unambiguously represents the sequence that differs from the original one. One may define three classes of error, depending on the kind of the false k- tuples present in the file. False negative k-tuples (which are not accompanied with the false.
15 positives) produce “deletions”. False positive k-tuples are producing “elongations (unequal crossing over)”. False positives accompanied with false negatives are the reason for generation of “insertions”, alone or combined with “deletions”. The deletions are produced when all of the k-tuples (or their majority) between two possible starts of the subfragments are false negatives. Since every position in the sequence is defined by k-
20 tuples, the occurrence of the deletions in a common case requires k consecutive false negatives. (With 10% of the false negatives and k=8, this situation takes place after every 108 elements). This situation is extremely infrequent even in mammalian genome sequencing using random libraries containing ten genome equivalents.

Elongation of the end of the sequence caused by false positive k-tuples is the
25 special case of “insertions”, since the end of the sequence can be considered as the endless linear array of false negative k-tuples. One may consider a group of false positive k-tuples producing subfragments longer than one k-tuple. Situations of this kind may be detected if subfragments are generated in overlapped fragments, like random physical fragments of the ordering library. An insertion, or insertion in place of a deletion, can
30 arise as a result of specific combinations of false positive and false negative k-tuples. In the first case. the number of consecutive false negatives is smaller than k. Both cases

require several overlapping false positive k-tuples. The insertions and deletions are mostly theoretical possibilities without sizable practical repercussions since the requirements in the number and specificity of false k-tuples are simply too high.

5 In every other situation of not meeting the theoretical requirement of the minimal number and the kind of the false positive and/or negatives, mistakes in the k-tuples content may produce only the lesser completeness of a generated sequence.

10 In SBH, a sample nucleic acid is sequenced by exposing the sample to a support-bound probe of known sequence and a labeled probe or probes in solution. Wherever the probes ligase is introduced into the mixture of probes and sample, such that, wherever a support has a bound probe and a labeled probe hybridized back to back along the sample, the two probes will be chemically linked by the action of the ligase. After washing, only chemically linked support-bound and labeled probes are detected by the presence of the labeled probe. By knowing the identity of the support-bound probe at a particular location in an array, and the identity of the labeled probe, a portion of the sequence of the sample may be determined by the presence of a label at a point in an array on a Format with a sample of three substrates. Not all of the sample to be sequenced may be a nucleic acid fragment or oligonucleotide of ten base pairs ("bp"). The sample is preferably four to one thousand bases in length.

20 The length of the probe is a fragment less than ten bases in length, and, preferably, is between four and nine bases in length. In this way, arrays of support-bound probes may include all oligonucleotides of a given length or may include only oligonucleotides selected for a particular test. Where all oligonucleotides of a given length are used, the number of central oligonucleotides may be calculated by 4^N where N is the length of the probe.

25

5.36 RE-USING SEQUENCING CHIPS

When ligation is employed in the sequencing process, then the ordinary oligonucleotide chip cannot be immediately reused. The inventors contemplate that this may be overcome in various ways.

30 One may employ ribonucleotides for the second probe, probe P, so that this probe may subsequently be removed by RNase treatment. RNase treatment may utilize RNase

A, an endoribonuclease that specifically attacks single-stranded RNA 3'-to pyrimidine residues and cleaves the phosphate linkage to the adjacent nucleotide. The end products are pyrimidine 3' phosphates and oligonucleotides with terminal pyrimidine 3' phosphates. RNase A works in the absence of cofactors and divalent cations.

5 To utilize an RNase, one would generally incubate the chip in any appropriate RNase-containing buffer, as described by Sambrook *et al.* (1989; incorporated herein by reference). The use of 30-50 μ l of RNase-containing buffer per 8 x 8 mm or 9 x 9mm array at 37°C for between 10 and 60 minutes is appropriate. One would then wash with hybridization buffer.

10 Although not widely applicable, one could also use the uracil base, as described by Craig *et al.* (1989), incorporated herein by reference, in specific embodiments. Destruction of the ligated probe combination, to yield a re-usable chip, would be achieved by digestion with *the E. coli* repair enzyme, uracil-DNA glycosylase which removes uracil from DNA.

15 One could also generate a specifically cleavable bond between the probes and then cleave the bond after detection. For example, this may be achieved by chemical ligation as described by Shabarova *et al.*, (1991) and Dolmnnaya et at, (1988), both references being specifically incorporated herein by reference.

20 Shabarova *et al.* (1991) describe the condensation of oligodeoxyribonucleotides with cyanogen bromide as a condensing agent. In their one step chemical ligation reaction, the oligonucleotides are heated to 97°C, slowly cooled to 0°C, then 1 μ l 10mM BrCN in acetonitrile is added.

25 Dolmnnaya *et al.* (1988) show how to incorporate phosphoramidite and pyrophosphate internucleotide bonds in DNA duplexes. They also use a chemical ligation method for modification of the sugar phosphate backbone of DNA, with a water-soluble carbodiimide (CDI) as a coupling agent. The selective cleavage of a phosphoamide bond involves contact with 15% CH₃COOH for 5 mm at 95°C. The selective cleavage of a pyrophosphate bond involves contact with a pyridine-water mixture (9:1) and freshly distilled (CF₃CO)₂O.

30

5.37 DIAGNOSTICS - SCORING KNOWN MUTATIONS OR FULL GENE RESEQUENCING

In a simple case, the goal may be to discover whether selected, known mutations
 5 occur in a DNA segment. Less than 12 probes may suffice for this purpose, for example,
 5 probes positive for one allele, 5 positive for the other, and 2 negative for both. Because
 of the small number of probes to be scored per sample, large numbers of samples may be
 analyzed in parallel. For example, with 12 probes in 3 hybridization cycles, 96 different
 genomic loci or gene segments from 64 patient may be analyzed on one 6 x 9 in
 10 membrane containing 12 x 24 subarrays each with 64 dots representing the same DNA
 segment from 64 patients. In this example, samples may be prepared in sixty-four 96-well
 plates. Each plate may represent one patient, and each well may represent one of the
 DNA segments to be analyzed. The samples from 64 plates may be spotted in four
 replicas as four quarters of the same membrane.

15 A set of 12 probes may be selected by single channel pipetting or by a single pin
 transferring device (or by an array of individually-controlled pipets or pins) for each of
 the 96 segments, and the selected probes may be arrayed in twelve 96-well plates. Probes
 may be labelled, if they are not prelabelled, and then probes from four plates may be
 mixed with hybridization buffer and added to the subarrays preferentially by a 96-channel
 20 pipeting device. After one hybridization cycle it is possible to strip off previously-
 applied probes by incubating the membrane at 37° to 55°C in the preferably undiluted
 hybridization or washing buffer.

The likelihood that probes positive for one allele are positive and probes positive
 for the other allele are negative may be used to determine which of the two alleles is
 25 present. In this redundant scoring scheme, some level (about 10%) of errors in
 hybridization of each probe may be tolerated.

An incomplete set of probes may be used for scoring most of the alleles,
 especially if the smaller redundancy is sufficient, e.g., one or two probes which prove the
 presence or absence in a sample of one of the two alleles. For example, with a set of four
 30 thousand 8-mers there is a 91% chance of finding at least one positive probe for one of
 the two alleles for a randomly selected locus. The incomplete set of probes may be
 optimized to reflect G+C content and other biases in the analyzed samples.

For full gene sequencing, genes may be amplified in an appropriate number of segments. For each segment, a set of probes (about one probe per 2-4 bases) may be selected and hybridized. These probes may identify whether there is a mutation anywhere in the analyzed segments. Segments (*i.e.*, subarrays which contain these segments) where one or more mutated sites are detected may be hybridized with additional probes to find the exact sequence at the mutated sites. If a DNA sample is tested by every second 6-mer, and a mutation is localized at the position that is surrounded by positively hybridized probes TGCAA and TATTCC and covered by three negative probes: CAAAC, AAATA and ACTAT, the mutated nucleotides must be A and/or C occurring in the normal sequence at that position. They may be changed by a single base mutation, or by a one or two nucleotide deletion and/or insertion between bases AA, AC or CT.

One approach is to select a probe that extends the positively hybridized probe TGCAA for one nucleotide to the right, and which extends the probe TATTCC one nucleotide to the left. With these 8 probes (GCAAA, GCAAT, GCAAC, GCAAG and ATATTC, TTATTC, CTATTC, GTATTC) two questionable nucleotides are determined.

The most likely hypothesis about the mutation may be determined. For example, A is found to be mutated to G. There are two solutions satisfied by these results. Either replacement of A with G is the only change or there is in addition to that change an insertion of some number of bases between newly determined G and the following C. If the result with bridging probes is negative these options may then be checked first by at least one bridging probe comprising the mutated position (AAGCTA) and with an additional 8 probes: CAAAG, CAAAGT, CAAAGC, CAAAGG and ACTAT, TCTAT, CCTAT, GCTAT. There are many other ways to select mutation-solving probes.

In the case of diploid, particular comparisons of scores for the test samples and homozygotic control may be performed to identify heterozygotes (see above). A few consecutive probes are expected to have roughly twice smaller signals if the segment covered by these probes is mutated on one of the two chromosomes.

5.38 IDENTIFICATION OF GENES (MUTATIONS) RESPONSIBLE FOR GENETIC DISORDERS AND OTHER TRAITS

Using universal sets of longer probes (8-mers or 9-mers) on immobilized arrays of samples, DNA fragments as long as 5-20 kb may be sequenced without subcloning.

Furthermore, the speed of sequencing readily may be about 10 million

bp/day/hybridization instrument. This performance allows for resequencing a large

5 fraction of human genes or the human genome repeatedly from scientifically or medically interesting individuals. To resequence 50% of the human genes, about 100 million bp is checked. That may be done in a relatively short period of time at an affordable cost.

This enormous resequencing capability may be used in several ways to identify mutations and/or genes that encode for disorders or any other traits. Basically, mRNAs

10 (which may be converted into cDNAs) from particular tissues or genomic DNA of patients with particular disorders may be used as starting materials. From both sources of DNA, separate genes or genomic fragments of appropriate length may be prepared either by cloning procedures or by *in vitro* amplification procedures (for example by PCR). If cloning is used, the minimal set of clones to be analyzed may be selected from the

15 libraries before sequencing. That may be done efficiently by hybridization of a small number of probes, especially if a small number of clones longer than 5 kb is to be sorted. Cloning may increase the amount of hybridization data about two times, but does not require tens of thousands of PCR primers.

In one variant of the procedure, gene or genomic fragments may be prepared by

20 restriction cutting with enzymes like Hga I which cuts DNA in following way: GACGC(N5')/CTGCG(N10'). Protruding ends of five bases are different for different fragments. One enzyme produces appropriate fragments for a certain number of genes. By cutting cDNA or genomic DNA with several enzymes in separate reactions, every gene of interest may be excised appropriately. In one approach, the cut DNA is

25 fractionated by size. DNA fragments prepared in this way (and optionally treated with Exonuclease III which individually removes nucleotides from the 3' end and increases length and specificity of the ends) may be dispensed in the tubes or in multiwell plates. From a relatively small set of DNA adapters with a common portion and a variable protruding end of appropriate length, a pair of adapters may be selected for every gene

30 fragment that needs to be amplified. These adapters are ligated and then PCR is performed by universal primers. From 1000 adapters, a million pairs may be generated,

thus a million different fragments may be specifically amplified in the identical conditions with a universal pair of primers complementary to the common end of the adapters.

5 If a DNA difference is found to be repeated in several patients, and that sequence change is nonsense or can change function of the corresponding protein, then the mutated gene may be responsible for the disorder. By analyzing a significant number of individuals with particular traits, functional allelic variations of particular genes could be associated by specific traits.

10 This approach may be used to eliminate the need for very expensive genetic mapping on extensive pedigrees and has special value when there is no such genetic data or material.

5.39 SCORING SINGLE NUCLEOTIDE POLYMORPHISMS IN GENETIC MAPPING

15 Techniques disclosed in this application are appropriate for an efficient identification of genomic fragments with single nucleotide polymorphisms (SNUPs). In 10 individuals by applying the described sequencing process on a large number of genomic fragments of known sequence that may be amplified by cloning or by *in vitro* amplification, a sufficient number of DNA segments with SNUPs may be identified. The polymorphic fragments are further used as SNUP markers. These markers are either 20 mapped previously (for example they represent mapped STSs) or they may be mapped through the screening procedure described below.

SNUPs may be scored in every individual from relevant families or populations by amplifying markers and arraying them in the form of the array of subarrays. Subarrays contain the same marker amplified from the analyzed individuals. For each marker, as in 25 the diagnostics of known mutations, a set of 6 or less probes positive for one allele and 6 or less probes positive for the other allele may be selected and scored. From the significant association of one or a group of the markers with the disorder, chromosomal position of the responsible gene(s) may be determined. Because of the high throughput and low cost, thousands of markers may be scored for thousands of individuals. This 30 amount of data allows localization of a gene at a resolution level of less than one million bp as well as localization of genes involved in polygenic diseases. Localized genes may

be identified by sequencing particular regions from relevant normal and affected individuals to score a mutation(s).

PCR is preferred for amplification of markers from genomic DNA. Each of the markers require a specific pair of primers. The existing markers may be convertible or new markers may be defined which may be prepared by cutting genomic DNA by Hga I type restriction enzymes, and by ligation with a pair of adapters.

SNUP markers can be amplified or spotted as pools to reduce the number of independent amplification reactions. In this case, more probes are scored per one sample. When 4 markers are pooled and spotted on 12 replica membranes, then 48 probes (12 per marker) may be scored in 4 cycles.

5.40 DETECTION AND VERIFICATION OF IDENTITY OF DNA FRAGMENTS

DNA fragments generated by restriction cutting, cloning or *in vitro* amplification (e.g. PCR) frequently may be identified in a experiment. Identification may be performed by verifying the presence of a DNA band of specific size on gel electrophoresis.

Alternatively, a specific oligonucleotide may be prepared and used to verify a DNA sample in question by hybridization. The procedure developed here allows for more efficient identification of a large number of samples without preparing a specific oligonucleotide for each fragment. A set of positive and negative probes may be selected from the universal set for each fragment on the basis of the known sequences. Probes that are selected to be positive usually are able to form one or a few overlapping groups and negative probes are spread over the whole insert.

This technology may be used for identification of STSs in the process of their mapping on the YAC clones. Each of the STSs may be tested on about 100 YAC clones or pools of YAC clones. DNAs from these 100 reactions possibly are spotted in one subarray. Different STSs may represent consecutive subarrays. In several hybridization cycles, a signature may be generated for each of the DNA samples, which signature proves or disproves existence of the particular STS in the given YAC clone with necessary confidence.

To reduce the number of independent PCR reactions or the number of independent samples for spotting, several STSs may be amplified simultaneously in a reaction or PCR samples may be mixed, respectively. In this case more probes have to be scored per one dot. The pooling of STSs is independent of pooling YACs and may be used on single YACs or pools of YACs. This scheme is especially attractive when several probes labelled with different colors are hybridized together.

In addition to confirmation of the existence of a DNA fragment in a sample, the amount of DNA may be estimated using intensities of the hybridization of several separate probes or one or more pools of probes. By comparing obtained intensities with intensities for control samples having a known amount of DNA, the quantity of DNA in all spotted samples is determined simultaneously. Because only a few probes are necessary for identification of a DNA fragment, and there are N possible probes that may be used for DNA N bases long, this application does not require a large set of probes to be sufficient for identification of any DNA segment. From one thousand 8-mers, on average about 30 full matching probes may be selected for a 1000 bp fragment.

5.41 IDENTIFICATION OF INFECTIOUS DISEASE ORGANISMS AND THEIR VARIANTS

DNA-based tests for the detection of viral, bacterial, fungal and other parasitic organisms in patients are usually more reliable and less expensive than alternatives. The major advantage of DNA tests is to be able to identify specific strains and mutants, and eventually be able to apply more effective treatment. Two applications are described below.

The presence of 12 known antibiotic resistance genes in bacterial infections may be tested by amplifying these genes. The amplified products from 128 patients may be spotted in two subarrays and 24 subarrays for 12 genes may then be repeated four times on a 8 x 12 cm membrane. For each gene, 12 probes may be selected for positive and negative scoring. Hybridizations may be performed in 3 cycles. For these tests, a much smaller set of probes is most likely to be universal. For example, from a set of one thousand 8-mers, on average 30 probes are positive in 1000 bp fragments, and 10 positive probes are usually sufficient for a highly reliable identification. As described in Section

5.22, several genes may be amplified and/or spotted together and the amount of the given DNA may be determined. The amount of amplified gene may be used as an indicator of the level of infection.

Another example involves possible sequencing of one gene or the whole genome of an HIV virus. Because of rapid diversification, the virus poses many difficulties for selection of an optimal therapy. DNA fragments may be amplified from isolated viruses from up to 64 patients and resequenced by the described procedure. On the basis of the obtained sequence the optimal therapy may be selected. If there is a mixture of two virus types of which one has the basic sequence (similar to the case of heterozygotes), the mutant may be identified by quantitative comparisons of its hybridization scores with scores of other samples, especially control samples containing the basic virus type only. Scores twice as small may be obtained for three to four probes that cover the site mutated in one of the two virus types present in the sample (see above).

15 **5.42 FORENSIC AND PARENTAL IDENTIFICATION**

Sequence polymorphisms make an individual genomic DNA unique. This permits analysis of blood or other body fluids or tissues from a crime scene and comparison with samples from criminal suspects. A sufficient number of polymorphic sites are scored to produce a unique signature of a sample. SBH may easily score single nucleotide polymorphisms to produce such signatures.

A set of DNA fragments (10-1000 mer) may be amplified from samples and suspects. DNAs from samples and suspects representing one fragment are spotted in one or several subarrays and each subarray may be replicated 4 times. In three cycles, 12 probes may determine the presence of allele A or B in each of the samples, including suspects, for each DNA locus. Matching the patterns of samples and suspects may lead to discovery of the suspect responsible for the crime.

The same procedure may be applicable to prove or disprove the identity of parents of a child. DNA may be prepared and polymorphic loci amplified from the child and adults; patterns of A or B alleles may be determined by hybridization for each. Comparisons of the obtained patterns, along with positive and negative controls, aide in the determination of familial relationships. In this case, only a significant portion of the

alleles need match with one parent for identification. Large numbers of scored loci allow for the avoidance of statistical errors in the procedure or of masking effects of *de novo* mutations.

5.43 ASSESSING GENETIC DIVERSITY OF POPULATIONS OR SPECIES AND BIOLOGICAL DIVERSITY OF ECOLOGICAL NICHES

Measuring the frequency of allelic variations on a significant number of loci (for example, several genes or entire mitochondrial DNA) permits development of different types of conclusions, such as conclusions regarding the impact of the environment on the genotypes, history and evolution of a population or its susceptibility to diseases or extinction, and others. These assessments may be performed by testing specific known alleles or by full resequencing of some loci to be able to define *de novo* mutations which may reveal fine variations or presence of mutagens in the environment.

Additionally, biodiversity in the microbial world may be surveyed by resequencing evolutionarily conserved DNA sequences, such as the genes for ribosomal RNAs or genes for highly conservative proteins. DNA may be prepared from the environment and particular genes amplified using primers corresponding to conservative sequences. DNA fragments may be cloned preferentially in a plasmid vector (or diluted to the level of one molecule per well in multiwell plates and then amplified *in vitro*). Clones prepared this way may be resequenced as described above. Two types of information are obtained. First of all, a catalogue of different species may be defined as well as the density of the individuals for each species. Another segment of information may be used to measure the influence of ecological factors or pollution on the ecosystem. It may reveal whether some species are eradicated or whether the abundance ratios among species is altered due to the pollution. The method also is applicable for sequencing DNA from fossils.

5.44 DETECTION OR QUANTIFICATION OF NUCLEIC ACID SPECIES

DNA or RNA species may be detected and quantified by employing a probe pair including an unlabeled probe fixed to a substrate and a labeled probe in a solution. The species may be detected and quantified by exposure to the unlabeled probe in the presence of the labeled probe and ligase. Specifically, the formation of an extended probe

by ligation of the labeled and unlabeled probe on the sample nucleic acid backbone is indicative of the presence of the species to be detected. Thus, the presence of label at a specific point in the array on the substrate after removing unligated labeled probe indicates the presence of a sample species while the quantity of label indicates the expression level of the species.

Alternatively, one or more unlabeled probes may be arrayed on a substrate as first members of pairs with one or more labeled probes to be introduced in solution.

According to one method, multiplexing of the label on the array may be carried out by using dyes which fluoresce at distinguishable wavelengths. In this manner, a mixture of cDNAs applied to an array with pairs of labeled and unlabeled probes specific for species to be identified may be examined for the presence of and expression level of cDNA species. According to a preferred embodiment this approach may be carried out to sequence portions of cDNAs by selecting pairs of unlabeled and labeled probes pairs comprising sequences which overlap along the sequence of a cDNA to be detected.

Probes may be selected to detect the presence and quantity of particular pathogenic organisms genome by including in the composition selected probe pairs which appear in combination only in target pathogenic genome organisms. Thus, while no single probe pair may necessarily be specific for the pathogenic organism genome, the combination of pairs is. Similarly, in detecting or sequencing cDNAs, it might occur that a particular probe is not be specific for a cDNA or other type of species. Nevertheless, the presence and quantity of a particular species may be determined by a result wherein a combination of selected probes situated at distinct array locations is indicative of the presence of a particular species.

An infectious agent with about 10kb or more of DNA may be detected using a support-bound detection chip without the use of polymerase chain reaction (PCR) or other target amplification procedures. According to other methods, the genomes of infectious agents including bacteria and viruses are assayed by amplification of a single target nucleotide sequence through PCR and detection of the presence of target by hybridization of a labelled probe specific for the target sequence. Because such an assay is specific for only a single target sequence it therefore is necessary to amplify the gene by methods such as PCR to provide sufficient target to provide a detectable signal.

According to this example, an improved method of detecting nucleotide sequences characteristic of infectious agents through a Format 3-type reaction is provided wherein a solid phase detection chip is prepared which comprises an array of multiple different immobilized oligonucleotide probes specific for the infectious agent of interest:

- 5 A single dot comprising a mixture of many unlabeled probes complementary to the target nucleic acid concentrates the label specific to a species at one location thereby improving sensitivity over diffuse or single probe labeling. Such multiple probes may be of overlapping sequences of the target nucleotide sequence but may also be non-overlapping sequences as well as non-adjacent. Such probes preferably have a length of about 5 to 12
10 nucleotides.

- A nucleic acid sample exposed to the probe array and target sequences present in the sample will hybridize with the multiple immobilized probes. A pool of multiple labeled probes selected to specifically bind to the target sequences adjacent to the immobilized probes is then applied with the sample to an array of unlabeled
15 oligonucleotide probe mixtures. Ligase enzyme is then applied to the chip to ligate the adjacent probes on the sample. The detection chip is then washed to remove unhybridized and unligated probe and sample nucleic acids and the presence of sample nucleic acid may be determined by the presence or absence of label. This method provides reliable sample detection with about a 1000-fold reduction of molarity of the sample agent.

- 20 As a further aspect of the invention, the signal of the labelled probes may be amplified by means such as providing a common tail to the free probe which itself comprises multiple chromogenic, enzymatic or radioactive labels or which is itself susceptible to specific binding by a further probe agent which is multiply labelled. In this way, a second round of signal amplification may be carried out. Labeled or unlabeled
25 probes may be used in a second round of amplification. In this second round of amplification, a lengthy DNA sample with multiple labels may result in an increased amplification intensity signal between 10 to 100 fold which may result in a total signal amplification of 100,000 fold. Through the use of both aspects of this example, an intensity signal approximately 100,000 fold may give a positive result of probe-DNA
30 ligation without having to employ PCR or other amplification procedures.

According to a further aspect of the invention an array or super array may be prepared which consists of a complete set of probes, for example 4096 6-mer probes. Arrays of this type are universal in a sense that they can be used for detection or partial to complete sequencing of any nucleic acid species. Individual spots in an array may contain
5 single probe species or mixtures of probes, for example N(1-3) B(4-6) N(1-3) type of mixtures that are synthesized in the single reaction (N represents all four nucleotides, B one specific nucleotide and where the associated numbers are a range of numbers of bases *i.e.*, 1-3 means "from one to three bases"). These mixtures provide stronger signal
10 for a nucleic acid species present at low concentration by collecting signal from different parts of the same long nucleic acid species molecule. The universal set of probes may be subdivided in many subsets which are spotted as unit arrays separated by barriers that prevent spreading of hybridization buffer with sample and labeled probe(s).

For detection of a nucleic acid species with a known sequence one of more oligonucleotide sequences comprising both unlabelled fixed and labeled probes in
15 solution may be selected. Labeled probes are synthesized or selected from the presynthesized complete sets of, for example, 7-mers. The labeled probes are added to corresponding unit arrays of fixed probes such that a pair of fixed and labeled probes will adjacently hybridize to the target sequence such that upon administration of ligase the probes will be covalently bound.

20 If a unit array contains more than one fixed probe (as separated spots or within the same spot) that are positive in a given nucleic acid species all corresponding labeled probes may be mixed and added to the same unit array. The mixtures of labeled probes are even more important when mixtures of nucleic acid species are tested. One example of a complex mixture of nucleic acid species are mRNAs in one cell or tissue.

25 According to one embodiment of the invention unit arrays of fixed probes allow use of every possible immobilized probe with cocktails of a relatively small number of labeled probes. More complex cocktails of labeled probes may be used if a multiplex labeling scheme is implemented. Preferred multiplexing methods may use different fluorescent dyes or molecular tags that may be separated by mass spectroscopy.

30 Alternatively, according to a preferred embodiment of the invention, relatively short fixed probes may be selected which frequently hybridize to many nucleic acid

sequence allow the pooling of free or solution (nonbound) 5-mers for treatment of each subarray, without a loss of sequence information. In a preferred embodiment, 16 probes are pooled for each subarray, and all possible 5-mers are represented in 64 total pools of free 5-mers. Thus, all possible 10-mers may be probed against a DNA sample using

5 1024 subarrays (16 subarrays for each pool of free 5-mers).

The target DNA in this embodiment represents two-600 bp segments of the HIV virus. These 600 bp segments are represented by pools of 60 overlapping 30-mers (the 30-mers overlap each adjacent 30 mer by 20 nucleotides). The pools of 30-mers mimic a target DNA that has been treated using techniques well known in the art to shear, digest,

10 and/or random PCR the target DNA to produce a random pool of very small fragments.

As described above in the previous Format III examples, the free 5-mers are labeled with radioactive isotopes, biotin, fluorescent dyes, etc. The labeled free 5-mers are then hybridized along with the bound 5-mers to the target DNA, and ligated. In a preferred embodiment, 300-1000 units of ligase are added to the reaction. The

15 hybridization conditions were worked out following the teachings of the previous examples. Following ligation and removal of the target DNA and excess free probe, the array is assayed to determine the location of labeled probes (using the techniques described in the examples above).

The known DNA sequence of the target, and the known free and bound 5-mers in each subarray, predict which bound 5-mers will be ligated to a labeled free 5-mer in each subarray. The signal from 20 of these predicted dots were lost and 20 new signals were gained for each change in the target DNA from the predicted sequence. The overlapping sequence of the bound 5-mers in these ten new dots identifies which free, labeled 5-mer is bound in each new dot.

25 Using the described methods, arrays and pools of free, labeled 5-mers, the test HIV DNA sequence was probed with all possible 10mers. Using this Format III approach, we properly identified the "wild-type" sequence of the segments tested, as well as several sequence "mutants" that were introduced into these segments.

5.46 SEQUENCING OF REPETITIVE DNA SEQUENCES

30 Repetitive DNA sequences in the target DNA are sequenced with "spacer oligonucleotides" in a modified Format III approach. Spacer oligonucleotides of varying

lengths of the repetitive DNA sequence (the repeating sequence is identified on a first SBH run) are hybridized to the target DNA along with a first known adjoining oligonucleotide and a second known, or group of possible oligonucleotides adjoining the other side of the spacer (known from the first SBH run). When a spacer matching the length of the repetitive DNA segment is hybridized to the target, the two adjacent oligonucleotides can be ligated to the spacer. If the first known oligonucleotide is fixed to a substrate, and the second known or possible oligonucleotide(s) is labeled, a bound ligation product including the labeled second known or possible oligonucleotide(s) is formed when a spacer of the proper length is hybridized to the target DNA.

10 **5.47 SEQUENCING THROUGH BRANCH POINTS WITH FORMAT III SBH**

Branch points in the target DNA are sequenced using a third set of oligonucleotides and a modified Format III approach. After a first SBH run, several branch points may be identified when the sequence is compiled. These can be solved by hybridizing oligonucleotide(s) that overlap partially with one of the known sequences leading into the branch point and then hybridizing to the target an additional oligonucleotide that is labeled and corresponds to one of the sequences that comes out of the branch point. When the proper oligonucleotides are hybridized to the target DNA, the labeled oligonucleotide can be ligated to the other(s). In a preferred embodiment, a first oligonucleotide that is offset by one to several nucleotides from the branch point is selected (so that it reads into one of the branch sequences), a second oligonucleotide reading from the first and into the branch point sequence is also selected, and a set of third oligonucleotides that correspond to all the possible branch sequences with an overlap of the branch point sequence by one or a few nucleotides (corresponding to the first oligonucleotide) is selected. These oligonucleotides are hybridized to the target DNA, and only the third oligonucleotide with the proper branch sequence (that matches the branch sequence of the first oligonucleotide) will produce a ligation product with the first and second oligonucleotides.

30 **5.48 MULTIPLEXING PROBES FOR ANALYZING A TARGET NUCLEIC ACID**

Sets of probes are labeled with different labels so that each probe of a set can be differentiated from the other probes in the set. Thus, the set of probes may be contacted with target nucleic acid in a single hybridization reaction without the loss of any probe information. In preferred embodiments, the different labels are different radioisotopes, or
 5 different fluorescent labels, or different EMLs. These sets of probes may be used in either Format I, Format II or Format III SBH.

In Format I SBH, the set of differently labeled probes are hybridized to target nucleic acid which is fixed to a substrate under conditions that allow differentiation between perfect matches one base-pair mismatches. Specific probes which bind to the
 10 target nucleic acid are identified by their different labels and perfect matches are determined, at least in part, from this binding information.

In Format II SBH, the target nucleic acids are labeled with different probes and hybridized to arrays of probes. Specific target nucleic acids which bind to the probes are identified by their different labels and perfect matches are determined, at least in part,
 15 form this binding information.

In Format III SBH, the set of differently labeled probes and fixed probes are hybridized to a target nucleic acid under conditions that allow perfect matches to be differentiated from one base-pair mismatches. Labeled probes that are adjacent on the target to a fixed probe are bound to the fixed probe, and these products are detected and
 20 differentiated by their different labels.

In a preferred embodiment, the different labels are EMLs, which can be detected by electron capture mass spectrometry (EC-MS). EMLs may be prepared from a variety of backbone molecules, with certain aromatic backbones being particularly preferred, *e.g.*, see Xu *et al.*, J. Chromatog. 764:95-102 (1997). The EML is attached to a probe in a
 25 reversible and stable manner, and after the probe is hybridized to target nucleic acid, the EML is removed from the probe and identified by standard EC-MS (*e.g.*, the EC-MS may be done by a gas chromatograph-massspectrometer).

5.49 DETECTION OF LOW FREQUENCY TARGET NUCLEIC ACIDS

Format III SBH has sufficient discrimination power to identify a sequence that is
 30 present in a sample at 1 part to 99 parts of a similar sequence that differs by a single

nucleotide. Thus, Format III can be used to identify a nucleic acid present at a very low concentration in a sample of nucleic acids, *e.g.*, a sample derived from blood.

In one embodiment, the two sequences are for cystic fibrosis and the sequences differ from each other by a deletion of three nucleotides. Probes for the two sequences were as follows, probes distinguishing the deletion from wild type were fixed to a substrate, and a labeled contiguous probe was common to both. Using these targets and probes, the deletion mutant could be detected with Format III SBH when it was present at one part to ninety nine parts of the wild-type.

5.50 POLAROID APPARATUS AND METHOD FOR ANALYZING A TARGET NUCLEIC ACID

An apparatus for analyzing a nucleic acid can be constructed with two arrays of nucleic acids, and an optional material that prevents the nucleic acids of the two arrays from mixing until such mixing is desired. The arrays of the apparatus may be supported by a variety of substrates, including but not limited to, nylon membranes, nitrocellulose membranes, or other materials disclosed above. In preferred embodiments, one of the substrate is a membrane separated into sectors by hydrophobic strips, or a suitable support material with wells which may contain a gel or sponge. In this embodiment, probes are placed on a sector of the membrane, or in the well, the gel, or sponge, and a solution (with or without target nucleic acids) is added to the membrane or well so that the probes are solubilized. The solution with the solubilized probes is then allowed to contact the second array of nucleic acids. The nucleic acids may be, but are not limited to, oligonucleotide probes, or target nucleic acids, and the probes or target nucleic acids may be labeled. The nucleic acids may be labeled with any labels conventionally used in the art, including but not limited to radioisotopes, fluorescent labels or electrophore mass labels.

The material which prevents mixing of the nucleic acids may be disposed between the two arrays in such a way that when the material is removed the nucleic acids of the two arrays mix together. This material may be in the form of a sheet, membrane, or other barrier, and this material may be comprised of any material that prevents mixing of the nucleic acids.

This apparatus may be used in Format I SBH as follows: a first array of the apparatus has target nucleic acids that are fixed to the substrate, and a second array of the apparatus has nucleic acid probes that are labeled and can be removed to interrogate the target nucleic acid of the first array. The two arrays are optionally separated by a
5 sheet of material that prevents the probes from contacting the target nucleic acid, and when this sheet is removed, the probes can interrogate the target. After appropriate incubation, and (optionally) washing steps the array of targets may be read to determine which probes formed perfect matches with the target. This reading may be automated or can be done manually (e.g. by eye with an autoradiogram). In format II SBH, the
10 procedure followed would be similar to that described above except the target is labeled and the probes are fixed.

Alternatively the apparatus may be used in Format III SBH as follows: to arrays of nucleic acid probes are formed, the nucleic acid probes of either or both arrays may be labeled and one of the arrays may be fixed to its substrate. The two arrays are separated
15 by a sheet of material that prevents the probes from mixing. A Format II reaction is initiated by adding target nucleic acid and removing the sheet allowing the probes to mix with each other and the target. Probes which bind to adjacent sites on the target are bound together (e.g., by base stacking interactions or by covalently joining the
backbones), and the results are read to determine which probes bound to the target at
20 adjacent sites. When one set of probes is fixed to the substrate, the fixed array can be read to determine which probes from the other array are bound together with the fixed probes. As with the method above, this reading may be automated (e.g., with an ELISA reader) or can be done manually (e.g., by eye with an autoradiogram).

6.0 EXAMPLES

Selected tables are provided on the CD-ROM, supplied concurrently with this application. The entirety of the contents of the CD-ROM are intended to be a part of this application, and are incorporated by reference. The electronic file name, where appropriate,
5 follows the first reference to the table throughout the application.

6.1 The 748 Gene Family

Novel Contigs

The novel contigs of the invention, were assembled from novel expressed sequence tags (EST's) isolated by methods described herein (*e.g.*, SBH), and in some
10 cases sequences obtained from one or more public databases. The inserts for the cDNA libraries from which the novel ESTs were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts. These samples were spotted onto nylon membranes and interrogated with oligonucleotide probes to give sequence signatures. The clones were clustered into groups of similar or identical
15 sequences, and single representative clones were selected from each group for gel sequencing. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the
20 novel ESTs. The novel contigs of the invention, were assembled from the novel ESTs and, in some cases, sequences obtained from one or more public databases. The sequences for the resulting contigs from the 748 gene family are designated as 748 SEQ ID NO: 1-45,196 and are provided in the Sequence Listing.

6.2 The 752 Gene Family

Novel Contigs

The novel contigs of the invention, were assembled from novel expressed sequence tags (EST's) isolated by methods described herein (*e.g.*, SBH), and in some
30 cases sequences obtained from one or more public databases. The inserts for the cDNA libraries from which the novel ESTs were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts. These samples were

spotted onto nylon membranes and interrogated with oligonucleotide probes to give sequence signatures. The clones were clustered into groups of similar or identical sequences, and single representative clones were selected from each group for gel sequencing. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel ESTs. The novel contigs of the invention, were assembled from the novel ESTs and, in some cases, sequences obtained from one or more public databases. The sequences for the resulting contigs from the 752 gene family are designated as 752 SEQ ID NO: 1-13,192 and are provided in the Sequence Listing.

6.3 The 778 Gene Family

Novel Contigs

The novel contigs of the invention, were assembled from novel expressed sequence tags (ESTs) isolated by methods described herein (*e.g.*, SBH), and in some cases sequences obtained from one or more public databases. The inserts for the cDNA libraries from which the novel ESTs were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts. These samples were spotted onto nylon membranes and interrogated with oligonucleotide probes to give sequence signatures. The clones were clustered into groups of similar or identical sequences, and single representative clones were selected from each group for gel sequencing. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel ESTs. The novel contigs of the invention, were assembled from the novel ESTs and, in some cases, sequences obtained from one or more public databases. The sequences for the resulting contigs from the 778 gene family are designated as 778 SEQ ID NO: 1-94 and are provided in the Sequence Listing.

6.4 The 779 Gene Family

Novel Contigs

The novel contigs of the invention, were assembled from sequences that were obtained from cDNA libraries by methods described herein (*e.g.*, SBH). Briefly, clones
 5 from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences, and single representative clones were selected from each group for gel sequencing. The inserts for the cDNA libraries from which the sequences were obtained were amplified with PCR using primers specific
 10 for the vector sequences which flank the inserts, or isolated from plasmid preparations. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol, as well as internal primers in both the forward and reverse direction. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction. In some
 15 cases all of a signature cluster was sequenced to generate overlapping clones to assemble the contigs.

Chromatograms were base called and assembled using a software suite from Washington University, MO containing three applications designated PHRED, PEIRAP, and CONSED. The sequences for the resulting contigs for the 779 gene family are
 20 designated as 779 SEQ ID NO: 1-128 and are provided in the Sequence Listing.

Additionally, contig sequences were BLASTed against Hyseq's database to to determine adequate sequence homology for addition to the contigs. Full length clones of the entire message were obtained either by identifying clones which contained the beginning of the open reading frame and fully sequenced and verified against the contig.
 25 If no clones were available containing the full length sequence, PCR was used to generate an amplicon from tissue libraries and the entire length sequenced and verified against the contig.

6.5 The 782 Gene Family

Novel Contigs

30 A novel contig of the invention was assembled from sequences that were obtained from a cDNA library by methods described herein (*e.g.*, SBH). Briefly, clones from cDNA

libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The inserts for the cDNA libraries from which the sequences were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts, or isolated from plasmid preparations. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol, as well as internal primers in both the forward and reverse direction. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction. In all cases all of a signature cluster was sequenced to generate overlapping clones to assemble the contigs. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting contigs for the 782 gene family are designated as 782 SEQ ID NO: 1-10,451 and are provided in the attached Sequence Listing. inserts was then deduced in a typical Sanger sequencing protocol. The inserts of the library were, amplified with PCR using 5 primers specific for vector sequences which flank the inserts.

The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 782 SEQ ID NO: 1-10,451 are shown in Table 2, and identified as Table2(782).doc on the enclosed compact disc.

6.6 The 784 Gene Family

Novel Contigs

Table 3 (identified as Table3(784).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (784 SEQ ID NO: 1-10,289) of the present invention, and their corresponding nucleotide locations to each of 748 SEQ ID NO: 1-10,289. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 3 is a higher number than the predicted end nucleotide of Table 3, then the amino acid sequence is derived from the complementary strand of the indicated SEQ ID NO. The locations of the predicted beginning and end nucleotides correlate to the nucleotide sequence of the indicated SEQ ID NO., not its complementary strand.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 3 or from six frame translations of 784 SEQ ID NO: 1-10,289; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 784 SEQ ID NO: 1-10,289; or (b) polynucleotides that hybridize to the

complement of the polynucleotids of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in Table 3 or from six frame translations of 784 SEQ ID NO: 1-10,289, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

The contigs or the nucleic acids of the present invention, designated as 784 SEQ ID NO: 1-10,289 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 4 (identified as Table4(784).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 784 SEQ ID NO: 1-10,289).

5 The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The
10 nearest neighbor results for 784 SEQ ID NO: 1-10,289 are shown in the Table 5, infra.

6.7 **The 785 Gene Family**

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared
15 from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA
libraries were spotted on nylon membrane filters and screened with oligonucleotide
20 probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using
25 a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described above, and in some cases sequences
30 obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three

applications designated PJRED, PHRAP, and CONSED. The sequences for the resulting contigs are designated as 785 SEQ ID NO: 1-3,796 and are provided in the Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling
5 additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with
10 BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using Fastxy algorithm. Fastxy is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and
15 contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 785 SEQ ID NO: 1-3,796 are shown in Table 6 (identified as Table6(785).doc on the enclosed CD), *infra*.

The nucleotide sequence within the assembled contigs that codes for signal peptide sequences and their cleavage sites can be determined from using Neural network
20 SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrick Nielson, Jacob Englebrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein
25 Engineering, vol. 10, no. 1, pp. 1-6 (1997) incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et. al., reference, are obtained from each assembled contig. Table 7 sets forth the nucleotide sequence range for each sequence of 785 SEQ ID NO: 1-3,796 that encodes a corresponding forty-five amino acid sequence containing the signal peptide sequence and its cleavage site, the maximum S
30 score and the mean S score obtained for each sequence. Not all forty-five amino acids in the sequence may comprise the signal peptide.

6.8 The 787 Gene Family

Table 8 (identified as Table8(787).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (787 SEQ ID NO: 1-3960) of the present invention, and their corresponding nucleotide locations to each of 787 SEQ ID NO: 1-3960. Table 8 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 8 is a higher number than the predicted end nucleotide of Table 8, then the amino acid sequence is derived from the complementary strand of the indicated SEQ ID NO. The locations of the predicted beginning and end nucleotides correlate to the nucleotide sequence of the indicated SEQ ID NO., not its complementary strand.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 8 or from six frame translations of 787 SEQ ID NO: 1-3960; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 787 SEQ ID NO: 1-3960; or (b) polynucleotides that hybridize to the complement of the

polynucleotids of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in Table 8 or from six frame translations of 787 SEQ ID NO: 1-3960, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Novel Contigs

The contigs or the nucleic acids of the present invention, designated as 787 SEQ ID NO: 1-3960 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences

into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 9 (identified as Table9(787).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 787 SEQ ID NO: 1-3960).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 787 SEQ ID NO: 1-3960 are shown in the Table 10, (identified as Table10(787).doc on the enclosed CD) infra.

6.9 The 788 Gene Family

Table 11 (identified as Table11(788).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (788 SEQ ID NO: 1-14,074) of the present invention, and their corresponding nucleotide locations to each of 788 SEQ ID NO: 1-14,074. Table 11 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 11 is a higher number than the

predicted end nucleotide of Table 11, then the amino acid sequence is derived from the complementary strand of the indicated SEQ ID NO. The locations of the predicted beginning and end nucleotides correlate to the nucleotide sequence of the indicated SEQ ID NO., not its complementary strand.

5 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 11 or from six frame translations of 788 SEQ ID NO: 1-14,074; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six
10 frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 788 SEQ ID NO: 1-14,074; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in
15 Table 11 or from six frame translations of 788 SEQ ID NO: 1-14,074, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the
20 genetically engineered cells (*e.g.* host cells) of the invention.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared 20 from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using
25 primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing. In some cases the 5' sequence of the amplified inserts was then deduced using a typical
30 Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied

Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Novel Contigs

5 The novel contigs of the invention were assembled from sequences that were
obtained from a cDNA library by methods described above, and in some cases sequences
obtained from one or more public databases. The sequences for the resulting contigs are
designated as 788 SEQ ID NO: 1-14,074 and are provided in the attached Sequence
Listing; The contigs were assembled using an EST sequence as a seed. Then a recursive
10 algorithm was used to extend the seed EST into an extended assemblage, by pulling
additional sequences from different databases (*i.e.*, Hyseq's database containing EST
sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this
assemblage. The algorithm terminated when there was no additional sequences from the
above databases that would extend the assemblage. Inclusion of component sequences
15 into the assemblage was based on a BLASTN hit to the extending assemblage with
BLAST score greater than 300 and percent identity greater than 95%.

Table 12 (identified as Table12(788).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 788 SEQ ID NO: 1-14,074).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 788 SEQ ID NO: 1-14,074 are shown in the Table 13, (identified as Table13(788).doc on the enclosed CD) infra.

6.10 The 789 Gene Family

30 Table 14 (identified as Table14(789).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (789

SEQ ID NO: 1-6,391) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-6,391. Table 14 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which
 5 selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a
 10 probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest
 15 open reading frame.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using
 20 primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a
 25 typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

30 Novel Contigs

The novel contigs or the nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting contigs are designated as 789 SEQ ID NO: 1-6,391 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UriGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95 %.

Table 15 (identified as Table15(789).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 789 SEQ ID NO: 1-6,391).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 789 SEQ ID NO: 1-6,391 are shown in the Table 16, (identified as Table16(789).doc on the enclosed CD) infra.

6.11 The 790 Gene Family

Table 17 (identified as Table17(790).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (790 SEQ ID NO: 1-30,553) of the present invention, and their corresponding start and stop nucleotide location to each of 790 SEQ ID NO: 1-30,553. Table 17 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide

obtained by using a software program called FASTY (available from
<http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of
 translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in
 Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a
 5 polypeptide obtained by using a software program called GenScan for human/vertebrate
 sequences (available from Stanford University, Office of Technology Licensing) that
 predicts the polypeptide based on a probabilistic model of gene structure/compositional
 properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein
 by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary
 10 software program that translates the novel polynucleotide and its complementary strand
 into six possible amino acid sequences (forward and reverse frames) and chooses the
 polypeptide with the longest open reading frame.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared
 from various human tissues and in some cases isolated from a genomic library derived
 15 from human chromosome using standard PCR, SBH sequence signature analysis and
 Sanger sequencing techniques. The inserts of the library were amplified with PCR using
 primers specific for the vector sequences which flank the inserts. Clones from cDNA
 libraries were spotted on nylon membrane filters and screened with oligonucleotide
 probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups
 20 of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a
 typical Sanger sequencing protocol. PCR products were purified and subjected to
 fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using
 a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In
 25 some cases RACE (Random Amplification of cDNA Ends) was performed to further
 extend the sequence in the 5' direction.

Novel Contigs

The contigs or the nucleic acids of the present invention, designated as 790 SEQ
 ID NO: 1-30,553 were assembled using an EST sequence from Hyseq's database as a
 30 seed. A recursive algorithm was used to extend the seed EST into an extended
 assemblage, by pulling additional sequences from different databases (*e.g.*, Hyseq's

database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 10.3, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there were no additional sequences from the databases that will extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 18 (identified as Table18(790).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 790 SEQ ID NO:1-30,553).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 1.15, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 790 SEQ ID NO: 1-30,553 are shown in the Table 19, (identified as Table19(790).doc on the enclosed CD) infra.

6.12 The 791 Gene Family

Table 20 (identified as Table20(791).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (791 SEQ ID NO: 1-5,822) of the present invention, and their corresponding nucleotide locations to each of 791 SEQ ID NO: 1-5,822. Table 20 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J.

Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Novel Contigs

The contigs or the nucleic acids of the present invention, designated as 791 SEQ ID NO: 1-5,822 were assembled using an EST sequence from Hyseq's database as a seed. A recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*e.g.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there were no additional sequences from the databases that will extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 21 (identified as Table21(791).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 791 SEQ ID NO: 1-5,822).

5 The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The
10 nearest neighbor results for 791 SEQ ID NO: 1-5,822 are shown in the Table 22, (identified as Table22(791).doc on the enclosed CD) infra.

6.13 **The 792 Gene Family**

Table 23 sets forth the novel predicted polypeptides (including proteins) encoded
15 by the novel polynucleotides (792 SEQ ID NO: 1-8,502) of the present invention, and their corresponding nucleotide locations to each of 792 SEQ ID NO: 1-8,502. Table 23 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of
20 translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional
25 properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

30 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 23 or from six

frame translations of 792 SEQ ID NO: 1-8,502; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 792 SEQ ID NO: 1-8,502; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in Table 23 or from six frame translations of 792 SEQ ID NO: 1-8,502, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75 %, 80%, 85 %, 90%, 95 %, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Novel Contigs

The contigs or the nucleic acids of the present invention, designated as 792 SEQ ID NO: 1-8,502 were assembled using an EST sequence from Hyseq's database as a seed. A recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*e.g.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there were no additional sequences from the databases that will extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 24 shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 792 SEQ ID NO 1-8,502).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 792 SEQ ID NO: 1-8,502 are shown in the Table 25, infra.

TABLE 5 Nearest neighbor (FastA v. Genbank, Genpept release 114)

SEQ ID NO.	ACCESSION NO.	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
1	L27428	Homo sapiens reverse transcriptase	253	32.129
2	X97675	Homo sapiens plakophilin 2b	167	50.794
3	U49082	Homo sapiens transporter protein	1001	56.122
4	U17247	Saccharomyces cerevisiae Imhlp	164	25.217
5	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	320	26.144
6	AF080234	Human endogenous retrovirus K polymerase	330	46.774
7	M13101	Rattus norvegicus unknown protein	265	49.398
8	M12140	Homo sapiens envelope protein	458	40.865
9	U49974	Homo sapiens mariner transposase	545	78.571
10	AB014549	Homo sapiens KIAA0649 protein	588	81.818
11	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	266	65.789
12	AB007903	Homo sapiens KIAA0443	1527	65.445
13	X78933	Homo sapiens zinc finger protein	465	65.979
14	AF081111	Mus musculus domesticus ORF2	276	63.158
15	AF081111	Mus musculus domesticus ORF2	178	46.341
16	AB012223	Canis familiaris ORF2	271	49.485
17	X03725	Mus musculus ORF 2 (466 aa)	222	43.902
18	U49974	Homo sapiens mariner transposase	870	71.491
19	D49677	Homo sapiens U2AF1-RS2	476	67.391
20	AJ001714	Homo sapiens Myosin-IXA	261	58.750
21	U93572	Homo sapiens putative p150	295	50.000
22	AB012223	Canis familiaris ORF2	182	43.434
23	X53581	Rattus norvegicus ORF4	176	40.230
24	L27428	Homo sapiens reverse transcriptase	223	35.714
25	U93568	Homo sapiens putative p150	227	65.574
26	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	285	52.542
27	AF003535	Homo sapiens ORF2-like protein	252	42.149
28	AF123881	multiple sclerosis associated retrovirus element gag polyprotein	549	84.821
29	AF123881	multiple sclerosis associated retrovirus element gag polyprotein	391	62.500
30	AB022046	Cynops pyrrhogaster alpha1 type II collagen	151	35.294
31	AF015539	Mytilus edulis precollagen P	265	32.950
32	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	367	57.983
33	AL032660	Caenorhabditis elegans predicted using Genefinder	930	37.174
34	AJ005073	Mus musculus Alix	2666	88.565
35	AL117237	Homo sapiens hypothetical protein	523	72.656
36	U93570	Homo sapiens p40	190	33.333
37	U09116	Homo sapiens ORF2, encodes a reverse transcriptase homolog	248	47.107
38	M34651	Pseudorabies virus ORF-3 protein	159	40.206
39	L76559	Drosophila melanogaster mus308	271	51.724
40	X06745	Homo sapiens DNA polymerase alpha-	382	68.317

		subunit (AA 1 - 1462)		
41	U83119	Rattus norvegicus ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH	161	39.831
42	U89959	Arabidopsis thaliana Similar to yeast general negative regulator of transcription subunit 1	527	38.435
43	AB012223	Canis familiaris ORF2	337	38.122
44	X52235	Homo sapiens ORFII	248	46.429
45	U93574	Homo sapiens putative p150	250	47.706
46	AB012223	Canis familiaris ORF2	361	45.802
47	M13002	Mus musculus 2855 is the position of the first start codon in ORF 2; putative	149	40.000
48	X65551	Homo sapiens antigen of the monoclonal antibody Ki-67	224	76.471
49	X03725	Mus musculus ORF 2 (466 aa)	291	45.536
50	U23857	Herpesvirus papio EBNA1	125	36.782
51	AF003535	Homo sapiens ORF2-like protein	220	42.029
52	AF003535	Homo sapiens ORF2-like protein	233	42.574
53	AB012223	Canis familiaris ORF2	357	53.077
54	X03145	Homo sapiens pot. ORF I	270	50.538
55	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	198	39.000
56	M64793	Rattus norvegicus salivary proline-rich protein	194	35.115
57	AF167320	Mus musculus zinc finger protein ZFP113	742	55.026
58	U83086	Dictyostelium discoideum Lima	200	29.126
59	Z72499	Homo sapiens herpesvirus associated ubiquitin-specific protease (HAUSP)	588	69.173
60	AF078828	Homo sapiens talin	557	71.429
61	L18966	Bos taurus pyruvate dehydrogenase phosphatase	2169	90.685
62	AF081114	Mus musculus domesticus ORF2	288	42.157
63	AF041330	Bodo saltans NADH dehydrogenase subunit 5	166	38.053
64	AF149422	Homo sapiens unknown	207	41.228
65	L27428	Homo sapiens reverse transcriptase	170	40.230
66	AF003535	Homo sapiens ORF2-like protein	292	56.731
67	AJ001563	Homo sapiens immunoglobulin heavy chain, constant region	554	77.876
68	AB012223	Canis familiaris ORF2	225	38.000
69	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	148	41.379
70	U83303	Homo sapiens line-1 reverse transcriptase	139	39.474
71	X03145	Homo sapiens pot. ORF I	217	41.509
72	AF003535	Homo sapiens ORF2-like protein	197	44.231
73	U83303	Homo sapiens line-1 reverse transcriptase	314	56.140
74	X52235	Homo sapiens ORFII	202	52.830
75	L49380	Homo sapiens transcription factor ZFM1	232	28.261
76	AF078035	Homo sapiens translation initiation factor IF2	385	62.376
77	M34059	Homo sapiens beta-globin	283	75.000
78	M11841	simian type D virus 1 pol protein	234	37.879
79	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	190	40.000

80	M22333	Homo sapiens unknown protein	215	42.857
81	D86850	Homo sapiens HADHB	163	58.491
82	M22334	Homo sapiens unknown protein	230	60.563
83	S80119	Rattus sp. reverse transcriptase homolog	264	48.000
84	AF081114	Mus musculus domesticus ORF2	213	47.826
85	U09116	Homo sapiens ORF2, encodes a reverse transcriptase homolog	244	42.857
86	AJ010479	Homo sapiens kinesin-like protein	464	69.091
87	X61296	Rattus norvegicus open reading frame 2	240	41.085
88	Z24734	Meloidogyne incognita cuticular collagen	165	34.416
89	U72069	Homo sapiens karyopherin beta2	538	67.361
90	M55409	Homo sapiens pancreatic tumor-related protein	273	59.494
91	X07881	Homo sapiens proline-rich protein G1	205	38.182
92	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	428	84.043
93	D89053	Homo sapiens Acyl-CoA synthetase 3	683	66.667
94	AF006514	Homo sapiens CHD2	293	58.242
95	X59841	Homo sapiens homeobox protein	648	70.130
96	M74816	Homo sapiens sulfated glycoprotein-2	413	76.829
97	X58251	Mus musculus pro-alpha-2(I) collagen	190	31.579
98	Z71173	Mus musculus inositol 1,4,5-trisphosphate receptor type 2	375	66.667
99	S80119	Rattus sp. reverse transcriptase homolog	183	40.625
100	U22055	Homo sapiens 100 kDa coactivator	402	76.667
101	X14690	Homo sapiens lambda HuHIT1-13	209	51.899
102	AF003535	Homo sapiens ORF2-like protein	170	34.234
103	M22333	Homo sapiens unknown protein	214	43.519
104	L11672	Homo sapiens zinc finger protein	685	44.033
105	M22333	Homo sapiens unknown protein	261	43.750
106	AB002312	Homo sapiens KIAA0314	433	69.903
107	X55777	Homo sapiens put. ORF	309	68.056
108	AF009668	multiple sclerosis associated retrovirus polyprotein	410	60.377
109	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	532	76.364
110	AB012223	Canis familiaris ORF2	269	41.497
111	L06147	Homo sapiens golgin-95	752	57.752
112	X61048	Hydra sp. mini-collagen	141	42.391
113	L27428	Homo sapiens reverse transcriptase	286	45.299
114	X82153	Homo sapiens Cathepsin O	308	54.167
115	D13629	Homo sapiens KIAA0004	169	42.000
116	AF123881	multiple sclerosis associated retrovirus element gag polyprotein	409	41.071
117	AB019602	Homo sapiens IDN3-B	237	53.012
118	AF155099	Homo sapiens NY-REN-18 antigen	237	47.423
119	AB020660	Homo sapiens KIAA0853 protein	153	31.304
120	AJ249625	Paracentrotus lividus Chaperonin	413	63.208
121	M22334	Homo sapiens unknown protein	282	49.565
122	X70391	Mus musculus inter-alpha-inhibitor H1 chain	170	77.778

123	D88899	Mus musculus kidney-derived aspartic protease-like protein	242	66.071
124	U93572	Homo sapiens p40	159	30.833
125	AL117200	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	193	38.095
126	AL117200	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	183	37.349
127	AJ388555	Canis familiaris hypothetical protein	1720	75.703
128	L27428	Homo sapiens reverse transcriptase	226	37.313
129	U93567	Homo sapiens putative p150	470	49.524
130	AL050060	Homo sapiens hypothetical protein	286	64.000
131	Y12713	Mus musculus Gag polyprotein	270	44.444
132	M58704	Homo sapiens 12-lipoxygenase	306	60.204
133	L19713	Homo sapiens dematin	236	68.182
134	L36120	Medicago sativa proline rich protein	172	39.655
135	L26245	Homo sapiens effector cell protease receptor 1	259	47.619
136	AB028997	Homo sapiens KIAA1074 protein	286	44.697
137	AF075575	Homo sapiens dysferlin	242	59.701
138	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .	163	45.652
139	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	485	47.584
140	AB012223	Canis familiaris ORF2	323	46.226
141	X97630	Homo sapiens serine/threonine protein kinase	322	39.474
142	D83776	Homo sapiens The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.	1932	53.103
143	U80846	Caenorhabditis elegans No definition line found	163	28.070
144	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	521	69.079
145	X13885	Nicotiana tabacum extensin (AA 1-620)	293	26.138
146	AB012223	Canis familiaris ORF2	352	44.509
147	AF003535	Homo sapiens ORF2-like protein	248	47.423
148	AB012223	Canis familiaris ORF2	276	51.685
149	AB014574	Homo sapiens KIAA0674 protein	4403	96.296
150	X98494	Homo sapiens M phase phosphoprotein 10	254	74.194
151	AB012223	Canis familiaris ORF2	482	47.514
152	M80537	Drosophila melanogaster fat protein	549	35.043
153	X51622	Caenorhabditis elegans collagen	213	36.702
154	X87629	Homo sapiens nicotinic acetylcholine receptor	138	29.365
155	AB011126	Homo sapiens KIAA0554 protein	294	46.207
156	X55126	Mus musculus Zfp-29	522	44.907
157	M61120	Homo sapiens loricrin	183	32.240
158	U02313	Mus musculus protein kinase	238	51.807
159	AB002342	Homo sapiens KIAA0344	299	32.203
160	AF003535	Homo sapiens ORF2-like protein	246	47.573
161	U95090	Homo sapiens F19541 1	1239	59.950
162	X52235	Homo sapiens ORFII	405	54.478

163	AB012223	Canis familiaris ORF2	448	51.748
164	AB017600	Haliotis discus collagen pro alpha-chain	173	28.992
165	M13002	Mus musculus 2855 is the position of the first start codon in ORF 2; putative	381	60.177
166	X71602	Nicotiana tabacum extensin	164	36.364
167	AL117200	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	304	34.641
168	X52235	Homo sapiens ORFII	231	39.024
169	M31524	Saccharomyces cerevisiae PRP16 peptide (put. helicase); putative	337	34.254
170	AB012223	Canis familiaris ORF2	444	52.841
171	AB012223	Canis familiaris ORF2	626	40.294
172	M92040	Strongylocentrotus purpuratus alpha-1 collagen	234	30.213
173	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1	896	85.625
174	M63595	Xenopus laevis alpha-1 type II collagen	351	30.116
175	AF085809	Mus musculus synapsin Ib	205	33.880
176	AC004794	Homo sapiens Acetolactate synthase	253	49.180
177	AL049482	Arabidopsis thaliana putative protein	487	42.366
178	U09413	Homo sapiens zinc finger protein ZNF135	906	53.138
179	AL023781	Schizosaccharomyces pombe N-terminal acetyltransferase 1	816	41.212
180	Y14685	Arabidopsis thaliana polynucleotide phosphorylase	61	41.379
181	M80341	Homo sapiens ORF2 contains a reverse transcriptase domain.; ORF2	477	51.282
182	AF003131	Caenorhabditis elegans C. elegans UNC-89 (GB:U33058) (NID:g1160355)	282	25.153
183	AL022374	Streptomyces coelicolor putative ABC transporter	181	40.299
184	U93569	Homo sapiens putative p150	886	55.294
185	U93568	Homo sapiens putative p150	256	38.583
186	X64697	Homo sapiens titin	1535	82.724
187	AB025259	Mus musculus granuphilin-b	201	31.210
188	D14663	Homo sapiens KIAA0107	346	66.055
189	AJ007798	Homo sapiens nuclear protein SA3	734	59.041
190	AB018281	Homo sapiens KIAA0738 protein	566	40.876
191	U07973	Gallus gallus alpha-1 collagen type III	207	30.189
192	M35547	Human herpesvirus 4 LF3 gene product	294	27.523
193	U53445	Homo sapiens DOC1	201	28.205
194	U76618	Mus musculus N-RAP	2955	83.422
195	M25984	Gallus gallus alpha-2 type I collagen	305	28.634
196	U41557	Caenorhabditis elegans proline and glycine-rich	437	35.018
197	AB028997	Homo sapiens KIAA1074 protein	311	50.000
198	U59694	Homo sapiens zinc finger protein basonuclin	362	44.853
199	Y10392	Human endogenous retrovirus K gag protein	761	49.550
200	AF167320	Mus musculus zinc finger protein ZFP113	536	52.288
201	X92485	Plasmodium vivax pval	269	59.036
202	U47856	Araneus diadematus fibroin-4	204	29.588
203	AB020708	Homo sapiens KIAA0901 protein	406	29.260
204	AF056936	Plasmodium falciparum mature parasite-	240	21.245

		infected erythrocyte surface antigen		
205	Z75330	Homo sapiens nuclear protein SA-1	194	48.810
206	X92887	Human endogenous retrovirus K pol/env	693	41.833
207	X13885	Nicotiana tabacum extensin (AA 1-620)	239	31.274
208	AC005990	Arabidopsis thaliana Strong similarity to PFAM PF00069 Eukaryotic protein kinase domain.	255	34.545
209	U93563	Homo sapiens putative p150	1103	53.670
210	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	301	28.918
211	AF133730	Rattus norvegicus Slit2	339	29.730
212	AL080123	Homo sapiens hypothetical protein	627	47.391
213	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1440	56.587
214	U35245	Rattus norvegicus vacuolar protein sorting homolog r-vps33b	951	64.800
215	AB007860	Homo sapiens KIAA0400	242	27.511
216	AJ010585	Rattus rattus PTB-like protein	1304	80.216
217	M27878	Homo sapiens DNA binding protein	1721	69.252
218	U59655	Pithecia pithecia MHC class I Pipi-G*04	431	69.474
219	AF159296	Lycopersicon esculentum extensin-like protein	340	33.333
220	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	287	61.458
221	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	325	26.979
222	X06021	Xenopus laevis Xfin protein (AA 1 - 1350)	1093	36.266
223	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	323	64.646
224	AF052663	Xenopus laevis gamma-tubulin interacting protein	294	29.528
225	AB017600	Haliotis discus collagen pro alpha-chain	252	29.487
226	AB023065	Rattus norvegicus O-sialoglycoprotease	431	61.429
227	M22334	Homo sapiens unknown protein	364	38.438
228	U41557	Caenorhabditis elegans proline and glycine-rich	143	30.530
229	S57132	Homo sapiens type XVI collagen alpha 1 chain, alpha 1 (XVI)	237	29.860
230	U97553	murine herpesvirus 68 unknown	262	32.899
231	X89453	Rattus norvegicus DRPLA	201	27.869
232	AL118514	Streptomyces coelicolor A3(2) DNA polymerase III subunit gamma	163	27.059
233	D29642	Homo sapiens KIAA0053	312	41.290
234	AF153062	Canis familiaris type I collagen pre-pro-alpha1(I) chain	218	33.333
235	AF032103	Homo sapiens ataxin-7	313	39.216
236	AB002319	Homo sapiens KIAA0321	179	36.275
237	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	519	71.930
238	U87607	Rattus norvegicus putative RNA binding protein 1	299	46.667
239	X53581	Rattus norvegicus ORF3	797	49.858
240	Z11922	Canis familiaris Ran	383	81.579
241	M77194	Rat leukemia virus polymerase	261	44.094
242	Z34465	Zea mays extensin-like protein	292	32.527

243	AF017178	Homo sapiens pro alpha 1(I) collagen	185	29.344
244	AC008075	Arabidopsis thaliana F24J5.4	193	34.932
245	U41557	Caenorhabditis elegans histidine-rich	190	31.646
246	U76618	Mus musculus N-RAP	1470	47.599
247	AC004561	Arabidopsis thaliana putative proline-rich protein	219	28.041
248	X07441	Turnip yellow mosaic virus 69K ORF (AA 1-628)	153	30.085
249	AB012223	Canis familiaris ORF2	341	48.592
250	AF000657	Arabidopsis thaliana hypothetical protein	249	28.718
251	AB020629	Homo sapiens KIAA0822 protein	1072	64.103
252	AL118514	Streptomyces coelicolor A3(2) DNA polymerase III subunit gamma	163	35.811
253	X66358	Homo sapiens serine/threonine protein kinase	505	88.571
254	U09413	Homo sapiens zinc finger protein ZNF135	1102	45.498
255	AL079308	Streptomyces coelicolor putative serine/threonine protein kinase	168	42.593
256	AF169388	Mus musculus alpha 4 collagen IV	240	27.609
257	U93564	Homo sapiens putative p150	260	37.727
258	M12140	Homo sapiens envelope protein	395	59.322
259	AC004955	Homo sapiens supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan	268	64.103
260	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	517	30.081
261	M26927	Gibbon leukemia virus pol polyprotein	557	50.754
262	AB011152	Homo sapiens KIAA0580 protein	712	44.747
263	X87226	Jaculus orientalis NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)	214	47.321
264	U44091	Rattus norvegicus atrophin-1 related protein	178	33.511
265	Z98980	Schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog 1	227	26.070
266	Z79694	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST yk552a12.3 comes from this gene	158	29.333
267	AF144627	Mus musculus SLIT1	377	29.368
268	D00824	Gallus gallus alpha 1 chain of type XII collagen	110	40.566
269	AB011414	Homo sapiens Kruppel-type zinc finger protein	792	56.650
270	X52046	Mus musculus type III collagen	481	32.472
271	M11723	Homo sapiens coagulation factor XII	1618	81.379
272	M22334	Homo sapiens unknown protein	755	45.455
273	X69490	Homo sapiens titin	214	65.574
274	M22334	Homo sapiens unknown protein	360	50.000
275	U35022	Rattus norvegicus cis-Golgi matrix protein GM130	323	47.097
276	X03725	Mus musculus ORF 2 (466 aa)	287	48.855
277	L08811	Drosophila melanogaster adherin	662	32.822
278	K02444	Oryctolagus cuniculus beta-myosin heavy	385	46.753

		chain		
279	AB018312	Homo sapiens KIAA0769 protein	435	43.541
280	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	196	35.065
281	AB011164	Homo sapiens KIAA0592 protein	758	82.468
282	AF045239	Homo sapiens brain expressed ring finger protein	310	28.205
283	AL110218	Homo sapiens hypothetical protein	473	63.380
284	U10281	Sus scrofa gastric mucin	188	24.706
285	U93570	Homo sapiens putative p150	305	53.968
286	U56964	Caenorhabditis elegans weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386)	766	31.866
287	U70136	Homo sapiens megakaryocyte stimulating factor; MSF	208	23.928
288	Z78279	Rattus norvegicus Collagen alpha1	194	29.042
289	AF085185	Acanthamoeba castellanii Myosin-IA	217	35.377
290	M33509	Homo sapiens HLA-B-associated transcript 2 (BAT2)	197	25.791
291	AC006530	Homo sapiens unknown	207	82.222
292	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	279	33.333
293	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	225	21.692
294	X53556	Bos taurus type X collagen	175	28.221
295	M92913	Nephila clavipes dragline silk fibroin	319	28.778
296	U37012	Homo sapiens cleavage and polyadenylation specificity factor	781	88.194
297	L21990	Homo sapiens spliceosomal protein	240	35.542
298	AJ006754	Yarrowia lipolytica hypothetical protein	164	36.496
299	U49974	Homo sapiens mariner transposase	599	69.128
300	AF153062	Canis familiaris type I collagen pre-pro-alpha1(I) chain	308	32.845
301	AF055904	Myxococcus xanthus unknown	213	32.014
302	X13804	Rattus sp. heavy neurofilament polypeptide (854 AA)	246	23.618
303	AF000198	Caenorhabditis elegans Similar to cuticular collagen	159	44.048
304	U97553	murine herpesvirus 68 unknown	191	28.994
305	M13101	Rattus norvegicus unknown protein	274	44.444
306	AF144573	Mesocricetus auratus Mx-interacting protein kinase PKM	3766	97.222
307	AB012223	Canis familiaris ORF2	337	52.713
308	D70831	Homo sapiens Zinc-finger protein	630	55.208
309	U97553	murine herpesvirus 68 unknown	317	33.631
310	Y17832	Human endogenous retrovirus K pol protein	1047	61.686
311	D31763	Homo sapiens ha0946 protein is Kruppel-related.	574	50.000
312	X51394	Xenopus laevis APEG precursor protein	226	32.068
313	Y10392	Human endogenous retrovirus K gag protein	273	44.144
314	AC007842	Homo sapiens BC331191 1	1005	74.129
315	D63881	Homo sapiens KIAA0160 gene product is	1100	68.106

		novel.		
316	U35376	Homo sapiens repressor transcriptional factor	773	57.014
317	X65964	Homo sapiens nestin	3614	99.313
318	M82977	Bos taurus alpha-collagen	228	29.528
319	M14123	Homo sapiens pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative	3111	70.629
320	AF004211	Mus musculus paired-like homeodomain containing protein	335	40.606
321	AL080125	Homo sapiens hypothetical protein	1468	62.893
322	M13101	Rattus norvegicus unknown protein	288	35.784
323	L11672	Homo sapiens zinc finger protein	270	40.120
324	AF084642	Mus musculus cellular retinaldehyde-binding protein; CRALBP	507	34.496
325	M12140	Homo sapiens envelope protein	432	48.966
326	AB015438	Cynops pyrrhogaster alpha 1 type I collagen	293	31.635
327	X98705	Homo sapiens collagen type I alpha 1	347	32.548
328	X15332	Homo sapiens alpha-1 (III) collagen	289	30.361
329	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	269	75.510
330	Z54238	Caenorhabditis elegans T28C6.1	184	41.667
331	AB012223	Canis familiaris ORF2	671	42.784
332	U09413	Homo sapiens zinc finger protein ZNF135	978	60.996
333	AL031985	Homo sapiens dJ228H13.3 (zinc finger protein)	936	72.928
334	AB000462	Homo sapiens SH3 binding protein	249	47.273
335	D80009	Homo sapiens KIAA0187	569	60.804
336	U41021	Caenorhabditis elegans C. elegans mec-2 (GB:U26735)	239	39.552
337	AJ243460	Leishmania major proteophosphoglycan	231	27.246
338	U23484	Caenorhabditis elegans weakly similar to serine/threonine protein kinase	667	35.840
339	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	437	59.690
340	U41557	Caenorhabditis elegans proline and glycine-rich	444	33.679
341	AB012223	Canis familiaris ORF2	279	39.806
342	X52235	Homo sapiens ORFII	369	56.897
343	AF108843	Homo sapiens env protein	762	56.696
344	X16711	Homo sapiens COL2A1	289	31.186
345	AJ012371	Homo sapiens NAALADase L protein	819	72.512
346	AB001535	Homo sapiens similar to C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF54D1.5. similar to trp and trp-like proteins	888	38.795
347	M15103	Plasmodium cynomolgi circumsporozoite antigen	125	24.402
348	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	470	25.698
349	AF081111	Mus musculus domesticus ORF2	301	38.255
350	L07924	Mus musculus guanine nucleotide dissociation stimulator	249	31.799
351	L35601	Drosophila melanogaster ankyrin	247	25.092

352	D88764	Rana catesbeiana alpha 2 type I collagen	258	28.231
353	D10354	Rattus rattus alanine aminotransferase	516	53.439
354	AB014561	Homo sapiens KIAA0661 protein	46	35.294
355	U97553	murine herpesvirus 68 unknown	254	31.701
356	L27428	Homo sapiens reverse transcriptase	228	43.810
357	AB012223	Canis familiaris ORF2	227	49.451
358	AC003682	Homo sapiens R28830 1	669	54.067
359	AF006466	Mus musculus lymphocyte specific formin related protein	421	52.071
360	AF015539	Mytilus edulis precollagen P	235	29.258
361	Z77664	Unknown predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST CEMSC43F comes from	208	39.623
362	Y07752	Volvox carteri pherophorin-S	239	41.053
363	K02623	Drosophila melanogaster tropomyosin isoform 33 (9C)	212	36.774
364	D86983	Homo sapiens similar to D.melanogaster peroxidasin(U11052)	450	29.442
365	AL021747	Schizosaccharomyces pombe hypothetical protein	388	31.599
366	AB020671	Homo sapiens KIAA0864 protein	681	82.677
367	K01228	Homo sapiens alpha 1 (I) chain propeptide	217	32.258
368	AF003535	Homo sapiens ORF2-like protein	357	54.902
369	Z11974	Mus musculus macrophage mannose receptor precursor	249	27.014
370	AF070651	Homo sapiens zinc finger protein 4	246	40.000
371	AF068749	Mus musculus sphingosine kinase	362	65.657
372	AB012223	Canis familiaris ORF2	364	51.938
373	AF169633	Mus musculus alpha 2 delta calcium channel subunit	332	44.633
374	U80846	Caenorhabditis elegans No definition line found	237	24.710
375	X16711	Homo sapiens COL2A1	431	29.918
376	AC004460	Homo sapiens similar to golgi antigen; similar to Q08379 (PID:g2498401)	412	59.124
377	M20789	Homo sapiens alpha-1 type I collagen	169	34.921
378	AF027735	Nephila clavipes minor ampullate silk protein MiSp1	298	30.977
379	AF003535	Homo sapiens ORF2-like protein	513	63.704
380	X83413	Human herpesvirus 6 U88	328	36.649
381	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	773	70.225
382	AF020261	Santalum album proline rich protein	194	39.200
383	AC002535	Arabidopsis thaliana putative G-beta-repeat containing protein, 5' partial	503	25.473
384	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	191	27.717
385	X98330	Homo sapiens ryanodine receptor 2	216	41.176
386	AF145705	Mus musculus T2K protein kinase homolog	972	80.342
387	Z49125	Unknown similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession)	312	31.356
388	X03725	Mus musculus ORF 2 (466 aa)	270	45.185
389	M31627	Homo sapiens X box binding protein-1	458	68.148
390	L07545	Leishmania tarentolae A 'c' was inserted	212	27.490

		after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression		
391	U93572	Homo sapiens putative p150	486	45.509
392	AJ000496	Rattus norvegicus cyclic nucleotide-gated channel beta subunit	298	36.604
393	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	351	24.477
394	M13100	Rattus norvegicus unknown protein	231	37.838
395	AB012223	Canis familiaris ORF2	300	42.553
396	U35376	Homo sapiens repressor transcriptional factor	521	40.940
397	AL050022	Homo sapiens hypothetical protein	312	35.060
398	AF038564	Homo sapiens atrophin-1 interacting protein 4	472	69.811
399	X61295	Rattus norvegicus L1 retroposon, a portion of its ORF2 sequence	413	42.922
400	AF064604	Homo sapiens KE03 protein	1279	50.785
401	U93181	Homo sapiens nuclear dual-specificity phosphatase	1716	55.626
402	AF081111	Mus musculus domesticus ORF2	598	44.156
403	U00978	Mus musculus type I inosine monophosphate dehydrogenase	1626	83.537
404	U67056	Acanthamoeba castellanii myosin I heavy chain kinase	222	29.478
405	L15419	Caenorhabditis elegans col-40 collagen	196	35.681
406	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	783	79.268
407	X51394	Xenopus laevis APEG precursor protein	141	32.584
408	AJ223069	Mus musculus TCF-3 protein	1337	86.307
409	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	339	29.250
410	X51616	Volvox carteri SULFATED SURFACE GLYCOPROTEIN 185	224	37.190
411	U96113	Homo sapiens WWP1	157	28.916
412	X83413	Human herpesvirus 6 U88	270	34.118
413	Z34465	Zea mays extensin-like protein	306	29.032
414	U24246	Drosophila melanogaster I71-7	228	36.232
415	U08020	Mus musculus collagen pro-alpha-1 type I chain	369	32.374
416	X83413	Human herpesvirus 6 U88	402	65.049
417	Z67990	Caenorhabditis elegans similar to cuticle collagen	246	35.829
418	AL078635	Amycolatopsis orientalis putative WD-repeat containing protein	142	28.571
419	U43541	Mus musculus laminin beta 2	507	43.023
420	Z70756	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST EMBL:D66041 comes from this gene; cDNA EST EMBL:D66295 comes from this gene; cDNA EST EMBL:D69679 comes from	114	27.632

		this gene; cDNA EST EMBL:D70027 comes from this gene		
421	M22333	Homo sapiens unknown protein	268	49.275
422	AB012223	Canis familiaris ORF2	292	42.520
423	AL117201	Caenorhabditis elegans predicted using Genefinder	187	25.934
424	U97553	murine herpesvirus 68 unknown	379	32.599
425	U09116	Homo sapiens ORF2, encodes a reverse transcriptase homolog	361	40.686
426	AF169388	Mus musculus alpha 4 collagen IV	292	28.723
427	Y17832	Human endogenous retrovirus K pol protein	850	59.817
428	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	275	33.007
429	AB008372	Oncorhynchus mykiss alpha 2 type I collagen	186	30.485
430	U93568	Homo sapiens putative p150	555	49.772
431	AB012223	Canis familiaris ORF2	195	40.000
432	X04758	Homo sapiens pro- alpha (V)collagen (AA 1099)	220	30.078
433	U80076	Rattus norvegicus RIN1	326	36.493
434	AC002398	Homo sapiens F25965 3	533	69.697
435	AF000198	Caenorhabditis elegans Similar to cuticular collagen	272	31.600
436	AF114486	Drosophila melanogaster Zimp-B	273	30.114
437	AL021811	Arabidopsis thaliana putative protein	816	51.154
438	Z69368	Schizosaccharomyces pombe hypothetical divergent repeat-containing protein	178	31.285
439	U73819	Mus musculus polypeptide GalNAc transferase-T4	366	40.838
440	X86019	Homo sapiens SH3-domain interacting protein	190	32.000
441	AJ004801	Bovine herpesvirus type 1.1 immediate-early transactivator protein (cell nucleus)	112	30.539
442	M60172	Gallus gallus novel collagen protein	319	29.730
443	AB013464	Mus musculus cytohesin 1	378	48.810
444	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 ..	205	33.158
445	U97553	murine herpesvirus 68 unknown	213	29.355
446	AB014608	Homo sapiens KIAA0708 protein	960	79.670
447	AL031231	Streptomyces coelicolor hypothetical protein SC3C3.03c	158	30.435
448	AF081110	Mus musculus domesticus ORF2	285	48.259
449	AF081111	Mus musculus domesticus ORF2	227	40.141
450	AF132480	Mus musculus Ese2 protein	2336	90.226
451	AB002304	Homo sapiens KIAA0306	1459	74.656
452	AF067607	Caenorhabditis elegans Similar to cuticular collagen; C18H7.3	253	31.343
453	AB011370	Mus musculus Ankhzn	2127	76.231
454	Z78279	Rattus norvegicus Collagen alpha1	223	32.472
455	AF115480	Mus musculus cAMP-dependent Rap1 guanine-nucleotide exchange factor	230	32.308
456	M22334	Homo sapiens unknown protein	1085	58.544

457	L40459	Mus musculus latent transforming growth factor-beta binding protein	2128	89.969
458	AF116556	Arabidopsis thaliana putative transcription factor	171	37.059
459	M22333	Homo sapiens unknown protein	174	30.137
460	AB023203	Homo sapiens KIAA0986 protein	165	46.591
461	AF003535	Homo sapiens ORF2-like protein	492	54.301
462	X51394	Xenopus laevis APEG precursor protein	194	33.333
463	Y07752	Volvox carteri pherophorin-S	305	45.918
464	Y18314	Homo sapiens paraplegin-like protein	323	40.952
465	Z67990	Caenorhabditis elegans similar to cuticle collagen	216	40.476
466	L43619	Homo sapiens polycystic kidney disease 1 protein	162	34.266
467	X56805	Gallus gallus procKr2	168	33.577
468	AB012223	Canis familiaris ORF2	535	40.397
469	AC008075	Arabidopsis thaliana Contains PF 00069 Eukaryotic protein kinase domain.	181	38.462
470	U58736	Caenorhabditis elegans Similar to cuticular collagen	245	33.333
471	AB012223	Canis familiaris ORF2	200	43.269
472	AF053091	Drosophila melanogaster eyelid	315	29.968
473	AB015440	Rana catesbeiana alpha 1 type I collagen	270	27.672
474	Z98980	Schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog 1	172	31.416
475	AF090866	Mus musculus CDO	1473	47.119
476	L76559	Drosophila melanogaster mus308	477	30.484
477	AC002528	Homo sapiens alpha2(I) collagen	212	28.060
478	AL033534	Schizosaccharomyces pombe serine-rich protein	253	35.065
479	X15120	Pseudorabies virus immediate-early protein (AA 1-1460)	105	25.869
480	AF071172	Homo sapiens HERC2	615	85.000
481	Z70208	Caenorhabditis elegans predicted using Genefinder; similar to collagen	199	31.088
482	U44091	Rattus norvegicus atrophin-1 related protein	227	32.168
483	M13002	Mus musculus 2855 is the position of the first start codon in ORF 2; putative	344	52.212
484	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	244	32.154
485	U07629	Drosophila melanogaster beta-heavy-spectrin	228	30.052
486	U93563	Homo sapiens putative p150	595	50.649
487	Z34465	Zea mays extensin-like protein	250	31.383
488	AB020686	Homo sapiens KIAA0879 protein	318	34.884
489	M11897	Mus musculus proline-rich salivary protein	234	28.571
490	M12100	Mus musculus proline-rich protein MP-3	227	36.585
491	AF045567	Xenopus laevis nucleoporin Nup153 homolog	94	24.335
492	AF003535	Homo sapiens ORF2-like protein	370	44.805
493	U35376	Homo sapiens repressor transcriptional factor	903	62.312
494	AF109907	Homo sapiens S164	350	40.361

495	X52046	Mus musculus type III collagen	212	35.417
496	D42063	Homo sapiens RanBP2 (Ran-binding protein 2)	354	48.588
497	D50926	Homo sapiens The KIAA0136 gene product is novel.	315	58.491
498	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	218	58.974
499	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	665	76.744
500	Y10392	Human endogenous retrovirus K protease	582	72.581
501	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	276	69.841
502	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	231	45.926
503	X52495	Glycine max DNA-directed RNA polymerase	248	39.153
504	L32162	Homo sapiens transcription factor	247	36.816
505	X53599	Mus musculus formin	320	44.898
506	Y11871	Arabidopsis thaliana Oxal protein	330	26.710
507	M12099	Mus musculus proline-rich protein	240	37.500
508	L22557	Rattus norvegicus calmodulin-binding protein	930	79.803
509	Z74615	Homo sapiens prepro-alpha1(I) collagen	312	30.227
510	AF038554	Homo sapiens density regulated protein drp1	752	88.281
511	M74165	Gallus gallus tensin	77	28.125
512	U81788	Drosophila melanogaster kinesin-73	625	45.174
513	AF074086	Homo sapiens envelope	956	55.814
514	M94131	Homo sapiens mucin	265	41.333
515	AL110151	Homo sapiens hypothetical protein	361	36.269
516	U42471	Mus musculus Wiscott-Aldrich Syndrome protein homolog	228	41.600
517	AL021841	Mycobacterium tuberculosis PE PGRS	190	33.880
518	AB018263	Homo sapiens KIAA0720 protein	421	53.788
519	D38024	Homo sapiens ORF	293	45.985
520	X69838	Homo sapiens G9a	809	46.885
521	AB025412	Mus musculus Ten-m3	518	78.095
522	AL050276	Homo sapiens hypothetical protein	270	55.072
523	X65165	Volvox carteri extensin	233	33.838
524	Z93393	Caenorhabditis elegans Y48E1B.2b	326	26.300
525	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	222	35.233
526	Y17832	Human endogenous retrovirus K env protein	339	43.103
527	AF116463	Streptomyces lincolnensis unknown	183	33.649
528	K03205	Homo sapiens salivary proline-rich protein precursor	182	34.586
529	M96943	Homo sapiens profilaggrin	248	27.817
530	Z34465	Zea mays extensin-like protein	213	29.680
531	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	218	35.628
532	U00048	Caenorhabditis elegans No definition line found	520	32.759
533	AF020261	Santalum album proline rich protein	233	31.579
534	AC002310	Homo sapiens Unknown gene product	907	65.929
535	AJ243997	Homo sapiens ERIC1	264	50.355
536	U32189	Oryctolagus cuniculus histidine-rich glycoprotein precursor	291	47.458

537	AF003535	Homo sapiens ORF2-like protein	355	44.000
538	AB012223	Canis familiaris ORF2	219	38.211
539	L11672	Homo sapiens zinc finger protein	1730	42.364
540	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	337	38.538
541	M34225	Homo sapiens cytokeratin 8	580	72.603
542	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	167	27.559
543	U40953	Caenorhabditis elegans No definition line found	206	31.746
544	AF029310	Rattus norvegicus vanilloid receptor subtype 1	348	39.735
545	X03145	Homo sapiens pot. ORF I	227	34.395
546	U35376	Homo sapiens repressor transcriptional factor	917	51.136
547	U93564	Homo sapiens putative p150	254	47.222
548	X83413	Human herpesvirus 6 U88	257	41.606
549	AF030430	Mus musculus semaphorin VIA	531	43.644
550	AF018082	Homo sapiens type XVIII collagen	298	30.162
551	AB028997	Homo sapiens KIAA1074 protein	701	49.811
552	U07973	Gallus gallus alpha-1 collagen type III	184	28.829
553	U93563	Homo sapiens putative p150	278	36.508
554	X53581	Rattus norvegicus ORF3	487	64.800
555	U93568	Homo sapiens putative p150	228	42.424
556	Z14015	Nicotiana tabacum pistil extensin like protein	187	29.302
557	X55995	Rattus norvegicus dimethylglycine dehydrogenase	1412	91.111
558	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	155	25.652
559	AF042800	Homo sapiens suppressor of white apricot homolog 2	1369	67.204
560	AF109907	Homo sapiens S171	450	47.849
561	AL033534	Schizosaccharomyces pombe serine-rich protein	159	24.759
562	X53581	Rattus norvegicus ORF4	310	47.107
563	AB015438	Cynops pyrrhogaster alpha 1 type I collagen	534	29.097
564	AC003973	Homo sapiens ZNF91L	662	49.794
565	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	461	57.432
566	AB012223	Canis familiaris ORF2	420	45.789
567	U43360	Peromyscus maniculatus reverse transcriptase	339	48.592
568	AF003535	Homo sapiens ORF2-like protein	267	57.732
569	D38548	Homo sapiens The ha0936 gene product is novel.	421	34.247
570	M22334	Homo sapiens unknown protein	299	46.053
571	X83413	Human herpesvirus 6 U88	407	42.593
572	AF055904	Myxococcus xanthus unknown	150	38.889
573	K03204	Homo sapiens salivary proline-rich protein precursor	220	36.310
574	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	368	65.979
575	X51394	Xenopus laevis APEG precursor protein	317	34.091
576	M22334	Homo sapiens unknown protein	631	51.101

577	X90569	Homo sapiens elastic titin	270	35.455
578	X51394	Xenopus laevis APEG precursor protein	263	31.773
579	AB008372	Oncorhynchus mykiss alpha 2 type I collagen	266	31.116
580	AE001727	Thermotoga maritima conserved hypothetical protein	226	28.571
581	U08020	Mus musculus collagen pro-alpha-1 type I chain	179	32.203
582	AJ132099	Homo sapiens VNN1 protein	944	70.936
583	AB020629	Homo sapiens KIAA0822 protein	1552	70.904
584	M76671	Lycopersicon esculentum extensin (class II)	238	31.361
585	AC004144	Homo sapiens R34001 1	1611	78.571
586	D31909	Pneumocystis carinii ORF-3	210	32.857
587	AB012223	Canis familiaris ORF2	213	39.695
588	AL117200	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	320	25.123
589	M83179	Gallus gallus alpha-3 type IX collagen	218	28.713
590	X03725	Mus musculus ORF 2 (466 aa)	262	41.880
591	Z78018	Caenorhabditis elegans predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene	1258	36.444
592	Z34465	Zea mays extensin-like protein	238	30.556
593	Z68760	Homo sapiens Similarity to Human ankaryin (SW:ANKB_HUMAN); cDNA EST EMBL:D34286 comes from this gene; cD	362	37.952
594	AB028236	Tricholoma matsutake Pol (reverse transcriptase-RNase H-integrase)	172	31.111
595	AF053745	Mus dunni endogenous virus gag protein	205	37.615
596	X92887	Human endogenous retrovirus K pol/env	586	64.493
597	AB002321	Homo sapiens KIAA0323	1358	85.169
598	L32973	Mus musculus This ORF is capable of encoding 432 aa which is similar to thymidylate kinases especially at two domains: the p-loop or catalytic site and the substrate binding site; ORF	1011	80.952
599	M22333	Homo sapiens unknown protein	418	46.000
600	AF033811	Moloney murine leukemia virus Pr180	359	50.376
601	AF026954	Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr	797	72.131
602	M13100	Rattus norvegicus unknown protein	286	41.781
603	D42043	Homo sapiens The ha2022 gene product is novel.	1232	75.746
604	AL110188	Homo sapiens hypothetical protein	657	50.746
605	U41557	Caenorhabditis elegans proline and glycine-rich	255	30.154
606	M95610	Homo sapiens alpha-2 IX collagen	152	29.795
607	AC004221	Homo sapiens R29144 1	144	27.500
608	AL031588	Homo sapiens dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsrl (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEGF2)	1006	75.622
609	AC004460	Homo sapiens similar to golgi antigen;	571	78.448

		similar to Q08379 (PID:g2498401)		
610	L12016	Rattus norvegicus tricarboxylate transport protein	593	64.671
611	X69838	Homo sapiens G9a	426	63.910
612	U08020	Mus musculus collagen pro-alpha-1 type I chain	268	35.401
613	X83429	Bombyx mori alpha-tubulin	741	81.119
614	AJ238221	Homo sapiens RNA polymerase III subunit	175	64.815
615	M58378	Homo sapiens synapsin Ib	175	35.616
616	AB015440	Rana catesbeiana alpha 1 type I collagen	251	31.657
617	AJ001038	Mus musculus M-protein	1798	45.704
618	D70831	Homo sapiens Zinc-finger protein	563	63.504
619	U49830	Caenorhabditis elegans coded for by C. elegans cDNA yk14e10.3; similar to S. pombe cell division control protein 16, CDC16 (SP:CC16_SCHPO, P36618) and to S. cerevisiae cell cycle arrest protein BUB2 (SP:BUB2_YEAST, P26448)	628	34.571
620	AL021366	Homo sapiens cICK0721Q.4.1 (PHD finger protein 1) (isoform 1)	443	39.791
621	L03427	Homo sapiens basonuclin	327	32.510
622	U93570	Homo sapiens putative p150	287	39.355
623	Z75550	Caenorhabditis elegans weak similarity with BRKA gene from Bordetella Pertussis; cDNA EST EMBL:T01060 comes from this gene; cDNA EST EMBL:T01361 comes from this gene	588	49.524
624	AL022537	Arabidopsis thaliana putative protein	222	31.950
625	AF098511	Xenopus laevis Scythe	274	46.479
626	K03475	Homo sapiens pulmonary surfactant-associated protein	181	46.078
627	AB020629	Homo sapiens KIAA0822 protein	1415	72.107
628	Z73619	Saccharomyces cerevisiae ORF YPL263c	386	27.132
629	Z78279	Rattus norvegicus Collagen alpha1	202	26.866
630	AF068706	Homo sapiens gamma2-adaptin	254	64.198
631	Z22964	Caenorhabditis elegans a2(IV) collagen	156	34.300
632	U23181	Caenorhabditis elegans final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein	223	36.150
633	AB015440	Rana catesbeiana alpha 1 type I collagen	331	28.466
634	AB014564	Homo sapiens KIAA0664 protein	513	58.140
635	AF092449	Heterodera glycines mucin-like protein	143	26.804
636	M63596	Xenopus laevis alpha-1 type II' collagen	298	32.249
637	AL031231	Streptomyces coelicolor hypothetical protein SC3C3.03c	187	29.365
638	AF077000	Rattus norvegicus protein tyrosine phosphatase TD14	319	33.968
639	D88440	Gallus gallus high molecular mass nuclear antigen	177	22.642
640	M92913	Nephila clavipes dragline silk fibroin	185	31.278
641	Z74615	Homo sapiens prepro-alpha1(I) collagen	306	29.108
642	U41387	Homo sapiens Gu protein	843	60.484
643	Z92546	Homo sapiens bK65A6.1	1700	90.175

644	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	365	44.390
645	L36381	Neisseria gonorrhoeae putative	181	38.462
646	D38162	Mus musculus mouse a1(XI) collagen chain	176	37.264
647	AF055904	Myxococcus xanthus unknown	192	33.166
648	AB023222	Homo sapiens KIAA1005 protein	472	37.805
649	U43200	Boreogadus saida antifreeze glycopeptide AFGP polyprotein precursor	149	40.157
650	U43200	Boreogadus saida antifreeze glycopeptide AFGP polyprotein precursor	232	31.687
651	AF071172	Homo sapiens HERC2	797	81.765
652	AF098788	Gallus gallus nuclear calmodulin-binding protein	2383	61.111
653	U47855	Araneus diadematus fibroin-3	386	28.099
654	AF083334	Antheraea pernyi fibroin	256	33.923
655	L02897	Canis familiaris beta-spectrin	164	27.962
656	U93572	Homo sapiens putative p150	377	55.814
657	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	266	33.562
658	L28125	Podospira anserina beta transducin-like protein	316	26.525
659	AF031588	Homo sapiens WASP interacting protein	266	30.102
660	AC006135	Arabidopsis thaliana putative vicilin storage protein (globulin-like)	389	41.618
661	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	230	22.689
662	AL033514	Caenorhabditis elegans Y75B8A.12	510	41.441
663	X12928	Triticum aestivum HMW glutenin subunit 5 (AA 1-848)	312	30.033
664	U93564	Homo sapiens putative p150	933	62.195
665	U93572	Homo sapiens putative p150	338	48.673
666	Y12713	Mus musculus Gag polyprotein	288	45.528
667	M13100	Rattus norvegicus unknown protein	239	42.056
668	AF000298	Caenorhabditis elegans weak similarity to collagens; glycine- and proline-rich	246	29.562
669	M19419	Mus musculus proline-rich salivary protein	261	38.743
670	X53581	Rattus norvegicus ORF3	332	54.491
671	Y10392	Human endogenous retrovirus K gag protein	273	44.144
672	X61294	Rattus norvegicus L1 retroposon, a portion of its ORF2 sequence	291	38.144
673	U43360	Peromyscus maniculatus reverse transcriptase	215	45.614
674	U93572	Homo sapiens putative p150	396	57.554
675	AF081113	Mus musculus domesticus ORF1	188	45.370
676	U49974	Homo sapiens mariner transposase	590	72.222
677	AF083384	Homo sapiens 45kDa splicing factor; SPF 45	654	73.649
678	Y17833	Human endogenous retrovirus K gag protein	277	44.860
679	X67863	Mus musculus T2	179	37.857
680	X59244	Homo sapiens ZNF43	519	50.282
681	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	194	41.538
682	U64849	Caenorhabditis elegans Contains	974	44.475

		similarity to Pfam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1		
683	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	273	31.429
684	X01469	Plasmodium lophurae histidine-rich protein	298	56.410
685	AB012223	Canis familiaris ORF2	290	54.545
686	Z92546	Homo sapiens bK65A6.1	411	43.333
687	Z81515	Unknown cDNA EST EMBL:T01055 comes from this gene; cDNA EST EMBL:D74980 comes from this gene; cDNA	328	24.746
688	AF067607	Caenorhabditis elegans Similar to cuticular collagen; C18H7.3	183	30.594
689	X17403	human herpesvirus 5 HCMVUL61	185	31.188
690	AF036145	Homo sapiens meningioma-expressed antigen 5	675	70.909
691	AJ132828	Spermatozopsis similis p210 protein	229	30.802
692	X58251	Mus musculus pro-alpha-2(I) collagen	201	26.974
693	X63134	Zea mays hydroxyproline-rich glycoprotein	195	26.210
694	X56044	Mus musculus protein Htf9C	1143	63.023
695	Z34465	Zea mays extensin-like protein	188	32.800
696	V01555	Human herpesvirus 4 BRLF1 reading frame, (immediate?) early gene, acts as transcription activator.	164	30.319
697	AB012223	Canis familiaris ORF2	540	46.377
698	AF081111	Mus musculus domesticus ORF2	727	46.201
699	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	347	61.538
700	AF003535	Homo sapiens ORF2-like protein	328	49.032
701	Z84476	Homo sapiens dJ25J6.4 (ret finger protein)	292	32.639
702	U34781	Anthopleura elegantissima Antho-LWamidII preprohormone	300	32.584
703	L26953	Homo sapiens chromosomal protein	199	68.000
704	D12983	Pyrococcus furiosus DNA polymerase	1140	96.923
705	AB014596	Homo sapiens KIAA0696 protein	723	86.232
706	AF030131	Mus musculus Plenty of SH3s; POSH	132	25.328
707	L29029	Chlamydomonas reinhardtii amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	205	33.846
708	X83413	Human herpesvirus 6 U88	213	40.299
709	Z81503	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene	130	30.151
710	D13645	Homo sapiens KIAA0020	641	80.435
711	U94855	Homo sapiens translation initiation factor 3 47 kDa subunit	276	75.556
712	AC007192	Homo sapiens P85B_HUMAN; PTDINS-3-KINASE P85-BETA	1055	77.432
713	D83146	Mus musculus Six5	327	53.600
714	M60832	Homo sapiens alpha-2 type VIII collagen	200	33.673

715	L48440	Rattus norvegicus collagen alpha 1 type II	286	33.639
716	L48440	Rattus norvegicus collagen alpha 1 type II	283	29.070
717	AB012223	Canis familiaris ORF2	343	37.727
718	U09367	Homo sapiens zinc finger protein ZNF136	605	59.494
719	AL078579	Arabidopsis thaliana putative proline-rich protein	186	33.333
720	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	1796	73.351
721	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	213	29.618
722	U07973	Gallus gallus alpha-1 collagen type III	190	30.837
723	AL050306	Homo sapiens dJ475B7.2 (novel protein)	217	52.381
724	M13100	Rattus norvegicus unknown protein	234	58.333
725	AB012223	Canis familiaris ORF2	337	52.713
726	X64698	Homo sapiens titin	1055	84.314
727	AF041449	Homo sapiens advillin; p92	267	60.204
728	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	503	69.748
729	U10281	Sus scrofa gastric mucin	198	28.326
730	X64322	Chironomus tentans BR1	223	45.349
731	AF043636	Plasmodium chabaudi circumsporozoite protein	345	55.682
732	AE000114	Escherichia coli possible synthesis of cofactor for carnitine racemase and dehydratase	955	93.038
733	U93569	Homo sapiens putative p150	362	46.296
734	AF104328	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog	186	45.263
735	AB032552	Schizosaccharomyces pombe mipl	1068	61.355
736	AL079348	Streptomyces coelicolor putative serine-threonine protein kinase	195	34.010
737	X54162	Homo sapiens 64 Kd autoantigen	460	48.876
738	U93572	Homo sapiens putative p150	352	48.734
739	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 ..	188	37.931
740	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	164	27.500
741	AF151865	Homo sapiens CGI-107 protein	556	73.050
742	AF094519	Mus musculus diaphanous-related formin; p134 mDia2	1533	87.500
743	U22376	Homo sapiens alternatively spliced product using exon 13A	372	55.200
744	L17318	Rattus norvegicus proline-rich proteoglycan	252	46.154
745	AF153604	Homo sapiens ubiquitin-specific protease homolog	224	48.673
746	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	489	39.405
747	L27428	Homo sapiens reverse transcriptase	241	45.528
748	AF003522	Homo sapiens Delta	501	75.000
749	U76759	Mus musculus nuclear protein NIP45	533	57.778
750	AJ000517	Homo sapiens spinocerebellar ataxia 7	1214	42.626

751	U07786	Sus scrofa beta actin	537	69.118
752	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	813	67.797
753	AC006264	Arabidopsis thaliana unknown protein	335	45.217
754	Z98979	Schizosaccharomyces pombe tat binding homolog	526	49.333
755	AF006522	Homo sapiens immunoglobulin heavy chain variable region	379	76.056
756	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1	2886	98.670
757	U40342	Mus musculus ninein	660	64.072
758	AF055077	Homo sapiens zinc finger protein 42	595	32.447
759	M12100	Mus musculus proline-rich protein MP-3	207	48.810
760	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	413	46.970
761	X53581	Rattus norvegicus ORF2	188	42.718
762	U40342	Mus musculus ninein	1779	76.903
763	AC003027	Arabidopsis thaliana lcl prt_seq No definition line found	277	41.406
764	U88549	Mus musculus OL-protocadherin	760	89.516
765	U45958	Nicotiana glauca pistil extensin-like protein	182	32.800
766	U55816	Rattus norvegicus furosemide-sensitive K-Cl cotransporter	5046	98.710
767	D30612	Homo sapiens repressor protein	1280	42.786
768	AB011135	Homo sapiens KIAA0563 protein	1104	77.193
769	AB029014	Homo sapiens KIAA1091 protein	9111	99.852
770	X83413	Human herpesvirus 6 U88	253	48.673
771	X03145	Homo sapiens pot. ORF V	212	39.286
772	AB023183	Homo sapiens KIAA0966 protein	407	98.485
773	X15334	Homo sapiens creatine kinase B	195	56.667
774	M98502	Mus musculus pMLZ-4	677	63.571
775	AF003535	Homo sapiens ORF2-like protein	175	50.602
776	AF109905	Mus musculus Hsc70t	355	88.060
777	U90126	Bos taurus ABC transporter	230	35.294
778	U09411	Homo sapiens zinc finger protein ZNF132	611	65.873
779	U49974	Homo sapiens mariner transposase	494	77.670
780	D86974	Homo sapiens KIAA0220	1169	97.238
781	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	669	79.699
782	AB014607	Homo sapiens KIAA0707 protein	396	75.309
783	M62626	Homo sapiens homeobox protein	264	74.545
784	L01790	Drosophila melanogaster potential zinc-finger domains centered at aa 135 and aa 364; 43 kDa protein; putative	743	48.230
785	AL080157	Homo sapiens hypothetical protein	352	77.632
786	L01790	Drosophila melanogaster potential zinc-finger domains centered at aa 135 and aa 364; 43 kDa protein; putative	673	50.249
787	X83413	Human herpesvirus 6 U88	47	41.379
788	X94082	Xenopus laevis KLP2 protein	497	39.844
789	AB006628	Homo sapiens KIAA0290	414	44.898
790	X78932	Homo sapiens zinc finger protein	361	53.043
791	U93909	Cercopithecine herpesvirus 15 nuclear antigen EBNA-1	137	41.379
792	AB002304	Homo sapiens KIAA0306	910	73.729

793	AJ000517	Homo sapiens spinocerebellar ataxia 7	890	43.280
794	L22858	Autographa californica nucleopolyhedrovirus AcOrf-91 peptide	201	51.515
795	A09561	synthetic construct human serum albumin	1295	99.487
796	U00029	Saccharomyces cerevisiae Yhr217cp	169	45.946
797	AB005803	Homo sapiens histidine-rich glycoprotein	244	43.038
798	U25725	Homo sapiens AH antigen	1128	98.333
799	D63487	Homo sapiens The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8.	349	69.512
800	AJ222801	Homo sapiens neutral sphingomyelinase	250	73.214
801	AL035652	Homo sapiens dJ1J6.1 (topoisomerase (DNA) I)	165	92.000
802	S38742	Homo sapiens HOX11 homeodomain=HOX11	351	74.684
803	S70011	Rattus sp. tricarboxylate carrier	226	43.119
804	AB028948	Homo sapiens KIAA1025 protein	607	75.652
805	U95760	Drosophila melanogaster Sno	1513	50.763
806	AF164610	Homo sapiens Gag protein	786	55.399
807	AJ001189	Homo sapiens oligophrenin 1	355	68.966
808	L20315	Mus musculus MPS1 protein	1517	77.899
809	AF132480	Mus musculus Ese2 protein	1515	89.057
810	D70831	Homo sapiens Zinc-finger protein	462	67.890
811	M21582	Trypanosoma cruzi chagas antigen	177	51.639
812	X65165	Volvox carteri extensin	293	41.463
813	AF155095	Homo sapiens NY-REN-2 antigen	379	51.773
814	AF093140	Mus musculus tip associating protein	192	77.500
815	X52472	Triticum aestivum proline-rich protein	339	30.876
816	Y18890	Human endogenous retrovirus K env protein	490	60.345
817	U41107	Caenorhabditis elegans No definition line found	308	28.571
818	AF092091	Rattus norvegicus cp431	478	46.667
819	AE001406	Plasmodium falciparum predicted membrane associated protein	166	38.136
820	AB020709	Homo sapiens KIAA0902 protein	939	55.516
821	X03725	Mus musculus ORF 2 (466 aa)	348	52.414
822	Z70310	Caenorhabditis elegans R11A8.7b	1729	53.875
823	U35376	Homo sapiens repressor transcriptional factor	547	73.451
824	AL031177	Homo sapiens dJ889M15.3 (novel protein)	434	32.800
825	Y17832	Human endogenous retrovirus K pol protein	1176	60.201
826	AJ010641	Drosophila melanogaster Dof protein	186	24.042
827	AF045454	Cavia porcellus phospholipase B	1279	60.942
828	AB020678	Homo sapiens KIAA0871 protein	1181	66.182
829	Y14318	Homo sapiens peroxisomal ABC-transporter	201	56.250
830	AB014607	Homo sapiens KIAA0707 protein	902	77.436
831	AC003007	Homo sapiens Unknown gene product (partial)	2180	91.733
832	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	316	80.000
833	AL080091	Homo sapiens hypothetical protein	402	59.223
834	M19538	Cricetulus griseus RNA polymerase II largest subunit	171	27.917

835	M87049	Escherichia coli similar to putative regulatory protein AtsB of Klebsiella pneumoniae	1020	100.000
836	Z83868	Rattus norvegicus serine/threonine kinase	2896	91.268
837	AF102855	Rattus norvegicus synaptic SAPAP-interacting protein Synamon	871	58.621
838	AB029022	Homo sapiens KIAA1099 protein	1091	64.583
839	M22334	Homo sapiens unknown protein	934	67.143
840	AF030131	Mus musculus Plenty of SH3s; POSH	2810	87.500
841	U50157	Homo sapiens cAMP-specific phosphodiesterase HPDE4D1 variant	573	83.333
842	Y09788	Homo sapiens mucin	219	30.052
843	AB023226	Homo sapiens KIAA1009 protein	756	75.410
844	D50857	Homo sapiens DOCK180 protein	1779	69.211
845	X58826	Drosophila melanogaster RNA polymerase III second-largest subunit	841	69.110
846	AB018353	Homo sapiens KIAA0810 protein	191	53.731
847	AJ011928	Drosophila melanogaster Fidiidine	377	37.056
848	Z50144	Rattus norvegicus kynurenine/alpha-aminoadipate aminotransferase	337	62.821
849	AL009197	Schizosaccharomyces pombe putative pre-mRNA splicing factor ATP-dependent RNA helicase	251	47.619
850	U06713	Rattus norvegicus SM-20	750	66.129
851	Z70310	Caenorhabditis elegans R11A8.7b	1310	57.487
852	U32498	Rattus norvegicus rsec8	2904	95.238
853	U35376	Homo sapiens repressor transcriptional factor	1212	78.281
854	AF081941	Rattus norvegicus soluble adenylyl cyclase	230	30.682
855	AF012252	Gallus gallus Coch-5B2	626	46.632
856	AB027757	Cicer arietinum NADPH oxidoreductase homolog	886	43.817
857	S74902	Homo sapiens P2U nucleotide receptor	197	34.375
858	D50928	Homo sapiens The KIAA0138 gene product is novel.	539	38.971
859	X67704	Drosophila melanogaster sperm protein	196	38.393
860	X99145	Canis familiaris overexpressed in thyroid tissue after TSH stimulation	1278	84.100
861	AJ006278	Mus musculus acetylglucosaminyltransferase-like protein	1759	70.637
862	AC007651	Arabidopsis thaliana Hypothetical protein	247	27.155
863	X05562	Homo sapiens alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon)	1095	100.000
864	Y09945	Rattus norvegicus putative integral membrane transport protein	1254	53.867
865	X66957	Homo sapiens hexokinase type 1	701	73.239
866	AB007938	Homo sapiens KIAA0469 protein	296	31.841
867	L20303	Gallus gallus actin filament-associated protein	230	41.758
868	L08240	Homo sapiens located at OATL1	484	40.183
869	D86947	Pseudomonas aeruginosa chemotactic	186	26.923

		transducer		
870	AF043697	Caenorhabditis elegans contains similarity to NAD(P)H oxidases	307	38.889
871	Z46861	Saccharomyces cerevisiae Met30p	179	37.209
872	U09413	Homo sapiens zinc finger protein ZNF135	538	51.049
873	U95760	Drosophila melanogaster Sno	1513	50.763
874	AL022165	Homo sapiens dJ71L16.5 (KIAA0267 LIKE putative Na(+)/H(+) exchanger)	1207	73.462
875	AF038615	Caenorhabditis elegans No definition line found	272	23.145
876	U72194	Mus musculus muskulin	1156	90.722
877	M62324	Homo sapiens modulator recognition factor I	828	75.401
878	AB023202	Homo sapiens KIAA0985 protein	397	48.649
879	AL117472	Homo sapiens hypothetical protein	905	94.904
880	AC006017	Homo sapiens similar to ALR; similar to AAC51735 (PID:g2358287)	2584	98.718
881	AF079974	Mus musculus Rac GTPase-activating protein	2441	86.998
882	Z83868	Rattus norvegicus serine/threonine kinase	2896	91.268
883	U09367	Homo sapiens zinc finger protein ZNF136	761	65.089
884	Z19555	Unknown predicted using Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:	2310	65.483
885	L11316	Mus musculus ect2	1642	97.287
886	AC006123	Homo sapiens KIAA0616 protein	307	33.831
887	X76013	Homo sapiens glutamyl-tRNA synthetase	4984	99.597
888	AB020721	Homo sapiens KIAA0914 protein	852	50.177
889	X83413	Human herpesvirus 6 U88	205	30.769
890	AB019003	Mus musculus MRP5	609	50.691
891	U67056	Acanthamoeba castellanii myosin I heavy chain kinase	363	35.125
892	U47661	Lupinus luteus proline-rich protein PRP2 precursor	184	40.397
893	AL050298	Homo sapiens hypothetical protein	1751	98.881
894	AB020718	Homo sapiens KIAA0911 protein	611	63.265
895	AB017498	Homo sapiens Lipoprotein Receptor Related Protein 5	1453	75.962
896	AB001735	Mus musculus ADAMTS-1	309	34.783
897	X78933	Homo sapiens zinc finger protein	582	58.333
898	AC006942	Homo sapiens Human alpha-adaptin A homolog	423	78.571
899	D79994	Homo sapiens similar to ankyrin of Chromatium vinosum.	395	32.231
900	L20302	Gallus gallus actin filament protein	244	28.082
901	X87224	Canis familiaris ribosome receptor	5288	81.853
902	AB014568	Homo sapiens KIAA0668 protein	558	75.940
903	X90849	Gallus gallus polybromo 1 protein	2365	95.767
904	AB002384	Homo sapiens KIAA0386	526	29.011
905	U07609	Rattus norvegicus brain specific Na+-dependent inorganic phosphate cotransporter	383	90.909
906	AB011127	Homo sapiens KIAA0555 protein	2001	60.036
907	X90587	Homo sapiens Rod cGMP phosphodiesterase	513	60.221

908	X69063	Mus musculus erythroid ankyrin	475	33.813
909	AB029016	Homo sapiens KIAA1093 protein	499	40.549
910	AF117754	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240	497	43.627
911	X58288	Homo sapiens protein-tyrosine phosphatase	5123	99.870
912	D49489	Homo sapiens human P5	274	50.000
913	U68380	Gallus gallus csdp	1158	61.888
914	D78255	Mus musculus PAP-1	1261	92.821
915	U13642	Caenorhabditis elegans exon 5 similar to transmembrane domain of S. cerevisiae zinc resistance protein	351	38.860
916	X73874	Homo sapiens phosphorylase kinase	1161	93.137
917	X52127	Mus musculus domesticus testis-specific protein, clone 46	244	34.746
918	L36434	Mus musculus basic domain/leucine zipper transcription factor	225	39.860
919	Z17238	Rattus norvegicus glutamate receptor subtype delta-1	848	77.297
920	U09413	Homo sapiens zinc finger protein ZNF135	779	51.042
921	U73200	Mus musculus p116Rip	3211	88.328
922	AC004528	Homo sapiens R32184 3	2194	95.342
923	AF067165	Homo sapiens zinc finger protein 3	491	62.992
924	U66707	Rattus norvegicus densin-180	271	31.832
925	U41538	Caenorhabditis elegans proline rich	226	36.066
926	AF071544	Spinacia oleracea ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	195	30.147
927	Z95334	Schizosaccharomyces pombe hypothetical protein	2386	52.191
928	AF007872	Homo sapiens torsinB	235	43.011
929	AF151847	Homo sapiens CGI-89 protein	796	56.784
930	AL031848	Homo sapiens dJ20208.1 (novel rat Espin LIKE protein containing Ank repeats)	171	41.304
931	AF053356	Homo sapiens leucin rich neuronal protein	1259	99.490
932	U37501	Mus musculus laminin alpha 5 chain	449	53.289
933	AL031447	Homo sapiens dJ126A5.2.1 (novel protein) (isoform 1)	176	26.370
934	AJ010901	Homo sapiens MUC4	276	25.872
935	AJ007395	Homo sapiens QA79 membrane protein	547	63.699
936	AF064254	Homo sapiens very long-chain acyl-CoA synthetase homolog 1; VLCS-H1	454	81.720
937	U28377	Escherichia coli ORF_f246; alternate name yggE'; orf6 of X14436	430	94.521
938	U37248	Homo sapiens alpha-mannosidase	363	52.113
939	L20319	Rattus norvegicus developmentally regulated protein	639	76.336
940	AB007895	Homo sapiens KIAA0435	988	64.502
941	U22815	Homo sapiens LAR-interacting protein 1a	976	68.254
942	AF043695	Caenorhabditis elegans similar to the protein phosphates 2c family	259	30.435
943	D86560	Schizosaccharomyces pombe carboxypeptidase Y	183	31.783

944	AB015289	Gallus gallus BASH	191	42.857
945	X65165	Volvox carteri extensin	235	39.806
946	AB023216	Homo sapiens KIAA0999 protein	1157	79.661
947	AF010403	Homo sapiens ALR	180	36.029
948	AF003535	Homo sapiens ORF2-like protein	176	52.459
949	Z99271	Caenorhabditis elegans similar to zinc metallopeptidase (M8 family); cDNA EST EMBL:C07771 comes from this gene; cDNA EST EMBL:C09261 comes from this gene; cDNA EST yk259c1.5 comes from this gene	495	40.506
950	Y17920	Drosophila melanogaster CALO protein	741	42.525
951	AF074086	Homo sapiens polymerase	2590	84.774
952	D86983	Homo sapiens similar to D.melanogaster peroxidase (U11052)	1173	67.568
953	U13152	Mesocricetus auratus guanine nucleotide-binding protein beta 5	2174	85.158
954	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	179	76.316
955	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1	2886	98.670
956	Y11710	Homo sapiens collagen type XIV	1892	100.000
957	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	316	80.000
958	X52046	Mus musculus type III collagen	260	32.215
959	AF149422	Homo sapiens unknown	329	42.537
960	AF037364	Homo sapiens paraneoplastic neuronal antigen MA1	289	36.810
961	U15784	Mus musculus Shcp52	216	45.098
962	AB029290	Homo sapiens actin binding protein ABP620	1780	100.000
963	AF057140	Homo sapiens cargo selection protein TIP47	511	38.095
964	U29156	Mus musculus involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	1321	95.516
965	X67863	Mus musculus T2	182	37.895
966	AB029014	Homo sapiens KIAA1091 protein	9111	99.852
967	AB014568	Homo sapiens KIAA0668 protein	558	75.940
968	AF017777	Drosophila melanogaster misato	654	30.948
969	AF071186	Mus musculus WW domain binding protein 11	230	35.915
970	AC004865	Homo sapiens similar to KIAA0319; similar to AB002317 (PID:g2224579)	1715	93.857
971	AF109719	Mus musculus BAT2	1132	36.805
972	AC007019	Arabidopsis thaliana hypothetical protein	648	37.183
973	AF003739	Caenorhabditis elegans No definition line found	412	51.402
974	AJ000517	Homo sapiens spinocerebellar ataxia 7	890	43.280
975	AF016252	Rattus norvegicus Spinophilin	2415	98.947
976	Z70208	Caenorhabditis elegans predicted using Genefinder; similar to collagen	165	34.459
977	AJ010482	Homo sapiens Myopodin protein	699	36.627

978	U92072	Rattus norvegicus m-tomosyn	1148	94.505
979	Z74037	Caenorhabditis elegans predicted using Genefinder; similar to collagen	203	30.366
980	U55816	Rattus norvegicus furosemide-sensitive K-Cl cotransporter	729	83.436
981	Z46259	Saccharomyces cerevisiae NO348	273	26.923
982	U26397	Rattus norvegicus inositol polyphosphate 4-phosphatase	384	28.378
983	AB002320	Homo sapiens KIAA0322	930	94.231
984	AB020678	Homo sapiens KIAA0871 protein	1181	66.182
985	AB026190	Homo sapiens Kelch motif containing protein	930	47.975
986	X56044	Mus musculus protein Htf9C	400	39.037
987	AF109907	Homo sapiens S164	317	27.341
988	AB000215	Rattus norvegicus CCA1 protein	1516	89.615
989	AF091457	Rattus norvegicus zinc finger protein RIN ZF	1474	81.851
990	AC006193	Arabidopsis thaliana Hypothetical Protein	481	32.155
991	D86966	Homo sapiens similar to human ZFY protein.	544	46.023
992	U22818	Cricetulus griseus mutant sterol regulatory element binding protein-2	729	74.342
993	AB017614	Mus musculus OASIS protein	724	64.062
994	D87682	Homo sapiens similar to a C.elegans protein encoded in cosmid T26A5.	1380	80.135
995	M17921	human herpesvirus 1 latency associated transcript (LAT) ORF-2	266	56.818
996	AF151821	Homo sapiens CGI-63 protein	180	85.294
997	AF128625	Homo sapiens CDC42-binding protein kinase beta	5379	99.509
998	U43194	Mus musculus rhophilin	1007	45.966
999	AF009039	Homo sapiens synaptojanin	180	34.127
1000	AF005036	Mus musculus secretory carrier membrane protein	584	55.705
1001	U02289	Caenorhabditis elegans GTPase-activating protein	650	42.606
1002	X52022	Homo sapiens collagen type VI, alpha 3 chain	412	50.758
1003	U22376	Homo sapiens alternatively spliced product using exon 13A	322	71.622
1004	AF032103	Homo sapiens ataxin-7	833	44.702
1005	U56732	Rattus norvegicus KRAB/zinc finger suppressor protein 1	1459	50.336
1006	AJ010949	Mus musculus calcium channel alpha-2-delta-C subunit	604	49.444
1007	M16591	Homo sapiens protein-tyrosine kinase	234	89.583
1008	U28831	Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies	2221	95.263
1009	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	1283	56.051
1010	U76992	Homo sapiens Tat-SF1	410	48.000
1011	U93872	Kaposi's sarcoma-associated herpesvirus ORF 73, contains large complex repeat CR 73	164	25.874
1012	Z75543	Caenorhabditis elegans cDNA EST EMBL:M89063 comes from this gene; cDNA EST yk384f1.3 comes	250	32.773

		from this gene; cDNA EST yk384f1.5 comes from this gene		
1013	M25393	Homo sapiens protein tyrosine phosphatase	996	91.617
1014	X90569	Homo sapiens elastic titin	1746	82.390
1015	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	226	69.811
1016	AF187961	Schizosaccharomyces pombe ubiquitin carboxyl-terminal hydrolase	498	30.311
1017	AF186461	Rattus norvegicus ring finger protein Fxy	53	30.233
1018	AL035526	Arabidopsis thaliana extensin-like protein	222	36.196
1019	X65165	Volvox carteri extensin	223	40.458
1020	X98411	Homo sapiens myosin-IE	192	33.140
1021	Z81561	Caenorhabditis elegans cDNA EST yk338f6.5 comes from this gene; cDNA EST EMBL:D75296 comes from this gene	279	33.333
1022	Y17833	Human endogenous retrovirus K pol protein	813	85.034
1023	Z74035	Unknown similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D32547 comes from this gene	237	22.492
1024	Z14020	Nicotiana tabacum Pistil extensin like protein, partial CDS only	188	50.649
1025	AC002310	Homo sapiens Unknown gene product	187	56.140
1026	X90849	Gallus gallus polybromo 1 protein	2869	86.614
1027	D13896	Rattus norvegicus cytoplasmic dynein heavy chain	1642	98.540
1028	U09116	Homo sapiens ORF1, encodes a 40 kDa product	371	50.407
1029	U23519	Caenorhabditis elegans No definition line found	278	31.343
1030	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	331	46.847
1031	AB014511	Homo sapiens KIAA0611 protein	976	65.339
1032	Y10392	Human endogenous retrovirus K gag protein	706	43.983
1033	L25050	Homo sapiens serine/proline-rich protein	521	57.396
1034	AB006624	Homo sapiens KIAA0286	433	31.897
1035	AF055636	Homo sapiens leucine-rich glioma-inactivated protein precursor	934	52.459
1036	U66707	Rattus norvegicus densin-180	807	84.049
1037	AF096896	Drosophila melanogaster pushover	294	33.333
1038	AF139185	Rattus norvegicus myomegalin	208	30.366
1039	Z11527	Drosophila melanogaster CYS3HIS finger protein	389	51.754
1040	X87342	Homo sapiens Human giant larvae homologue	1057	95.181
1041	Z97184	Homo sapiens BING1	784	96.992
1042	Y09022	Homo sapiens Not56-like protein	1062	90.217
1043	AB018325	Homo sapiens KIAA0782 protein	202	43.363
1044	AF155101	Homo sapiens putative kruppel-related zinc finger protein NY-REN-23 antigen	740	42.388
1045	AP000058	Aeropyrum pernix 246aa long hypothetical protein	252	41.818
1046	X65165	Volvox carteri extensin	257	46.250
1047	AC003080	Homo sapiens Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539)	2058	99.068
1048	AL110151	Homo sapiens hypothetical protein	352	37.288
1049	U25116	Dictyostelium discoideum cytoplasmic dynein intermediate chain	187	29.655
1050	D28863	Anthocidaris crassispina dynein intermediate chain 3	1166	71.193
1051	X12609	Homo sapiens anion transport protein (AA 1 -	245	45.390

		911)		
1052	Z54327	Caenorhabditis elegans C26D10.4	451	33.028
1053	U82808	Homo sapiens muscle-specific serine kinase 1	233	78.000
1054	AB002384	Homo sapiens KIAA0386	241	25.566
1055	AF117814	Mus musculus odd-skipped related 1 protein	984	94.156
1056	AF151840	Homo sapiens CGI-82 protein	363	45.890
1057	AL117448	Homo sapiens hypothetical protein	1107	74.180
1058	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LAbEIT@EMBL-Heidelberg.DE	969	98.658
1059	M26312	Oryctolagus cuniculus unknown protein	190	36.220
1060	AB020662	Homo sapiens KIAA0855 protein	520	37.808
1061	M27878	Homo sapiens DNA binding protein	721	71.852
1062	U22058	Mus musculus ADAM 4 protein precursor	689	63.704
1063	AF003622	Drosophila melanogaster A-kinase anchor protein DAKAP550	947	62.128
1064	AF017368	Mus musculus faciogenital dysplasia protein 2	2115	86.301
1065	X83413	Human herpesvirus 6 U88	550	55.645
1066	AF040642	Caenorhabditis elegans contains similarity to transacylases	800	35.476
1067	U88157	Rattus norvegicus PAM COOH-terminal interactor protein 10a	541	73.171
1068	AF155117	Homo sapiens NY-REN-62 antigen	1320	69.470
1069	AC002310	Homo sapiens Unknown gene product	187	56.140
1070	L09190	Homo sapiens trichohyalin	239	21.471
1071	X57017	Saccharomyces cerevisiae acetylglutamate kinase	418	27.020
1072	AB028978	Homo sapiens KIAA1055 protein	394	35.455
1073	U97553	murine herpesvirus 68 unknown	234	30.065
1074	L16507	Sus scrofa formiminotransferase-cyclodeaminase	776	90.076
1075	AB028997	Homo sapiens KIAA1074 protein	263	40.940
1076	X15769	Mus musculus U1RNA-associated 70-kDa protein	142	30.075
1077	X61296	Rattus norvegicus open reading frame 2	309	47.794
1078	AF181627	Drosophila melanogaster BcDNA.GH04120	699	37.669
1079	Z71408	Saccharomyces cerevisiae ORF YNL132w	1757	65.541
1080	Z47747	Homo sapiens NFkB1	322	100.000
1081	U50078	Homo sapiens p532	1085	77.209
1082	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	893	49.801
1083	AB007859	Homo sapiens KIAA0399	805	99.213
1084	AL023704	Schizosaccharomyces pombe putative translocation elongation factor-Tu family	800	32.688
1085	AF081568	Mus musculus delta tubulin	61	56.522
1086	AF181645	Drosophila melanogaster BcDNA.GH12144	207	36.567
1087	AL021747	Schizosaccharomyces pombe hypothetical protein	349	21.492
1088	AB023216	Homo sapiens KIAA0999 protein	1157	79.661
1089	AF130441	Arabidopsis thaliana UVB-resistance protein UVR8	347	33.766
1090	AE001399	Plasmodium falciparum GAF domain protein (cyclic nt signal transduct.)	203	34.058
1091	AF082556	Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase	299	38.462
1092	S66427	Homo sapiens retinoblastoma binding protein 1, RBP1	603	63.576

1093	X51591	Homo sapiens beta-myosin heavy chain (1151 AA)	158	26.846
1094	AB002335	Homo sapiens KIAA0337	193	60.294
1095	AB007950	Homo sapiens KIAA0481 protein	316	43.931
1096	AF109719	Mus musculus BAT2	1119	36.714
1097	AB028982	Homo sapiens KIAA1059 protein	1244	74.900
1098	AF076183	Rattus norvegicus cytosolic sorting protein PACS-1a	1620	95.849
1099	U74586	Rattus norvegicus double-stranded RNA specific adenosine deaminase	393	68.478
1100	X83413	Human herpesvirus 6 U88	334	40.909
1101	AF159356	Rattus norvegicus Munc13-4 protein	4605	87.377
1102	AF039690	Homo sapiens antigen NY-CO-8	2056	78.465
1103	AF082664	Gallus gallus interferon alpha/beta receptor 1	242	28.782
1104	J02459	bacteriophage lambda exonuclease	886	96.528
1105	U79142	Sus scrofa putative inhibitor of apoptosis	471	39.024
1106	AB012223	Canis familiaris ORF2	203	52.941
1107	AB029014	Homo sapiens KIAA1091 protein	9111	99.852
1108	D86214	Mus musculus Ca2+ dependent activator protein for secretion	1702	93.141
1109	Z93393	Unknown Similarity with snail BR-1 protein (Swiss Prot accession number Q25112); cDNA EST EMBL:D371	673	31.447
1110	AC005048	Homo sapiens laminin beta precursor; similar to AAB92586 (PID:g2708707)	770	40.625
1111	U93909	Cercopithecine herpesvirus 15 nuclear antigen EBNA-1	172	41.525
1112	AF031939	Mus musculus RalBP1-associated EH domain protein Repl1	2397	95.968
1113	U72972	Sus scrofa calcium/calmodulin-dependent protein kinase II isoform gamma-E	1737	98.195
1114	AC005142	Arabidopsis thaliana putative calcium channel	296	25.705
1115	AF091457	Rattus norvegicus zinc finger protein RIN ZF	468	52.703
1116	AL050019	Homo sapiens hypothetical protein	793	89.041
1117	D89285	Mesocricetus auratus inter-alpha-trypsin inhibitor heavy chain 1	1086	35.727
1118	AC004594	Homo sapiens Ca2+ dependent activator protein for secretion; similar to D86214 (NID:g1398903)	1891	98.936
1119	AB002323	Homo sapiens KIAA0325	3563	99.821
1120	Z98595	Schizosaccharomyces pombe hypothetical protein	477	28.155
1121	Z35719	Unknown cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA	487	40.574
1122	U96131	Homo sapiens HPV16 E1 protein binding protein	937	70.270
1123	D87433	Homo sapiens KIAA0246	219	32.479
1124	AC005534	Homo sapiens supported by human ESTs AA412402 (NID:g2070990) NH44021 (NID:g1182549), mouse EST AA065933 (NID:g1562789), and genscan	223	72.222
1125	AF068748	Mus musculus sphingosine kinase	557	50.289
1126	AB020664	Homo sapiens KIAA0857 protein	507	40.293
1127	AC007660	Arabidopsis thaliana putative RNA helicase	491	37.201
1128	M69183	Plasmodium falciparum mature-parasite-infected erythrocyte surface antigen	284	51.923
1129	AF114378	Mus musculus cypher1	219	44.144
1130	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	145	40.000

1131	AF149093	Mus musculus zinc finger ZF-12	399	50.394
1132	Z68106	Caenorhabditis elegans F41E7.1	187	26.036
1133	Y17920	Drosophila melanogaster CALO protein	491	35.798
1134	Z98047	Homo sapiens dJ162H14.1 (FIBULIN 1 like protein)	316	36.757
1135	U20217	Mus musculus fibrillin-2	1020	74.556
1136	AB010247	Mus musculus Ring3	196	34.286
1137	U13152	Mesocricetus auratus guanine nucleotide-binding protein beta 5	1165	82.096
1138	Y14946	Homo sapiens SPIN protein	234	52.941
1139	D13309	Rattus sp. DNA binding protein B	208	41.026
1140	AB018348	Homo sapiens KIAA0805 protein	987	53.962
1141	AF019887	Mus musculus metalloprotease-disintegrin meltrin beta	1508	80.385
1142	AL031177	Homo sapiens dJ889M15.3 (novel protein)	434	32.800
1143	AF132209	Homo sapiens prepro-major basic protein homolog	358	54.000
1144	AF072372	Mus musculus lysosomal trafficking regulator 2	960	94.156
1145	AF181646	Drosophila melanogaster BcDNA.GH12326	279	36.429
1146	L05186	Homo sapiens focal adhesion kinase	219	74.419
1147	X03145	Homo sapiens pot. ORF II	233	52.874
1148	Y18890	Human endogenous retrovirus K pol protein	807	84.416
1149	X83413	Human herpesvirus 6 U88	314	51.852
1150	X05472	Rattus norvegicus ORF 3	194	46.053
1151	U40342	Mus musculus ninein	1799	76.903
1152	D90713	Escherichia coli Hypothetical protein in hrsA 3' region .	727	96.639
1153	AE000464	Escherichia coli formate dehydrogenase-O, major subunit	894	92.199
1154	D37918	Escherichia coli Reverse transcriptase like protein	427	85.714
1155	D90719	Escherichia coli ORF ID:o207#4	843	90.000
1156	D90704	Escherichia coli Penicillin-binding protein 2 (pbp-2) .	838	99.174
1157	AJ002735	Klebsiella oxytoca initiation factor IF2-alpha	1252	93.953
1158	AF083501	Macaca mulatta rhadinovirus 17577 latent nuclear antigen	169	44.086
1159	AF043636	Plasmodium chabaudi circumsporozoite protein	237	63.830
1160	AF087573	Homo sapiens DNA fragmentation factor DFF35	369	61.017
1161	AL034352	Schizosaccharomyces pombe putative phosphodiesterase-nucleotide pyrophosphatase precursor	391	31.746
1162	Y17793	Mus musculus Dutt1 protein	1969	61.075
1163	X03557	Homo sapiens 56-KDa protein (aa 1-478)	1225	62.581
1164	U41662	Rattus norvegicus neuroligin 2	1931	98.662
1165	AB026190	Homo sapiens Kelch motif containing protein	275	46.789
1166	AL021481	Unknown similar to Phosphoglucosyltransferase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168	719	43.494
1167	AF079974	Mus musculus Rac GTPase-activating protein	307	53.333
1168	U79716	Homo sapiens Human Reelin	745	84.034
1169	AC008075	Arabidopsis thaliana F24J5.4	167	35.000
1170	X13916	Homo sapiens LDL-receptor related precursor (AA -19 to 4525)	766	87.603
1171	X75296	Homo sapiens TUP1 like enhancer of SPLIT gene 1	256	59.016
1172	U70935	Peromyscus maniculatus reverse transcriptase	163	29.371

1173	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	543	73.043
1174	AB020629	Homo sapiens KIAA0822 protein	508	71.698
1175	D50927	Homo sapiens The KIAA0137 gene product is related to Arabidopsis thaliana protein kinase (TOUSLED).	390	93.846
1176	AF111423	Xenopus laevis chromosome condensation protein XCAP-G	177	57.447
1177	AB023188	Homo sapiens KIAA0971 protein	362	79.452
1178	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	232	51.899
1179	S61070	Homo sapiens reverse transcriptase homolog=pol {retroviral element}	453	75.758
1180	AF046001	Homo sapiens zinc finger transcription factor	187	59.016
1181	AB028981	Homo sapiens KIAA1058 protein	480	64.078
1182	X01455	Reticuloendotheliosis virus C end of pol protein (reverse transcriptase)	237	34.314
1183	L13391	Homo sapiens helix-loop-helix phosphoprotein	482	70.940
1184	AB011152	Homo sapiens KIAA0580 protein	185	74.359
1185	AC006233	Arabidopsis thaliana hypothetical protein	175	41.111
1186	X62681	Gallus gallus limb deformity protein	408	57.377
1187	Z14093	Homo sapiens branched chain decarboxylase alpha subunit	739	85.106
1188	X97999	Homo sapiens transcription factor IID	203	37.008
1189	M85168	Homo sapiens glycogen debranching enzyme	251	57.447
1190	X90569	Homo sapiens elastic titin	365	75.610
1191	U80736	Homo sapiens CAGF9	743	90.323
1192	U35376	Homo sapiens repressor transcriptional factor	678	74.590
1193	U90215	Rattus norvegicus polysialyltransferase	225	59.155
1194	AB011169	Homo sapiens KIAA0597 protein	211	96.429
1195	U48736	Homo sapiens serine/threonine-protein kinase PRP4h	269	71.667
1196	AF026169	Homo sapiens SALF	245	82.500
1197	U93570	Homo sapiens p40	173	37.895
1198	X13621	Homo sapiens HNP-3 defensin (AA 1- 94)	205	71.795
1199	U51432	Homo sapiens nuclear protein Skip	280	77.193
1200	AL050037	Homo sapiens hypothetical protein	355	56.731
1201	AF076783	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 1kb	312	73.134
1202	AF085691	Homo sapiens multidrug resistance-associated protein 3A	626	39.858
1203	AF069603	Homo sapiens myosin light chain kinase isoform 3B	228	70.455
1204	AB007945	Homo sapiens KIAA0476 protein	529	46.269
1205	AF083037	Homo sapiens A-kinase anchoring protein AKAP350	292	96.000
1206	X01469	Plasmodium lophurae histidine-rich protein	214	45.283
1207	AF145705	Mus musculus T2K protein kinase homolog	841	77.381
1208	X78933	Homo sapiens zinc finger protein	407	57.732
1209	AF042169	Homo sapiens putative ATP-dependent mitochondrial RNA helicase	420	65.421
1210	X06596	Homo sapiens complement protein C1s precursor	318	58.065
1211	D38595	Homo sapiens inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP)	406	65.909
1212	L16558	Homo sapiens ribosomal protein L7	318	81.967
1213	Z79757	Unknown Similarity to Candida CDC4 gene	35	42.857

		(TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cD		
1214	U42580	Paramecium bursaria Chlorella virus 1 Pro-, Lys-rich, PAPK (30x); similar to wheat Pro-, Lys-rich protein, GenBank Accession Number X52472	174	29.661
1215	U93570	Homo sapiens putative p150	145	37.778
1216	D50487	Homo sapiens RNA helicase (HRH1)	331	58.416
1217	M20471	Homo sapiens clathrin light-chain a	292	88.679
1218	AF049910	Homo sapiens TACC1	392	85.333
1219	D80009	Homo sapiens KIAA0187	443	77.174
1220	Z26653	Homo sapiens laminin M chain (merosin)	351	79.167
1221	M96264	Homo sapiens galactose-1-phosphate uridyl transferase	252	58.333
1222	AL050373	Homo sapiens hypothetical protein	194	73.333
1223	A69020	unidentified PROTEASE	485	41.808
1224	V00488	Homo sapiens alpha globin	466	69.725
1225	AL008723	Homo sapiens dJ90G24.4 (SAAT1 (low affinity sodium glucose cotransporter (sodium:solute symporter family)))	152	41.429
1226	AL110218	Homo sapiens hypothetical protein	287	92.000
1227	U02032	Homo sapiens ribosomal protein L23a	291	56.977
1228	M13100	Rattus norvegicus unknown protein	196	35.345
1229	M12140	Homo sapiens envelope protein	567	46.067
1230	D30648	Homo sapiens flavoprotein subunit of complex II	440	64.286
1231	AB020629	Homo sapiens KIAA0822 protein	125	46.667
1232	M69297	Homo sapiens ORF 3	163	33.333
1233	M62419	Mus musculus clathrin-associated protein	214	52.308
1234	A15293	Homo sapiens Mature HSA	473	73.267
1235	U83908	Homo sapiens nuclear antigen H731	307	70.588
1236	L28010	Homo sapiens HnRNP F protein	283	85.714
1237	X53414	Homo sapiens L- alanine:glyoxylate aminotransferase	244	77.778
1238	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	341	46.552
1239	M19938	Homo sapiens fructose-6-phosphate,2-kinase: fructose-2, 6-bisphosphatase	185	60.417
1240	X84157	Homo sapiens subunit of the dimeric cap binding complex CBC	405	70.652
1241	AB029008	Homo sapiens KIAA1085 protein	331	59.223
1242	X01677	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase	467	72.549
1243	U09367	Homo sapiens zinc finger protein ZNF136	467	52.500
1244	AC006128	Homo sapiens Human homolog of Mus musculus wizS protein	559	70.732
1245	X15005	Homo sapiens pot. lamimin-binding protein (AA 1 - 300)	570	68.595
1246	S63654	Mus sp. type VII collagen	278	50.000
1247	M10905	Homo sapiens fibronectin	172	36.264
1248	D13635	Homo sapiens KIAA0010	566	79.279
1249	AB028948	Homo sapiens KIAA1025 protein	553	75.221
1250	D45131	Homo sapiens basigin	471	65.741
1251	AF015308	Homo sapiens nucleolar protein	311	68.354
1252	AL049557	Homo sapiens dJ773A18.2 (PROBABLE ATP-DEPENDENT RNA HELICASE P47 HOMOLOG)	456	58.333

1253	U88629	Homo sapiens RNA polymerase II elongation factor ELL2	171	93.103
1254	AF098788	Gallus gallus nuclear calmodulin-binding protein	1980	64.389
1255	AF077207	Homo sapiens HSPC021	279	51.456
1256	M13100	Rattus norvegicus unknown protein	441	56.250
1257	U93568	Homo sapiens putative p150	206	36.000
1258	AB014571	Homo sapiens KIAA0671 protein	861	58.009
1259	D16815	Homo sapiens EAR-1r	172	70.968
1260	AF167320	Mus musculus zinc finger protein ZFP113	640	66.923
1261	Z95334	Schizosaccharomyces pombe hypothetical protein	267	60.976
1262	X01455	Reticuloendotheliosis virus C end of pol protein (reverse transcriptase)	217	36.364
1263	AJ243460	Leishmania major proteophosphoglycan	232	32.468
1264	D63481	Homo sapiens The KIAA0147 gene product is related to adenyl cyclase.	1027	57.597
1265	U41559	Caenorhabditis elegans No definition line found	223	26.606
1266	U76846	Arabidopsis thaliana ubiquitin-specific protease	217	30.108
1267	D63481	Homo sapiens The KIAA0147 gene product is related to adenyl cyclase.	1027	57.597
1268	X52235	Homo sapiens ORFII	243	60.870
1269	AF019082	Borrelia burgdorferi virulent strain associated lipoprotein	261	29.150
1270	U49379	Homo sapiens diacylglycerol kinase epsilon DGK	159	83.333
1271	AC007228	Homo sapiens BC37295 2 (partial)	598	37.037
1272	AF091090	Homo sapiens unknown	200	93.333
1273	X69490	Homo sapiens titin	2362	98.939
1274	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	528	71.560
1275	AF078933	Homo sapiens WAIT-1	403	87.879
1276	Y16241	Homo sapiens nebulin	2397	65.306
1277	AB018348	Homo sapiens KIAA0805 protein	327	51.042
1278	AJ242979	Homo sapiens KIAA0461/245 protein	592	61.202
1279	D89660	Rattus norvegicus peroxisome assembly factor-2	257	83.333
1280	U67056	Acanthamoeba castellanii myosin I heavy chain kinase	203	29.289
1281	AF072810	Homo sapiens transcription factor WSTF	380	84.000
1282	AB014607	Homo sapiens KIAA0707 protein	608	41.564
1283	AF052831	Trypanosoma cruzi unknown	134	36.111
1284	AC003038	Homo sapiens R30923 1	575	72.993
1285	D25215	Homo sapiens KIAA0032	214	33.010
1286	AF108843	Homo sapiens env protein	496	52.229
1287	AJ243460	Leishmania major proteophosphoglycan	184	29.851
1288	U89439	Bos taurus ubiquitin-like protein	46	25.641
1289	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	286	84.615
1290	X99211	Drosophila melanogaster ubiquitin-specific protease	589	39.373
1291	X53556	Bos taurus type X collagen	252	30.534
1292	AC002333	Arabidopsis thaliana SF16 isolog	180	32.192
1293	Y17832	Human endogenous retrovirus K pol protein	213	45.000
1294	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	192	35.766
1295	Z79752	Homo sapiens predicted using Genefinder; Similarity to Human RNA helicase (SW:P68_HUMAN); cDNA EST EMBL:	188	45.205

1296	Z22968	Homo sapiens M130 antigen	929	54.386
1297	AB007862	Homo sapiens KIAA0402	1117	82.126
1298	AB006755	Homo sapiens PCDH7 (BH-Pcdh)a	434	37.611
1299	AF180920	Homo sapiens cyclin ania-6a	295	29.500
1300	AF003385	Caenorhabditis elegans No definition line found	1156	37.434
1301	AL035311	Unknown 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end; 2-evidence=pred	484	36.564
1302	M92040	Strongylocentrotus purpuratus alpha-1 collagen	166	31.319
1303	AF003535	Homo sapiens ORF2-like protein	256	40.777
1304	L31840	Rattus norvegicus nuclear pore complex protein NUP107	513	85.714
1305	U97553	murine herpesvirus 68 unknown	191	37.143
1306	X00318	Homo sapiens apoferritin H chain	570	73.276
1307	D30648	Homo sapiens flavoprotein subunit of complex II	677	88.496
1308	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	274	54.321
1309	U01317	Homo sapiens G-gamma globin	559	70.492
1310	D79996	Homo sapiens KIAA0174	220	81.395
1311	Y17267	Mus musculus ubiquitin-conjugating enzyme	322	57.143
1312	D63881	Homo sapiens KIAA0160 gene product is novel.	3156	99.161
1313	D42150	Gallus gallus chicken cadherin-7	906	84.146
1314	M12140	Homo sapiens envelope protein	397	47.794
1315	AF007270	Arabidopsis thaliana contains similarity to myosin heavy chain	86	23.864
1316	U66561	Homo sapiens kruppel-related zinc finger protein	1607	57.067
1317	AF081144	Rattus norvegicus CL1AA	277	58.537
1318	M25984	Gallus gallus alpha-2 type I collagen	180	31.169
1319	X66363	Homo sapiens serine/threonine protein kinase	427	59.259
1320	AL022603	Arabidopsis thaliana putative protein	219	43.590
1321	Y11145	Pacifastacus leniusculus masquerade-like protein	174	27.919
1322	Y17833	Human endogenous retrovirus K pol protein	840	84.000
1323	Y17832	Human endogenous retrovirus K env protein	598	66.667
1324	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	748	49.770
1325	AJ004801	Bovine herpesvirus type 1.1 immediate-early transactivator protein with Zn finger (cell nucleus)	192	32.168
1326	X99753	Homo sapiens Arno protein (ARF exchange factor)	217	35.965
1327	M94065	Homo sapiens dihydroorotate dehydrogenase	409	72.917
1328	AF072758	Mus musculus fatty acid transport protein 3; FATP3	2164	80.653
1329	AJ006693	Homo sapiens ultra high sulfur keratin	182	28.155
1330	Y10256	Homo sapiens NIK, serine/threonine protein-kinase	74	22.989
1331	X79448	Homo sapiens type I	464	48.780
1332	AF071172	Homo sapiens HERC2	250	60.606
1333	U50193	Caenorhabditis elegans weak similarity to SP:YAD5_CLOAB (P33746) hypothetical protein and to PIR:C48583 stress-inducible protein STI1	640	31.579
1334	AB012223	Canis familiaris ORF2	228	37.963
1335	AF106682	Homo sapiens spindlin	1009	93.168
1336	U07358	Homo sapiens serine/threonine protein kinase	718	37.353
1337	AF016507	Homo sapiens C-terminal binding protein 2	786	83.916
1338	L15309	Homo sapiens zinc finger protein	574	74.138

1339	AB024075	Homo sapiens B120	906	47.826
1340	M12140	Homo sapiens envelope protein	508	54.615
1341	U09413	Homo sapiens zinc finger protein ZNF135	1034	60.090
1342	AF074086	Homo sapiens envelope	699	71.533
1343	M11902	Mus musculus proline-rich salivary protein	221	33.582
1344	D50464	Mus musculus SDR2	263	28.636
1345	X57527	Homo sapiens alpha 1(VIII) collagen	201	33.125
1346	AC004890	Homo sapiens similar to zinc finger proteins; similar to AAC01956 (PID:g2843171)	240	30.405
1347	L04159	Plasmodium falciparum 3' end., gene product	151	24.519
1348	AL096846	Schizosaccharomyces pombe similar to yeast DEC1 mitochondrial inheritance and actin cytoskeleton organisation protein	281	22.651
1349	AC002389	Homo sapiens GAPDH-2 like	262	47.525
1350	AC005498	Homo sapiens R31665 2	160	43.284
1351	M63595	Xenopus laevis alpha-1 type II collagen	238	27.397
1352	AL035472	Mycobacterium leprae putative protein synthesis initiation factor 2	172	35.780
1353	M25984	Gallus gallus alpha-2 type I collagen	180	31.169
1354	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	813	66.509
1355	Z24725	Homo sapiens mitogen inducible gene mig-2	1952	91.437
1356	M11052	Mus musculus envelope polyprotein precursor	176	34.375
1357	AF132180	Drosophila melanogaster unknown	338	31.792
1358	D31883	Homo sapiens similar to an actin bundling protein, dematn.	399	54.074
1359	AL117200	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	208	37.719
1360	AF146040	Cavia porcellus endothelial nitric oxide synthase	185	30.986
1361	AC002310	Homo sapiens Unknown gene product	630	52.151
1362	M64791	Rattus norvegicus salivary proline-rich protein	201	32.308
1363	AL021747	Schizosaccharomyces pombe hypothetical protein	205	55.172
1364	X53581	Rattus norvegicus ORF2	165	49.123
1365	Y08715	Mus musculus vascular cadherin-2	1317	78.599
1366	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	244	82.927
1367	U83590	Rattus norvegicus PAR interacting protein	1542	68.421
1368	U12390	Cloning vector pSport1 beta-galactosidase alpha peptide	176	44.928
1369	U01351	Homo sapiens glucocorticoid receptor alpha-2	758	93.443
1370	X51591	Homo sapiens beta-myosin heavy chain (1151 AA)	286	53.271
1371	AF009668	multiple sclerosis associated retrovirus polyprotein	393	47.143
1372	AB002348	Homo sapiens KIAA0350	2009	84.896
1373	M30023	orf virus ORF2	167	35.252
1374	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1474	57.100
1375	Z49651	Saccharomyces cerevisiae ORF YJR151c	168	27.363
1376	AC002365	Homo sapiens APXL	266	42.991
1377	AB015440	Rana catesbeiana alpha 1 type I collagen	320	29.470
1378	AF176688	Rattus norvegicus sodium/calcium/potassium exchanger NCKX1	191	33.113
1379	Y15635	Homo sapiens ABCR	200	42.391
1380	X75926	Mus musculus abcl	2263	55.857
1381	V01555	Human herpesvirus 4 BYRF1, encodes EBNA-2	181	31.707

		(Dambaugh et al, 1984; Dillner et al, 1984)		
1382	AF015454	Xenopus laevis ER1	613	51.485
1383	X16468	Homo sapiens prepropeptide (AA 1-1418)	200	29.911
1384	D80004	Homo sapiens KIAA0182	640	90.000
1385	M11902	Mus musculus proline-rich salivary protein	199	33.793
1386	D86969	Homo sapiens similar to Human zinc-finger protein, BR140 (P1:JC2069)	1479	68.403
1387	AL033534	Schizosaccharomyces pombe serine-rich protein	176	30.061
1388	AF167320	Mus musculus zinc finger protein ZFP113	789	55.140
1389	Z68335	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST EMBL:D68967 comes from this gene; cDNA EST EMBL:D69298 comes from this gene; cDNA EST EMBL:D69331 comes from this gene; cDNA EST EMBL:D70368 comes from this gene	157	35.514
1390	Z69361	Caenorhabditis elegans Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene	199	40.000
1391	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	197	38.793
1392	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	184	48.077
1393	M57551	Pseudomonas aeruginosa transcription regulatory protein	156	37.000
1394	AF016687	Caenorhabditis elegans Similar to cuticular collagen; coded for by C. elegans cDNA yk69e4.5	181	35.652
1395	M83822	Homo sapiens beige-like protein	413	82.192
1396	AF085185	Acanthamoeba castellanii Myosin-IA	226	42.400
1397	U87318	Xenopus laevis NaDC-2	1500	56.041
1398	Y15491	Pongo pygmaeus fertilin alpha protein	973	94.161
1399	AB002321	Homo sapiens KIAA0323	2351	99.403
1400	X75926	Mus musculus abcl1	2263	55.857
1401	M18247	Feline leukemia virus gag-pol precursor polyprotein gPr80	259	36.792
1402	Z97340	Arabidopsis thaliana extensin like protein	144	39.344
1403	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	184	46.377
1404	S80119	Rattus sp. reverse transcriptase homolog	379	53.608
1405	AF071172	Homo sapiens HERC2	299	88.636
1406	AF134304	Homo sapiens Scar2	190	31.967
1407	L06863	Cricetulus griseus type VII collagen	164	33.333
1408	AF032872	Rattus norvegicus potassium channel regulatory protein KChAP	229	84.091
1409	M37759	Mus musculus serine 1 ultra high sulfur protein	284	40.336
1410	S74439	Bombyx mori=silkworms, Peptide Partial, 633 aa silk fibroin heavy chain {C-terminal}	426	40.314
1411	D80009	Homo sapiens KIAA0187	323	57.944
1412	M12140	Homo sapiens envelope protein	316	71.186
1413	M13100	Rattus norvegicus unknown protein	263	64.516
1414	AF116463	Streptomyces lincolnensis unknown	219	33.173
1415	U00039	Escherichia coli No definition line found	796	97.561
1416	AB017614	Mus musculus OASIS protein	1919	92.652
1417	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2	180	25.532
1418	D87459	Homo sapiens Similar to Volvox carteri extensin	204	35.766

		(S22697)		
1419	U33834	Homo sapiens helicase	350	52.713
1420	AB007871	Homo sapiens KIAA0411	668	60.938
1421	Z48149	Saccharomyces cerevisiae similarity with H. polymorpha hypothetical protein in LEU2 region	169	32.432
1422	K03207	Homo sapiens salivary proline-rich protein precursor	177	33.077
1423	AC002563	Homo sapiens putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5501	99.166
1424	AJ004832	Homo sapiens neuropathy target esterase	1205	79.762
1425	X64346	Saimiriine herpesvirus 2 ORF 73; ECLF1	221	29.070
1426	Y08986	Brassica napus oleosin-like protein	190	36.842
1427	M99063	Homo sapiens cytokeratin 2	372	54.348
1428	AF099976	Mus musculus schlafen4	710	47.012
1429	D13636	Homo sapiens KIAA0011	374	41.579
1430	AJ245569	Mus musculus hypothetical protein	249	67.273
1431	AF139744	Streptococcus pyogenes serum opacity factor precursor	144	31.304
1432	D70831	Homo sapiens Zinc-finger protein	710	59.016
1433	X52235	Homo sapiens ORFII	197	42.667
1434	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2	534	82.569
1435	AL049608	Arabidopsis thaliana extensin-like protein	160	37.662
1436	AB014514	Homo sapiens KIAA0614 protein	347	73.973
1437	AF043944	Mytilus edulis nongradient byssal precursor	223	31.092
1438	U44898	Homo sapiens SNAP45 subunit	301	54.237
1439	X89383	Rattus norvegicus SNF1-related kinase	308	73.684
1440	AF097183	Cryptosporidium parvum unknown	238	33.735
1441	AF055904	Myxococcus xanthus unknown	225	29.082
1442	X53581	Rattus norvegicus ORF1	200	40.506
1443	AF043297	Chlamydomonas reinhardtii poly(A) binding protein RB47	192	32.484
1444	D29766	Rattus norvegicus Crk-associated substrate, p130	1853	86.420
1445	M27878	Homo sapiens DNA binding protein	734	74.265
1446	AF057557	Homo sapiens anti-Fas-induced apoptosis	196	63.462
1447	AJ133125	Mus musculus immunity associated protein 38	315	48.387
1448	U64608	Caenorhabditis elegans coded for by C. elegans cDNA yk173c12.5	334	34.706
1449	AF053356	Homo sapiens leucin rich neuronal protein	886	90.972
1450	AB014584	Homo sapiens KIAA0684 protein	209	77.083
1451	AB018293	Homo sapiens KIAA0750 protein	1090	50.146
1452	Z78064	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST EMBL:D69730 comes from this gene	151	31.544
1453	U12134	Homo sapiens RAD52	223	69.091
1454	U07973	Gallus gallus alpha-1 collagen type III	134	30.597
1455	AL080141	Homo sapiens hypothetical protein	1117	67.293
1456	AL031323	Schizosaccharomyces pombe putative transcription or splicing factor	162	28.571
1457	U43585	Mus musculus protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	280	57.143
1458	AB029335	Halocynthia roretzi HrPET-3	238	32.738
1459	U82982	Cavia porcellus GEC-3	227	38.679

1460	Z19574	Homo sapiens cytokeratin 17	178	61.364
1461	AB014521	Homo sapiens KIAA0621 protein	936	64.390
1462	AJ131526	Mus musculus TEF-5	156	68.293
1463	AB022927	Oryctolagus cuniculus hyperpolarization activated cation channel	186	31.280
1464	U64608	Caenorhabditis elegans coded for by C. elegans cDNA yk173c12.5	334	34.706
1465	X70944	Homo sapiens PTB-associated splicing factor	231	30.366
1466	AJ243460	Leishmania major proteophosphoglycan	221	33.173
1467	U81788	Drosophila melanogaster kinesin-73	257	61.538
1468	U14635	Caenorhabditis elegans similar to GABA and glycine receptors	681	34.925
1469	M24355	Homo sapiens filaggrin	518	34.014
1470	M12140	Homo sapiens envelope protein	497	50.345
1471	X97675	Homo sapiens plakophilin 2b	186	77.778
1472	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	211	54.688
1473	U42471	Mus musculus Wiscott-Aldrich Syndrome protein homolog	226	39.669
1474	AF001305	Pneumocystis carinii f. sp. carinii protease 1	195	27.485
1475	X75931	Bos taurus Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit	2445	98.660
1476	AF084521	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2	1552	94.286
1477	X83413	Human herpesvirus 6 U88	175	41.509
1478	AF164612	Homo sapiens envelope protein	334	41.221
1479	AF115435	Rattus norvegicus syntaxin 17	234	62.338
1480	AC002563	Homo sapiens putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5501	99.166
1481	D13644	Homo sapiens protein related N-terminus of the oncogene	238	84.444
1482	AF009243	Homo sapiens proline-rich Gla protein 2	333	94.118
1483	D25538	Homo sapiens KIAA0037	387	76.389
1484	Y17137	Mus musculus mCASK-A	237	79.167
1485	AE000789	Borrelia burgdorferi B. burgdorferi predicted coding region BBI16	218	29.885
1486	AF146531	Homo sapiens bridging integrator-2	175	64.286
1487	AB023161	Homo sapiens KIAA0944 protein	566	56.954
1488	AB018288	Homo sapiens KIAA0745 protein	524	39.837
1489	AL021929	Mycobacterium tuberculosis PPE	193	37.500
1490	AB028998	Homo sapiens KIAA1075 protein	386	57.692
1491	AF124435	Danio rerio p55-related MAGUK protein DLG3	776	82.482
1492	X65546	Mycobacterium leprae proline-rich antigen	145	44.186
1493	AB023178	Homo sapiens KIAA0961 protein	1615	79.061
1494	Z46791	Caenorhabditis elegans similar to collagen	188	35.849
1495	AF085185	Acanthamoeba castellanii Myosin-IA	205	35.811
1496	J05499	Rattus norvegicus L-glutamine amidohydrolase	1327	79.259
1497	AL021492	Unknown similar to Glycosyl transferases; cDNA EST EMBL:D33950 comes from this gene; cDNA EST EMB	246	33.143
1498	U27459	Homo sapiens hORC2L	213	60.000
1499	U50078	Homo sapiens p532	333	88.679
1500	AE000351	Escherichia coli orf, hypothetical protein	899	98.473
1501	X69089	Homo sapiens 165kD protein	374	62.766
1502	L19201	Escherichia coli glutamine synthetase	1255	93.564

1503	D90846	Escherichia coli Acriflavin resistance protein F (EnvD protein) .	1619	96.617
1504	AE000248	Escherichia coli persistence to inhibition of murein or DNA biosynthesis, DNA-binding regulator	1335	94.340
1505	D90730	Escherichia coli MukB protein	1416	94.515
1506	D90709	Escherichia coli YhhI protein	784	90.152
1507	X69089	Homo sapiens 165kD protein	196	70.455
1508	AB004659	Acidiphilium multivorum ArsB	621	80.488
1509	X73143	Escherichia coli NikA	885	95.620
1510	L10328	Escherichia coli f772	641	90.909
1511	D90731	Escherichia coli Asparaginyl-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS) .	485	94.872
1512	X57560	Escherichia coli pspB protein	294	86.000
1513	D90716	Escherichia coli Hypothetical 54.3 kd protein in lpd-3 5' region (orf2) .	716	94.737
1514	D90748	Escherichia coli Virulence membrane protein phoQ .	844	90.789
1515	X16531	Escherichia coli oxyR gene product 34kD protein (AA 1-305)	853	91.096
1516	AB011180	Homo sapiens KIAA0608 protein	560	63.566
1517	AB012725	Mus musculus zinc finger protein	943	91.447
1518	AB018274	Homo sapiens KIAA0731 protein	527	67.500
1519	AL035632	Unknown /prediction=(method:"genefinder", version:"084", score:"113.36"); /prediction=(meth	573	59.028
1520	Z11518	Homo sapiens histidyl-tRNA synthetase	2152	100.000
1521	U08350	Sus scrofa E-selectin	187	30.392
1522	AF007170	Homo sapiens unknown	154	85.714
1523	AF160798	Rattus norvegicus calcium transporter CaT1	1513	90.041
1524	D63478	Homo sapiens The KIAA0144 gene product is novel .	155	84.615
1525	AJ133120	Rattus norvegicus Proline rich synapse associated protein 2	606	80.189
1526	A58331	Homo sapiens unnamed protein product	831	99.115
1527	U39060	Mus musculus glucocorticoid receptor interacting protein 1	219	84.091
1528	U71273	Sus scrofa glucosidase II	704	60.667
1529	Y00826	Rattus norvegicus gp210 (AA 1-1886)	258	84.444
1530	U66707	Rattus norvegicus densin-180	558	60.432
1531	M18907	Homo sapiens nifedipine oxidase	654	81.967
1532	AB020716	Homo sapiens KIAA0909 protein	318	89.583
1533	AF156856	Mus musculus cytosolic sialic acid 9-O-acetylcetylesterase	268	72.917
1534	U86074	Homo sapiens tesmin	662	76.577
1535	Z19550	Homo sapiens N-acetylglucosaminide beta-1,6-N-acetylglucosaminyltransferase	339	52.128
1536	AL096749	Homo sapiens DKFZp434G153	271	36.522
1537	AF156529	Mus musculus Mx2 interacting nuclear target protein	179	100.000
1538	AB009024	Homo sapiens capping enzyme 1B	157	100.000
1539	U13019	Caenorhabditis elegans No definition line found	426	56.731
1540	AB002370	Homo sapiens KIAA0372	263	97.436
1541	U39940	Sinorhizobium meliloti choline sulfatase	254	35.417

1542	D78572	Mus musculus membrane glycoprotein	747	65.000
1543	M63180	Homo sapiens threonyl-tRNA synthetase	174	42.500
1544	Z68011	Unknown Similarity to Xenopus F-spondin precursor (PIR Acc. No. A47723); cDNA EST EMBL:D33135 comes	191	33.708
1545	U37373	Xenopus laevis up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region	387	81.250
1546	AL096768	Homo sapiens dJ858B16.1.2 (KIAA0542 (isoform 2))	176	83.333
1547	AF022962	Mus musculus Sec8	194	93.939
1548	Z81467	Caenorhabditis elegans cDNA EST EMBL:D32693 comes from this gene; cDNA EST EMBL:D35405 comes from this gene; cDNA EST yk307c10.5 comes from this gene	510	52.632
1549	AF023261	Human endogenous retrovirus K pol-env	412	54.167
1550	U59287	Gallus gallus paranemin	162	57.895
1551	AC002332	Arabidopsis thaliana putative NAD(P)-dependent cholesterol dehydrogenase	303	39.412
1552	Z68297	Unknown Similarity to Yeast TAT-binding homolog 7 (SW:TBP7_YEAST); cDNA EST EMBL:D37124 comes from	259	34.375
1553	AF064553	Mus musculus NSD1 protein	640	90.526
1554	AF151877	Homo sapiens CGI-119 protein	323	84.375
1555	M97662	Rattus norvegicus beta-alanine synthase	255	80.000
1556	AF067226	Homo sapiens cGMP phosphodiesterase A4	205	55.172
1557	AB018274	Homo sapiens KIAA0731 protein	497	67.857
1558	D86566	Homo sapiens NOTCH4	307	100.000
1559	D87326	Mus musculus GSG2	328	42.069
1560	U09413	Homo sapiens zinc finger protein ZNF135	618	68.376
1561	L28167	Mus musculus zinc finger protein	674	78.947
1562	X91788	Homo sapiens Icln protein	639	100.000
1563	D87127	Homo sapiens translocation protein-1	520	62.205
1564	U17342	Thermus sp. serine proteinase	262	41.121
1565	D80005	Homo sapiens KIAA0183	55	46.667
1566	AB014594	Homo sapiens KIAA0694 protein	366	52.212
1567	AF099032	Homo sapiens embryonic ectoderm development protein short isoform	208	76.190
1568	U95171	Drosophila melanogaster microtubule associated protein	229	25.191
1569	AF064748	Mus musculus S3-12	569	79.464
1570	A36790	unidentified LIGHT CHAIN VARIABLE REGION C21-L3	154	96.000
1571	AF017152	Mus musculus Shc binding protein	234	83.333
1572	AF095136	Homo sapiens protein O-mannosyl-transferase 1	1351	89.474
1573	AF165161	Homo sapiens FLASH	732	100.000
1574	AL008637	Homo sapiens NCF4	247	83.333
1575	AB007931	Homo sapiens KIAA0462 protein	151	83.333
1576	AF055291	Rattus norvegicus signal transducer and activator of transcription 4	238	97.059
1577	AL031667	Homo sapiens dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	440	78.889
1578	AF143946	Homo sapiens transcriptional activator SRCAP	963	98.675
1579	AF022256	Mus musculus corneal proteoglycan, keratocan	221	37.069

1580	X67052	Gallus gallus c-Rml	301	95.745
1581	AC006539	Homo sapiens BC39498 2	584	63.866
1582	AL080156	Homo sapiens hypothetical protein	260	38.462
1583	S67826	Homo sapiens immunoglobulin heavy chain variable region	549	67.568
1584	Z68760	Homo sapiens Similarity to Human ankaryin (SW:ANKB_HUMAN); cDNA EST EMBL:D34286 comes from this gene; cD	306	38.655
1585	Z70271	Unknown Similarity to Yeast E1-E2 ATPase (SW:YED1_YEAST); cDNA EST EMBL:D37634 comes from this gene	709	44.737
1586	AB018334	Homo sapiens KIAA0791 protein	175	84.848
1587	AF091624	Drosophila melanogaster Pelle associated protein Pellino	420	60.952
1588	AB004884	Homo sapiens PKU-alpha	161	70.588
1589	U52193	Mus musculus phosphoinositide 3-kinase	922	99.259
1590	M80902	Homo sapiens AHNAK nucleoprotein	686	79.032
1591	AB019440	Homo sapiens immunogloblin heavy chain variable region	643	81.250
1592	X60155	Homo sapiens zinc finger 41	788	63.473
1593	Y17793	Mus musculus Dutt1 protein	546	56.522
1594	AB007876	Homo sapiens KIAA0416	459	43.382
1595	D63850	Mus musculus hepatoma-derived growth factor	182	27.439
1596	AJ010949	Mus musculus calcium channel alpha-2-delta-C subunit	1093	97.605
1597	U34360	Homo sapiens LAF-4	211	82.353
1598	V00401	Gallus gallus collagen	559	54.861
1599	AC006266	Arabidopsis thaliana hypothetical protein	147	46.667
1600	U35371	Rattus norvegicus neural cell adhesion protein BIG-2 precursor	690	93.519
1601	J02635	Rattus norvegicus prealpha-2-macroglobulin	304	41.667
1602	U03969	Tripneustes gratilla dynein heavy chain isotype 1B	694	76.515
1603	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	193	35.246
1604	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	677	83.761
1605	D86983	Homo sapiens similar to D.melanogaster peroxidasin(U11052)	236	35.115
1606	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	571	57.724
1607	D87437	Homo sapiens KIAA0250	165	96.429
1608	X51394	Xenopus laevis APEG precursor protein	305	47.619
1609	X72473	Homo sapiens Ig kappa light chain (VJC)	376	82.609
1610	AF132726	Mus musculus FLASH	396	60.606
1611	X69942	Mus musculus enhancer-trap-locus-1	233	94.872
1612	L24907	Rattus norvegicus protein kinase I	157	89.286
1613	M98326	Homo sapiens valyl-tRNA synthetase	584	71.930
1614	AL031667	Homo sapiens dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	545	100.000
1615	D90188	Homo sapiens phSR2	201	78.125
1616	AJ004810	Zea mays cytochrome P450 monooxygenase	159	68.293
1617	U93872	Kaposi's sarcoma-associated herpesvirus ORF 73, contains large complex repeat CR 73	149	31.298

1618	X79233	Mus musculus EWS	175	74.194
1619	Z54216	Unknown similar to DNAJ protein; cDNA EST EMBL:T00334 comes from this gene; cDNA EST EMBL:T01898 co	255	41.237
1620	AF159295	Homo sapiens serine/threonine protein kinase Kp78 splice variant CTAK75a	164	71.795
1621	AJ012376	Homo sapiens ATP-binding cassette transporter-1 (ABC-1)	181	33.043
1622	AL031432	Homo sapiens dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins)	168	80.645
1623	Z49144	Oryctolagus cuniculus multidrug resistance-associated protein 2	513	48.125
1624	Z97628	Homo sapiens Similarity to Human GC-rich DNA-binding factor (GCF) (SW:P16383); cDNA EST yk238e11.3 comes	178	31.624
1625	U58134	Mus musculus poly(A) polymerase VI	242	97.297
1626	U93181	Homo sapiens nuclear dual-specificity phosphatase	240	48.889
1627	Z80220	Unknown similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST	289	27.326
1628	U31961	Drosophila melanogaster ORF2	199	37.931
1629	M63438	Homo sapiens , gene product	518	81.188
1630	X92653	Drosophila melanogaster unknown product	340	50.459
1631	Z25535	Homo sapiens nuclear pore complex protein hnup153	283	100.000
1632	AL031667	Homo sapiens dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	531	67.544
1633	AF017806	Mus musculus Zn-15 transcription factor	713	94.690
1634	U09116	Homo sapiens ORF2, encodes a reverse transcriptase homolog	198	56.604
1635	X94082	Xenopus laevis KLP2 protein	191	90.323
1636	AF062187	Homo sapiens immunoglobulin heavy chain variable region	653	88.073
1637	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LBEIT@EMBL-Heidelberg.DE	488	97.403
1638	AF165310	Homo sapiens ATP cassette binding transporter 1	179	42.424
1639	Z93785	Caenorhabditis elegans similar to Protein phosphatase 2C (2 domains); cDNA EST yk279g8.5 comes from this gene	202	56.250
1640	AF127979	Homo sapiens lambda 2 immunoglobulin light chain variable region	481	74.747
1641	AB007939	Homo sapiens KIAA0470 protein	197	93.750
1642	D26067	Homo sapiens KIAA0033	208	96.970
1643	U04267	Gossypium barbadense proline-rich cell wall protein	210	44.578
1644	AB018311	Homo sapiens KIAA0768 protein	1321	43.644
1645	A65888	unidentified PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA)-99	182	100.000
1646	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	279	78.571

1647	U18973	Drosophila melanogaster protein disulfide isomerase	189	30.328
1648	AF080229	Human endogenous retrovirus K polymerase	537	68.644
1649	AC006530	Homo sapiens unknown	186	44.286
1650	AF055634	Homo sapiens transmembrane receptor UNC5C	347	100.000
1651	U35376	Homo sapiens repressor transcriptional factor	533	67.273
1652	AL031230	Homo sapiens dJ73M23.3 (KIAA0319)	198	63.043
1653	X06148	Rattus norvegicus ribosomal protein L5 (AA 1-297)	411	86.301
1654	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	271	84.783
1655	U90543	Homo sapiens butyrophilin	274	38.333
1656	AC007660	Arabidopsis thaliana putative serine/threonine protein kinase	336	29.304
1657	U95171	Drosophila melanogaster microtubule associated protein	340	49.057
1658	A07400	Homo sapiens villin	229	100.000
1659	X65165	Volvox carteri extensin	177	36.449
1660	AB014574	Homo sapiens KIAA0674 protein	186	68.085
1661	AJ005897	Homo sapiens JM5	347	71.429
1662	U23502	Plasmodium chabaudi chabaudi POM1	487	46.012
1663	D88154	Homo sapiens villin-like protein	209	96.970
1664	X06956	Homo sapiens alpha-tubulin	481	93.671
1665	AF070470	Mus musculus SPARC-related protein	1803	96.578
1666	S75578	Homo sapiens 4-aminobutyrate aminotransferase	279	97.674
1667	Z68297	Unknown Similarity to Yeast TAT-binding homolog 7 (SW:TBP7_YEAST); cDNA EST EMBL:D37124 comes from	732	82.540
1668	AF076183	Rattus norvegicus cytosolic sorting protein PACS-1a	957	98.675
1669	U00483	Macaca mulatta mucin	148	48.387
1670	AJ130711	Homo sapiens QA79 membrane protein, splice product airm-2	481	48.864
1671	U50040	Homo sapiens signaling inositol polyphosphate 5 phosphatase SIP-110	210	97.222
1672	AB005541	Rattus rattus PCTAIRE3	1106	92.222
1673	X06290	Homo sapiens apolipoprotein (a) (AA -19 to 4529)	375	78.788
1674	Y17737	Canis familiaris albumin	157	52.000
1675	Z12168	Canis familiaris stimulatory GTP binding protein	1211	88.614
1676	D16626	Homo sapiens histidase	198	79.487
1677	AB018268	Homo sapiens KIAA0725 protein	216	100.000
1678	AB004885	Homo sapiens PKU-beta	172	92.593
1679	Z26876	Homo sapiens ribosomal protein	24	57.143
1680	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR	362	82.540
1681	AF151827	Homo sapiens CGI-69 protein	299	78.571
1682	AB002299	Homo sapiens KIAA0301	272	64.286
1683	AF060076	Mus musculus polyhomeotic 2 protein	245	67.797
1684	AF015911	Rattus norvegicus NAC-1 protein	796	97.541
1685	AJ243997	Homo sapiens ERIC1	167	96.667
1686	AF118023	Homo sapiens SH3 domain-binding protein SNP70	441	86.957
1687	X69086	Homo sapiens utrophin (dystrophin related)	200	22.326

		protein)		
1688	AF016903	Homo sapiens agrin precursor	476	39.394
1689	L13923	Homo sapiens fibrillin	220	83.333
1690	X89858	Drosophila melanogaster actin binding protein	184	64.865
1691	U31629	Mus musculus unknown	201	65.789
1692	U68233	Homo sapiens farnesol receptor HRR-1	204	100.000
1693	AB011370	Mus musculus Ankhzn	148	100.000
1694	M74165	Gallus gallus tensin	589	65.714
1695	AB020662	Homo sapiens KIAA0855 protein	225	59.322
1696	AL117237	Homo sapiens hypothetical protein	597	90.816
1697	AF042191	Danio rerio paraxial protocadherin; PAPC	439	50.382
1698	U08813	Oryctolagus cuniculus 597 aa protein related to Na/glucose cotransporters	220	94.444
1699	U40342	Mus musculus ninein	495	68.103
1700	AF039698	Homo sapiens antigen NY-CO-33	746	39.523
1701	M90656	Homo sapiens gamma-glutamylcysteine synthetase	215	100.000
1702	AF166261	Xenopus laevis nuclear protein Sojo	360	55.856
1703	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	545	76.577
1704	AF129756	Homo sapiens NG26	272	75.000
1705	D44497	Homo sapiens human p57	368	80.000
1706	U97189	Caenorhabditis elegans strong similarity to thw P13/P14 family of kinases	141	29.412
1707	AL117204	Caenorhabditis elegans predicted using Genefinder	202	40.845
1708	AF017275	Mus musculus growth factor independence-1B	594	77.679
1709	D26069	Homo sapiens KIAA0041	227	23.963
1710	Z81525	Unknown cDNA EST yk361e11.5 comes from this gene; cDNA EST yk222c8.3 comes from this gene; cDNA EST	372	41.026
1711	D10627	Mus musculus zinc finger protein	576	54.412
1712	X69942	Mus musculus enhancer-trap-locus-1	1250	96.373
1713	AC007204	Homo sapiens BC273239 1	691	60.927
1714	AF016448	Caenorhabditis elegans No definition line found	564	41.791
1715	U56732	Rattus norvegicus KRAB/zinc finger suppressor protein 1	903	66.667
1716	X64228	Homo sapiens putative oncogene	273	92.000
1717	AF064553	Mus musculus NSD1 protein	1556	69.429
1718	AF028789	Homo sapiens UNC-119b	199	67.500
1719	L01986	Homo sapiens trithorax	227	97.297
1720	U09413	Homo sapiens zinc finger protein ZNF135	537	62.963
1721	Z66568	Schizosaccharomyces pombe hypothetical trp-asp repeats containing protein	461	54.237
1722	X69942	Mus musculus enhancer-trap-locus-1	698	96.296
1723	AF038007	Homo sapiens FIC1	480	84.615
1724	M86664	Equine herpesvirus 1 membrane glycoprotein	166	25.150
1725	Z26634	Homo sapiens ankyrin B (440 kDa)	312	33.898
1726	AF082556	Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase	2343	82.082
1727	AB029290	Homo sapiens actin binding protein ABP620	674	51.515
1728	Z66511	Unknown similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST CEMSA01F comes fr	201	36.364
1729	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LBEIT@EMBL-	1637	99.209

		Heidelberg.DE		
1730	X90569	Homo sapiens elastic titin	1831	99.286
1731	Z48045	Caenorhabditis elegans sre-2	320	25.664
1732	Z22968	Homo sapiens M130 antigen	944	63.043
1733	AJ132751	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III	685	70.073
1734	AB014577	Homo sapiens KIAA0677 protein	740	65.409
1735	U32305	Caenorhabditis elegans No definition line found	272	51.899
1736	AL080125	Homo sapiens hypothetical protein	422	53.543
1737	U06641	Homo sapiens UDP glucuronosyltransferase	420	80.769
1738	M31013	Homo sapiens nonmuscle myosin heavy chain (NMHC)	329	95.918
1739	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LBEIT@EMBL-Heidelberg.DE	1114	99.412
1740	U64598	Caenorhabditis elegans weakly similar to S. cervisiae PTM1 precursor (SP:P32857)	316	45.045
1741	Z21507	Homo sapiens human elongation factor-1-delta	388	76.190
1742	Z19092	Oryctolagus cuniculus trichohyalin	207	26.038
1743	Z75536	Caenorhabditis elegans similar to DnaJ domain; cDNA EST yk398h12.5 comes from this gene; cDNA EST yk250d6.5 comes from this gene	326	39.264
1744	D80003	Homo sapiens KIAA0181	2675	99.761
1745	AE001032	Archaeoglobus fulgidus purine NTPase, putative	212	22.901
1746	AL080141	Homo sapiens hypothetical protein	1943	74.347
1747	AF000195	Caenorhabditis elegans similar to oxysterol-binding proteins	272	63.768
1748	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	228	76.744
1749	Z81029	Unknown Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes	19	75.000
1750	AB029012	Homo sapiens KIAA1089 protein	198	80.952
1751	AF078856	Homo sapiens p47	393	50.400
1752	U97002	Caenorhabditis elegans similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1	389	51.200
1753	U09411	Homo sapiens zinc finger protein ZNF132	889	61.497
1754	Z47811	Unknown similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes f	345	28.205
1755	U29096	Caenorhabditis elegans coded for by C. elegans cDNA yk44f2.5; similar to P59 protein (HSP binding immunophilin) and to TPR domain	622	32.768
1756	Z68297	Unknown cDNA EST EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA	593	47.847
1757	Z27079	Unknown cDNA EST CEMSF67FB comes from this gene; cDNA EST CEMSF67R comes from this gene; cDNA EST y	497	35.039
1758	AL035601	Arabidopsis thaliana putative protein	241	27.811
1759	AJ005821	Homo sapiens X-like 1 protein	507	51.299

1760	AB026190	Homo sapiens Kelch motif containing protein	264	42.478
1761	AL021768	Arabidopsis thaliana putative protein	321	28.947
1762	U90920	Homo sapiens PTPL1-associated RhoGAP	909	47.097
1763	U76373	Mus musculus skm-BOP1	960	96.403
1764	M12130	Mus musculus RNA polymerase II	377	88.060
1765	AF144477	Homo sapiens myotilin	645	98.947
1766	AB005549	Rattus norvegicus atypical PKC specific binding protein	875	79.412
1767	AF020261	Santalum album proline rich protein	176	34.444
1768	X17617	Mus musculus zinc finger protein (AA 1-580)	658	48.148
1769	U39850	Caenorhabditis elegans coded for by C. elegans cDNA yk131g12.5	207	29.221
1770	M84911	Pseudomonas aeruginosa ORF located downstream of mmsAB operon, has sequence similarity to an acetyl-CoA synthetase; ORF1; putative	670	59.006
1771	AF051944	Gallus gallus Xin	326	42.857
1772	AB002388	Homo sapiens KIAA0390	480	34.557
1773	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LBEIT@EMBL-Heidelberg.DE	932	99.301
1774	AB023178	Homo sapiens KIAA0961 protein	919	59.906
1775	AF051945	Mus musculus Xin	526	61.194
1776	AL117666	Homo sapiens hypothetical protein	285	100.000
1777	L16547	Bos taurus chloride channel protein	441	74.725
1778	U05204	Oryctolagus cuniculus preproacrosin	188	59.459
1779	AF167320	Mus musculus zinc finger protein ZFP113	807	56.633
1780	AL080125	Homo sapiens hypothetical protein	1297	56.592
1781	U50413	Mus musculus phosphoinositide 3-kinase p85alpha	501	94.595
1782	Z98601	Schizosaccharomyces pombe hypothetical protein	334	31.500
1783	Y17267	Mus musculus ubiquitin-conjugating enzyme	1650	98.450
1784	AF056977	Penicillium chrysogenum hypothetical protein	329	36.806
1785	X64418	Drosophila melanogaster kurz protein	458	48.611
1786	X79828	Mus musculus NK10	1285	94.054
1787	AB018270	Homo sapiens KIAA0727 protein	1715	57.683
1788	Z70310	Caenorhabditis elegans R11A8.7b	1732	59.785
1789	AF036706	Caenorhabditis elegans No definition line found	495	41.000
1790	AB005549	Rattus norvegicus atypical PKC specific binding protein	2594	88.791
1791	AF015454	Xenopus laevis ER1	185	64.286
1792	X52943	Homo sapiens ATF-a protein (AA 1-483)	391	100.000
1793	U97006	Caenorhabditis elegans No definition line found	406	43.671
1794	M20031	Homo sapiens V-III-J region	383	95.312
1795	AF079765	Mus musculus enhancer of polycomb	616	96.000
1796	Z71180	Caenorhabditis elegans similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene	731	44.141
1797	AB023216	Homo sapiens KIAA0999 protein	809	95.935
1798	AL022600	Schizosaccharomyces pombe hypothetical protein	428	40.860
1799	U34932	Rattus norvegicus Fos-related antigen	300	68.421
1800	Y00062	Homo sapiens precursor polypeptide (AA -23 to 1120)	203	82.857
1801	U35376	Homo sapiens repressor transcriptional factor	2183	78.358

1802	AF053091	Drosophila melanogaster eyelid	661	40.741
1803	AF000198	Caenorhabditis elegans weak similarity to HSP90	48	60.000
1804	AL031583	Unknown /prediction=(method:"genefinder", version:"084", score:"120.68"); /prediction=(meth	634	52.885
1805	U41538	Caenorhabditis elegans No definition line found	668	47.748
1806	X90565	Saccharomyces cerevisiae MYO2	475	43.860
1807	X78926	Homo sapiens zinc finger protein	601	67.213
1808	AB007931	Homo sapiens KIAA0462 protein	1180	97.895
1809	AB014570	Homo sapiens KIAA0670 protein	223	24.229
1810	Y15197	Mus musculus microtubule-associated protein, MAP-115	339	26.036
1811	X86683	Drosophila melanogaster deep orange (dor)	358	40.909
1812	AF151014	Xenopus laevis small Rho-like GTPase Rnd1	265	86.047
1813	U17989	Homo sapiens GS2NA	243	84.091
1814	Y16790	Homo sapiens keratin type I	345	36.585
1815	AF191252	Homo sapiens guanosin-diphosphatase like protein	614	63.636
1816	AB011094	Homo sapiens KIAA0522 protein	322	35.714
1817	AB026190	Homo sapiens Kelch motif containing protein	438	39.196
1818	A63605	unidentified unnamed protein product	1057	100.000
1819	AF102129	Rattus norvegicus KPL2	1094	88.660
1820	AL021086	Unknown /prediction=(method:"genefinder", version:"084", score:"147.90"); /match=(desc:"LI	297	60.811
1821	M61185	Bos taurus glutamic acid-rich protein	217	52.174
1822	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	1335	90.868
1823	AB023215	Homo sapiens KIAA0998 protein	567	35.385
1824	AB001772	Ciona savignyi PEM-5	211	45.588
1825	D42043	Homo sapiens The ha2022 gene product is novel.	240	23.019
1826	U93872	Kaposi's sarcoma-associated herpesvirus ORF 73, contains large complex repeat CR 73	322	27.451
1827	AC005614	Homo sapiens F23269 2	635	64.463
1828	AB002374	Homo sapiens KIAA0376	600	47.964
1829	AF019236	Dictyostelium discoideum TipD	146	37.288
1830	M12140	Homo sapiens envelope protein	297	48.421
1831	D90756	Escherichia coli Hypothetical protein in pth-prsA intergenic region .	878	100.000
1832	M64658	Oryctolagus cuniculus phosphorylase kinase beta-subunit	191	96.429
1833	Z78201	Unknown Similarity to E.coli 2-oxoglutarate dehydrogenase (SW:ODO1_ECOLI); cDNA EST EMBL:D32590 com	776	58.163
1834	AF065215	Homo sapiens cytosolic phospholipase A2 beta	559	45.506
1835	AJ248284	Pyrococcus abyssi chromosome segregation protein (smc1)	177	22.467
1836	D83776	Homo sapiens The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.	219	96.552
1837	X64346	Saimiriine herpesvirus 2 ORF 48; EDLF5; sim. to EBV BRRF2	720	66.355
1838	U93872	Kaposi's sarcoma-associated herpesvirus ORF 73, contains large complex repeat CR 73	218	20.952
1839	AC007138	Arabidopsis thaliana predicted protein of	191	50.000

		unknown function		
1840	Z75540	Unknown similar to BRCA1 C Terminus (BRCT) domain (4 domains); cDNA EST EMBL:D36641 comes from this	173	30.508
1841	X15657	Drosophila melanogaster Elf-1 protein (AA 1-1063)	374	58.163
1842	J03916	Escherichia coli phosphatidylserine decarboxylase	945	98.630
1843	U90880	Fugu rubripes zinc finger protein	665	92.632
1844	D63881	Homo sapiens KIAA0160 gene product is novel.	219	97.059
1845	U35376	Homo sapiens repressor transcriptional factor	706	73.134
1846	AB028978	Homo sapiens KIAA1055 protein	603	62.411
1847	AF126736	Homo sapiens ubiquitin processing protease	448	46.897
1848	Z73906	Caenorhabditis elegans cDNA EST EMBL:M88866 comes from this gene	168	36.145
1849	AL031032	Arabidopsis thaliana extensin-like protein	285	47.059
1850	AF181856	Rattus norvegicus tRNA selenocysteine associated protein	153	95.833
1851	AF055666	Mus musculus kinesin light chain 2	203	100.000
1852	Z12841	Oryctolagus cuniculus Phospholipase	1236	79.646
1853	M27878	Homo sapiens DNA binding protein	873	73.054
1854	AL031667	Homo sapiens dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	206	93.548
1855	AB023155	Homo sapiens KIAA0938 protein	955	59.615
1856	AF167320	Mus musculus zinc finger protein ZFP113	829	76.871
1857	AB000512	Gallus gallus cadherin-10	735	78.571
1858	AC004227	Homo sapiens KIAA001LB	2741	100.000
1859	M97639	Homo sapiens transmembrane receptor	840	87.591
1860	D63476	Homo sapiens The KIAA0142 gene is related to human KIAA0006 gene.	236	85.000
1861	AF091628	Mus musculus ERG-associated protein ESET	526	33.977
1862	AB023186	Homo sapiens KIAA0969 protein	581	31.343
1863	X78933	Homo sapiens zinc finger protein	1018	64.516
1864	AL049784	Homo sapiens hypothetical protein	1152	95.977
1865	Z48809	Unknown similarity to the yeast MET30 protein (PIR accession number S43750); cDNA EST EMBL:M89261 c	377	29.880
1866	AL050367	Homo sapiens hypothetical protein	378	46.400
1867	AJ242914	Mus musculus neurotrophin receptor interacting factor (NRIF1)	353	50.833
1868	AF043695	Caenorhabditis elegans Similar to mitochondrial carrier protein	287	37.778
1869	Z70310	Caenorhabditis elegans R11A8.7b	540	34.277
1870	D83146	Mus musculus Six5	825	81.935
1871	AB029290	Homo sapiens actin binding protein ABP620	1516	100.000
1872	AJ243806	Chlamydomonas reinhardtii 1-alpha dynein heavy chain	256	73.913
1873	AF004813	Homo sapiens electrogenic Na ⁺ bicarbonate cotransporter; NBC	700	74.453
1874	AF135440	Mus musculus huntington yeast partner C	270	97.500
1875	U18991	Homo sapiens retinal pigment epithelium-specific 61 kDa protein	293	33.333
1876	X74546	Escherichia coli LysR homologue A	935	100.000
1877	M67467	Macaca fuscata 3-beta-hydroxy-5-ene steroid	858	85.430

		dehydrogenase/delta-5-delta-4 isomerase		
1878	Z21707	Homo sapiens polypeptide	202	32.576
1879	U37775	Mus musculus tuberlin	349	69.231
1880	AF022729	Rattus norvegicus HNK-1 sulfotransferase	361	41.667
1881	AF081941	Rattus norvegicus soluble adenylyl cyclase	178	38.961
1882	AF004715	Homo sapiens jerky gene product homolog	328	41.270
1883	M60172	Gallus gallus novel collagen protein	342	48.696
1884	AF056617	Homo sapiens BWSCR2 associated zinc-finger protein BAZ1	825	70.440
1885	AL021482	Caenorhabditis elegans Y39A1B.2	269	36.220
1886	D63478	Homo sapiens The KIAA0144 gene product is novel.	312	45.455
1887	AJ131021	Mus musculus ribosomal protein S6 kinase 3	720	79.365
1888	U49974	Homo sapiens mariner transposase	158	64.865
1889	AF016448	Caenorhabditis elegans No definition line found	719	47.083
1890	AB008164	Homo sapiens ST1C2	234	94.444
1891	U27196	Gallus gallus zinc finger protein	250	41.304
1892	Y08564	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	546	63.303
1893	AL021492	Caenorhabditis elegans Y45F10D.11	230	51.429
1894	AF180728	Drosophila melanogaster sulfate transporter	429	36.709
1895	U88172	Caenorhabditis elegans No definition line found	202	25.000
1896	AL117626	Homo sapiens hypothetical protein	553	62.590
1897	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	1907	98.233
1898	AB023155	Homo sapiens KIAA0938 protein	726	66.111
1899	Y13367	Homo sapiens phosphoinositide 3-kinase	442	98.413
1900	AF083391	Homo sapiens putative WHSC1 protein	191	41.791
1901	AB007934	Homo sapiens KIAA0465 protein	1347	64.286
1902	X69490	Homo sapiens titin	1208	97.980
1903	AF117888	Homo sapiens myosin-IXa	1547	100.000
1904	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	856	98.485
1905	X69490	Homo sapiens titin	926	99.281
1906	X69490	Homo sapiens titin	1687	100.000
1907	X69089	Homo sapiens 165kD protein	598	36.630
1908	AB029290	Homo sapiens actin binding protein ABP620	1524	61.039
1909	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	1635	100.000
1910	AB014601	Homo sapiens KIAA0701 protein	390	40.909
1911	AL031230	Homo sapiens dJ73M23.3 (KIAA0319)	258	41.129
1912	M32865	Homo sapiens Ku protein subunit	187	100.000
1913	AF038007	Homo sapiens FIC1	547	63.971
1914	D10712	Mus musculus nedd-1 protein	614	92.079
1915	D26069	Homo sapiens KIAA0041	156	29.921
1916	Z66496	Unknown cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA	240	28.387
1917	AF140360	Homo sapiens histone acetyltransferase	159	100.000

1918	D42046	Homo sapiens The ha3631 gene product is related to S.cerevisiae protein encoded in chromosome VIII.	299	97.917
1919	AF125386	Drosophila melanogaster L82C	226	31.532
1920	D16611	Homo sapiens coproporphyrinogen oxidase	207	75.610
1921	AB028958	Homo sapiens KIAA1035 protein	402	48.000
1922	X79131	Mus musculus IB3/5-polyptide	1535	78.105
1923	U72192	Homo sapiens lysosomal trafficking regulator LYST	160	100.000
1924	AF027955	Mus musculus G protein-coupled receptor	754	60.221
1925	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	226	34.307
1926	U10401	Caenorhabditis elegans No definition line found	391	30.741
1927	U87965	Mus musculus putative G-protein	337	50.000
1928	AB023157	Homo sapiens KIAA0940 protein	519	39.241
1929	AF016191	Rattus norvegicus potassium channel	629	97.917
1930	Z71264	Unknown predicted using Genefinder; Weak similarity to Mouse T-complex-associated-testes-expressed-	325	33.908
1931	J05194	Oryctolagus cuniculus myosin light chain kinase (EC 2.7.1.-)	1077	97.590
1932	AF124396	Danio rerio R-cadherin precursor	389	41.722
1933	U79587	Homo sapiens immunoglobulin V-region light chain	320	79.032
1934	AF035537	Homo sapiens DNA polymerase zeta	285	89.583
1935	U93181	Homo sapiens nuclear dual-specificity phosphatase	183	52.941
1936	AF129756	Homo sapiens BAT2	793	40.568
1937	D89677	Mus musculus Kryn	2393	78.005
1938	Z93372	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk345d5.5 comes from this gene; cDNA EST yk345d5.3 comes from this gene	746	48.052
1939	AF104414	Mus musculus large tumor suppressor 1	944	78.261
1940	AB002376	Homo sapiens KIAA0378	780	76.220
1941	L20303	Gallus gallus actin filament-associated protein	582	37.370
1942	AJ133521	Drosophila buzzatii protease, reverse transcriptase, ribonuclease H, integrase	228	29.787
1943	L38620	Mus musculus mSin3A gene product	809	100.000
1944	Z71264	Unknown predicted using Genefinder; Weak similarity to Mouse T-complex-associated-testes-expressed-	462	34.812
1945	X15187	Homo sapiens precursor polypeptide (AA -21 to 782)	1761	97.112
1946	D78572	Mus musculus membrane glycoprotein	184	50.000
1947	D87077	Homo sapiens KIAA0240	483	93.750
1948	AE000699	Aquifex aeolicus chromosome assembly protein homolog	143	22.414
1949	AJ131244	Homo sapiens Sec24A protein	433	95.161
1950	U09820	Homo sapiens helicase II	259	100.000
1951	AB030502	Xenopus laevis XDRP1	729	82.576
1952	M74165	Gallus gallus tensin	464	45.276
1953	AE000142	Escherichia coli putative transport protein	1049	98.246
1954	AF025467	Caenorhabditis elegans contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	181	43.548
1955	A56817	unidentified unnamed protein product	255	53.571
1956	AF060246	Mus musculus zinc finger protein 106	1295	80.543

1957	X75342	Homo sapiens Shb	335	42.636
1958	M74165	Gallus gallus tensin	1269	87.879
1959	AB002384	Homo sapiens KIAA0386	676	54.545
1960	AF017112	Mus musculus non-erythrocyte beta spectrin	170	100.000
1961	X12492	Homo sapiens CTF-1 factor (AA 1 - 499)	1087	95.906
1962	Z11527	Drosophila melanogaster CYS3HIS finger protein	742	74.219
1963	J02974	Acanthamoeba castellanii myosin IB heavy chain	183	37.000
1964	X90840	Homo sapiens axonal transporter of synaptic vesicles	1904	99.647
1965	M27266	Mus musculus p59fyn	168	25.424
1966	L40459	Mus musculus latent transforming growth factor-beta binding protein	1279	88.701
1967	Z48583	Unknown similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623	267	42.553
1968	AF181631	Drosophila melanogaster BcDNA.GH04929	245	28.481
1969	S48472	Felis catus arylsulfatase B, ARSB	727	57.838
1970	Z70683	Unknown Weak similarity to Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 c	326	47.273
1971	AF078790	Caenorhabditis elegans No definition line found	159	25.564
1972	Z22642	Homo sapiens PO-GA	214	28.488
1973	X56203	Plasmodium falciparum liver stage antigen	314	23.566
1974	X73882	Homo sapiens microtubule associated protein	298	38.776
1975	Z71178	Unknown similar to pro-collagen domains; cDNA EST EMBL:D27978 comes from this gene; cDNA EST EMBL:D	380	40.411
1976	D10627	Mus musculus zinc finger protein	747	56.287
1977	U09413	Homo sapiens zinc finger protein ZNF135	1082	52.797
1978	AF106682	Homo sapiens spindlin	770	75.159
1979	AL023781	Schizosaccharomyces pombe N-terminal acetyltransferase 1	686	40.876
1980	U53332	Caenorhabditis elegans No definition line found	190	30.769
1981	AF111169	Homo sapiens unknown	1357	77.741
1982	U41164	Rattus norvegicus Cys2/His2 zinc finger protein	1089	75.879
1983	AJ131720	Homo sapiens alpha integrin binding protein 80	2396	98.652
1984	U69262	Mus musculus matrilin-2 precursor	2150	86.765
1985	AC007193	Homo sapiens Putative homolog of hypoxia inducible factor three alpha	1849	95.172
1986	AF113131	Homo sapiens host cell factor homolog LCP	481	51.969
1987	L20450	Mus musculus DNA-binding protein	703	63.699
1988	AE000798	Methanobacterium thermoautotrophicum O-linked GlcNAc transferase	185	31.293
1989	AB011414	Homo sapiens Kruppel-type zinc finger protein	780	82.222
1990	S79915	Drosophila sp. Hls=155 kda putative DE-H type RNA-dependent ATPase-helicase/RNA localizing protein	335	27.037
1991	Z48241	Caenorhabditis elegans similar to coiled coil domains; cDNA EST yk302g12.5 comes from this gene; cDNA EST yk365d10.5 comes from this gene; cDNA EST yk461c1.5 comes from this gene	166	23.316
1992	AF012942	Dictyostelium discoideum Held	580	50.532
1993	U39851	Caenorhabditis elegans coded for by C. elegans cDNA yk121e3.3; coded for by C. elegans cDNA yk121e3.5; coded for by C. elegans cDNA cm06g4	511	43.367

1994	AF067622	Caenorhabditis elegans Contains similarity to Pfam domain: PF00628 (PHD), Score=36.7, E-value=1.7e-07, N=2	320	32.227
1995	AJ003112	Homo sapiens doublecortin	202	28.947
1996	AL109832	Schizosaccharomyces pombe putative gtpase activating protein	433	35.484
1997	D87908	Mus musculus nuclear protein np95	1561	85.057
1998	AB014538	Homo sapiens KIAA0638 protein	238	36.774
1999	M95762	Rattus norvegicus GABA transporter	791	92.913
2000	Z49967	Unknown cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA	238	41.837
2001	U78180	Homo sapiens sodium channel 2	794	56.281
2002	AB011094	Homo sapiens KIAA0522 protein	940	95.946
2003	L25055	Escherichia coli NADH dehydrogenase	440	98.413
2004	AF126867	Mus musculus calpain-like protease	1088	73.585
2005	L02897	Canis familiaris beta-spectrin	241	49.315
2006	X85214	Mus musculus ox40	1059	100.000
2007	D13159	Escherichia coli transaldolase	821	98.450
2008	AF064604	Homo sapiens KE03 protein	493	54.264
2009	X52574	Mus musculus GTP binding protein	363	50.420
2010	AF060503	Homo sapiens zinc finger protein	780	83.453
2011	D78174	Mus musculus Zic4 protein	1436	92.453
2012	L07736	Rattus norvegicus carnitine palmitoyltransferase I	1292	55.828
2013	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha	184	28.431
2014	M80537	Drosophila melanogaster fat protein	180	28.767
2015	AF100956	Mus musculus Bing1	367	41.497
2016	AF047659	Caenorhabditis elegans No definition line found	331	52.336
2017	AF005654	Homo sapiens actin-binding double-zinc-finger protein	1835	96.471
2018	S62941	Homo sapiens Ps 2=basic proline-rich protein(PRB1L precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor) {C-terminal}	263	33.929
2019	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	269	35.507
2020	AB029013	Homo sapiens KIAA1090 protein	1055	67.633
2021	AL080125	Homo sapiens hypothetical protein	777	68.387
2022	U75276	Homo sapiens TFIIB related factor hBRF	172	96.154
2023	D90714	Escherichia coli Aldose 1-epimerase (EC 5.1.3.3) (mutarotase).	1371	97.156
2024	AF015297	Human herpesvirus 6 (strain Uganda-1102) IE2hom	194	24.583
2025	D87743	Homo sapiens Similar to Human Na ⁺ /H ⁺ exchanger 2 (A57644)	193	57.692
2026	AB001735	Mus musculus ADAMTS-1	546	54.286
2027	U94585	Homo sapiens requiem homolog	1231	59.044
2028	AL031583	Unknown /prediction=(method:"genefinder", version:"084", score:"120.68"); /prediction=(meth	274	42.857
2029	AF057019	Dictyostelium discoideum interaptin	194	20.866
2030	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	773	98.214
2031	U09413	Homo sapiens zinc finger protein ZNF135	998	55.459

2032	U13766	Murine leukemia virus gag-pol polyprotein	159	46.154
2033	U28831	Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies	518	82.524
2034	AF038599	Sus scrofa env protein	196	25.000
2035	D63476	Homo sapiens The KIAA0142 gene is related to human KIAA0006 gene.	210	75.610
2036	Z18361	Ovis aries trichohyalin	243	23.514
2037	AB002303	Homo sapiens KIAA0305	252	38.043
2038	AB015629	Homo sapiens type II membrane protein similar to HIV gp120-binding C-type lectin	637	78.231
2039	Y12400	Drosophila melanogaster putative organic cation transporter	470	42.222
2040	X78925	Homo sapiens zinc finger protein	816	57.592
2041	X06704	Homo sapiens trk-2h polypeptide	301	89.130
2042	L26507	Mus musculus myocyte nuclear factor	2438	97.268
2043	U05681	Homo sapiens homologous to members of the I-kappa B family; protein binds NF-kappa B proteins	236	35.036
2044	M55169	Homo sapiens tripeptidyl peptidase II	339	96.154
2045	U53420	Rattus norvegicus sodium-calcium exchanger form 3	894	95.652
2046	U84248	Aedes aegypti blood meal-induced protein	630	57.042
2047	AF121781	Homo sapiens unknown	244	25.201
2048	AF045022	Bos taurus phosphatidic acid-preferring phospholipase A1	1521	98.696
2049	AB023178	Homo sapiens KIAA0961 protein	687	60.248
2050	Z68760	Homo sapiens Similarity to Human ankaryin (SW:ANKB_HUMAN); cDNA EST EMBL:D34286 comes from this gene; cD	365	40.141
2051	D87433	Homo sapiens KIAA0246	1430	47.103
2052	AF104260	Homo sapiens hiwi	395	39.412
2053	AF032668	Rattus norvegicus rsec15	897	98.561
2054	AC007228	Homo sapiens BC37295 1	1253	65.748
2055	Z93239	Unknown predicted using Genefinder; cDNA EST EMBL:D68680 comes from this gene; cDNA EST yk212g2.5 c	288	51.899
2056	U09874	Mus musculus SKD3	1468	92.500
2057	Y10601	Homo sapiens ankyrin-like protein	285	97.619
2058	U09411	Homo sapiens zinc finger protein ZNF132	689	60.839
2059	AB023163	Homo sapiens KIAA0946 protein	747	99.115
2060	AF109906	Mus musculus NG22	481	25.778
2061	AF075587	Homo sapiens protein associated with Myc	373	98.214
2062	AF041382	Drosophila melanogaster microtubule binding protein D-CLIP-190	316	33.588
2063	AF055636	Homo sapiens leucine-rich glioma-inactivated protein precursor	649	51.813
2064	AF115509	Homo sapiens LRR FLI-I interacting protein 2	214	100.000
2065	AB011532	Rattus norvegicus MEGF6	1378	74.762
2066	AF051945	Mus musculus Xin	990	77.835
2067	AB023209	Homo sapiens KIAA0992 protein	857	67.582
2068	AF069300	Arabidopsis thaliana contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637)	261	34.483
2069	AL050134	Homo sapiens hypothetical protein	402	38.418
2070	S60312	Mus sp. DMR-N9 {C-terminal}	512	70.370

2071	AF005050	Homo sapiens aspartyl aminopeptidase	255	82.609
2072	AB000113	Rattus norvegicus cationic amino acid transporter 3	1304	85.281
2073	AC005954	Homo sapiens ZO-3	807	100.000
2074	Z78543	Caenorhabditis elegans predicted using Genefinder	310	32.663
2075	AC003026	Homo sapiens Multiple drug resistance gene MRP1 (5' partial)	556	67.500
2076	M80537	Drosophila melanogaster fat protein	482	37.727
2077	L32162	Homo sapiens transcription factor	283	60.526
2078	U38620	Gallus gallus cSH-PTP2	766	94.118
2079	X65157	Mus musculus desmoyokin	271	39.855
2080	AB029290	Homo sapiens actin binding protein ABP620	766	63.542
2081	AB002347	Homo sapiens KIAA0349	216	75.000
2082	X62528	Rattus norvegicus ribonuclease inhibitor	578	42.347
2083	L40933	Homo sapiens phosphoglucomutase-related protein	369	100.000
2084	Z81051	Homo sapiens predicted using Genefinder; Similarity in 3' end to Human KIAA0173 protein (TR:Q14679); cDN	219	42.254
2085	U50078	Homo sapiens p532	388	88.235
2086	D86604	Mus musculus Bach2	1079	92.982
2087	AB026190	Homo sapiens Kelch motif containing protein	377	42.857
2088	AF119816	Oryctolagus cuniculus sodium bicarbonate cotransporter	694	88.235
2089	AE000350	Escherichia coli putative ATP-binding component of a transport system	1186	98.953
2090	AC005065	Homo sapiens determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735)	589	52.874
2091	AJ010973	Homo sapiens DEDD protein	186	40.244
2092	AF117210	Homo sapiens host cell factor 2	191	36.905
2093	AB013605	Mus musculus Per3	669	46.275
2094	X64346	Saimiriine herpesvirus 2 ORF 73; ECLF1	179	26.829
2095	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	173	38.202
2096	U55042	Bos taurus myosin X	1676	89.726
2097	AJ010949	Mus musculus calcium channel alpha-2-delta-C subunit	306	92.453
2098	AB020715	Homo sapiens KIAA0908 protein	400	47.863
2099	M28231	Drosophila melanogaster neuroglial precursor	287	32.370
2100	Y17048	Rattus norvegicus caldendrin	269	48.611
2101	D32210	Mus musculus cell surface protein	4497	93.557
2102	X86368	Mus musculus transcription factor	835	72.222
2103	AF023450	Homo sapiens Down syndrome cell adhesion molecule	720	70.064
2104	AL031118	Homo sapiens dJ153G14.3 (novel C2H2 type Zinc Finger protein)	159	22.656
2105	AF082556	Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase	313	32.800
2106	U32517	Saccharomyces cerevisiae Ydr324cp	296	36.691
2107	AC005005	Homo sapiens similar to phosphatidylinositol (4,5)bisphosphate 5-phosphatase; match to PID:g1399105	1949	98.592
2108	J04526	Rattus norvegicus hexokinase	983	74.611
2109	AL032626	Unknown cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this	472	39.130

		gene; cDN		
2110	U20105	Rattus norvegicus synaptotagmin VI	1371	92.444
2111	U55816	Rattus norvegicus furosemide-sensitive K-Cl cotransporter	4723	98.462
2112	AF038554	Homo sapiens density regulated protein drp1	233	97.143
2113	X56203	Plasmodium falciparum liver stage antigen	304	26.737
2114	AF071172	Homo sapiens HERC2	385	90.476
2115	AB018280	Homo sapiens KIAA0737 protein	173	96.429
2116	L21998	Homo sapiens mucin	408	22.769
2117	AB000275	Homo sapiens DAP-2	369	83.333
2118	AF151110	Mus musculus COPI protein	203	96.552
2119	AB002379	Homo sapiens KIAA0381	329	50.000
2120	J05499	Rattus norvegicus L-glutamine amidohydrolase	393	100.000
2121	U49974	Homo sapiens mariner transposase	252	78.000
2122	J03796	Homo sapiens erythroid protein 4.1 isoform B	233	29.412
2123	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	655	55.224
2124	D90828	Escherichia coli Lysostaphin precursor (EC 3.5.1.-).	946	100.000
2125	D90825	Escherichia coli ORF ID:o334#5; similar to	84	41.176
2126	AL096883	Homo sapiens hypothetical protein	327	27.376
2127	AB015484	Dugesia japonica myosin heavy chain	175	24.891
2128	U23516	Caenorhabditis elegans No definition line found	407	33.476
2129	AB023148	Homo sapiens KIAA0931 protein	523	97.531
2130	AF047347	Homo sapiens adaptor protein X11alpha	265	90.698
2131	D87436	Homo sapiens Similar to Human KIAA0188 protein	234	100.000
2132	AC003040	Arabidopsis thaliana putative nicotinate phosphoribosyltransferase	1483	44.241
2133	U73199	Mus musculus Rho-guanine nucleotide exchange factor	1694	72.654
2134	X95190	Homo sapiens branched chain acyl-CoA oxidase	273	97.561
2135	AB023212	Homo sapiens KIAA0995 protein	259	89.362
2136	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	249	39.706
2137	AB028997	Homo sapiens KIAA1074 protein	809	49.123
2138	U82761	Homo sapiens S-adenosyl homocysteine hydrolase homolog	189	100.000
2139	A63607	unidentified unnamed protein product	1113	100.000
2140	D87445	Homo sapiens KIAA0256	198	100.000
2141	AL009171	Drosophila melanogaster 62D9.a	2515	66.415
2142	D42063	Homo sapiens RanBP2 (Ran-binding protein 2)	1014	96.875
2143	L08505	Rattus norvegicus dynein heavy chain	2612	98.272
2144	AF056116	Fugu rubripes All-1 related protein	1045	69.444
2145	AF181639	Drosophila melanogaster BcDNA.GH09358	300	35.333
2146	AL031324	Schizosaccharomyces pombe membrane atpase	630	50.256
2147	Z97211	Schizosaccharomyces pombe kinesin-like protein	321	51.515
2148	AB002379	Homo sapiens KIAA0381	302	48.276
2149	AB002374	Homo sapiens KIAA0376	1155	100.000
2150	AF007116	Mus musculus cadherin 7 precursor	1048	93.373
2151	Z98866	Unknown predicted using Genefinder; cDNA EST yk261h2.3 comes from this gene; cDNA EST yk261h2.5 com	174	29.508
2152	AF043643	Xenopus laevis NF-protocadherin	665	43.396
2153	U81036	Rattus norvegicus ankyrin binding cell adhesion molecule neurofascin	722	84.848

2154	X62379	Mus musculus formin, isoform IV	744	73.203
2155	U29156	Mus musculus involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	1290	86.047
2156	X12517	Homo sapiens C protein (AA 1-159)	247	93.750
2157	D10171	Mus musculus glutamate receptor channel subunit delta-1	1458	97.391
2158	AB028997	Homo sapiens KIAA1074 protein	324	57.303
2159	Y14946	Homo sapiens SPIN protein	870	78.286
2160	AF084396	synthetic construct calmodulin mutant SYNCAM30	153	26.667
2161	AJ243460	Leishmania major proteophosphoglycan	249	30.488
2162	AF091457	Rattus norvegicus zinc finger protein RIN ZF	471	27.716
2163	AF151863	Homo sapiens CGI-105 protein	238	91.667
2164	X70326	Homo sapiens MacMARCKS	68	33.333
2165	U13766	Murine leukemia virus gag-pol polyprotein	159	46.154
2166	D32064	Homo sapiens 2-oxoglutarate dehydrogenase	2420	81.840
2167	X98055	Mus musculus glutathione S-transferase theta	302	65.753
2168	Y16610	Homo sapiens paraplegin	368	98.305
2169	AC006530	Homo sapiens unknown	214	86.486
2170	Y15895	Drosophila melanogaster ubiquitin activating enzyme	215	47.143
2171	U02476	Sus scrofa NADPH oxidase heavy chain subunit	182	39.130
2172	AC005053	Homo sapiens match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112)	370	46.078
2173	U49114	Homo sapiens prohormone convertase 5 precursor	208	93.750
2174	AF001434	Homo sapiens Hpast	1306	80.000
2175	Y17867	Homo sapiens tenascin-X	2768	99.263
2176	Z77663	Caenorhabditis elegans cDNA EST yk221b11.5 comes from this gene; cDNA EST yk221b11.3 comes from this gene; cDNA EST yk614h5.3 comes from this gene	306	26.873
2177	AF055985	Onchocerca volvulus pyrrolidone-rich antigen	116	38.776
2178	AF070065	Rattus norvegicus Citron-K kinase	388	94.828
2179	A56817	unidentified unnamed protein product	389	44.304
2180	M37190	Homo sapiens ras inhibitor	319	46.610
2181	D90790	Escherichia coli ORF ID:o279#8; similar to	970	100.000
2182	AL050156	Homo sapiens hypothetical protein	189	100.000
2183	M81787	Gallus gallus , gene product	245	32.090
2184	X51829	Mus musculus MyD116 protein (AA 1-657)	168	40.000
2185	AF075461	Mus musculus ADP-ribosylation factor-directed GTPase activating protein isoform a	1131	94.220
2186	L07599	Homo sapiens ribosomal protein S6 kinase 3	182	64.583
2187	U55042	Bos taurus myosin X	1149	97.159
2188	S57132	Homo sapiens type XVI collagen alpha 1 chain, alpha 1 (XVI)	517	45.355
2189	L26335	Cavia porcellus zinc finger protein	617	50.602
2190	D42041	Homo sapiens The ha1225 gene product is related to human alpha-glucosidase.	226	100.000
2191	AC004240	Homo sapiens match to Z43555 (NID:g572788)	994	99.338
2192	AB020665	Homo sapiens KIAA0858 protein	1454	100.000
2193	AB007407	Mus musculus myeloid zinc finger protein-2	185	68.182
2194	AB018333	Homo sapiens KIAA0790 protein	857	45.954
2195	A68194	unidentified unnamed protein product	793	92.424
2196	U14003	Escherichia coli apparent frameshift in GenBank	940	100.000

		Accession Number X55662		
2197	U92949	Mus musculus kinesin motor protein	2353	83.641
2198	D80004	Homo sapiens KIAA0182	246	90.476
2199	AF058693	Mus musculus M-RdgB2 retinal degeneration protein B subtype 2	212	76.190
2200	AF143946	Homo sapiens transcriptional activator SRCAP	929	97.857
2201	AB014557	Homo sapiens KIAA0657 protein	499	30.400
2202	AF058693	Mus musculus M-RdgB2 retinal degeneration protein B subtype 2	1255	81.858
2203	AF050183	Rattus norvegicus GTPase activating protein SynGAP-c	979	94.969
2204	D21239	Homo sapiens C3G protein	174	89.655
2205	AF125964	Caenorhabditis elegans contains similarity to collagens	249	33.333
2206	U20281	Gallus gallus cell division cycle control protein 37	356	46.491
2207	X05173	Escherichia coli NR(II) (glnL gene product) (AA 1-349)	792	100.000
2208	D70831	Homo sapiens Zinc-finger protein	727	63.576
2209	X78932	Homo sapiens zinc finger protein	794	80.000
2210	U87305	Rattus norvegicus transmembrane receptor UNC5H1	796	90.000
2211	M74094	Schizosaccharomyces pombe mitotic control protein	207	27.128
2212	AL022018	Unknown /prediction=(method:"genscan", version:"1.0", score:"294.38"); /match=(desc:"THIAZ	413	55.140
2213	AF081825	Rattus norvegicus sodium-dependent high-affinity dicarboxylate transporter	980	91.358
2214	X74904	Gallus gallus alpha-2-macroglobulin receptor	1086	57.795
2215	AF016903	Homo sapiens agrin precursor	1538	95.902
2216	AF038564	Homo sapiens atrophin-1 interacting protein 4	219	39.286
2217	Z75712	Unknown Similarity with yeast gene L3502.1 (TREMBL ID G609424); cDNA EST EMBL:D33317 comes from thi	45	25.000
2218	Z75537	Caenorhabditis elegans Similarity to Aspergillus acid phosphatase (TR:G755244)	396	47.934
2219	U74586	Rattus norvegicus double-stranded RNA specific adenosine deaminase	688	89.286
2220	M19501	Escherichia coli formylglycineamide ribonucleotide synthetase (EC 6.3.5.3)	814	96.032
2221	M96625	Gallus gallus cardiac muscle tensin	1139	53.165
2222	D25215	Homo sapiens KIAA0032	492	50.694
2223	AF006465	Mus musculus B cell antigen receptor Ig beta associated protein 1	941	80.838
2224	AF125455	Caenorhabditis elegans No definition line found	349	37.368
2225	AL035634	Homo sapiens dJ403L10.1 (SNX9 (Sorting Nexin 9))	555	49.718
2226	Z81125	Unknown cDNA EST yk422g1.5 comes from this gene; cDNA EST yk192c4.5 comes from this gene; cDNA EST	304	26.688
2227	AF176688	Rattus norvegicus sodium/calcium/potassium exchanger NCKX1	216	32.632
2228	X52022	Homo sapiens collagen type VI, alpha 3 chain	2313	99.180
2229	AB004906	Ipomoea purpurea transposase	227	21.290
2230	AL023799	Homo sapiens dJ322P7.1 (zinc finger)	561	64.138

2231	D38255	Homo sapiens CAB1	226	24.176
2232	AL009171	Drosophila melanogaster 62D9.o	1052	59.109
2233	AF060500	Homo sapiens liver specific transporter	803	53.219
2234	Y14946	Homo sapiens SPIN protein	224	100.000
2235	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase precursor	375	33.945
2236	Z68753	Unknown predicted using Genefinder; Similarity to Glucose-repressible alcohol dehydrogenase transc	293	43.269
2237	AJ004832	Homo sapiens neuropathy target esterase	1350	72.830
2238	Z80220	Unknown similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST	182	25.882
2239	AB000216	Rattus norvegicus CCA3	1343	61.747
2240	Y17832	Human endogenous retrovirus K env protein	616	63.636
2241	AB009024	Homo sapiens capping enzyme 1B	240	97.297
2242	D50455	Rattus norvegicus phospholipase C delta4	195	84.375
2243	AB002377	Homo sapiens KIAA0379	241	29.949
2244	AL033534	Schizosaccharomyces pombe serine-rich protein	214	28.934
2245	U09367	Homo sapiens zinc finger protein ZNF136	570	60.800
2246	AF019380	Arabidopsis thaliana putative phosphatidylinositol-4-phosphate 5-kinase	172	35.714
2247	U07817	Dictyostelium discoideum glutamine-asparagine rich protein	164	25.532
2248	AF078786	Caenorhabditis elegans No definition line found	210	32.836
2249	X94335	Saccharomyces cerevisiae YOR3348c	198	26.500
2250	AF100960	Rattus norvegicus protocadherin	282	39.161
2251	AF140674	Homo sapiens zinc metalloprotease ADAMTS6	372	44.030
2252	AF094508	Homo sapiens dentin phosphoryn	166	19.870
2253	AJ010045	Mus musculus guanine nucleotide-exchange factor	1262	69.811
2254	D86971	Homo sapiens no similarities to reported gene products	192	27.717
2255	AF134918	Mus musculus semaphorin subclass 4 member G	952	92.517
2256	AF179369	Mus musculus insulin-like growth factor binding protein 5 protease	517	52.071
2257	D37793	Mus musculus synaptotagminII/IP4BP	348	63.636
2258	AF167320	Mus musculus zinc finger protein ZFP113	626	63.281
2259	AL049688	Homo sapiens hypothetical protein	493	39.512
2260	AB023151	Homo sapiens KIAA0934 protein	2089	73.500
2261	X14805	Mus musculus DNA methyltransferase 1	201	55.814
2262	AL035403	Homo sapiens bK134P22.1 (novel protein similar to mouse Immunoglobulin superfamily protein BL2)	552	50.968
2263	U35376	Homo sapiens repressor transcriptional factor	890	65.922
2264	AB002298	Homo sapiens KIAA0300	1347	99.519
2265	AF056302	Drosophila melanogaster eIF-2alpha kinase	338	48.214
2266	U28373	Saccharomyces cerevisiae Ydr365cp	638	37.500
2267	AC003682	Homo sapiens ZNF134	649	49.162
2268	S66427	Homo sapiens retinoblastoma binding protein 1, RBP1	476	47.399
2269	AL121800	Drosophila melanogaster BACN5I9.i	237	28.916
2270	U10281	Sus scrofa gastric mucin	205	24.497
2271	AF111168	Homo sapiens unknown	882	52.000
2272	AL021997	Homo sapiens dJ874C20.1 (Zinc Finger Protein ZFP47 LIKE)	427	63.636

2273	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	929	73.301
2274	Z68302	Caenorhabditis elegans ZK792.8	280	36.000
2275	AL049667	Homo sapiens hypothetical protein	760	98.305
2276	AF007157	Homo sapiens unknown	139	78.125
2277	X12593	Mus musculus mkr4	1169	71.493
2278	Z46970	Leishmania mexicana secreted acid phosphatase 2 (SAP2)	141	30.667
2279	X82153	Homo sapiens Cathepsin O	233	64.286
2280	U64675	Homo sapiens sperm membrane protein BS-63	437	95.714
2281	U80227	Mus musculus ELL	181	34.615
2282	AC004943	Homo sapiens alpha-fetoprotein enhancer-binding protein; 99% identical to A41948 (PID:g283975)	599	68.992
2283	U82535	Homo sapiens fatty acid amide hydrolase	224	69.388
2284	X97674	Homo sapiens transcriptional intermediary factor 2	336	100.000
2285	AC004991	Homo sapiens ATM-like; similar to AL022373 (PID:g3036812)	452	98.529
2286	L19102	Rattus norvegicus sodium dependent sulfate transporter	719	53.171
2287	AB007901	Homo sapiens HH0601 cDNA clone for KIAA0441 has an 82-bp deletion at positions between 1455 and 1538 of the sequence of KIAA0441.	220	100.000
2288	AB023624	Rattus norvegicus SCOP	1147	88.325
2289	Z72499	Homo sapiens herpesvirus associated ubiquitin-specific protease (HAUSP)	474	100.000
2290	U80953	Caenorhabditis elegans weakly similar in serine repeat region to rat thyroxine-binding globulin (PIR:A39567) and to D. melanogaster ecdysone-inducible protein E75-C (SP:E75C DROME, P13055)	547	32.961
2291	M63510	Rattus norvegicus uromodulin	445	50.000
2292	AF081158	Rattus norvegicus CL3BB	308	72.308
2293	AB020684	Homo sapiens KIAA0877 protein	224	67.308
2294	U10556	Saccharomyces cerevisiae Yhr074wp	343	76.562
2295	U75321	Mus musculus chromaffin granule ATPase II homolog	601	67.391
2296	M58583	Homo sapiens precerebellin	212	54.237
2297	AF083339	Mus musculus double-stranded RNA-binding zinc finger protein JAZ	358	47.934
2298	AB011370	Mus musculus Ankhzn	816	98.496
2299	U23514	Caenorhabditis elegans similar to S. cerevisiae SSD1 protein (SP:SSD1_YEAST, P24276) and to E. coli VACB and Ribonuclease II genes	315	39.231
2300	AB029034	Homo sapiens KIAA1111 protein	230	34.021
2301	AB014600	Homo sapiens KIAA0700 protein	2128	99.689
2302	U81035	Rattus norvegicus ankyrin binding cell adhesion molecule neurofascin	942	94.000
2303	U58203	Mus musculus Lsc	563	42.424
2304	AF047714	Mus musculus melastatin	681	60.784
2305	Z79598	Unknown cDNA EST EMBL:D34748 comes from this gene; cDNA EST yk218e6.5 comes from this gene; cDNA ES	217	23.894
2306	AB023658	Rattus norvegicus Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha	754	87.402

2307	AL031583	Unknown /prediction=(method:"genefinder", version:"084", score:"120.68"); /prediction=(meth	384	48.872
2308	AB014566	Homo sapiens KIAA0666 protein	245	28.492
2309	AF071787	Homo sapiens melastatin 1	322	33.523
2310	Z35597	Unknown Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:	303	46.875
2311	AF063936	Homo sapiens putative neuronal cell adhesion molecule	235	94.444
2312	S46622	Homo sapiens calcineurin A catalytic subunit, calmodulin-dependent protein phosphatase catalytic subunit, CaM-PrP catalytic subunit	167	100.000
2313	AB007298	Homo sapiens hGLI2	754	69.799
2314	D37918	Escherichia coli Reverse transcriptase like protein	1144	100.000
2315	AC005600	Homo sapiens PKD1	1113	100.000
2316	U41543	Unknown Similar to Rat trg gene product; coded for by C. elegans cDNA yk31e7.5; coded for by C. ele	250	28.994
2317	AC005600	Homo sapiens tuberin	641	94.340
2318	X97675	Homo sapiens plakophilin 2b	226	69.231
2319	U93872	Kaposi's sarcoma-associated herpesvirus ORF 73, contains large complex repeat CR 73	290	28.629
2320	Z12840	Oryctolagus cuniculus protein of unknown function	792	78.231
2321	X97675	Homo sapiens plakophilin 2b	166	92.308
2322	D64000	Synechocystis sp. hypothetical protein	231	33.333
2323	AF023459	Haliotis rufescens lustrin A	235	27.232
2324	AP000058	Aeropyrum pernix 246aa long hypothetical protein	257	34.247
2325	AF145634	Drosophila melanogaster BcDNA.GH06193	356	33.047
2326	U10281	Sus scrofa gastric mucin	205	21.849
2327	AF176069	Homo sapiens ubiquilin	409	52.941
2328	U09367	Homo sapiens zinc finger protein ZNF136	1331	59.819
2329	AF006465	Mus musculus B cell antigen receptor Ig beta associated protein 1	275	29.474
2330	AF060152	Homo sapiens METH1 protein	431	43.796
2331	M81591	Mus musculus CD10 neutral endopeptidase 24.11	576	58.462
2332	L08505	Rattus norvegicus dynein heavy chain	1620	99.177
2333	AC005169	Arabidopsis thaliana hypothetical protein	79	38.235
2334	AJ000517	Homo sapiens spinocerebellar ataxia 7	402	51.493
2335	AF017433	Homo sapiens putative transcription factor CR53	392	65.306
2336	U41663	Rattus norvegicus neuroligin 3	1003	95.597
2337	AB020678	Homo sapiens KIAA0871 protein	1157	59.871
2338	X70514	Mus musculus nodal	640	64.238
2339	AC002328	Arabidopsis thaliana F2202.20	226	43.678
2340	M77697	Caenorhabditis elegans acid-rich protein	237	31.847
2341	AF143946	Homo sapiens transcriptional activator SRCAP	293	39.394
2342	AF098504	Caenorhabditis elegans contains similarity to protein kinases (Pfam: pkinase.hmm, score: 149.36)	338	40.449
2343	U88181	Caenorhabditis elegans similar to glycerol kinase	632	44.340
2344	AB014532	Homo sapiens KIAA0632 protein	1956	100.000

2345	M24282	Gallus gallus alpha-3 collagen type VI	220	24.667
2346	X99384	Mus musculus paladin	1033	80.208
2347	AF144629	Mus musculus SLIT3	405	31.967
2348	AF033339	Caenorhabditis briggsae UNC-45	195	23.897
2349	AB018293	Homo sapiens KIAA0750 protein	1097	84.896
2350	X54135	Homo sapiens protein-tyrosine phosphatase	729	79.433
2351	AB012033	Mus musculus keratin 6 alpha	641	71.014
2352	M98776	Homo sapiens keratin 1	602	62.805
2353	AB000216	Rattus norvegicus CCA3	201	46.512
2354	Z46241	Unknown carboxyl terminus of the predicted protein shows similarity to chimaerin; cDNA EST EMBL:Z14	602	45.685
2355	AB018348	Homo sapiens KIAA0805 protein	1146	76.168
2356	U81453	Mus musculus myosin VIIa	722	55.959
2357	J04425	Gallus gallus type VI collagen, alpha-2 subunit	433	42.857
2358	U39573	Homo sapiens salivary peroxidase	203	93.333
2359	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	240	65.574
2360	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	1192	87.156
2361	U48363	Mus musculus alpha-NAC, muscle-specific form gp220	472	37.860
2362	M87306	Tetrahymena thermophila micronuclear linker histone polyprotein	192	24.567
2363	AF031834	Caenorhabditis elegans GLY4; ppGaNtase	423	41.714
2364	X69490	Homo sapiens titin	1246	98.980
2365	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	1478	98.298
2366	X90569	Homo sapiens elastic titin	207	94.286
2367	AF051944	Gallus gallus Xin	301	38.462
2368	AB005047	Homo sapiens SH3 binding protein	475	42.162
2369	AC004974	Homo sapiens spa-1-like; similar to AF026504 (PID:g2555183)	888	66.176
2370	U37591	Homo sapiens similar to the following EST sequences: GenBank Accession Numbers T96213 and T96131; 3'UTR nmd sequence found in U30998	518	42.424
2371	X56203	Plasmodium falciparum liver stage antigen	210	27.273
2372	AL022326	Homo sapiens dJ333H23.1.1 (60S Ribosomal Protein L3)	372	96.552
2373	U25739	Mus musculus YSPL-1 form 2	228	49.351
2374	Z93244	Homo sapiens bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	125	77.273
2375	U09413	Homo sapiens zinc finger protein ZNF135	904	54.338
2376	AF162681	Drosophila melanogaster maroon-like protein	327	37.419
2377	X78933	Homo sapiens zinc finger protein	747	77.344
2378	AF168795	Rattus norvegicus schlafen-4	601	38.060
2379	AE000799	Methanobacterium thermoautotrophicum O-linked GlcNAc transferase	235	29.560
2380	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	196	23.973
2381	AC004877	Homo sapiens sco-spondin-mucin-like; similar to	1073	92.453

		P98167 (PID:g1711548); details of intron/exon structure uncertain		
2382	AF060246	Mus musculus zinc finger protein 106	2195	72.837
2383	AF132478	Mus musculus Esel protein	211	27.155
2384	AF115480	Mus musculus cAMP-dependent Rap1 guanine-nucleotide exchange factor	168	34.177
2385	AF135440	Mus musculus huntington yeast partner C	3683	95.608
2386	AL049481	Arabidopsis thaliana putative protein	334	48.148
2387	AC002451	Homo sapiens pyruvate dehydrogenase kinase isoform 4	251	100.000
2388	AB007897	Homo sapiens KIAA0437	587	42.308
2389	AF016679	Caenorhabditis elegans No definition line found	199	26.776
2390	AB023139	Homo sapiens KIAA0922 protein	423	98.276
2391	Z71264	Caenorhabditis elegans similar to C2 domain	176	27.815
2392	AF053368	Mus musculus lysyl oxidase-related protein 2	1945	95.053
2393	U16726	Chlamydomonas reinhardtii histone H1	164	32.258
2394	AF098066	Homo sapiens squamous cell carcinoma antigen recognized by T cell	530	39.437
2395	AB017615	Mus musculus Eos protein	1081	93.642
2396	AB000199	Rattus norvegicus CCA2 protein	312	82.456
2397	Z73428	Caenorhabditis elegans similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene	553	67.797
2398	AF032668	Rattus norvegicus rsec15	931	94.667
2399	AF094520	Mus musculus NET1 homolog	305	40.909
2400	D87450	Homo sapiens Similar to D.melanogaster parallel sister chromatids protein	1273	83.333
2401	L04159	Plasmodium falciparum 3' end., gene product	163	26.738
2402	AJ388557	Canis familiaris zinc finger protein	968	45.918
2403	Z33905	Homo sapiens 43kD Acetylcholine receptor-associated protein (Rapsyn)	972	98.592
2404	AB018317	Homo sapiens KIAA0774 protein	267	95.556
2405	AF012273	Mus musculus rho-type GTPase-activating protein rhoGAPX-1	893	43.731
2406	AF109906	Mus musculus G9A	1276	58.140
2407	U40410	Caenorhabditis elegans C54G7.4 gene product	226	28.571
2408	X51760	Homo sapiens zinc finger protein (583 AA)	391	54.310
2409	M61199	Homo sapiens cleavage signal 1 protein	260	86.364
2410	AC002336	Arabidopsis thaliana hypothetical protein	211	32.759
2411	AF186273	Homo sapiens leucine-rich repeats containing F-box protein FBL3	249	30.994
2412	AC005614	Homo sapiens F23269 2	701	58.974
2413	U03976	Tripneustes gratilla dynein heavy chain isotype 5C	494	73.958
2414	AF061758	Gallus gallus poly(A) polymerase II	1460	83.794
2415	AF184226	Drosophila melanogaster BcDNA.GH09045	793	38.692
2416	AB012223	Canis familiaris ORF2	288	71.186
2417	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	256	66.102
2418	L09742	Carassius auratus gene, complete cds., gene product	146	40.449
2419	AF038007	Homo sapiens FIC1	701	51.643
2420	Z73424	Caenorhabditis elegans C44B9.1	352	26.254
2421	AF117675	Homo sapiens nebulin	183	71.053
2422	X64697	Homo sapiens titin	1593	98.016

2423	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LAbEIT@EMBL-Heidelberg.DE	953	100.000
2424	X90569	Homo sapiens elastic titin	1126	98.830
2425	AF060246	Mus musculus zinc finger protein 106	574	89.362
2426	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LAbEIT@EMBL-Heidelberg.DE	1391	100.000
2427	X90569	Homo sapiens elastic titin	3791	99.307
2428	U41534	Caenorhabditis elegans Contains similarity to Pfam domain: PF00271 (helicase_C), Score=49.0, E-value=3.3e-11, N=1	332	37.500
2429	AB014542	Homo sapiens KIAA0642 protein	455	54.610
2430	AB029335	Halocynthia roretzi HrPET-3	243	36.641
2431	AB029018	Homo sapiens KIAA1095 protein	584	49.038
2432	AL031733	Homo sapiens dJ455J7.1 (cellular repressor of E1A-stimulated genes CREG)	443	39.416
2433	X14355	Homo sapiens FcRI b form (AA 1-344)	154	39.241
2434	AB011370	Mus musculus Ankhzn	193	96.774
2435	Z70269	Unknown predicted using Genefinder; Similarity to Yeast hypothetical protein YHG1 (SW:YHG1 YEAST);	501	58.400
2436	X97650	Mus musculus myosin-I	878	90.411
2437	U11843	Homo sapiens fructose transporter	356	65.333
2438	AC003007	Homo sapiens KIAA0220	333	100.000
2439	U91318	Homo sapiens pM5 (3' partial)	246	70.968
2440	AC003681	Homo sapiens match to AB002369 (NID:g2224682)	295	60.606
2441	D87845	Homo sapiens platelet-activating factor acetylhydrolase 2	202	83.333
2442	Z22181	Caenorhabditis elegans cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene	199	34.641
2443	Z83225	Caenorhabditis elegans similar to ankyrin domain; cDNA EST yk219g4.5 comes from this gene; cDNA EST yk590g11.3 comes from this gene; cDNA EST yk598d5.3 comes from this gene	266	35.075
2444	AF045640	Caenorhabditis elegans No definition line found	385	47.518
2445	AB018336	Homo sapiens KIAA0793 protein	230	34.711
2446	AB011116	Homo sapiens KIAA0544 protein	628	70.714
2447	AC006550	Unknown Identical to gb U12536 3-methylcrotonyl-CoA carboxylase precursor protein from Arabidopsi	677	55.191
2448	X64697	Homo sapiens titin	903	99.259
2449	Y18204	Equus caballus high affinity immunoglobulin E receptor alpha subunit	198	50.943
2450	AB028954	Homo sapiens KIAA1031 protein	177	45.283
2451	AF040944	Mus musculus P140	413	41.317
2452	AL021392	Homo sapiens dJ439F8.2 (novel KIAA0279 LIKE cadherin domain protein (similar to mouse Celsr1, rat MEGF2))	191	32.090
2453	AL022322	Homo sapiens bK228A9.1 (85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2)	175	100.000
2454	Z67990	Caenorhabditis elegans similar to cuticle	167	37.705

		collagen		
2455	U41543	Unknown Similar to Rat trg gene product; coded for by C. elegans cDNA yk31e7.5; coded for by C. ele	199	28.571
2456	D87908	Mus musculus nuclear protein np95	244	62.963
2457	Z73428	Caenorhabditis elegans similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene	604	69.697
2458	Z50142	Schizosaccharomyces pombe unknown	213	34.821
2459	AF169411	Rattus norvegicus PAPIN	423	92.537
2460	M96629	Canis familiaris homologue to sec61	570	95.604
2461	AF098070	Drosophila melanogaster Lis1 homolog	153	25.166
2462	Z99708	Arabidopsis thaliana actin interacting protein	628	71.875
2463	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	208	48.276
2464	S45710	Homo sapiens Fc gamma receptor	254	36.496
2465	X90849	Gallus gallus polybromo 1 protein	2241	88.525
2466	AB023230	Homo sapiens KIAA1013 protein	1012	58.582
2467	AF067136	Homo sapiens protein phosphatase-1 regulatory subunit 7 alpha2	203	37.374
2468	U24070	Rattus norvegicus Munc13-1	1637	83.013
2469	Y00826	Rattus norvegicus gp210 (AA 1-1886)	1915	86.604
2470	AB002365	Homo sapiens KIAA0367	321	53.846
2471	U41552	Caenorhabditis elegans No definition line found	460	33.955
2472	AF083424	Ateline herpesvirus 3 orf 48	275	29.082
2473	Y16008	Mus musculus neuronal-STOP protein	1523	60.227
2474	M30270	Torpedo californica electromotor neuron-associated protein	507	54.225
2475	AF173829	Mus musculus neuropathy target esterase homolog	1046	68.778
2476	AF057019	Dictyostelium discoideum interaptin	183	21.918
2477	AF145690	Drosophila melanogaster BcDNA.LD28657	787	60.317
2478	L39891	Homo sapiens polycystic kidney disease-associated protein	772	96.748
2479	X58681	Saccharomyces cerevisiae the product of PRP22 gene acts late in the splicing of yeast pre-messenger RNA, mediating the release of the spliced mRNA from the spliceosome	171	59.524
2480	D86966	Homo sapiens similar to human ZFY protein.	437	48.630
2481	AB029035	Homo sapiens KIAA1112 protein	505	63.248
2482	U43194	Mus musculus rhophilin	215	36.290
2483	AF087697	Rattus norvegicus dlq 3	175	89.655
2484	AB014533	Homo sapiens KIAA0633 protein	2237	99.707
2485	X86683	Drosophila melanogaster deep orange (dor)	355	29.218
2486	AB025411	Mus musculus Ten-m2	1087	98.137
2487	AF019380	Arabidopsis thaliana putative phosphatidylinositol-4-phosphate 5-kinase	295	38.261
2488	X15430	Dictyostelium discoideum gelation factor (AA 1 - 857)	243	37.097
2489	AB014600	Homo sapiens KIAA0700 protein	298	88.462
2490	X80535	Rattus rattus thyrotropin-releasing hormone degrading enzyme	921	94.521
2491	AB002086	Rattus norvegicus p47	308	41.129
2492	X53959	Drosophila melanogaster slit protein	228	35.211
2493	AF055357	Arabidopsis thaliana respiratory burst oxidase	238	54.386

		protein D		
2494	U22376	Homo sapiens alternatively spliced product using exon 13A	464	80.233
2495	AB023230	Homo sapiens KIAA1013 protein	1385	76.357
2496	AJ007395	Homo sapiens QA79 membrane protein	440	49.689
2497	AL021497	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk673c5.3 comes from this gene	254	36.585
2498	Z54308	Schizosaccharomyces pombe putative major facilitator superfamily protein	642	42.435
2499	AJ242914	Mus musculus neurotrophin receptor interacting factor (NRIF1)	245	54.688
2500	AB023227	Homo sapiens KIAA1010 protein	766	29.806
2501	AF151847	Homo sapiens CGI-89 protein	285	52.500
2502	Z49212	Saccharomyces cerevisiae unknown	277	45.217
2503	Z23024	Homo sapiens rhoGAP protein	159	37.500
2504	U67322	Homo sapiens HBV associated factor	216	74.419
2505	U44731	Mus musculus purine nucleotide binding protein	676	70.629
2506	U62967	Homo sapiens Na ⁺ /nucleoside cotransporter	263	95.000
2507	AL035701	Homo sapiens dJ8B1.3 (similar to PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1)	420	38.068
2508	Z81557	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk265g6.3 comes from this gene; cDNA EST yk265g6.5 comes from this gene; cDNA EST yk656g4.3 comes from this gene	292	52.439
2509	X96618	Mus musculus novel stromal cell protein	214	76.190
2510	AF117892	Homo sapiens aspartic-like protease	482	89.024
2511	AJ007395	Homo sapiens QA79 membrane protein	194	73.810
2512	U15131	Homo sapiens p126	427	37.959
2513	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	209	32.164
2514	AL031324	Schizosaccharomyces pombe beta transducin	478	38.021
2515	U81788	Drosophila melanogaster kinesin-73	1309	67.961
2516	Y13245	Moraxella sp. NAD-dependent formate dehydrogenase	748	72.078
2517	L33861	Heliocidaris erythrogramma fibropellin Ia	540	41.209
2518	AJ243535	Synechococcus elongatus possible thiophene and furan oxidation protein	242	37.778
2519	AC002394	Homo sapiens Gene product with similarity to dynein beta subunit	749	59.538
2520	AL117610	Homo sapiens hypothetical protein	359	58.904
2521	Z78417	Caenorhabditis elegans cDNA EST EMBL:D27838 comes from this gene; cDNA EST EMBL:D27837 comes from this gene; cDNA EST yk315g9.5 comes from this gene	289	23.367
2522	AF101361	Drosophila melanogaster Abnormal X segregation	318	36.242
2523	K02581	Homo sapiens thymidine kinase (EC 2.7.1.21)	192	96.667
2524	X61276	Streptococcus pyogenes ML2.1	192	27.354
2525	L07911	Mus musculus DNA-binding protein	141	33.333
2526	AF098066	Homo sapiens squamous cell carcinoma antigen recognized by T cell	457	52.174
2527	AJ223324	Homo sapiens MAX.3 cell surface antigen	207	33.333
2528	AF127374	Streptomyces lavendulae unknown	586	38.645
2529	AF181626	Drosophila melanogaster BcDNA.GH03694	480	40.171
2530	AF184921	Rattus norvegicus ion transporter protein	299	45.055
2531	Z36233	Mus musculus sialoadhesin	394	70.130

2532	S62035	Homo sapiens Ras-specific guanine nucleotide-releasing factor, H-GRF55=CDC25 homolog	251	100.000
2533	AB023202	Homo sapiens KIAA0985 protein	247	61.017
2534	U63809	Homo sapiens prostate apoptosis response protein par-4	313	97.959
2535	AC004794	Homo sapiens F02569 2	141	41.791
2536	AF003134	Caenorhabditis elegans strong similarity to the CDC2/CDX subfamily of ser/thr protein kinases	532	54.483
2537	L06147	Homo sapiens golgin-95	226	51.000
2538	L06898	Actinomyces viscosus sialidase	174	30.657
2539	AC004997	Unknown match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and	266	97.436
2540	X79568	Homo sapiens protein-tyrosine-phosphatase	630	97.826
2541	AJ388557	Canis familiaris zinc finger protein	973	61.137
2542	D86491	Xenopus laevis Nfrl	947	77.273
2543	U19361	Petromyzon marinus NF-180	164	30.769
2544	U25739	Mus musculus YSPL-1 form 2	367	80.303
2545	AF040642	Caenorhabditis elegans contains similarity to transacylases	498	39.583
2546	AF061026	Mus musculus leucine zipper-EF-hand containing transmembrane protein 1	376	60.870
2547	U13836	Mus musculus vacuolar adenosine triphosphatase subunit Acl16	1439	61.891
2548	D87467	Homo sapiens Similar to a C.elegans guanine nucleotide releasing factor homolog (S4 2368)	189	90.323
2549	U70825	Rattus norvegicus 5-oxo-L-prolinase	269	74.000
2550	M37760	Mus musculus serine 2 ultra high sulfur protein	441	49.123
2551	AB028978	Homo sapiens KIAA1055 protein	198	37.500
2552	U75686	Homo sapiens polyadenylate binding protein	725	59.140
2553	AC004755	Homo sapiens fos37502 2	4609	99.156
2554	D86970	Homo sapiens similar to myosin heavy chain: Containing ATP/GTP-binding site motif A(P-loop)	247	89.130
2555	U63818	Xenopus laevis RING finger protein	251	37.037
2556	L12147	Mus musculus early B-cell factor	1727	96.269
2557	AB014551	Homo sapiens KIAA0651 protein	287	100.000
2558	D83703	Homo sapiens peroxisome assembly factor-2	242	100.000
2559	X05418	Homo sapiens keratin type II (AA1-215)	178	46.753
2560	AB005549	Rattus norvegicus atypical PKC specific binding protein	963	88.125
2561	Z32683	Unknown cDNA EST EMBL:Z14902 comes from this gene; cDNA EST EMBL:M89155 comes from this gene; cDNA	327	30.293
2562	U81006	Homo sapiens p76	394	100.000
2563	X07695	Homo sapiens cytokeratin 4 (408 AA)	507	60.902
2564	U78516	Homo sapiens cAMP-regulated guanine nucleotide exchange factor II	557	33.333
2565	X97818	Mus musculus samaphorin G	914	93.793
2566	AF003384	Caenorhabditis elegans weak similarity to the peptidase family A2	343	39.130
2567	AB028959	Homo sapiens KIAA1036 protein	554	60.448
2568	D90272	Tachypleus tridentatus limulus factor C precursor	202	35.789
2569	AL021154	Homo sapiens dJ15005.1 (transcription factor E2F-2)	188	83.333

2570	D84296	Homo sapiens TPRDIII	863	89.189
2571	X15573	Homo sapiens 1-phosphofructokinase	236	62.264
2572	AC002310	Homo sapiens Unknown gene product	604	100.000
2573	AF041373	Rattus norvegicus clathrin assembly protein short form	445	60.800
2574	M64780	Rattus norvegicus agrin	267	38.614
2575	X74818	Homo sapiens AHNAK-related protein	290	35.948
2576	X15657	Drosophila melanogaster Elf-1 protein (AA 1-1063)	229	46.429
2577	AB018281	Homo sapiens KIAA0738 protein	469	52.817
2578	AF151843	Homo sapiens CGI-85 protein	278	78.182
2579	U41558	Caenorhabditis elegans No definition line found	422	48.361
2580	Y09945	Rattus norvegicus putative integral membrane transport protein	498	50.000
2581	AF100960	Rattus norvegicus protocadherin	518	58.088
2582	AF104260	Homo sapiens hiwi	268	36.607
2583	AB018258	Homo sapiens KIAA0715 protein	881	55.981
2584	U20086	Mus musculus NF2d9	317	97.959
2585	D90734	Escherichia coli Helicase (EC 3.6.1.-) IV.	517	96.386
2586	Y12781	Homo sapiens transducin (beta) like 1 protein	303	80.000
2587	AF058446	Gallus gallus histone macroH2A1.2	225	26.027
2588	U19463	Mus musculus A20 protein	174	56.098
2589	AL022271	Unknown similar to Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases; cDNA EST yk	279	40.952
2590	AB007864	Homo sapiens KIAA0404	345	47.573
2591	AB011535	Homo sapiens MEGF1	184	100.000
2592	AF030430	Mus musculus semaphorin VIa	487	98.630
2593	U14635	Caenorhabditis elegans similar to GABA and glycine receptors	511	43.011
2594	M28880	Homo sapiens ankyrin	224	94.444
2595	AF064553	Mus musculus NSD1 protein	311	95.349
2596	Z93241	Homo sapiens dJ222E13.3.2 (PUTATIVE partial isoform 2)	204	90.625
2597	Z70310	Caenorhabditis elegans R11A8.7b	267	39.416
2598	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	5272	99.137
2599	AF099974	Mus musculus schlafen3	242	37.984
2600	AF117754	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240	426	95.588
2601	D25538	Homo sapiens KIAA0037	251	100.000
2602	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	793	80.916
2603	M33874	Xenopus laevis Xotch protein	285	44.444
2604	Z78417	Caenorhabditis elegans cDNA EST EMBL:D27838 comes from this gene; cDNA EST EMBL:D27837 comes from this gene; cDNA EST yk315g9.5 comes from this gene	260	29.596
2605	M76720	Xenopus laevis egg-specific protein	523	64.516
2606	U76764	Homo sapiens CD97	415	64.130
2607	U92072	Rattus norvegicus m-tomosyn	1290	98.396
2608	U23516	Caenorhabditis elegans No definition line found	249	41.414
2609	Z70038	Caenorhabditis elegans cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene	543	37.949

2610	Z24680	Homo sapiens garp	271	84.615
2611	Z70038	Caenorhabditis elegans cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene	793	38.292
2612	M21389	Homo sapiens keratin type II	295	58.333
2613	AL023777	Schizosaccharomyces pombe rna binding protein	241	59.016
2614	U21317	Caenorhabditis elegans similar to YBS4_YEAST (P38244) hypothetical 47.8 kD protein in HSP26-SEC18 intergenic region	196	28.986
2615	Y12781	Homo sapiens transducin (beta) like 1 protein	1121	93.939
2616	AF097887	Rattus norvegicus Chp	1103	98.780
2617	M77003	Mus musculus glycerol-3-phosphate acyltransferase	237	35.032
2618	L08811	Drosophila melanogaster adherin	656	53.804
2619	U20217	Mus musculus fibrillin-2	1007	66.477
2620	Z38112	Caenorhabditis elegans E03A3.6	231	30.827
2621	Z26653	Homo sapiens laminin M chain (merosin)	191	32.283
2622	AF155117	Homo sapiens NY-REN-62 antigen	355	50.000
2623	AF104260	Homo sapiens hiwi	682	55.495
2624	U03979	Tripneustes gratilla dynein heavy chain isotype 7B	1034	82.386
2625	AF113614	Cricetulus griseus Toll-like receptor 2	176	31.973
2626	D83390	Gallus gallus connectin/titin	193	29.371
2627	U09413	Homo sapiens zinc finger protein ZNF135	894	65.405
2628	M92443	Homo sapiens zinc finger protein 41	591	44.920
2629	AF002251	Rattus norvegicus Maxp1	1052	87.027
2630	AF062256	Homo sapiens immunoglobulin heavy chain variable region	633	75.591
2631	D12621	Homo sapiens cytochrome P-450LTBV	1152	90.526
2632	U97002	Caenorhabditis elegans similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1	690	53.125
2633	AF121081	Mus musculus cAMP inducible 2 protein	1113	80.905
2634	AC005567	Homo sapiens FAA	228	100.000
2635	D90727	Escherichia coli Hypothetical protein Y	732	100.000
2636	D90811	Escherichia coli ORF ID:o320#13; similar to	1006	97.403
2637	AE000232	Escherichia coli orf, hypothetical protein	981	100.000
2638	AL117518	Homo sapiens hypothetical protein	179	68.571
2639	AF101315	Caenorhabditis elegans No definition line found	146	47.727
2640	U28377	Escherichia coli ORF f329	1430	98.190
2641	D90713	Escherichia coli TolA protein.	880	100.000
2642	AF030430	Mus musculus semaphorin VIa	1910	90.820
2643	AB028997	Homo sapiens KIAA1074 protein	189	64.286
2644	U00039	Escherichia coli No definition line found	940	100.000
2645	D90239	Homo sapiens glycine decarboxylase precursor	167	100.000
2646	S80905	Homo sapiens Con1-salivary concanavalin-A binding protein {exon 3}	195	26.891
2647	AB029324	Rattus norvegicus TIP120-family protein TIP120B	1743	91.549
2648	Y08260	Mus musculus cytoplasmic polyadenylation element-binding protein (CPEB)	1313	93.137

2649	AF100960	Rattus norvegicus protocadherin	555	57.246
2650	M86444	Sus scrofa moesin B	892	96.429
2651	AL032684	Schizosaccharomyces pombe 60s ribosomal protein l2	506	58.400
2652	D90739	Escherichia coli Orf1 5' of phoH.	448	100.000
2653	AL031540	Schizosaccharomyces pombe hypothetical ATP binding protein	261	29.956
2654	U00006	Escherichia coli similar to O.berteriana mitochon. protein involved in cytochrome c biogenesis	896	99.248
2655	D90227	Escherichia coli ATP-binding protein	580	100.000
2656	Y07752	Volvox carteri pherophorin-S	238	61.702
2657	AB002331	Homo sapiens KIAA0333	230	30.952
2658	AB011532	Rattus norvegicus MEGF6	1100	72.115
2659	AF098993	Caenorhabditis elegans No definition line found	362	37.662
2660	U75361	Rattus norvegicus Munc13-3	782	81.690
2661	AB000893	Mus musculus synaptotagmin 3	1341	97.549
2662	AC006593	Arabidopsis thaliana unknown protein	221	29.104
2663	U53445	Homo sapiens DOC1	435	40.642
2664	X92591	Mus musculus transcription factor	194	40.625
2665	AC007519	Arabidopsis thaliana F16N3.15	263	26.606
2666	AF052042	Rattus norvegicus zinc finger protein Y1	563	76.316
2667	U81259	Pseudomonas aeruginosa carbamoylphosphate synthetase large subunit	181	76.316
2668	U35376	Homo sapiens repressor transcriptional factor	617	74.775
2669	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	826	100.000
2670	AJ006486	Mus musculus RNA binding protein	178	92.857
2671	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	1021	99.412
2672	AF034611	Homo sapiens intrinsic factor-B12 receptor precursor; cubilin	503	26.196
2673	X75603	Pleurodeles waltl fibroblast growth factor receptor 3	536	32.738
2674	Z75527	Caenorhabditis elegans predicted using Genefinder; Similarity to Human ARNT interacting protein (TR:G1144013)	560	28.820
2675	U88167	Caenorhabditis elegans contains similarity to C2 domains	557	29.268
2676	AF102875	Mus musculus mismatch-specific thymine-DNA glycosylate	156	95.652
2677	AF053700	Homo sapiens deltex	250	40.952
2678	AB002377	Homo sapiens KIAA0379	2295	68.738
2679	D13635	Homo sapiens KIAA0010	203	96.667
2680	AB018274	Homo sapiens KIAA0731 protein	601	82.524
2681	D80001	Homo sapiens similar to hypothetical protein D4478 of S.cerevisiae.	833	100.000
2682	U84725	Mus musculus GATA-5 cardiac transcription factor	687	77.600
2683	AF003535	Homo sapiens ORF2-like protein	320	78.947
2684	U12336	Rattus rattus acetylcholine receptor alpha 9	293	69.841

		subunit		
2685	U50078	Homo sapiens p532	430	97.183
2686	D38582	Escherichia coli FhiA	1092	96.591
2687	D90828	Escherichia coli Pyruvate kinase (EC 2.7.1.40)	793	100.000
2688	U00039	Escherichia coli No definition line found	820	100.000
2689	M80458	Escherichia coli biotin carboxylase	522	100.000
2690	U14003	Escherichia coli vacB gene product	993	93.671
2691	D90725	Escherichia coli ORF ID:o212#3	1008	99.342
2692	M18747	Escherichia coli glutamate synthase large subunit (EC 2.6.1.53)	716	98.230
2693	D90840	Escherichia coli Transcriptional activator protein MetR.	745	100.000
2694	D90876	Escherichia coli dihydrodipicolinate synthase (EC 4.2.1.52)	498	97.403
2695	AE000412	Escherichia coli putative transport	1123	98.315
2696	M11689	Escherichia coli positive regulatory protein	436	100.000
2697	L08399	Escherichia coli peripheral membrane protein	1199	98.907
2698	D90699	Escherichia coli Sensor protein copS (EC 2.7.3.-).	938	100.000
2699	X69089	Homo sapiens 165kD protein	339	100.000
2700	L13601	Escherichia coli homoserine kinase	749	100.000
2701	D90868	Escherichia coli PUTATIVE PEPTIDASE IN GCVT-SPOIIIAA INTERGENIC REGION (EC 3.4.-.-).	693	97.273
2702	Z19601	Escherichia coli ORF, trpS. Hall C.V., van Cleemput M., Muench K.H., Yanofsky C.; J. Biol. Chem. 257(11):6132-6136(1982)	538	68.800
2703	D90701	Escherichia coli Aspartate transaminase (EC 2.6.1.1)	860	89.189
2704	U70214	Escherichia coli hypothetical	540	100.000
2705	D90824	Escherichia coli Probable ATP-dependent helicase dinG homolog.	909	98.582
2706	K01174	Escherichia coli DnaB replication protein (dnaB)	834	100.000
2707	D90812	Escherichia coli FixC protein.	765	98.319
2708	M38777	Escherichia coli htpG ORF	870	99.286
2709	U00006	Escherichia coli matches PS00443: Glutamine amidotransferases class-II active site	775	82.432
2710	AE000443	Escherichia coli orf, hypothetical protein	1135	98.765
2711	M37702	Escherichia coli queA	774	90.152
2712	AE000406	Escherichia coli putative ATP-binding component of a transport system	340	100.000
2713	L10328	Escherichia coli similar to R. meliloti nodulation protein D; similar to lysR class of regulatory proteins	610	93.000
2714	D13159	Escherichia coli transaldolase	452	100.000
2715	X71917	Escherichia coli glutamate decarboxylase	1162	98.182
2716	D90721	Escherichia coli Transmembrane protein dppC	488	100.000
2717	D38504	Escherichia coli formaldehyde dehydrogenase	959	99.301
2718	D90746	Escherichia coli SocA3 protein	648	95.192
2719	AJ224871	Escherichia coli GTPase	1178	95.745
2720	X14152	Escherichia coli SrmB protein	802	93.985
2721	D10483	Escherichia coli baiF homolog (PIR:F37844)	966	99.324
2722	D90744	Escherichia coli Flagellar hook-associated protein 1 (hap1)	617	100.000
2723	X53696	Escherichia coli glutamate-1-semialdehyde 2,1-	757	100.000

		aminomutase		
2724	M13457	Escherichia coli nmpC	818	97.541
2725	AE000391	Escherichia coli putative transport protein	392	100.000
2726	X04890	Escherichia coli threonine deaminase	1170	98.913
2727	D90836	Escherichia coli Invasin.	773	90.370
2728	D90878	Escherichia coli polyphosphate kinase (EC 2.7.4.1)	284	97.826
2729	X13141	Escherichia coli ugpE protein (AA 1-281)	841	91.489
2730	AE000341	Escherichia coli orf, hypothetical protein	1479	99.078
2731	U82598	Escherichia coli hypothetical protein	510	95.000
2732	D90801	Escherichia coli Mlc protein.	1038	96.319
2733	L03845	Escherichia coli glyoxylate carboligase	896	94.521
2734	M19501	Escherichia coli formylglycineamide ribonucleotide synthetase (EC 6.3.5.3)	888	98.462
2735	U43568	Brugia malayi microfilarial sheath protein SHP1	178	48.077
2736	AE000362	Escherichia coli putative glucarate dehydratase	1646	98.361
2737	D90701	Escherichia coli Hypothetical protein 200 (entA 3' region)	1342	99.024
2738	D90825	Escherichia coli ORF ID:o334#8; similar to	936	94.156
2739	D10483	Escherichia coli secA protein	829	96.269
2740	D90888	Escherichia coli PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYR-SENSITIVE (EC 4.1.2.15) (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE).	840	97.674
2741	D90823	Escherichia coli 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (b-IPM dehydrogenase) (ImdH) (3-IPM-DH).	815	100.000
2742	D10483	Escherichia coli hsp70 protein	965	100.000
2743	U14003	Escherichia coli ORF f543	765	95.276
2744	U00006	Escherichia coli similar to E. coli pyruvate formate-lyase activating enzyme	874	100.000
2745	D90732	Escherichia coli Hypothetical protein K	1269	100.000
2746	X72298	Escherichia coli homolog to ccl1 protein from Rhodobacter capsulatus	399	98.413
2747	AF009204	Homo sapiens PSD-95/SAP90-associated protein-2	278	97.619
2748	X15237	Escherichia coli AmpD protein (AA 1-183)	756	98.165
2749	D90803	Escherichia coli Sensor protein RstB (EC 2.7.3.-).	758	100.000
2750	U82598	Escherichia coli CitG homolog	820	100.000
2751	D90849	Escherichia coli D-mannonate oxidoreductase (EC 1.1.1.57) (Fructuronate reductase).	1346	99.495
2752	D90702	Escherichia coli Sensor kinase Cita	457	100.000
2753	U14003	Escherichia coli ORF f260	743	100.000
2754	M24905	Escherichia coli recE	1123	99.415
2755	D90777	Escherichia coli Copper amine oxidase precursor (EC 1.4.3.6) (Tyramine oxidase).	876	100.000
2756	M13495	Escherichia coli UvrA protein	934	97.333
2757	D90788	Escherichia coli Alcohol dehydrogenase I (EC 1.1.1.1) (ADH I).	1133	100.000
2758	D90783	Escherichia coli Tyrosine aminotransferase (EC 2.6.1.5) (L-tyrosine:2-oxoglutarate aminotransferase) (TAT).	448	98.551
2759	D90741	Escherichia coli MdoG protein.	257	100.000
2760	D90887	Escherichia coli similar to	706	100.000

2761	D13328	Escherichia coli Uronate isomerase	1155	99.438
2762	AE000249	Escherichia coli putative LACI-type transcriptional regulator	436	100.000
2763	D85613	Escherichia coli 30KD protein, similar to ADHX-RAT	188	100.000
2764	D90865	Escherichia coli LONG-CHAIN FATTY ACID TRANSPORT PROTEIN PRECURSOR (OUTER MEMBRANE FADL PROTEIN) (OUTER MEMBRANE FLP PROTEIN).	189	84.848
2765	D90716	Escherichia coli Molybdenum cofactor biosynthesis protein A.	628	94.624
2766	U28377	Escherichia coli ORF o219; alternate name yghB	761	100.000
2767	U93405	Escherichia coli 2,4-dienoyl-CoA reductase	775	95.868
2768	U00007	Escherichia coli yohG	672	94.872
2769	M38288	Escherichia coli RNA polymerase beta subunit (rpoC) (EC 2.7.7.6)	436	97.143
2770	X59460	Escherichia coli penicillin-binding protein 4 (PBP4)	786	97.414
2771	L19346	Escherichia coli urf1	919	97.222
2772	X13002	Escherichia coli exonuclease III	554	98.718
2773	AE000399	Escherichia coli orf, hypothetical protein	857	98.561
2774	D90715	Escherichia coli Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase).	485	97.368
2775	M24148	Escherichia coli 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	933	100.000
2776	U28377	Escherichia coli ORF f413	359	92.982
2777	U28379	Escherichia coli alternate name ygiP; ORF 310	716	97.248
2778	M32793	Escherichia coli amylomaltase (malQ)	780	100.000
2779	D90756	Escherichia coli 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase	406	86.301
2780	M87625	Escherichia coli cobalamin-independent methionine synthase	805	98.333
2781	AE000475	Escherichia coli B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of metE and metF	1042	98.171
2782	AE000144	Escherichia coli putative enzyme	642	100.000
2783	M84805	Escherichia coli proton-glutamate	870	97.222
2784	AE000395	Escherichia coli putative tagatose-6-phosphate aldose/ketose isomerase	789	99.174
2785	M38777	Escherichia coli htpG ORF	658	100.000
2786	Y00544	Escherichia coli PufX protein	1000	100.000
2787	V00267	Escherichia coli reading frame gamma	369	93.939
2788	U82664	Escherichia coli similar to E. coli ydhB	868	97.826
2789	D90825	Escherichia coli ORF ID:o334#7; similar to	1601	100.000
2790	D90715	Escherichia coli Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase).	536	86.598
2791	D10483	Escherichia coli 4-coumarate-CoA homolog (PIR:S01667)	461	100.000
2792	D83536	Escherichia coli DNA polymerase III, alpha chain (EC 2.7.7.7).	1178	99.432
2793	M12858	Escherichia coli beta-cystathionase	787	100.000
2794	L03845	Escherichia coli glyoxylate carboligase	771	100.000
2795	D90880	Escherichia coli IMP dehydrogenase (EC 1.1.1.205)	1051	93.750

2796	X04341	Escherichia coli recF protein	1087	99.379
2797	X76979	Escherichia coli orf303	486	93.976
2798	X54945	Escherichia coli product appears to be membrane bound	786	98.305
2799	D90791	Escherichia coli ORF ID:o280#4; similar to	1029	98.137
2800	AE000415	Escherichia coli putative transport	735	100.000
2801	D90868	Escherichia coli PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-FRU).	859	100.000
2802	D83536	Escherichia coli Lipid-a-disaccharide synthase (EC 2.4.1.182).	721	99.115
2803	D90842	Escherichia coli ORF ID:o352#3; similar to	786	96.800
2804	X14152	Escherichia coli SrmB protein	712	97.321
2805	D90703	Escherichia coli Lipoprotein RlpA precursor.	1239	100.000
2806	D90758	Escherichia coli hyothetical protein (purT region)	775	99.099
2807	AE000136	Escherichia coli putative enzyme	1185	100.000
2808	AB000275	Homo sapiens DAP-2	182	100.000
2809	X04619	Escherichia coli A protein (AA 1-388)	1555	100.000
2810	Y17108	Homo sapiens rhomboid-related protein	358	42.748
2811	AF071071	Mus musculus protein kinase Myak-S	540	47.312
2812	U06713	Rattus norvegicus SM-20	349	45.370
2813	U07817	Dictyostelium discoideum glutamine-asparagine rich protein	238	25.098
2814	Z49216	Homo sapiens mitoxantrone-resistance associated gene	338	84.211
2815	Z95334	Schizosaccharomyces pombe hypothetical protein	1206	41.880
2816	AB023186	Homo sapiens KIAA0969 protein	193	36.842
2817	AF009668	multiple sclerosis associated retrovirus polyprotein	376	53.097
2818	M23236	Mus musculus proline-rich protein	344	33.110
2819	AB028942	Homo sapiens KIAA1019 protein	6540	96.555
2820	D31885	Homo sapiens KIAA0069	1122	94.545
2821	L00923	Mus musculus myosin I	5487	96.445
2822	AF069307	Homo sapiens sodium-dependent multivitamin transporter	1050	52.535
2823	U93863	Mus musculus ribosomal protein L21	498	78.788
2824	AF081260	Mus musculus testis-specific chromodomain Y-like protein	628	61.988
2825	AF052573	Homo sapiens DNA polymerase theta	11511	99.773
2826	Z78144	Mus musculus unknown	508	70.769
2827	U09413	Homo sapiens zinc finger protein ZNF135	524	40.520
2828	AB014578	Homo sapiens KIAA0678 protein	6414	98.438
2829	AF102546	Homo sapiens dachshund	3539	93.944
2830	U22376	Homo sapiens alternatively spliced product using exon 13A	380	70.103
2831	M74002	Homo sapiens arginine-rich nuclear protein	458	30.311
2832	AF076250	Lytechinus variegatus hyalin	295	29.210
2833	Y11354	Homo sapiens subunit of RNA polymerase II transcription factor TFIID	6989	97.969
2834	AF074086	Homo sapiens envelope	697	56.571
2835	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1611	44.073
2836	M63311	Cricetulus sp. cAMP-dependent protein kinase	2226	97.436

		alpha-catalytic subunit		
2837	D70831	Homo sapiens Zinc-finger protein	1032	66.109
2838	U57347	Sus scrofa Sp1 transcription factor	267	57.143
2839	AF063243	Bos taurus ribosomal protein L30	407	76.000
2840	U93570	Homo sapiens p40	228	47.368
2841	AF183139	Cercopithecine herpesvirus 15 truncated type 2 EBNA2	202	30.303
2842	M13100	Rattus norvegicus unknown protein	373	42.857
2843	AF159297	Zea mays extensin-like protein	412	25.638
2844	M74027	Homo sapiens mucin	257	26.044
2845	AL080140	Homo sapiens hypothetical protein	4718	99.018
2846	AF104413	Homo sapiens large tumor suppressor 1	1861	92.759
2847	U35376	Homo sapiens repressor transcriptional factor	1288	53.352
2848	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	722	36.548
2849	D86980	Homo sapiens KIAA0227	340	36.481
2850	M34986	Homo sapiens erythropoietin receptor precursor	269	70.588
2851	U15174	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 3	508	66.667
2852	AL096751	Homo sapiens hypothetical protein	5007	99.493
2853	AL080170	Homo sapiens hypothetical protein	824	46.471
2854	X61280	Oryza sativa hydroxyproline-rich glycoprotein	181	39.623
2855	AB023191	Homo sapiens KIAA0974 protein	1166	87.054
2856	AB018288	Homo sapiens KIAA0745 protein	302	72.857
2857	AB014587	Homo sapiens KIAA0687 protein	7749	99.915
2858	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	352	49.541
2859	M73713	Homo sapiens pregnancy-specific beta-1-glycoprotein 5	362	70.588
2860	X94335	Saccharomyces cerevisiae YOR3348c	361	27.184
2861	AC004144	Homo sapiens R34001.1	6792	97.348
2862	AF038611	Caenorhabditis elegans contains similarity to sulphatases	784	28.440
2863	X92485	Plasmodium vivax pval	364	45.614
2864	U51723	Plasmodium vivax V-SERA 1	168	37.500
2865	AF083242	Homo sapiens HSPC024-iso	994	94.706
2866	U60416	Rattus norvegicus myr 6 myosin heavy chain	2689	93.407
2867	Z75713	Unknown cDNA EST EMBL:D36107 comes from this gene; cDNA EST yk208c1.3 comes from this gene; cDNA ES	298	24.127
2868	AJ004810	Zea mays cytochrome P450 monooxygenase	200	78.049
2869	AB007888	Homo sapiens KIAA0428	1169	59.365
2870	AL021748	Schizosaccharomyces pombe hypothetical protein	293	31.884
2871	Z81525	Unknown cDNA EST yk282b7.5 comes from this gene; cDNA EST EMBL:D28011 comes from this gene; cDNA ES	766	41.889
2872	X55656	Homo sapiens gamma-G globin	180	46.835
2873	AB029008	Homo sapiens KIAA1085 protein	3580	96.447
2874	AF045253	Mus musculus tousled-like kinase	370	77.778
2875	AF151827	Homo sapiens CGI-69 protein	1337	75.817
2876	M92443	Homo sapiens zinc finger protein 41	540	35.959
2877	AF155096	Homo sapiens NY-REN-6 antigen	2445	87.555
2878	AB014595	Homo sapiens KIAA0695 protein	4636	99.861
2879	U38847	Homo sapiens TAR RNA loop binding protein	10152	97.111
2880	U22376	Homo sapiens alternatively spliced product	474	74.257

		using exon 13A		
2881	AF029249	Mytilus edulis precollagen D	192	29.815
2882	U80837	Caenorhabditis elegans contains similarity to C2H2-type zinc fingers	382	36.257
2883	AF113615	Homo sapiens FH1/FH2 domain-containing protein FHOS	1228	54.743
2884	Z11115	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk281d4.5 comes from this gene; cDNA EST yk288c12.5 comes from this gene; cDNA EST yk406g11.5 comes from this gene	719	28.653
2885	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	434	50.000
2886	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	293	63.333
2887	X55995	Rattus norvegicus dimethylglycine dehydrogenase	1011	89.535
2888	AL035709	Arabidopsis thaliana putative protein	704	37.231
2889	U41387	Homo sapiens Gu protein	2182	64.794
2890	Y09060	murine herpesvirus 68 serine threonine rich glycoprotein	220	28.426
2891	AF125386	Drosophila melanogaster L82C	669	46.083
2892	Z81552	Caenorhabditis elegans similar to Thioredoxins; cDNA EST yk491h3.5 comes from this gene	704	36.494
2893	AF002592	Pterolebias xiphophorus cytochrome oxidase I	223	67.089
2894	U49973	Homo sapiens ORF1; MER37; putative transposase similar to pogo element	315	75.248
2895	AC006592	Arabidopsis thaliana unknown protein	243	26.648
2896	AB020684	Homo sapiens KIAA0877 protein	1161	71.795
2897	AL080125	Homo sapiens hypothetical protein	452	53.488
2898	AF041054	Mus musculus E1B 19K/Bcl-2-binding protein homolog	292	63.636
2899	AB020725	Homo sapiens KIAA0918 protein	400	35.548
2900	Z66563	Unknown Similarity to myosin; cDNA EST yk249a4.5 comes from this gene; cDNA EST yk270h6.5 comes fro	593	29.004
2901	U79260	Homo sapiens unknown	328	51.145
2902	AL032655	Caenorhabditis elegans predicted using Genefinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene; cDNA EST yk610f9.3 comes from this gene	372	32.827
2903	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	394	32.370
2904	U83176	Mus musculus ROSA26AS	323	23.451
2905	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	1006	66.814
2906	M94131	Homo sapiens mucin	291	24.758
2907	U27196	Gallus gallus zinc finger protein	1616	64.494
2908	AC004877	Homo sapiens zinc finger-like; similar to P52742 (PID:g1731411)	670	31.159
2909	AF167320	Mus musculus zinc finger protein ZFP113	786	67.702
2910	M23236	Mus musculus proline-rich protein	199	30.488
2911	AF184226	Drosophila melanogaster BcDNA.GH09045	894	37.915
2912	Z99271	Caenorhabditis elegans similar to zinc metalloproteinase (M8 family); cDNA EST EMBL:C07771 comes from this gene; cDNA EST EMBL:C09261 comes from this gene; cDNA EST yk259c1.5 comes from this gene	324	36.184
2913	Z72506	Unknown Similarity to Hydra RAS like protein	291	47.107

		RAS2 (SW:RAS2_HYDMA); cDNA EST EMBL:D72418 comes from		
2914	D67066	Bos taurus N-WASP	167	33.511
2915	X56044	Mus musculus protein Htf9C	2251	84.938
2916	X73974	Homo sapiens ribosomal protein L4	334	64.800
2917	U72882	Homo sapiens interferon-induced leucine zipper protein	1638	91.447
2918	X92352	Mus musculus homology to nucleosome assembly proteins; specifically expressed in neurons	373	33.422
2919	S67970	Homo sapiens ZNF75=KRAB zinc finger	1206	75.641
2920	AB017616	Mus musculus homologous to the yeast YGR163 gene	1923	81.989
2921	AL080141	Homo sapiens hypothetical protein	1134	54.695
2922	AF055084	Homo sapiens very large G-protein coupled receptor-1	11286	99.319
2923	AL050395	Homo sapiens hypothetical protein	846	88.506
2924	AF135440	Mus musculus huntington yeast partner C	384	68.041
2925	U07974	Gallus gallus unknown	175	28.105
2926	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	358	52.258
2927	Z78544	Caenorhabditis elegans predicted using Genefinder; Similarity to C.elegans Guanine nucleotide binding protein (WP:C14B1.4); cDNA EST yk567g12.3 comes from this gene	176	69.767
2928	S80119	Rattus sp. reverse transcriptase homolog	325	53.782
2929	M59227	Homo sapiens alpha-1 type III collagen	165	37.615
2930	AF039187	Schistosoma japonicum myosin	274	24.217
2931	Z68756	Homo sapiens Huntington Disease (HD) gene exon 1	171	35.632
2932	Y11770	Mus musculus very-long-chain acyl-CoA dehydrogenase	1714	47.430
2933	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	384	50.000
2934	U10414	Caenorhabditis elegans Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2	446	46.087
2935	AF040105	Homo sapiens RCL	517	67.647
2936	Z69635	Unknown Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this ge	705	49.393
2937	U22376	Homo sapiens alternatively spliced product using exon 13A	439	62.281
2938	X65120	Homo sapiens alpha1(X)collagen	487	36.424
2939	AF151825	Homo sapiens CGI-67 protein	1379	79.592
2940	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	1249	96.939
2941	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	438	77.895
2942	D50685	Trypanosoma cruzi trans-sialidase	274	41.709
2943	M33784	Dictyostelium discoideum protein-tyrosine kinase-2 (DPYK2)	299	30.449
2944	X53581	Rattus norvegicus ORF3	190	37.143
2945	S80119	Rattus sp. reverse transcriptase homolog	167	56.818
2946	U53153	Caenorhabditis elegans one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922)	513	34.756

2947	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	389	64.151
2948	AB020675	Homo sapiens KIAA0868 protein	8903	97.470
2949	AF067165	Homo sapiens zinc finger protein 3	728	52.423
2950	AB014580	Homo sapiens KIAA0680 protein	779	39.492
2951	U71601	Homo sapiens zinc finger protein zfp47	248	26.866
2952	M64793	Rattus norvegicus salivary proline-rich protein	266	30.943
2953	AF060173	Rattus norvegicus SV2 related protein	394	30.370
2954	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	413	67.647
2955	U79260	Homo sapiens unknown	356	71.429
2956	AF095155	Mus musculus C1q-related factor	310	33.000
2957	X91617	Mus musculus 5'-3' exonuclease	1721	56.593
2958	AC002505	Arabidopsis thaliana unknown protein	189	21.921
2959	AC006550	Arabidopsis thaliana Similar to gb U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF 00400 WD40, G-beta repeats. ESTs gb T43386 and gb AA395236 come from this gene.	528	33.542
2960	K02298	Rattus norvegicus chymotrypsin B	1644	91.288
2961	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	295	64.865
2962	AL080155	Homo sapiens hypothetical protein	2487	91.991
2963	AF020261	Santalum album proline rich protein	206	27.099
2964	Z69730	Schizosaccharomyces pombe putative ranbp7-importin-beta-cselp superfamily protein	445	24.756
2965	AF071103	Drosophila melanogaster myo-inositol-1-phosphate synthase	1866	61.169
2966	X70944	Homo sapiens PTB-associated splicing factor	1674	67.196
2967	AF095350	Homo sapiens RAB-like protein 2A	755	55.839
2968	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	746	43.987
2969	AL117452	Homo sapiens hypothetical protein	5690	97.068
2970	X59720	Saccharomyces cerevisiae YCR009c, len:265	264	26.446
2971	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	219	34.694
2972	AF078848	Homo sapiens BUP	985	62.136
2973	D87076	Homo sapiens similar to human bromodomain protein BR140 (JC2069)	3649	97.909
2974	AF056116	Fugu rubripes unknown	963	51.304
2975	AB011084	Homo sapiens KIAA0512 protein	523	34.426
2976	U73522	Homo sapiens AMSH	1185	53.736
2977	AF170708	Homo sapiens T-box protein TBX3	4480	98.207
2978	Z49068	Unknown similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D2	64	25.000
2979	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	410	71.579
2980	AB023160	Homo sapiens KIAA0943 protein	2508	99.728
2981	U70935	Peromyscus maniculatus reverse transcriptase	265	48.214
2982	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	397	51.462
2983	AF165161	Homo sapiens FLASH	6603	97.103
2984	D55696	Homo sapiens cysteine protease	172	54.237
2985	AJ005071	Gallus gallus Tapasin	315	34.091
2986	U30292	Mus musculus collagen type XIII alpha-1 chain	725	51.835
2987	AJ243459	Leishmania major proteophosphoglycan	324	31.414
2988	U85995	Homo sapiens unknown	2241	90.618
2989	U49082	Homo sapiens transporter protein	1046	54.785

2990	AB023209	Homo sapiens KIAA0992 protein	4871	95.460
2991	M14123	Homo sapiens pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative	8432	95.434
2992	M20789	Homo sapiens alpha-1 type I collagen	225	31.307
2993	D63876	Homo sapiens KIAA0154 gene product is related to mouse gamma adaptin.	4406	94.077
2994	X14401	Rattus rattus ribosomal protein L34	284	67.470
2995	AF167321	Mus musculus zinc finger protein ZFP235	1873	60.664
2996	AF159297	Zea mays extensin-like protein	404	27.051
2997	X95808	Homo sapiens X-linked mental retardation candidate gene	860	33.448
2998	U22376	Homo sapiens alternatively spliced product using exon 13A	361	65.591
2999	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	709	71.687
3000	AJ243459	Leishmania major proteophosphoglycan	186	29.461
3001	U97553	murine herpesvirus 68 unknown	281	28.708
3002	X56044	Mus musculus protein Htf9C	602	46.154
3003	Z46242	Caenorhabditis elegans similar to WD domain, G- beta repeat; cDNA EST yk283e3.3 comes from this gene; cDNA EST yk238e2.3 comes from this gene; cDNA EST yk283e3.5 comes from this gene; cDNA EST yk238e2.5 comes from this gene	1011	39.009
3004	X99252	Mus musculus arachidonate 12(S)-lipoygenase	3252	74.548
3005	X92485	Plasmodium vivax pval	181	51.613
3006	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	431	72.165
3007	D70831	Homo sapiens Zinc-finger protein	373	35.439
3008	D78255	Mus musculus PAP-1	810	56.391
3009	AB023163	Homo sapiens KIAA0946 protein	4478	98.802
3010	Y10746	Homo sapiens methyl-CpG binding protein	3952	99.102
3011	D25215	Homo sapiens KIAA0032	2351	55.199
3012	AF034746	Mus musculus LNXp70	260	82.812
3013	AL080196	Homo sapiens hypothetical protein	5255	99.264
3014	AF056116	Fugu rubripes unknown	381	36.715
3015	AF036699	Caenorhabditis elegans Similar to cuticular collagen; F58F6.2	180	29.956
3016	K03332	Human herpesvirus 4 nuclear antigen 2	227	28.800
3017	AB011084	Homo sapiens KIAA0512 protein	856	40.670
3018	U41534	Caenorhabditis elegans Contains similarity to Pfam domain: PF00271 (helicase_C), Score=49.0, E-value=3.3e-11, N=1	606	41.833
3019	V00148	Caenorhabditis elegans unnamed protein product	176	36.406
3020	U79260	Homo sapiens unknown	402	75.824
3021	AB022915	Mus musculus sif and Tiam1-like exchange factor	3634	84.978
3022	AJ001616	Mus musculus myeloid associated differentiation protein	237	39.623
3023	M12099	Mus musculus proline-rich protein	257	36.000
3024	AL035655	Schizosaccharomyces pombe hypothetical protein	471	40.693
3025	S79915	Drosophila sp. Hls=155 kda putative DE-H type RNA-dependent ATPase-helicase/RNA localizing protein	258	28.879
3026	AL031709	Homo sapiens c316G12.3 (novel protein)	1807	76.804
3027	AC006539	Homo sapiens BC39498 2	694	48.864
3028	AL110228	Homo sapiens hypothetical protein	4620	97.931
3029	AB020698	Homo sapiens KIAA0891 protein	3695	94.435
3030	AJ005890	Homo sapiens JMI	1043	86.301

3031	AJ388557	Canis familiaris zinc finger protein	1818	56.838
3032	V00147	Caenorhabditis elegans unnamed protein product	206	35.429
3033	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	385	61.111
3034	U22376	Homo sapiens alternatively spliced product using exon 13A	366	65.657
3035	U29154	Caenorhabditis elegans T07F12.1 gene product	451	31.939
3036	AL050396	Homo sapiens filamin	5534	77.814
3037	L01042	Homo sapiens TATA element modulatory factor	5656	99.460
3038	Z81503	Caenorhabditis elegans predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene	146	33.000
3039	D10627	Mus musculus zinc finger protein	756	58.730
3040	U93571	Homo sapiens p40	263	28.959
3041	AJ243459	Leishmania major proteophosphoglycan	270	36.123
3042	AL080159	Homo sapiens hypothetical protein	637	48.980
3043	Z77664	Unknown predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST CEMSC43F comes from	162	34.884
3044	AL079308	Streptomyces coelicolor putative serine/threonine protein kinase	194	31.795
3045	AB007887	Homo sapiens KIAA0427	325	29.221
3046	AB026190	Homo sapiens Kelch motif containing protein	480	26.882
3047	Y13374	Homo sapiens putative prenylated protein	966	82.530
3048	Y08766	Homo sapiens SF1-Bo isoform	86	29.101
3049	M80650	Caenorhabditis elegans alpha-collagen	206	31.414
3050	AJ242777	Mus musculus ABINs, A20-binding inhibitor of NF-kappa B activation (small)	567	36.503
3051	X71621	Saccharomyces cerevisiae hypothetical 58.9 kD protein	186	24.924
3052	X13885	Nicotiana tabacum extensin (AA 1-620)	274	24.568
3053	Y11395	Homo sapiens seventransmembrane-domain protein	1205	57.190
3054	AF156271	Homo sapiens RING finger protein terf	202	30.769
3055	V00148	Caenorhabditis elegans unnamed protein product	249	34.766
3056	U00025	Caenorhabditis elegans weak similarity to ATP synthase B chain	674	28.320
3057	AL080125	Homo sapiens hypothetical protein	525	61.268
3058	AF151827	Homo sapiens CGI-69 protein	1344	76.144
3059	AL080123	Homo sapiens hypothetical protein	528	30.366
3060	L11672	Homo sapiens zinc finger protein	442	26.448
3061	X74764	Homo sapiens protein-tyrosine kinase	5319	96.647
3062	AF149093	Mus musculus zinc finger ZF-12	354	59.036
3063	U79260	Homo sapiens unknown	242	56.180
3064	D31887	Homo sapiens KIAA0062	1316	50.000
3065	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	188	25.721
3066	D86966	Homo sapiens similar to human ZFY protein.	554	36.797
3067	X62681	Gallus gallus limb deformity protein	564	49.721
3068	AF087142	Homo sapiens TED protein	1040	41.016
3069	AF109906	Mus musculus NG22	720	30.270
3070	AB000459	Homo sapiens unnamed protein product	603	36.000
3071	X13885	Nicotiana tabacum extensin (AA 1-620)	383	31.976
3072	AF053356	Homo sapiens leucin rich neuronal protein	1429	67.016
3073	AB011164	Homo sapiens KIAA0592 protein	8471	97.791
3074	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	715	66.851

3075	AF039698	Homo sapiens antigen NY-CO-33	489	70.642
3076	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	476	50.228
3077	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	706	69.492
3078	M13100	Rattus norvegicus unknown protein	325	35.266
3079	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .	224	31.609
3080	AJ243459	Leishmania major proteophosphoglycan	177	25.858
3081	AF043944	Mytilus edulis nongradient byssal precursor	277	27.792
3082	S69693	Leishmania donovani, ssp. infantum, Ethiopian LV9, amastigote, Peptide, 236 aa stage-specific S antigen homolog=A2 {repetitive sequence}	226	36.076
3083	X79881	Rattus norvegicus aggrecan like protein/brevican	522	56.329
3084	AF039939	Canis familiaris type II collagen	94	44.444
3085	U04267	Gossypium barbadense proline-rich cell wall protein	143	27.749
3086	AC006220	Arabidopsis thaliana hypothetical protein	354	51.724
3087	X61295	Rattus norvegicus L1 retroposon, a portion of its ORF2 sequence	308	39.735
3088	AB029011	Homo sapiens KIAA1088 protein	4037	86.686
3089	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	419	71.134
3090	Z28201	Saccharomyces cerevisiae ORF YKL201c	151	27.273
3091	AB002336	Homo sapiens KIAA0338	6169	99.893
3092	AF159297	Zea mays extensin-like protein	284	25.967
3093	X92485	Plasmodium vivax pval	269	58.333
3094	AF060570	Mus musculus rig-1 protein	1698	73.156
3095	AF118223	Arabidopsis thaliana No definition line found	217	50.704
3096	U20107	Mus musculus synaptotagmin VIII	1134	69.922
3097	X51394	Xenopus laevis APEG precursor protein	376	36.861
3098	X79510	Homo sapiens protein-tyrosine-phosphatase	6982	97.056
3099	AF112299	Homo sapiens integral inner nuclear membrane protein MAN1	342	44.800
3100	Z28201	Saccharomyces cerevisiae ORF YKL201c	357	36.747
3101	U09367	Homo sapiens zinc finger protein ZNF136	577	52.717
3102	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	183	31.609
3103	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	385	57.692
3104	AB007447	Homo sapiens Fln29	165	62.745
3105	D13641	Homo sapiens mitochondrial outer membrane protein 19	416	75.962
3106	U41007	Caenorhabditis elegans similar to G beta repeats (PROSITE:PS00670)	280	37.226
3107	Z82268	Unknown predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from	227	35.971
3108	M73980	Homo sapiens TAN1	6446	98.970
3109	AC006293	Homo sapiens immunoglobulin-like transcript 10 protein	2290	88.060
3110	AF060248	Arabidopsis thaliana unknown	420	35.547
3111	X07881	Homo sapiens proline-rich protein G1	248	27.313
3112	U91318	Homo sapiens Gene product with similarity to Multidrug resistance protein MRP1	397	60.484
3113	U68488	Homo sapiens 5-hydroxytryptamine7 receptor	2150	82.989

		isoform d		
3114	AJ245587	Homo sapiens Kruppel-type zinc finger	247	35.648
3115	U33460	Homo sapiens DNA-directed RNA polymerase I, largest subunit	1923	98.371
3116	AF159297	Zea mays extensin-like protein	231	35.581
3117	AL035423	Homo sapiens dJ20I3.1 (brain mitochondrial carrier protein-1 (BMCP1))	932	86.982
3118	U22376	Homo sapiens alternatively spliced product using exon 13A	322	58.000
3119	AL117201	Caenorhabditis elegans predicted using Genefinder	228	26.063
3120	Z67990	Caenorhabditis elegans similar to cuticle collagen	217	29.097
3121	AF151840	Homo sapiens CGI-82 protein	463	42.000
3122	D14539	Homo sapiens LTG19	72	29.885
3123	U05227	Homo sapiens Rar protein	1386	66.460
3124	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	248	56.818
3125	U53155	Unknown Similar to cuticular collagen; coded for by C. elegans cDNA yk58e6.3; coded for by C. elegans	182	30.544
3126	K03208	Homo sapiens salivary proline-rich protein precursor	73	33.333
3127	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	199	53.333
3128	AB014578	Homo sapiens KIAA0678 protein	6383	98.242
3129	U49974	Homo sapiens mariner transposase	763	73.298
3130	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	230	52.475
3131	U15181	Mycobacterium leprae 4-coumarate-coA ligase	787	40.000
3132	X06956	Homo sapiens alpha-tubulin	2225	92.521
3133	U22376	Homo sapiens alternatively spliced product using exon 13A	448	65.179
3134	Z97336	Arabidopsis thaliana hypothetical protein	722	37.755
3135	AF045646	Caenorhabditis elegans contains similarity to collagens	138	29.646
3136	AC005360	Homo sapiens FAA	501	41.962
3137	Z35597	Unknown Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:	760	36.188
3138	M80344	Homo sapiens ORF1 codes for a 40 kDa product	333	50.450
3139	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	345	54.032
3140	L01775	Daucus carota proline-rich protein	273	35.211
3141	D90813	Escherichia coli ORF ID:o322#7; similar to	718	34.388
3142	AF063613	Homo sapiens 2'-5'oligoadenylate synthetase 3	7385	98.896
3143	J04974	Homo sapiens alpha-2 type XI collagen	196	29.435
3144	AF077538	Caenorhabditis elegans unknown	213	23.353
3145	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	332	59.048
3146	AF159297	Zea mays extensin-like protein	368	29.979
3147	M74027	Homo sapiens mucin	262	26.357
3148	U22376	Homo sapiens alternatively spliced product using exon 13A	399	73.494
3149	Z68215	Unknown similar to collagen; cDNA EST EMBL:D69371 comes from this gene; cDNA EST EMBL:D65671 comes	166	35.294
3150	M63798	Blaberus discoidalis cytochrome P450	653	50.711
3151	Z48045	Caenorhabditis elegans sre-2	1047	48.817
3152	AF104413	Homo sapiens large tumor suppressor 1	1687	72.566

3153	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	206	33.333
3154	L35013	Homo sapiens spliceosomal protein	215	32.877
3155	U24246	Drosophila melanogaster I71-7	302	28.926
3156	Z83232	Unknown cDNA EST EMBL:D26959 comes from this gene; cDNA EST EMBL:D26963 comes from this gene; cDNA	380	27.711
3157	AC007228	Homo sapiens BC37295 1	647	47.005
3158	U32447	Trypanosoma cruzi mucin-like protein	182	37.795
3159	U97006	Caenorhabditis elegans No definition line found	308	36.913
3160	AJ131535	Zea mays Hydroxyproline-rich Glycoprotein (HRGP)	204	22.464
3161	U48852	Cricetulus griseus HT protein	1918	76.453
3162	AF177758	Homo sapiens ubiquitin specific protease 16	1185	75.781
3163	U38252	Mus musculus fractionated X-irradiation-induced 29 thymoma	1015	60.702
3164	U76618	Mus musculus N-RAP	1163	48.603
3165	AF159297	Zea mays extensin-like protein	252	29.502
3166	U40029	Caenorhabditis elegans Contains similarity to Pfam domain: PF01060 (Worm_family_2), Score=203.8, E-value=8.6e-58, N=1	431	33.918
3167	M36912	Zea mays cell wall protein (put.); putative	245	30.072
3168	AF108843	Homo sapiens env protein	680	34.195
3169	AF022985	Unknown Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA	215	32.719
3170	AB028954	Homo sapiens KIAA1031 protein	2361	48.748
3171	M17802	Plasmodium falciparum circumsporozoite protein	213	28.676
3172	AF067165	Homo sapiens zinc finger protein 3	780	61.677
3173	U53154	Caenorhabditis elegans No definition line found	310	21.905
3174	Y12713	Mus musculus Gag polyprotein	516	43.210
3175	U95090	Homo sapiens F19541 1	1909	64.974
3176	X67156	Rattus norvegicus (S)-2-hydroxy-acid oxidase	1033	69.068
3177	S62936	Homo sapiens PRB1S precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor {C-terminal}	206	31.140
3178	M97347	Homo sapiens beta-1,6-N-acetylglucosaminyltransferase	343	72.973
3179	U60315	Molluscum contagiosum virus subtype 1 MC132L	484	41.429
3180	U58658	Homo sapiens unknown	257	62.162
3181	U93574	Homo sapiens putative p150	358	40.092
3182	U93571	Homo sapiens p40	409	42.941
3183	AC004235	Homo sapiens Myt1	359	51.163
3184	U40187	Caenorhabditis elegans C. elegans cuticle collagen col-8	169	31.472
3185	U79260	Homo sapiens unknown	288	58.696
3186	Z46787	Unknown cDNA EST EMBL:D75506 comes from this gene; cDNA EST EMBL:D72588 comes from this gene; cDNA	376	46.497
3187	U23514	Caenorhabditis elegans No definition line found	321	32.000
3188	U79260	Homo sapiens unknown	288	58.696
3189	U22376	Homo sapiens alternatively spliced product using exon 13A	445	56.115
3190	AC005175	Homo sapiens R31449 3	1854	57.739
3191	AJ010949	Mus musculus calcium channel alpha-2-delta-C	448	41.667

		subunit		
3192	U97553	murine herpesvirus 68 unknown	375	33.992
3193	L06147	Homo sapiens golgin-95	469	59.854
3194	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	438	77.895
3195	U97553	murine herpesvirus 68 unknown	197	31.276
3196	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	692	66.111
3197	X54162	Homo sapiens 64 Kd autoantigen	958	42.523
3198	S78234	Homo sapiens H-NUC=nuclear DNA binding protein	976	74.297
3199	U79260	Homo sapiens unknown	324	62.637
3200	AF152502	Homo sapiens protocadherin beta 9	1129	73.061
3201	AF006065	Fowlpox virus gag	296	31.474
3202	AF056617	Homo sapiens BWSCR2 associated zinc-finger protein BAZ1	1075	61.176
3203	U93566	Homo sapiens p40	263	47.706
3204	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	376	36.321
3205	M19503	Homo sapiens ORF1; putative	223	31.679
3206	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	434	26.087
3207	L11672	Homo sapiens zinc finger protein	864	43.077
3208	AJ225122	Mus musculus hyperpolarization-activated cation channel, HAC1	138	34.783
3209	AF071172	Homo sapiens HERC2	4696	97.127
3210	AB011532	Rattus norvegicus MEGF6	2066	74.143
3211	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	373	72.826
3212	U09116	Homo sapiens ORF1, encodes a 40 kDa product	238	39.706
3213	U85494	Zea mays LON1 protease	1881	56.238
3214	AF027973	Nephila clavipes flagelliform silk protein	430	29.014
3215	M17491	Mus musculus procollagen type I alpha chain	220	31.556
3216	AF132947	Homo sapiens CGI-13 protein	676	86.131
3217	U93564	Homo sapiens p40	227	28.571
3218	X69115	Homo sapiens ZNF37A	284	33.333
3219	AF045646	Caenorhabditis elegans contains similarity to collagens	182	34.363
3220	X63005	Mus musculus proline-rich protein	240	36.123
3221	AF132181	Drosophila melanogaster unknown	951	33.564
3222	AF081789	Mus musculus cell surface antigen AA4	359	28.053
3223	AF020261	Santalum album proline rich protein	210	29.811
3224	U09413	Homo sapiens zinc finger protein ZNF135	1531	53.753
3225	U22376	Homo sapiens alternatively spliced product using exon 13A	305	65.517
3226	AL023776	Schizosaccharomyces pombe hypothetical protein	363	26.359
3227	AL009196	Unknown /prediction=(method:"genefinder", version:"084", score:"59.41"); /prediction=(metho	858	37.209
3228	U09413	Homo sapiens zinc finger protein ZNF135	1801	58.093
3229	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	296	38.636
3230	M73980	Homo sapiens TAN1	10993	98.985
3231	AF181640	Drosophila melanogaster BcDNA.GH09817	553	45.575
3232	AF043642	Rattus norvegicus matrin cyclophilin	328	31.164
3233	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	212	33.163
3234	M73491	Mus musculus N-acetylglucosaminyltransferase I	499	37.193
3235	X55777	Homo sapiens put. ORF	261	60.526
3236	X15332	Homo sapiens alpha-1 (III) collagen	118	32.824
3237	X05830	Mus musculus ORF2 product	778	73.034

3238	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	416	71.134
3239	AF067946	Caenorhabditis elegans similar to Drosophila ring canal protein (kelch) (SW:Q04652)	376	25.683
3240	AF015037	Oryctolagus cuniculus endooligopeptidase A related protein; EOPA related protein	3012	90.154
3241	AF130441	Arabidopsis thaliana UVB-resistance protein UVR8	255	30.729
3242	U10281	Sus scrofa gastric mucin	199	24.405
3243	U93305	Homo sapiens triple LIM domain protein	406	47.863
3244	U20106	Rattus norvegicus synaptotagmin VII	1036	88.679
3245	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	359	66.337
3246	AF038963	Homo sapiens RNA helicase	584	31.690
3247	X92517	Saccharomyces cerevisiae N1751	291	29.614
3248	Z11773	Homo sapiens SRE-ZBP	2709	97.810
3249	AB011164	Homo sapiens KIAA0592 protein	8487	97.938
3250	M65014	Ovine pulmonary adenocarcinoma virus pol protein	377	41.358
3251	Z69635	Unknown Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this ge	536	40.728
3252	AB028987	Homo sapiens KIAA1064 protein	821	34.926
3253	U22376	Homo sapiens alternatively spliced product using exon 13A	398	78.824
3254	M14123	Homo sapiens pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative	781	33.830
3255	AJ010262	Mus musculus MT5-MMP protein	338	29.845
3256	U09366	Homo sapiens zinc finger protein ZNF133	1237	54.545
3257	AJ388557	Canis familiaris zinc finger protein	703	46.154
3258	U46068	Mus musculus von Ebner minor salivary gland protein	573	55.172
3259	U13766	Murine leukemia virus gag-pol polyprotein	794	29.542
3260	AF069307	Homo sapiens sodium-dependent multivitamin transporter	1040	52.765
3261	AF041082	Rattus norvegicus transmembrane receptor Robo1	312	26.518
3262	X87342	Homo sapiens Human giant larvae homologue	3108	95.609
3263	AF159297	Zea mays extensin-like protein	291	31.768
3264	D32050	Homo sapiens alanyl-tRNA synthetase	1303	37.074
3265	U22376	Homo sapiens alternatively spliced product using exon 13A	333	70.886
3266	D10923	Homo sapiens HM74	601	39.597
3267	AL023893	Drosophila melanogaster /prediction=(method:"genefinder", version:"084", score:"111.64"); /prediction=(method:"genscan", version:"1.0")	489	32.500
3268	D10280	Oryctolagus sp. myosin heavy chain	647	33.559
3269	L19267	Homo sapiens putative	3331	95.104
3270	AB014604	Homo sapiens KIAA0704 protein	3282	97.619
3271	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	463	43.443
3272	AF182946	Rattus norvegicus BRCA1-associated RING domain protein 1	305	31.621
3273	U09413	Homo sapiens zinc finger protein ZNF135	558	41.277
3274	U60416	Rattus norvegicus myr 6 myosin heavy chain	2703	93.187
3275	AF100318	Homo sapiens mitogen-activated protein kinase kinase kinase 6	183	40.268

3276	Z79757	Unknown Similarity to Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cD	201	22.659
3277	AF044924	Homo sapiens hook2 protein	773	48.630
3278	AB011096	Homo sapiens KIAA0524 protein	347	61.607
3279	M27685	Mus musculus ultra-high sulphur keratin	255	48.193
3280	AL117532	Homo sapiens hypothetical protein	5467	97.852
3281	AB017616	Mus musculus homologous to the yeast YGR163 gene	2208	96.089
3282	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	243	69.231
3283	AF072508	Homo sapiens envelope protein	165	43.182
3284	AL096811	Streptomyces coelicolor A3(2) putative acyl-CoA dehydrogenase	916	36.057
3285	AJ010046	Homo sapiens guanine nucleotide-exchange factor	2311	99.711
3286	U70932	Peromyscus leucopus reverse transcriptase	231	41.071
3287	U80735	Homo sapiens CAGF28	4578	97.312
3288	AL009147	Unknown /prediction=(method:"genscan", version:"1.0", score:"184.75"); /prediction=(method:	1309	49.883
3289	AJ000008	Homo sapiens PI3-kinase	9514	99.517
3290	AC004983	Homo sapiens similar to PID:g3877944	2934	94.456
3291	U15174	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 3	287	65.169
3292	AL117204	Caenorhabditis elegans predicted using Genefinder	301	35.047
3293	M13100	Rattus norvegicus unknown protein	216	53.750
3294	Z46241	Unknown carboxyl terminus of the predicted protein shows similarity to chimaerin; cDNA EST EMBL:Z14	582	33.038
3295	D89340	Rattus norvegicus dipeptidyl peptidase III	3642	87.106
3296	U22376	Homo sapiens alternatively spliced product using exon 13A	355	63.636
3297	AC004665	Arabidopsis thaliana unknown protein	270	24.756
3298	AF001958	Ambystoma tigrinum electrogenic Na ⁺ bicarbonate cotransporter; NBC	1829	56.031
3299	AF159297	Zea mays extensin-like protein	393	30.481
3300	U70932	Peromyscus leucopus reverse transcriptase	231	54.878
3301	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	625	58.768
3302	Z11773	Homo sapiens SRE-ZBP	2709	97.810
3303	AF071491	Homo sapiens potassium channel	5524	98.171
3304	X92485	Plasmodium vivax pval	259	48.980
3305	AF055084	Homo sapiens very large G-protein coupled receptor-1	11286	99.319
3306	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	287	70.130
3307	AF111169	Homo sapiens KIAA0759	1021	44.965
3308	D12485	Homo sapiens The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.	5619	93.545
3309	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	627	56.682
3310	Z79694	Caenorhabditis elegans predicted using Genefinder; similar to collagen	164	31.414
3311	X92485	Plasmodium vivax pval	335	64.516

3312	AC004005	Arabidopsis thaliana unknown protein	246	30.286
3313	D90886	Escherichia coli CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYLSERINE SYNTHASE).	880	86.335
3314	U79260	Homo sapiens unknown	288	58.696
3315	U22376	Homo sapiens alternatively spliced product using exon 13A	481	84.706
3316	U22376	Homo sapiens alternatively spliced product using exon 13A	417	73.913
3317	AL023702	Streptomyces coelicolor hypothetical protein SC1C3.11	420	39.524
3318	X91114	Gorilla gorilla interleukin-8 receptor type B	1216	86.036
3319	U22376	Homo sapiens alternatively spliced product using exon 13A	445	82.353
3320	AB023164	Homo sapiens KIAA0947 protein	9067	100.000
3321	X89985	Homo sapiens BCL7B	1109	96.629
3322	L08475	Xenopus laevis ubiquitin-like fusion protein	582	38.936
3323	Y07829	Homo sapiens RING finger protein	2983	97.516
3324	Z66519	Caenorhabditis elegans similar to Thiamine pyrophosphate enzymes; cDNA EST EMBL:D36315 comes from this gene; cDNA EST EMBL:D33464 comes from this gene	1141	44.550
3325	AC005581	Homo sapiens R31237 1, partial CDS	439	96.825
3326	U80082	Homo sapiens putative protein B2	5058	100.000
3327	AB011113	Homo sapiens KIAA0541 protein	7644	99.828
3328	AF061443	Rattus norvegicus G protein-coupled receptor LGR4	1574	91.603
3329	AC007168	Arabidopsis thaliana hypothetical protein	157	44.643
3330	AB002365	Homo sapiens KIAA0367	4745	99.860
3331	AL080173	Homo sapiens hypothetical protein	2968	100.000
3332	AF067864	Homo sapiens transferrin receptor 2 alpha	5197	99.501
3333	X64587	Mus musculus orf	3202	99.184
3334	U22232	Felis catus ribosomal protein S4	1702	99.237
3335	AB000910	Sus scrofa ribosomal protein	168	72.917
3336	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	6446	81.135
3337	AF094480	Homo sapiens cholesterol 24-hydroxylase	3332	100.000
3338	AB006622	Homo sapiens No similarities to any reported proteins	8935	100.000
3339	AB018273	Homo sapiens KIAA0730 protein	6572	99.801
3340	X03484	Homo sapiens raf protein (aa 1-648)	2262	88.993
3341	U87305	Rattus norvegicus transmembrane receptor UNC5H1	2655	93.119
3342	X97490	Mus musculus PNG protein	445	70.833
3343	M74509	Homo sapiens , gene product	541	87.255
3344	X98654	Homo sapiens homologue of Drosophila retinal degeneration B gene	7913	98.030
3345	AL035289	Homo sapiens hypothetical protein	5256	100.000
3346	AF132160	Drosophila melanogaster unknown	601	54.187
3347	M22332	Homo sapiens unknown protein	166	26.050
3348	AB020695	Homo sapiens KIAA0888 protein	4258	98.108
3349	AB012162	Homo sapiens APCL protein	14441	100.000
3350	AF011359	Bos taurus regulator of G-protein signaling 7	2957	98.874
3351	AL050321	Homo sapiens dJ717M23.1 (novel gene)	4999	99.868
3352	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B	329	86.441

		retroviruses and to class II HERVs		
3353	AF182946	Rattus norvegicus BRCA1-associated RING domain protein 1	449	41.711
3354	AB002299	Homo sapiens KIAA0301	13484	99.951
3355	L08483	Drosophila melanogaster ring canal protein	466	31.104
3356	AL080198	Homo sapiens hypothetical protein	4659	99.713
3357	X73874	Homo sapiens phosphorylase kinase	4572	98.770
3358	U21163	Ictalurus punctatus No definition line found	449	71.698
3359	AF083249	Homo sapiens Rb binding protein homolog	2736	98.265
3360	AB007931	Homo sapiens KIAA0462 protein	14285	98.466
3361	A01592	Homo sapiens haemoglobin A beta chain	329	81.159
3362	U41387	Homo sapiens Gu protein	5179	99.750
3363	X71997	Rattus norvegicus myosin I	4970	98.037
3364	AF071076	Homo sapiens Nup98-Nup96 precursor	11033	98.775
3365	AB006630	Homo sapiens KIAA0292	11483	99.883
3366	AF038554	Homo sapiens density regulated protein drp1	1548	98.745
3367	U29659	Human endogenous retrovirus pol gene product	206	42.708
3368	AB000884	Sus scrofa glutathione S-transferase	390	78.571
3369	AF151800	Homo sapiens CGI-41 protein	587	99.010
3370	AF151889	Homo sapiens CGI-131 protein	430	81.395
3371	AJ131581	Homo sapiens latrophilin-2	6260	94.515
3372	AF077030	Homo sapiens hypothetical 43.2 kDa protein	496	73.684
3373	D83776	Homo sapiens The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.	10130	99.081
3374	AF145681	Drosophila melanogaster BcDNA.LD23181	1099	36.813
3375	AL050022	Homo sapiens hypothetical protein	4172	99.675
3376	AF054284	Homo sapiens spliceosomal protein SAP 155	8400	98.471
3377	U72194	Mus musculus muskulin	1229	94.359
3378	Z70038	Homo sapiens Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from	436	38.298
3379	L14684	Rattus norvegicus elongation factor G	2295	86.885
3380	X96586	Homo sapiens FAN protein	4394	99.695
3381	AF076612	Homo sapiens chordin	5666	99.750
3382	AL080159	Homo sapiens hypothetical protein	2446	99.169
3383	AF139639	Oryctolagus cuniculus serum and glucocorticoid-regulated protein kinase	1791	67.990
3384	AC003058	Arabidopsis thaliana unknown protein	443	43.671
3385	AB019409	Homo sapiens unique gene expressed in fibroblasts of periodontal ligament	942	88.780
3386	AF125392	Homo sapiens insulin induced protein 2	1354	99.048
3387	AL050261	Homo sapiens hypothetical protein	296	58.333
3388	U44803	Rattus norvegicus ovarian-specific protein	1501	78.472
3389	X66285	Mus musculus HC1 ORF	207	43.243
3390	AC004542	Homo sapiens OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308)	2447	99.461
3391	AF067164	Homo sapiens zinc finger protein 2	1051	67.647
3392	Z78018	Caenorhabditis elegans predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene	1442	35.812
3393	AB011084	Homo sapiens KIAA0512 protein	963	43.026
3394	AB018288	Homo sapiens KIAA0745 protein	1002	63.248
3395	U12535	Homo sapiens epidermal growth factor receptor kinase substrate	1336	42.159

3396	AF009674	Homo sapiens axin	6111	99.667
3397	AF049528	Homo sapiens huntingtin-interacting protein HYPA/FBP11	2902	99.115
3398	D86978	Homo sapiens similar to a C.elegans protein encoded in cosmid K12D12 (Z49069)	13202	99.950
3399	Z15005	Homo sapiens CENP-E	3619	93.344
3400	AB011166	Homo sapiens KIAA0594 protein	5703	100.000
3401	AC007229	Homo sapiens dynamin II {AA 474- 866}	474	88.889
3402	D63487	Homo sapiens The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8.	4319	99.844
3403	AL032626	Caenorhabditis elegans predicted using Genefinder	322	47.826
3404	X63563	Homo sapiens RNA polymerase II 140 kDa subunit	4568	96.728
3405	D88315	Mus musculus tetracycline transporter-like protein	1371	70.279
3406	AB026257	Homo sapiens organic anion transporter OATP-C	1047	35.031
3407	AL080220	Homo sapiens hypothetical protein	2359	100.000
3408	AJ005898	Homo sapiens shal-type potassium channel	4209	99.691
3409	U03399	Homo sapiens T-complex protein 10A	801	74.011
3410	AF111170	Homo sapiens unknown	1357	100.000
3411	AB029032	Homo sapiens KIAA1109 protein	12865	99.898
3412	U22376	Homo sapiens alternatively spliced product using exon 13A	326	72.368
3413	X78926	Homo sapiens zinc finger protein	2804	98.500
3414	AF064254	Homo sapiens very long-chain acyl-CoA synthetase homolog 1; VLCS-H1	3003	96.473
3415	AF090834	Homo sapiens malonyl coenzyme A decarboxylase	3243	100.000
3416	D38521	Homo sapiens The ha0919 gene product is novel.	11907	99.333
3417	AF023674	Homo sapiens nephrocystin	4666	98.909
3418	D86957	Homo sapiens similar to Drosophila melanogaster septin (sep2).	2094	69.456
3419	L41686	Rattus norvegicus ORF	219	30.435
3420	AF062378	Mus musculus calmodulin-binding protein SHA1	1641	68.085
3421	Z36948	Unknown contains a valine and arginine rich domain, possesses weak similarity with the RNA binding	243	46.212
3422	AB014524	Homo sapiens KIAA0624 protein	13154	99.950
3423	X85991	Mus musculus semaphorin B	1768	78.916
3424	AC007018	Arabidopsis thaliana unknown protein	1778	42.653
3425	AB029040	Homo sapiens KIAA1117 protein	8856	99.927
3426	AB028956	Homo sapiens KIAA1033 protein	7779	100.000
3427	AB014576	Homo sapiens KIAA0676 protein	8297	99.367
3428	AF094508	Homo sapiens dentin phosphoryn	193	20.090
3429	AF094758	Homo sapiens nasopharyngeal epithelium specific protein 1	1779	98.940
3430	AC006135	Arabidopsis thaliana putative vicilin storage protein (globulin-like)	358	31.250
3431	AL110210	Homo sapiens hypothetical protein	6927	99.899
3432	M24401	Mus musculus zinc finger protein	527	29.032
3433	AB014534	Homo sapiens KIAA0634 protein	8726	99.244
3434	AF145632	Drosophila melanogaster BcDNA.GH06032	2127	51.073
3435	AF005632	Homo sapiens phosphodiesterase I/nucleotide pyrophosphatase beta	6023	99.543
3436	AB016930	Cricetulus griseus Phosphatidylglycerophosphate	3235	89.292

		synthase		
3437	AL031765	Unknown /prediction=(method:"genefinder", version:"084", score:"31.96"); /prediction=(metho	463	35.021
3438	AB023151	Homo sapiens KIAA0934 protein	6529	79.710
3439	AF155112	Homo sapiens NY-REN-50 antigen	1773	100.000
3440	AF124726	Homo sapiens acinusL	8287	99.070
3441	AF132180	Drosophila melanogaster unknown	796	36.267
3442	Z66524	Caenorhabditis elegans Homology with Squid retinal-binding protein (PIR Acc. No. A53057); cDNA EST yk463d10.3 comes from this gene; cDNA EST yk663h12.3 comes from this gene	1534	44.925
3443	AC007017	Arabidopsis thaliana putative RNA helicase A	936	40.690
3444	M26576	Homo sapiens alpha-1 type IV collagen	12444	99.880
3445	AC004381	Homo sapiens Unknown gene product	2096	76.321
3446	AF126867	Mus musculus calpain-like protease	1171	75.229
3447	X98411	Homo sapiens myosin-IE	1052	89.888
3448	AB018339	Homo sapiens KIAA0796 protein	7069	99.722
3449	U49829	Caenorhabditis elegans short region of weak similarity to human follicular variant translocation protein 1 precursor (FVT-1) (GB:X63657)	152	38.053
3450	AB007925	Homo sapiens KIAA0456 protein	7124	99.635
3451	AL110295	Schizosaccharomyces pombe hypothetical protein	173	44.156
3452	Z81569	Caenorhabditis elegans K11B4.2	188	33.663
3453	D86957	Homo sapiens similar to Drosophila melanogaster septin (sep2).	3283	100.000
3454	AF131739	Homo sapiens Unknown	354	48.077
3455	U62961	Homo sapiens succinyl CoA:3-oxoacid CoA transferase precursor	1658	75.802
3456	AF020760	Homo sapiens serine protease	2004	92.655
3457	AF152961	Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit	5752	99.665
3458	U89876	Mus musculus ALY	1419	93.562
3459	AF020261	Santalum album proline rich protein	264	41.060
3460	AC002544	Homo sapiens Unknown gene product splice form-1	1337	82.186
3461	AB029022	Homo sapiens KIAA1099 protein	1600	58.085
3462	U76638	Homo sapiens BRCA1-associated RING domain protein	284	29.231
3463	AF007152	Homo sapiens unknown	2948	100.000
3464	D80001	Homo sapiens similar to hypothetical protein D4478 of S.cerevisiae.	4857	98.558
3465	AB018347	Homo sapiens KIAA0804 protein	7881	99.423
3466	AL009266	Homo sapiens hypothetical protein	889	56.623
3467	Z38011	Mus musculus DMR-N9	902	51.203
3468	AB014557	Homo sapiens KIAA0657 protein	5242	100.000
3469	AF176069	Homo sapiens ubiquilin	3836	99.832
3470	AF139923	Mus musculus receptor-activated calcium channel	576	76.119
3471	AJ131244	Homo sapiens Sec24A protein	7090	99.907
3472	AF121858	Homo sapiens sorting nexin 8	2551	94.444
3473	AF042838	Homo sapiens MEK kinase 1	9864	99.666
3474	U62325	Homo sapiens FE65-like protein	4917	99.454
3475	AC007017	Arabidopsis thaliana putative RNA helicase A	1507	44.128
3476	AL050367	Homo sapiens hypothetical protein	5840	99.327
3477	Z82090	Unknown similar to Alpha-2-macroglobulin family	539	31.844

		(3 domains); cDNA EST EMBL:D67502 comes from this g		
3478	AL050156	Homo sapiens hypothetical protein	2269	100.000
3479	U05343	Mus musculus zinc finger protein PZF	1083	95.906
3480	U57368	Mus musculus EGF repeat transmembrane protein	4656	94.102
3481	L20900	Rattus norvegicus autoantigen p69	536	38.138
3482	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase	4297	99.848
3483	AF127142	Homo sapiens NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2,6-sialyltransferase alpha2,6-sialyltransferase	809	47.510
3484	D44480	Mus musculus MATH-2 protein	1674	99.592
3485	AF173937	Homo sapiens secreted protein of unknown function	1013	98.160
3486	AF059516	Homo sapiens tolloid-like 2 protein	7115	100.000
3487	AB018329	Homo sapiens KIAA0786 protein	6700	99.804
3488	AF055666	Mus musculus kinesin light chain 2	790	69.417
3489	AF073481	Homo sapiens polycystin-L	5199	99.009
3490	AF041483	Homo sapiens histone macroH2A1.2	180	86.842
3491	AL117626	Homo sapiens hypothetical protein	704	47.857
3492	D87742	Homo sapiens Similar to Human C219-reactive peptide (L34688)	7834	99.749
3493	X59131	Homo sapiens hypothetical protein	7217	99.634
3494	U11036	Homo sapiens Ibd1	355	97.297
3495	AB025258	Mus musculus granuphilin-a	680	38.344
3496	Y08134	Homo sapiens acid sphingomyelinase-like phosphodiesterase	3187	99.140
3497	AB017563	Homo sapiens IGSF4	242	56.757
3498	AB028983	Homo sapiens KIAA1060 protein	5731	99.887
3499	AF074091	Homo sapiens islet-brain 1	4770	98.312
3500	AF015287	Homo sapiens serine protease	1109	55.593
3501	AB007903	Homo sapiens KIAA0443	664	28.660
3502	AF056116	Fugu rubripes unknown	1400	57.398
3503	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038)	1188	98.953
3504	U32743	Haemophilus influenzae Rd fucose operon protein (fucU)	286	44.203
3505	Y08715	Mus musculus vascular cadherin-2	283	26.439
3506	Z73428	Unknown predicted using Genefinder; cDNA EST EMBL:T01774 comes from this gene; cDNA EST yk470a9.3 c	565	44.053
3507	AL080170	Homo sapiens hypothetical protein	2968	99.772
3508	AF151807	Homo sapiens CGI-49 protein	2752	99.532
3509	D88747	Arabidopsis thaliana AR401	450	39.336
3510	U47024	Mus musculus MEM3	3396	97.101
3511	Y09022	Homo sapiens Not56-like protein	1730	100.000
3512	AF116826	Homo sapiens putative protein-tyrosine kinase	4796	99.723
3513	U93181	Homo sapiens nuclear dual-specificity phosphatase	11068	99.000
3514	AB011180	Homo sapiens KIAA0608 protein	5244	99.871
3515	X73882	Homo sapiens microtubule associated protein	708	39.868
3516	AC004475	Homo sapiens F23858 1	3752	97.213
3517	D87071	Homo sapiens similar to C.elegans protein	693	56.054

		encoded in cosmid T20D3 (Z68220).		
3518	U93868	Homo sapiens RNA polymerase III subunit	447	46.196
3519	X84693	Mus musculus testis nuclear RNA binding protein	1245	88.444
3520	AF134726	Homo sapiens NG37	3676	98.435
3521	AF070594	Homo sapiens HNK-1 sulfotransferase	403	28.344
3522	AF121080	Mus musculus cAMP inducible 1 protein	2332	81.406
3523	AF141315	Homo sapiens alpha-1,4-N-acetylglucosaminyltransferase	336	36.301
3524	U72520	Mus musculus mena protein	1198	80.992
3525	AJ003125	Homo sapiens procollagen I N-proteinase	8516	99.422
3526	Z19585	Homo sapiens thrombospondin-4	2679	99.737
3527	AF111785	Homo sapiens myosin heavy chain IIx/d	12060	99.433
3528	U43148	Homo sapiens patched gene homolog; similar to Drosophila patched protein, Swiss-Prot Accession Number P18502; transmembrane protein; Method: conceptual translation supplied by author	364	70.930
3529	AB002361	Homo sapiens KIAA0363	9948	99.277
3530	D31886	Homo sapiens KIAA0066	6604	100.000
3531	AF062389	Rattus norvegicus kidney-specific protein	1795	78.593
3532	AB020716	Homo sapiens KIAA0909 protein	8247	98.464
3533	D89285	Mesocricetus auratus inter-alpha-trypsin inhibitor heavy chain 1	939	34.375
3534	AB023221	Homo sapiens KIAA1004 protein	1327	67.266
3535	D38231	Oryza sativa RWD	192	31.707
3536	AF071544	Spinacia oleracea ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	405	28.090
3537	AJ131245	Homo sapiens Sec24B protein	8242	99.370
3538	A48861	Homo sapiens unnamed protein product	410	40.711
3539	A31036	Nicotiana glauca PRP2	126	41.270
3540	AJ222636	Homo sapiens hypothetical protein	1372	100.000
3541	U80747	Homo sapiens CAGH3	256	97.619
3542	AB020716	Homo sapiens KIAA0909 protein	8247	98.464
3543	AF151822	Homo sapiens CGI-64 protein	591	96.386
3544	AB011665	Mus musculus BAZF	2205	87.569
3545	AL096881	Homo sapiens hypothetical protein	432	45.143
3546	U41060	Homo sapiens LIV-1 protein	483	45.087
3547	AF064748	Mus musculus S3-12	405	63.158
3548	AF032666	Rattus norvegicus rsec5	3300	90.893
3549	D50925	Homo sapiens The KIAA0135 gene is related to pim-1 oncogene.	8355	99.597
3550	U79260	Homo sapiens unknown	333	70.886
3551	AL022314	Homo sapiens dJ1170K4.1 (novel protein similar to KIAA0176 and mouse, worm and fly proteins)	1658	89.655
3552	AB020671	Homo sapiens KIAA0864 protein	7713	99.590
3553	AL031033	Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase (EC 4.2.1.70, Pseudouridylate Synthase, Uracil Hydrolase) LIKE protein)	2175	100.000
3554	AL009196	Unknown /prediction=(method:"genefinder", version:"084"); /prediction=(method:"genscan", ve	487	53.049
3555	AF132608	Homo sapiens histone deacetylase 5	7365	99.114
3556	U61538	Homo sapiens calcium-binding protein chp	221	31.928

3557	L07335	Homo sapiens putative	2166	99.085
3558	AB011173	Homo sapiens KIAA0601 protein	5852	100.000
3559	D79991	Homo sapiens putative hydrophobic domain in amino acid positions 373-390.	11158	99.712
3560	AF125451	Caenorhabditis elegans contains similarity to the NIFR3/SMM1 family	444	68.687
3561	U75467	Drosophila melanogaster Atu	599	54.974
3562	AL096750	Homo sapiens hypothetical protein	6025	93.699
3563	Y18314	Homo sapiens paraplegin-like protein	880	66.234
3564	AF177292	Homo sapiens genethonin 3	2211	100.000
3565	X97675	Homo sapiens plakophilin 2b	1407	99.556
3566	AL034399	Homo sapiens dA191P20.2 (novel Fibronectin type III domain containing protein similar to Ring finger protein MID1 (Midline 1))	2843	99.770
3567	S45936	Homo sapiens HTS1	1434	49.772
3568	AF045244	Klebsiella pneumoniae ribitol kinase	768	41.617
3569	AF155108	Homo sapiens NY-REN-41 antigen	1578	100.000
3570	AL022394	Homo sapiens dJ511B24.3 (KIAA0395 (probable Zinc Finger Homeobox protein))	3860	99.829
3571	X74654	Zea mays beta3 tubulin	876	33.698
3572	U17133	Rattus norvegicus ZnT-1	1945	81.671
3573	AJ010317	Fugu rubripes Sand	1593	68.232
3574	AB011180	Homo sapiens KIAA0608 protein	1272	77.366
3575	AF115313	Thermomonospora curvata PkWA	249	27.099
3576	X52138	Homo sapiens L7a protein	296	60.784
3577	AF097887	Rattus norvegicus Chp	840	61.321
3578	AC005005	Homo sapiens similar to phosphatidylinositol (4,5)bisphosphate 5-phosphatase; match to PID:g1399105	7224	99.905
3579	AF130366	Homo sapiens LISCH protein	4074	99.327
3580	AF045642	Caenorhabditis elegans No definition line found	446	29.762
3581	AF170723	Homo sapiens protein kinase STK10	435	43.386
3582	AL110124	Homo sapiens hypothetical protein	3965	99.836
3583	X62446	Gallus gallus PR 264	877	62.105
3584	AF119334	Homo sapiens zinc finger protein FOG-2	7618	99.298
3585	Y16187	Homo sapiens metalloproteinase	1830	98.127
3586	AF030430	Mus musculus semaphorin VIA	2240	91.826
3587	U73199	Mus musculus Rho-guanine nucleotide exchange factor	655	57.292
3588	AJ388553	Canis familiaris hypothetical protein	536	73.529
3589	AL050051	Homo sapiens hypothetical protein	774	100.000
3590	U66003	Xenopus laevis ADAM 13	1196	50.920
3591	AC006276	Homo sapiens R28379 3	452	56.376
3592	M31209	Gallus gallus skeletal muscle C-protein	374	35.096
3593	AF000657	Arabidopsis thaliana hypothetical protein	423	32.886
3594	AF152101	Homo sapiens paracellin-1	1810	98.168
3595	AB018253	Rattus norvegicus voltage-gated ca channel	2023	85.946
3596	D80005	Homo sapiens KIAA0183	7286	99.812
3597	AF015041	Homo sapiens NUMB-R protein	3525	99.625
3598	AF083384	Homo sapiens 45kDa splicing factor; SPF 45	1387	94.937
3599	AF067946	Caenorhabditis elegans similar to Drosophila ring canal protein (kelch) (SW:Q04652)	279	27.160
3600	U63648	Mus musculus p160 myb-binding protein	373	58.974
3601	L41690	Homo sapiens tumor necrosis factor receptor type 1 associated protein	2149	99.390

3602	U22376	Homo sapiens alternatively spliced product using exon 13A	445	82.353
3603	AC005896	Arabidopsis thaliana unknown protein	245	29.697
3604	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	162	60.870
3605	X06256	Homo sapiens integrin alpha 5 subunit precursor	7007	99.333
3606	U18018	Homo sapiens adenovirus E1A enhancer binding protein	3850	100.000
3607	U37439	Homo sapiens endoglin	4202	99.544
3608	AF003130	Caenorhabditis elegans No definition line found	324	35.088
3609	AB029041	Homo sapiens KIAA1118 protein	7413	99.485
3610	U29056	Mus musculus Src-like adapter protein	514	39.286
3611	AF136450	Homo sapiens goodpasture antigen-binding protein	4158	99.519
3612	AF074329	Mus musculus SH2-B PH domain containing signaling mediator 1 gamma isoform	3244	90.185
3613	AC006135	Arabidopsis thaliana putative vicilin storage protein (globulin-like)	258	26.642
3614	X52949	Giardia intestinalis unidentified reading frame; alternative codon use	207	36.257
3615	X82209	Homo sapiens MN1	3066	100.000
3616	AF132949	Homo sapiens CGI-15 protein	390	95.522
3617	AB028999	Homo sapiens KIAA1076 protein	5582	100.000
3618	L26335	Cavia porcellus zinc finger protein	899	93.333
3619	AB014553	Homo sapiens KIAA0653 protein	3829	99.821
3620	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	317	58.182
3621	U20780	Mus musculus ubiquitinating enzyme E2-230 kDa	906	86.420
3622	D25218	Homo sapiens KIAA0112	2639	100.000
3623	U10536	Pan paniscus MHC class I A	872	84.049
3624	L00352	Homo sapiens low density lipoprotein receptor	4599	99.850
3625	AL031228	Homo sapiens dJ1033B10.10 (membrane protein with histidine rich charge clusters (HKE4, RING5))	593	38.920
3626	AB000215	Rattus norvegicus CCA1 protein	387	84.932
3627	AL032660	Caenorhabditis elegans predicted using Genefinder	521	31.949
3628	L39211	Homo sapiens carnitine palmitoyltransferase I	608	53.293
3629	AF003130	Caenorhabditis elegans No definition line found	865	40.625
3630	AF057026	Rattus norvegicus protein kinase KID-1	1480	94.444
3631	U90143	Homo sapiens butyrophilin protein	207	33.813
3632	AB007883	Homo sapiens KIAA0423	10829	99.529
3633	AB023227	Homo sapiens KIAA1010 protein	8670	99.848
3634	Z94864	Schizosaccharomyces pombe hypothetical protein	384	36.923
3635	U22376	Homo sapiens alternatively spliced product using exon 13A	320	71.084
3636	AF111105	Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2	3994	98.546
3637	AF123880	multiple sclerosis associated retrovirus element unknown protein U5/1	317	79.032
3638	AB020720	Homo sapiens KIAA0913 protein	2943	98.633
3639	U15131	Homo sapiens p126	2467	64.726
3640	Y09631	Homo sapiens PIBF1 protein	643	79.452
3641	AL035263	Schizosaccharomyces pombe hypothetical protein	628	24.409

3642	AL050283	Homo sapiens hypothetical protein	976	54.015
3643	AF037454	Mus musculus ubiquitin protein ligase	5172	95.758
3644	AJ005891	Homo sapiens JM2	620	38.671
3645	AF149413	Arabidopsis thaliana contains similarity to protein kinase domains; Pfam PF00069, Score=15.8, E=0.0027, N=1	406	48.052
3646	M83297	Rattus norvegicus protein phosphatase 2A 55 kD regulatory subunit B	1912	78.919
3647	Z19152	Caenorhabditis elegans cDNA EST EMBL:T02216 comes from this gene; cDNA EST yk193b5.3 comes from this gene; cDNA EST yk193b5.5 comes from this gene	364	29.218
3648	U95044	Homo sapiens zinc finger protein	1472	82.449
3649	X92666	Bos taurus cysteine string protein	329	82.258
3650	AB002384	Homo sapiens KIAA0386	715	29.856
3651	Z99709	Caenorhabditis elegans cDNA EST EMBL:D73217 comes from this gene; cDNA EST yk478c5.3 comes from this gene; cDNA EST EMBL:M89187 comes from this gene	237	28.044
3652	U71383	Homo sapiens OB binding protein-2	578	96.809
3653	U09874	Mus musculus SKD3	3142	95.050
3654	U79260	Homo sapiens unknown	318	70.513
3655	D87458	Homo sapiens Similar to Human estrogen-responsive finger protein, efp (A49656)	3757	99.636
3656	AB014522	Homo sapiens KIAA0622 protein	8194	99.153
3657	D87470	Homo sapiens KIAA0280	784	53.252
3658	AF082657	Homo sapiens Era GTPase A protein	2941	99.774
3659	AF123344	Homo sapiens Kruppel-like zinc finger transcription factor	2537	99.155
3660	U23172	Caenorhabditis elegans No definition line found	197	40.206
3661	L25125	Mus musculus RNA helicase	533	100.000
3662	AL049955	Homo sapiens hypothetical protein	1060	87.958
3663	U21556	Homo sapiens similar to rat integral membrane glycoprotein, PIR Accession Number A40670	2083	91.193
3664	AC008075	Arabidopsis thaliana F24J5.4	224	35.075
3665	D86983	Homo sapiens similar to D.melanogaster peroxidase(U11052)	10048	99.466
3666	AB018313	Homo sapiens KIAA0770 protein	4841	100.000
3667	AB028989	Homo sapiens KIAA1066 protein	7056	99.625
3668	U13262	Mus musculus myelin gene expression factor	701	80.714
3669	X85019	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase	1777	52.008
3670	D87325	Mus musculus GSG1	471	45.588
3671	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	191	71.739
3672	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	289	78.689
3673	U41543	Unknown Similar to Rat trg gene product; coded for by C. elegans cDNA yk31e7.5; coded for by C. ele	881	45.652
3674	AL110490	Caenorhabditis elegans predicted using Genefinder	481	51.266
3675	U22376	Homo sapiens alternatively spliced product using exon 13A	445	82.353
3676	U22376	Homo sapiens alternatively spliced product using exon 13A	445	82.353

3677	X64995	Homo sapiens HGMP07J	856	55.469
3678	AB007862	Homo sapiens KIAA0402	11152	99.885
3679	AB002374	Homo sapiens KIAA0376	5532	99.548
3680	AB020671	Homo sapiens KIAA0864 protein	7713	99.590
3681	AC006201	Arabidopsis thaliana hypothetical protein	261	27.397
3682	AF124490	Homo sapiens ARF GTPase-activating protein GIT1	3300	96.507
3683	X75887	Bos taurus brevicin	5154	89.180
3684	AF036249	Mus musculus polymerase I-transcript release factor; PTRF	2102	93.817
3685	U95031	Homo sapiens sublingual gland mucin	6305	99.659
3686	U94991	Xenopus laevis transcription factor XLM01	535	77.451
3687	AC004021	Homo sapiens kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096)	582	32.773
3688	Z47811	Unknown similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D34519 comes from this gene	266	34.228
3689	AF117756	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP150	852	93.197
3690	Y07800	Oryctolagus cuniculus ryanodine receptor	760	91.597
3691	D86957	Homo sapiens similar to Drosophila melanogaster septin (sep2).	2094	69.456
3692	Z19555	Unknown predicted using Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:	2434	65.177
3693	X73608	Homo sapiens testican	2368	95.628
3694	AB014533	Homo sapiens KIAA0633 protein	8740	99.393
3695	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	333	70.588
3696	AL021816	Schizosaccharomyces pombe SPBC24E9.03c, unknown, len:251aa	207	34.694
3697	D50913	Homo sapiens The KIAA0123 gene product is related to rat general mitochondrial matrix processing protease (MPP).	3457	99.811
3698	D87930	Homo sapiens myosin phosphatase target subunit 1	532	34.483
3699	AJ133488	Bos taurus SCO-spondin	1570	79.377
3700	AJ001981	Homo sapiens OXA1L	3268	98.400
3701	AF061936	Homo sapiens diacylglycerol kinase iota	7093	99.438
3702	AL034417	Homo sapiens bK215D11.2 (similar to rat gene 33)	2219	98.176
3703	AL080143	Homo sapiens hypothetical protein	2615	96.649
3704	D78020	Rattus norvegicus NFI-A4	413	81.579
3705	AB001772	Ciona savignyi PEM-5	380	35.217
3706	AF133086	Homo sapiens membrane-type serine protease 1	5839	99.647
3707	AB020654	Homo sapiens KIAA0847 protein	4251	100.000
3708	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	165	46.154
3709	U37143	Homo sapiens cytochrome P450 monooxygenase CYP2J2	1025	43.056
3710	AF067972	Homo sapiens DNA cytosine methyltransferase 3 alpha	6312	99.233
3711	X83957	Homo sapiens nebulin	6801	98.712
3712	D10250	Homo sapiens alpha-fetoprotein enhancer binding protein	821	45.556
3713	AC004794	Homo sapiens F02569 2	1052	79.630

3714	AJ000644	Homo sapiens SPOP	933	71.635
3715	AC006029	Homo sapiens Similar to Sperm Surface Protein PH-20; Similar to P38568 (PID:585674)	3039	99.585
3716	X62528	Rattus norvegicus ribonuclease inhibitor	614	38.909
3717	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	843	64.362
3718	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	347	63.107
3719	M35297	Rattus norvegicus G-protein coupled receptor	286	75.385
3720	AB024400	Rattus norvegicus LAT4	832	57.627
3721	U79775	Homo sapiens NNP-1/Nop52	759	96.667
3722	Z83838	Homo sapiens GTPASE-ACTIVATING PROTEIN	2113	99.676
3723	U90653	Homo sapiens DHHC-domain-containing cysteine-rich protein	290	37.500
3724	AB029016	Homo sapiens KIAA1093 protein	815	54.122
3725	U10991	Homo sapiens G2	10859	99.764
3726	U41543	Unknown Similar to Rat trg gene product; coded for by C. elegans cDNA yk31e7.5; coded for by C. ele	948	41.289
3727	U76373	Mus musculus skm-BOP1	1636	91.760
3728	AF155595	Homo sapiens CoREST protein	3121	100.000
3729	AF167320	Mus musculus zinc finger protein ZFP113	877	72.189
3730	AB011089	Homo sapiens KIAA0517 protein	5113	99.114
3731	AC004542	Homo sapiens OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308)	580	77.778
3732	U80745	Homo sapiens CTG7a	2275	98.841
3733	Z75536	Caenorhabditis elegans similar to dynein heavy chain; cDNA EST EMBL:D27549 comes from this gene; cDNA EST EMBL:D34859 comes from this gene	244	35.385
3734	AJ002424	Rattus norvegicus p65 protein	1152	63.235
3735	L36434	Mus musculus basic domain/leucine zipper transcription factor	459	84.884
3736	D80005	Homo sapiens KIAA0183	7297	99.906
3737	U79263	Homo sapiens unknown	2128	99.115
3738	X55126	Mus musculus Zfp-29	648	39.858
3739	U81375	Homo sapiens equilibrative nucleoside transporter 1	510	36.965
3740	U22376	Homo sapiens alternatively spliced product using exon 13A	444	73.404
3741	AJ001531	Homo sapiens neurotrypsin	6316	99.657
3742	X66405	Mus musculus collagen alpha1 type VI-precursor	6248	90.578
3743	X66902	Mus musculus En-2/lacZ fusion protein	402	92.857
3744	AF121081	Mus musculus cAMP inducible 2 protein	395	90.000
3745	AB020671	Homo sapiens KIAA0864 protein	7713	99.590
3746	U75329	Homo sapiens serine protease	577	42.512
3747	D86980	Homo sapiens KIAA0227	447	63.793
3748	U22376	Homo sapiens alternatively spliced product using exon 13A	322	62.245
3749	AB023206	Homo sapiens KIAA0989 protein	5583	99.767
3750	X52949	Giardia intestinalis unidentified reading frame; alternative codon use	181	35.065
3751	AB011105	Homo sapiens KIAA0533 protein	10943	99.818
3752	L07809	Homo sapiens dynamin	323	77.049
3753	AB028957	Homo sapiens KIAA1034 protein	4933	98.558
3754	AF078165	Homo sapiens conductin	4436	98.678
3755	X52876	Gallus gallus myosin light chain kinase	263	38.312

3756	U23452	Caenorhabditis elegans No definition line found	355	40.397
3757	U80445	Unknown coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by	1584	45.819
3758	U80223	Drosophila melanogaster eukaryotic initiation factor eIF-2 alpha kinase; DGCN2	372	27.586
3759	U12392	Haematobia irritans putative ATPase	628	45.588
3760	Y15913	Homo sapiens COL1A1 and PDGFB fusion transcript	102	41.071
3761	AL050089	Homo sapiens hypothetical protein	5354	99.753
3762	AF063231	Mus musculus cytoplasmic dynein intermediate chain 2	3011	96.646
3763	AF151840	Homo sapiens CGI-82 protein	639	54.040
3764	AB014600	Homo sapiens KIAA0700 protein	7538	99.735
3765	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	425	75.610
3766	D42055	Homo sapiens KIAA0093 gene product is related to NEDD-4 protein.	6302	99.892
3767	M27685	Mus musculus ultra-high sulphur keratin	396	39.759
3768	AL031177	Homo sapiens dJ889M15.3 (novel protein)	366	30.534
3769	AF128527	Homo sapiens breast cancer associated gene 1 protein	768	42.663
3770	AL022393	Homo sapiens p373c6.1	3523	100.000
3771	U66496	Homo sapiens leptin receptor	265	63.380
3772	M34915	Bos taurus retina-specific 15.7 kDa protein	376	57.778
3773	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	1155	61.056
3774	D88750	Bacillus circulans beta-galactosidase	434	36.792
3775	Z50097	Drosophila melanogaster hdc protein	691	30.839
3776	U83246	Homo sapiens copine I	1011	53.667
3777	AB014516	Homo sapiens KIAA0616 protein	263	36.757
3778	AL031393	Homo sapiens dJ733D15.1 (Zinc-finger protein)	562	41.026
3779	Z24725	Homo sapiens mitogen inducible gene mig-2	4368	95.921
3780	U37376	Xenopus laevis MAM domain protein	1475	66.134
3781	AC007228	Homo sapiens BC37295 2 (partial)	1091	100.000
3782	AF124440	Homo sapiens MAGE tumor antigen D1	1496	57.176
3783	AF043695	Caenorhabditis elegans similar to the protein phosphates 2c family	732	37.789
3784	AL049733	Homo sapiens dJ875H3.1 (APK1 antigen)	1628	81.034
3785	AC006225	Arabidopsis thaliana putative multidrug resistance protein	948	45.723
3786	AB001636	Homo sapiens ATP-dependent RNA helicase #46	480	36.134
3787	U63839	Rattus norvegicus nucleoporin p58	701	94.017
3788	U75329	Homo sapiens serine protease	782	39.441
3789	AF127389	Rattus norvegicus putative taste receptor TR1	1201	43.715
3790	X80038	Homo sapiens Polio virus receptor protein	2979	99.560
3791	AF143003	Perca flavescens lysyl oxidase related protein homolog	1350	58.610
3792	S44213	Saccharomyces cerevisiae, Peptide, 323 aa YKL522=mitochondrial ADP/ATP carrier protein homolog	479	35.918
3793	AB018342	Homo sapiens KIAA0799 protein	4494	97.899
3794	Z29371	Oryctolagus cuniculus adenylyl cyclase type V	1178	100.000
3795	AF004715	Homo sapiens jerky gene product homolog	964	56.154
3796	AJ001403	Homo sapiens MUC5AC protein	7672	98.885
3797	X52875	Mus musculus Prx2	1371	88.845
3798	AF071172	Homo sapiens HERC2	533	32.626

3799	X75342	Homo sapiens Shb	3266	98.780
3800	M94362	Homo sapiens lamin B2	3268	99.806
3801	X67155	Homo sapiens mitotic kinase-like protein-1	4488	98.875
3802	AF132972	Homo sapiens CGI-38 protein	694	62.424
3803	U29156	Mus musculus involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	566	63.399
3804	AB011104	Homo sapiens KIAA0532 protein	10989	99.939
3805	AF088916	Homo sapiens emilin precursor	6793	99.902
3806	L41834	Ensis minor nuclear protein	466	31.944
3807	AF118889	Rattus norvegicus b-tomoyin isoform	2613	94.601
3808	L14009	Drosophila melanogaster zinc finger protein	294	39.655
3809	D38538	Anthocidaris crassispina dynein intermediate chain 2	320	61.250
3810	D79994	Homo sapiens similar to ankyrin of Chromatium vinosum.	352	54.918
3811	L04490	Homo sapiens NADH dehydrogenase (ubiquinone)	780	83.871
3812	M77003	Mus musculus glycerol-3-phosphate acyltransferase	1344	96.744
3813	U29501	Mus musculus Zfp67p	407	57.500
3814	AF055993	Homo sapiens mSin3A associated polypeptide p30	761	67.935
3815	AL080123	Homo sapiens hypothetical protein	828	60.317
3816	D80005	Homo sapiens KIAA0183	7297	99.906
3817	AL110490	Caenorhabditis elegans predicted using Genefinder	490	53.503
3818	L31840	Rattus norvegicus nuclear pore complex protein NUP107	3280	92.559
3819	D86976	Homo sapiens similar to C.elegans protein (Z37093)	7679	99.914
3820	X97230	Homo sapiens NK receptor	2968	98.621
3821	U22376	Homo sapiens alternatively spliced product using exon 13A	78	30.769
3822	Z97184	Homo sapiens BING1	2519	100.000
3823	AF041835	Homo sapiens laminin gamma 3 chain precursor	11183	99.685
3824	AF030430	Mus musculus semaphorin VIa	170	30.769
3825	AB014516	Homo sapiens KIAA0616 protein	323	31.915
3826	AB028948	Homo sapiens KIAA1025 protein	7802	100.000
3827	D88750	Bacillus circulans beta-galactosidase	433	36.792
3828	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	880	98.601
3829	D90716	Escherichia coli Hypothetical 18.7 kd protein in rhlE-dinG/rarB intergenic region (F160).	703	99.115
3830	AB018254	Homo sapiens KIAA0711 protein	285	31.818
3831	AC004010	Homo sapiens similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	3422	99.808
3832	D38538	Anthocidaris crassispina dynein intermediate chain 2	519	57.746
3833	D10355	Homo sapiens alanine aminotransferase	1410	67.230
3834	AF059611	Homo sapiens nuclear matrix protein NRP/B	1240	80.543
3835	D87467	Homo sapiens Similar to a C.elegans guanine nucleotide releasing factor homolog (S4 2368)	751	60.101
3836	AF022212	Homo sapiens Rho GTPase activating protein 6 isoform 2	4372	98.671
3837	AF135491	Mus musculus neuronal apoptosis inhibitory	364	23.143

		protein		
3838	AF089897	Homo sapiens topoisomerase-related function protein	701	72.414
3839	AC006951	Arabidopsis thaliana putative 3-oxoacyl carrier protein synthase II	1115	54.655
3840	AF104260	Homo sapiens hiwi	325	75.439
3841	X90849	Gallus gallus polybromo 1 protein	890	84.967
3842	AF045022	Bos taurus phosphatidic acid-preferring phospholipase A1	2411	91.847
3843	AC007661	Arabidopsis thaliana hypothetical protein	344	36.548
3844	AL080062	Homo sapiens hypothetical protein	2022	99.653
3845	D83536	Escherichia coli Acyl--UDP-n-acetylglucosamine o-acyltransferase (EC 2.3.1.129)	570	98.901
3846	AF115509	Homo sapiens LRR FLI-I interacting protein 2	2569	97.092
3847	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	261	80.000
3848	Z81143	Caenorhabditis elegans cDNA EST yk481g5.5 comes from this gene; cDNA EST yk508e4.3 comes from this gene	187	24.766
3849	AF181623	Drosophila melanogaster BcDNA.GH02974	494	43.655
3850	AF152097	Homo sapiens CGI-05 protein	3615	100.000
3851	AB018274	Homo sapiens KIAA0731 protein	7511	99.545
3852	X05472	Rattus norvegicus ORF 3	173	50.000
3853	D29954	Homo sapiens KIAA0056	9851	99.535
3854	AF126484	Homo sapiens CARD4	809	71.090
3855	AF151824	Homo sapiens CGI-66 protein	1228	81.304
3856	Z38102	Homo sapiens interleukin-11 receptor	197	87.500
3857	AF061346	Mus musculus Edp1 protein	195	59.091
3858	U58658	Homo sapiens unknown	291	51.546
3859	U70932	Peromyscus leucopus reverse transcriptase	150	43.137
3860	AB028997	Homo sapiens KIAA1074 protein	162	55.556
3861	AF028826	Homo sapiens Tax interaction protein 33	216	39.216
3862	AB012725	Mus musculus zinc finger protein	1900	84.046
3863	AF031835	Caenorhabditis elegans GLY5a; ppGaNTase	639	34.848
3864	A52806	unidentified unnamed protein product	1054	87.640
3865	X71666	Bos taurus calcineurin	366	75.641
3866	Z11793	Homo sapiens selenoprotein P	2557	99.475
3867	M29649	Otolemur crassicaudatus B-alpha-hemoglobin	169	41.772
3868	AF016448	Caenorhabditis elegans No definition line found	451	29.392
3869	AJ011856	Saccharomyces cerevisiae ORF Q0144	125	40.476
3870	A01592	Homo sapiens haemoglobin A beta chain	212	58.462
3871	V00662	Homo sapiens cytochrome oxidase I	1742	91.667
3872	U22232	Felis catus ribosomal protein S4	451	87.342
3873	AF159092	Homo sapiens syld709613 protein	447	77.273
3874	X85807	Saccharomyces cerevisiae ORF G6623	234	26.690
3875	U22961	Homo sapiens similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	289	91.837
3876	L06419	Homo sapiens lysyl hydroxylase	464	77.273
3877	AF041378	Homo sapiens cell death activator CIDE-A	260	44.444
3878	AL109630	Drosophila melanogaster BACR7A4.z	198	42.169
3879	D50134	Homo sapiens inward rectifying K channel	180	59.322
3880	U49439	Drosophila melanogaster ASH1	614	35.754
3881	AF081947	Mus musculus tektin	191	49.057
3882	AL034559	Plasmodium falciparum predicted using hexExon;	178	47.170

		MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa		
3883	M97662	Rattus norvegicus beta-alanine synthase	1836	86.469
3884	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006), AA823760 (NID:g2893628), AA215791 (NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)	3070	98.488
3885	AF163254	Homo sapiens adaptor protein DAPP1	320	90.196
3886	AB010710	Homo sapiens lectin-like oxidized LDL receptor	403	39.552
3887	L29029	Chlamydomonas reinhardtii amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	208	32.031
3888	X67863	Mus musculus T2	133	34.444
3889	AF028722	Mus musculus fetal globin inducing factor	915	80.347
3890	AF044208	Drosophila melanogaster Strabismus	1389	47.228
3891	D10712	Mus musculus nedd-1 protein	1450	78.397
3892	U07974	Gallus gallus unknown	349	34.528
3893	AF107295	Rattus norvegicus outer membrane protein	962	81.215
3894	M36912	Zea mays cell wall protein (put.); putative	247	31.073
3895	M23568	Mus musculus transmembrane protein	404	75.862
3896	AB002317	Homo sapiens KIAA0319	1066	50.309
3897	X92485	Plasmodium vivax pval	318	52.688
3898	X68060	Homo sapiens DNA topoisomerase II	10692	99.753
3899	U09366	Homo sapiens zinc finger protein ZNF133	1807	59.069
3900	X66366	Rattus norvegicus Gephyrin	2988	86.289
3901	AF113131	Homo sapiens host cell factor homolog LCP	1948	92.105
3902	AB023158	Homo sapiens KIAA0941 protein	259	53.425
3903	U23484	Caenorhabditis elegans similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 (SP:PR22_YEAST, P24384) and other DEAH subfamily members of the DEAD box family helicases	695	40.370
3904	Z98949	Homo sapiens bK125H2.1 (myosin heavy chain)	6922	99.813
3905	AL031174	Schizosaccharomyces pombe hypothetical protein	1088	40.222
3906	AC004925	Homo sapiens supported by human ESTs H23395 (NID:g892090) and AA126363 (NID:g1687976), mouse ESTs W83982 (NID:g1394952) and AA717633 (NID:g2729907), and Genscan	2042	98.697
3907	AF133124	Homo sapiens transcription factor IIIC63	2190	94.334
3908	AF074086	Homo sapiens envelope	781	53.266
3909	AF035285	Homo sapiens dihydroxyacetone phosphate acyltransferase	177	53.968
3910	AB018272	Homo sapiens KIAA0729 protein	1517	79.193
3911	AC008075	Arabidopsis thaliana F24J5.4	155	35.922
3912	U38904	Homo sapiens zinc finger protein C2H2-25	1179	61.905
3913	AF049099	Mus musculus SPAF	851	40.223
3914	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	340	64.865
3915	AL033125	Unknown 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end; 2-evidence=pred	245	29.907
3916	AJ002474	Rattus norvegicus Testis-specific A-kinase-anchoring-protein	244	26.106
3917	AB003503	Mus musculus Guanine Nucleotide Regulatory Protein	2849	95.730

3918	AF060539	Mus musculus channel interacting PDZ domain protein	710	82.014
3919	AF016427	Caenorhabditis elegans Contains similarity to Pfam domain: PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1	845	60.000
3920	Z30320	Plasmodium falciparum liver stage antigen-1	41	31.250
3921	AB009698	Homo sapiens hOAT1-2	168	51.786
3922	AF136234	Lytechinus variegatus microtubule-associated protein	482	35.371
3923	AF131833	Homo sapiens Unknown	312	69.014
3924	AF006064	Fowlpox virus protein kinase homolog	268	40.566
3925	M12140	Homo sapiens envelope protein	638	66.906
3926	AL022724	Homo sapiens dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	346	74.324
3927	AJ007798	Homo sapiens nuclear protein SA3	1098	92.090
3928	AF127374	Streptomyces lavendulae unknown	715	33.125
3929	Y15908	Homo sapiens DIA-12C protein	918	96.622
3930	M74824	Drosophila melanogaster D-E-A-D box protein	510	38.768
3931	A00279	synthetic construct Human serum albumin	519	67.857
3932	X78933	Homo sapiens zinc finger protein	1703	64.571
3933	AL117557	Homo sapiens hypothetical protein	628	64.671
3934	AF077040	Homo sapiens SIH003	167	92.308
3935	AF038963	Homo sapiens RNA helicase	564	32.749
3936	AB014579	Homo sapiens KIAA0679 protein	232	78.571
3937	AJ010045	Mus musculus guanine nucleotide-exchange factor	703	49.351
3938	AJ005021	Styela plicata intermediate filament protein IFB	188	25.294
3939	S48220	Homo sapiens type I 5' iodothyronine deiodinase, 5' DI	1696	99.593
3940	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog	324	28.631
3941	U22376	Homo sapiens alternatively spliced product using exon 13A	402	64.948
3942	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	315	58.621
3943	M93018	Rattus norvegicus , gene product	3698	95.805
3944	AL032657	Unknown predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 come	943	35.279
3945	U40411	Caenorhabditis elegans Similar to ubiquitin-conjugating enzyme.	254	41.837
3946	AF070572	Homo sapiens unknown	745	35.980
3947	X68314	Homo sapiens glutathione peroxidase-GI	1295	100.000
3948	J04801	Homo sapiens open reading frame A	321	86.207
3949	M77836	Homo sapiens pyrroline-5-carboxylate reductase	285	42.400
3950	AP000060	Aeropyrum pernix 143aa long hypothetical protein	169	37.681
3951	U12762	Caenorhabditis elegans prolyl 4-hydroxylase alpha subunit	249	52.239
3952	AB018274	Homo sapiens KIAA0731 protein	850	65.000
3953	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	174	31.677
3954	U24657	Myxococcus xanthus putative O-methyltransferase	371	39.205
3955	U13876	Caenorhabditis elegans similar to 4-hydroxybenzoate octaprenyltransferase	588	43.882

3956	Z37139	Unknown similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; c	514	64.865
3957	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	393	61.856
3958	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	338	56.383
3959	U56966	Caenorhabditis elegans coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	844	40.116
3960	Y14999	Drosophila melanogaster Bip2 protein	325	53.425
3961	M89471	gallid herpesvirus 1 MDV Eco Q protein	176	26.531
3962	U22376	Homo sapiens alternatively spliced product using exon 13A	379	60.825
3963	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038)	447	60.550
3964	L24907	Rattus norvegicus protein kinase I	311	63.636
3965	M97204	Drosophila melanogaster goliath protein	368	54.000
3966	U13644	Caenorhabditis elegans No definition line found	424	40.187
3967	AB023152	Homo sapiens KIAA0935 protein	4930	96.834
3968	AB020626	Homo sapiens KIAA0819 protein	294	50.000
3969	U22376	Homo sapiens alternatively spliced product using exon 13A	397	70.930
3970	D16593	Homo sapiens hippocalcin	190	68.750
3971	AB015630	Homo sapiens type II membrane protein	496	44.172
3972	X75342	Homo sapiens Shb	575	51.691
3973	U28993	Caenorhabditis elegans F22D3.2 gene product	256	26.244
3974	X64228	Homo sapiens putative oncogene	366	95.000
3975	L12351	Saccharomyces cerevisiae centromere/microtubule binding protein	154	59.524
3976	AF095737	Homo sapiens unknown	339	65.556
3977	Y09321	Homo sapiens TBP associated factor	352	96.491
3978	M12140	Homo sapiens envelope protein	1113	60.000
3979	AF132148	Drosophila melanogaster unknown	193	26.396
3980	AF010130	Mus musculus neuregulin-3	1435	78.397
3981	Z77660	Homo sapiens Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from th	754	50.000
3982	AL117662	Homo sapiens hypothetical protein	182	59.016
3983	X81380	Sus scrofa unnamed protein product	580	85.556
3984	AF151886	Homo sapiens CGI-128 protein	284	86.275
3985	U39621	Gallus gallus type V collagen	597	35.404
3986	U22376	Homo sapiens alternatively spliced product using exon 13A	294	59.770
3987	X61047	Hydra sp. mini-collagen	204	41.121
3988	AF003386	Caenorhabditis elegans No definition line found	236	24.242
3989	M80633	Rattus norvegicus adenylyl cyclase type IV	1363	92.478
3990	AF072508	Homo sapiens envelope protein	221	49.333
3991	AC004523	Homo sapiens F22329 1	1074	69.758
3992	AJ131243	Columba livia 5'-nucleotidase	382	71.084
3993	D38112	Homo sapiens cytochrome c oxidase subunit 3	1577	93.333
3994	AF125175	Homo sapiens angiopoietin-related protein-2	418	62.366
3995	S80119	Rattus sp. reverse transcriptase homolog	345	31.937
3996	AB023186	Homo sapiens KIAA0969 protein	268	44.231
3997	AF047695	Homo sapiens cap-binding protein 4EHP	338	30.890
3998	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent	238	48.780

		solute carrier		
3999	U72973	Sus scrofa calcium/calmodulin-dependent protein kinase II isoform gamma-G	613	66.447
4000	U23450	Caenorhabditis elegans No definition line found	252	28.994
4001	Z95584	Mycobacterium tuberculosis hypothetical protein Rv1158c	143	35.294
4002	U50929	Homo sapiens betaine:homocysteine methyltransferase	1061	76.166
4003	U22376	Homo sapiens alternatively spliced product using exon 13A	270	49.020
4004	U76846	Arabidopsis thaliana ubiquitin-specific protease	215	30.168
4005	M32865	Homo sapiens Ku protein subunit	221	85.366
4006	AJ235270	Rickettsia prowazekii PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (hemN)	709	34.188
4007	AB029022	Homo sapiens KIAA1099 protein	2590	75.940
4008	AB023210	Homo sapiens KIAA0993 protein	166	35.135
4009	Y13367	Homo sapiens phosphoinositide 3-kinase	667	79.310
4010	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	479	38.587
4011	U22376	Homo sapiens alternatively spliced product using exon 13A	296	61.842
4012	Z75331	Homo sapiens nuclear protein SA-2	563	69.065
4013	U60553	Homo sapiens carboxylesterase hCE-2	254	81.250
4014	L29457	Mus musculus dynamin	247	47.312
4015	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	371	70.667
4016	AL050321	Homo sapiens dJ717M23.1 (novel gene)	2757	94.533
4017	M18247	Feline leukemia virus gag-pol precursor polyprotein gPr80	394	31.780
4018	AE001691	Thermotoga maritima conserved hypothetical protein	189	33.333
4019	U22376	Homo sapiens alternatively spliced product using exon 13A	423	59.167
4020	Z97200	Homo sapiens dJ79C4.1.2 (Homeobox protein PMX-1 (PHOX1) isoform 2)	68	34.783
4021	S70011	Rattus sp. tricarboxylate carrier	2110	92.711
4022	Z37525	Xenopus laevis XDCoH	251	65.385
4023	X92485	Plasmodium vivax pval	232	58.929
4024	M19651	Rattus norvegicus fos-related antigen	137	33.684
4025	AJ010071	Homo sapiens TOM1-like protein	902	94.702
4026	AB020676	Homo sapiens KIAA0869 protein	478	46.707
4027	Y17833	Human endogenous retrovirus K env protein	417	47.863
4028	U15174	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 3	239	66.667
4029	AF132150	Drosophila melanogaster unknown	445	44.828
4030	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	358	63.158
4031	AF056116	Fugu rubripes unknown	955	70.732
4032	U22376	Homo sapiens alternatively spliced product using exon 13A	280	50.000
4033	K03036	Mus musculus alpha-1 type I procollagen	166	32.895
4034	X01068	Bombyx mori Hc-B chorion protein	282	63.077
4035	X71973	Homo sapiens phospholipid hydroperoxide glutathione peroxidase	1382	100.000
4036	V00662	Homo sapiens ATPase 6	1039	92.473

4037	AC005546	Homo sapiens R29425 1	2208	89.973
4038	X13459	Mus sp. laminin C-terminal fragment	921	65.581
4039	AF049588	Canis familiaris synapsin I	188	30.288
4040	AF027956	Homo sapiens G protein-coupled receptor	320	25.132
4041	AJ133120	Rattus norvegicus Proline rich synapse associated protein 2	847	93.382
4042	AL110226	Homo sapiens hypothetical protein	535	31.694
4043	AP000061	Aeropyrum pernix 235aa long hypothetical protein	170	30.337
4044	AF007826	Homo sapiens bax epsilon	165	50.000
4045	AF100426	Streptococcus parasanguinis fimbriae-associated protein Fap1	164	26.667
4046	Z82268	Unknown predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from	211	33.775
4047	AL049946	Homo sapiens hypothetical protein	1937	46.597
4048	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	364	64.198
4049	AJ001701	Homo sapiens deoxyhypusine synthase	488	81.720
4050	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	213	63.636
4051	X74370	Homo sapiens mucin	167	29.762
4052	D87908	Mus musculus nuclear protein np95	703	64.458
4053	X92485	Plasmodium vivax pval	230	47.826
4054	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	323	67.089
4055	Z71264	Caenorhabditis elegans similar to C2 domain	61	22.642
4056	AF108843	Homo sapiens env protein	348	72.727
4057	U22376	Homo sapiens alternatively spliced product using exon 13A	467	73.196
4058	M74055	Homo sapiens thromboxane synthase	203	82.051
4059	AL050382	Homo sapiens hypothetical protein	225	34.694
4060	AF132883	Caenorhabditis elegans UNC-52/Perlecan	384	32.240
4061	AB007930	Homo sapiens KIAA0461 peroteine	393	22.981
4062	Z35602	Caenorhabditis elegans similar to monoamine oxidase; cDNA EST EMBL:T01957 comes from this gene; cDNA EST yk324d6.3 comes from this gene; cDNA EST yk348h2.3 comes from this gene	528	38.168
4063	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	342	66.234
4064	X92485	Plasmodium vivax pval	140	63.889
4065	X92485	Plasmodium vivax pval	171	37.079
4066	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	141	50.000
4067	AB029018	Homo sapiens KIAA1095 protein	867	59.641
4068	AF145690	Drosophila melanogaster BcDNA.LD28657	1142	46.036
4069	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	716	34.574
4070	X78928	Homo sapiens zinc finger protein	183	34.694
4071	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	347	64.000
4072	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	174	28.571
4073	D87515	Rattus norvegicus aminopeptidase-B	1786	49.130
4074	AF015264	Rattus norvegicus golgi peripheral membrane protein p65	1576	72.997
4075	X58438	Mus musculus proline rich protein	231	31.333
4076	S67247	Homo sapiens smooth muscle myosin heavy chain isoform SMemb	197	38.554
4077	U22376	Homo sapiens alternatively spliced product using exon 13A	364	67.442
4078	AJ243460	Leishmania major proteophosphoglycan	189	31.278

4079	AJ248288	Pyrococcus abyssi hypothetical protein	378	39.394
4080	AJ388557	Canis familiaris zinc finger protein	1058	55.311
4081	AF041082	Rattus norvegicus transmembrane receptor Robo1	194	34.286
4082	AF181646	Drosophila melanogaster BcDNA.GH12326	300	31.847
4083	L36315	Mus musculus zinc finger protein	2474	89.367
4084	D70831	Homo sapiens Zinc-finger protein	1303	58.657
4085	AF083110	Homo sapiens sirtuin type 5	261	93.182
4086	AF072508	Homo sapiens envelope protein	370	79.221
4087	M38257	Escherichia coli ORF 235	696	99.057
4088	X05173	Escherichia coli NR(I) (glnG gene product) (AA 1-468)	995	98.065
4089	U88169	Caenorhabditis elegans similar to molybdoterin biosynthesis MOEB proteins	922	57.874
4090	AF105228	Bos taurus tuftelin	355	31.308
4091	AF169635	Sus scrofa Niemann-Pick C disease protein	478	59.167
4092	Z46793	Caenorhabditis elegans cDNA EST EMBL:D75782 comes from this gene; cDNA EST EMBL:D72838 comes from this gene; cDNA EST yk504a5.3 comes from this gene	244	23.858
4093	J03137	Bos taurus phospholipase C	7783	97.366
4094	AF146277	Homo sapiens adapter protein CMS	3820	100.000
4095	U09367	Homo sapiens zinc finger protein ZNF136	965	42.756
4096	D90907	Synechocystis sp. isoleucyl-tRNA synthetase	965	40.189
4097	U10435	Mus musculus Requiem	432	33.645
4098	X80111	Drosophila melanogaster synapse-associated protein	468	39.556
4099	AL032626	Caenorhabditis elegans predicted using Genefinder	735	51.031
4100	AF081258	Homo sapiens testis-specific chromodomain Y-like protein	3952	100.000
4101	D63877	Homo sapiens KIAA0157 gene product is novel.	2756	99.523
4102	AF116547	Homo sapiens cysteine sulfinic acid decarboxylase-related protein 3	3299	99.797
4103	AL031515	Streptomyces coelicolor hypothetical protein SC5C7.08	377	46.721
4104	Y10388	Homo sapiens Graf protein	293	41.667
4105	D61689	Mus musculus SOX-LZ	1146	96.591
4106	AL035424	Homo sapiens dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins)	2002	75.956
4107	AL035652	Homo sapiens dJ1J6.1 (topoisomerase (DNA) I)	179	100.000
4108	Z92770	Mycobacterium tuberculosis fadE2	267	56.627
4109	AL035524	Arabidopsis thaliana putative protein	498	50.993
4110	X01630	Homo sapiens argininosuccinate synthetase (aa 1-412)	151	100.000
4111	L24920	Pan troglodytes complement receptor 1	987	28.800
4112	AC002126	Homo sapiens R31240.1	655	100.000
4113	AL033377	Homo sapiens dJ287G14.2 (PUTATIVE novel seven transmembrane domain protein)	3224	100.000
4114	AB006533	Homo sapiens DNA helicase	553	77.477
4115	AF087697	Rattus norvegicus dlq 3	283	43.697
4116	AL021917	Homo sapiens dJ45P21.2 (butyrophilin)	613	98.889
4117	AF113136	Homo sapiens IL-1 receptor-associated-kinase-M; IRAK-M	2084	100.000

4118	AB023207	Homo sapiens KIAA0990 protein	533	37.968
4119	X58374	Drosophila melanogaster crn	2515	66.415
4120	Y08302	Homo sapiens mitogen-activated protein kinase phosphatase 4	1182	100.000
4121	AL031667	Homo sapiens dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	4841	100.000
4122	AB011121	Homo sapiens KIAA0549 protein	3094	99.787
4123	AF155115	Homo sapiens NY-REN-58 antigen	172	100.000
4124	AP000005	Pyrococcus horikoshii 149aa long hypothetical methylmalonyl-CoA decarboxylase gamma chain	225	38.554
4125	L48516	Homo sapiens paraoxonase-3	2210	98.534
4126	AC007292	Homo sapiens R31167 1, partial protein	2907	99.302
4127	D90746	Escherichia coli SocA3 protein	647	100.000
4128	AC005594	Homo sapiens R26984 1	608	100.000
4129	AF143536	Homo sapiens colon cancer-associated protein Mic1	3880	97.537
4130	U49082	Homo sapiens transporter protein	635	62.179
4131	AB018275	Homo sapiens KIAA0732 protein	5592	100.000
4132	M34059	Homo sapiens beta-globin	236	80.488
4133	D13637	Homo sapiens KIAA0012	267	34.307
4134	U90126	Bos taurus ABC transporter	468	60.870
4135	S61069	Homo sapiens reverse transcriptase homolog=pol {retroviral element}	271	75.806
4136	X66899	Homo sapiens RNA binding protein	440	100.000
4137	M34458	Homo sapiens lamin B	203	91.667
4138	J03998	Plasmodium falciparum glutamic acid-rich protein	153	30.645
4139	AE001394	Plasmodium falciparum predicted integral membrane protein	78	62.500
4140	AF036548	Rattus norvegicus RGC-32	683	91.304
4141	AF000423	Rattus norvegicus synaptotagmin XI	845	99.219
4142	X53773	Rattus norvegicus alpha-c large chain (AA 1-938)	1831	68.974
4143	A68194	unidentified unnamed protein product	4024	100.000
4144	AB011174	Homo sapiens KIAA0602 protein	6402	99.896
4145	AF035526	Mus musculus kanadaplin	2540	79.716
4146	AF023657	Rattus norvegicus endo-alpha-D-mannosidase	1590	68.285
4147	U62587	Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase	225	56.863
4148	AL049557	Homo sapiens dJ773A18.2 (PROBABLE ATP-DEPENDENT RNA HELICASE P47 HOMOLOG)	5454	99.879
4149	AF034745	Mus musculus LNXp80	2793	88.486
4150	AB020689	Homo sapiens KIAA0882 protein	6096	100.000
4151	L15313	Caenorhabditis elegans putative	743	70.667
4152	AF152311	Homo sapiens protocadherin alpha 3	6162	99.368
4153	U88908	Mus musculus inhibitor of apoptosis protein 1	223	41.667
4154	D13626	Homo sapiens KIAA0001	865	49.807
4155	X94912	Homo sapiens Pr22	252	92.857
4156	AF125568	Homo sapiens tumor suppressing STF cDNA 4	2239	99.392
4157	AL110239	Homo sapiens hypothetical protein	247	97.436
4158	U02082	Homo sapiens guanine nucleotide regulatory protein	822	43.910
4159	Z66496	Unknown cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this	240	28.387

		gene; cDNA		
4160	Z48615	Homo sapiens serine/threonine kinase with SH3 domain, leucine zipper domain and proline rich domain	275	43.846
4161	X66435	Homo sapiens Hydroxymethylglutaryl CoA Synthase	359	96.721
4162	Z49125	Unknown similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession	448	36.932
4163	AF072372	Mus musculus lysosomal trafficking regulator 2	1554	99.127
4164	M36501	Homo sapiens alpha-2-macroglobulin	642	44.643
4165	U41164	Rattus norvegicus Cys2/His2 zinc finger protein	721	86.957
4166	AL035678	Arabidopsis thaliana putative protein	2127	65.971
4167	AF078779	Rattus norvegicus putative four repeat ion channel	796	93.600
4168	Z28278	Saccharomyces cerevisiae ORF YKR053c	281	25.463
4169	AB028981	Homo sapiens KIAA1058 protein	2502	67.016
4170	AF007157	Homo sapiens unknown	2837	100.000
4171	Z77654	Caenorhabditis elegans predicted using Genefinder; Similarity to Drosophila RNA binding protein squid (SW:SQD_DROME); cDNA EST yk638a1.3 comes from this gene	215	34.483
4172	U62810	Mesocricetus auratus potassium channel Kv8.1	468	100.000
4173	X97999	Homo sapiens transcription factor IID	386	47.297
4174	A01592	Homo sapiens haemoglobin A beta chain	434	95.455
4175	AB001563	Homo sapiens RES4-22D	277	35.099
4176	AF103017	Homo sapiens uroporphyrinogen decarboxylase	248	77.273
4177	A01592	Homo sapiens haemoglobin A beta chain	382	86.567
4178	AB023207	Homo sapiens KIAA0990 protein	663	35.621
4179	Z83844	Homo sapiens similar to SH3-binding protein	372	98.214
4180	AF146688	Fugu rubripes sex comb on midleg-like 2 protein	188	40.000
4181	X13621	Homo sapiens HNP-3 defensin (AA 1- 94)	162	95.238
4182	AC002544	Homo sapiens Translation initiation factor eIF-p110	1750	98.893
4183	A01592	Homo sapiens haemoglobin A beta chain	434	92.754
4184	AF032668	Rattus norvegicus rsec15	411	73.810
4185	AF073299	Homo sapiens Na ⁺ /H ⁺ exchanger isoform 2	2255	100.000
4186	U25691	Mus musculus lymphocyte specific helicase	258	87.500
4187	S72008	Homo sapiens CDC10 homolog=hCDC10	199	94.286
4188	X16491	Dictyostelium discoideum spore coat protein sp96	198	29.240
4189	AJ001019	Homo sapiens ring finger protein	343	46.429
4190	AF125569	Homo sapiens tumor suppressing STF cDNA 6	589	100.000
4191	AB002321	Homo sapiens KIAA0323	5064	100.000
4192	L41560	Homo sapiens pterin-4a-carbinolamine dehydratase	319	67.105
4193	AB006625	Homo sapiens The human homolog of a mouse imprinted gene, Peg3.	7665	99.912
4194	AC004678	Homo sapiens R34094 1	292	93.878
4195	L13200	Caenorhabditis elegans putative	503	49.367
4196	AL032639	Unknown similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:C08103 comes from this ge	171	29.070
4197	U87318	Xenopus laevis NaDC-2	682	69.286
4198	AF111423	Xenopus laevis chromosome condensation protein XCAP-G	1706	54.386

4199	X76092	Homo sapiens DNA binding protein RFX3	3080	99.785
4200	U06631	Homo sapiens homologous to mouse gene PC326:GenBank Accession Number M95564	350	39.735
4201	AL080123	Homo sapiens hypothetical protein	978	64.000
4202	AC005395	Arabidopsis thaliana hypothetical protein	503	35.176
4203	X83544	Homo sapiens DAP-3	247	97.368
4204	AF099013	Homo sapiens glucocorticoid modulatory element binding protein-1	3686	100.000
4205	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C	3537	99.809
4206	AC002131	Arabidopsis thaliana Similar to seryl-tRNA synthetase gb U10400 from S cerevisiae. EST gb N96627 comes from this gene.	374	49.573
4207	AL080088	Homo sapiens hypothetical protein	1464	99.533
4208	AL031427	Homo sapiens dJ167A19.4 (novel protein)	146	92.000
4209	L10326	Rattus norvegicus GTP-binding protein alpha-s subunit	154	100.000
4210	AB028944	Homo sapiens KIAA1021 protein	5116	99.742
4211	Z50194	Homo sapiens PQ-rich protein	208	52.174
4212	AC006042	Homo sapiens supported by human ESTs AI681256.1 (NID:g4891438), N32168.1 (NID:g1152567) , and genscan	1016	100.000
4213	X67337	Homo sapiens Human pre-mRNA cleavage factor I 68 kDa subunit	370	65.169
4214	AF034803	Homo sapiens liprin-beta2	581	95.604
4215	U22376	Homo sapiens alternatively spliced product using exon 13A	264	77.358
4216	AF117758	Homo sapiens secreted frizzled-related protein 5	2253	100.000
4217	AF096300	Homo sapiens HPK/GCK-like kinase HGK	1707	92.958
4218	AF043250	Homo sapiens mitochondrial outer membrane protein	1319	64.561
4219	Z81505	Unknown similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene	1156	57.045
4220	L04656	Homo sapiens carbonic anhydrase-related protein VIII	220	94.118
4221	AC004084	Homo sapiens similar to GTPase-activating proteins; 35% similar to JC5047 (PID:g2136083)	1268	81.200
4222	A01573	synthetic construct cystatin C	314	92.000
4223	AB014579	Homo sapiens KIAA0679 protein	1735	98.872
4224	AF087433	Rattus norvegicus leprecan	3317	92.075
4225	AL034488	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:C08771 comes from this gene; cDNA EST EMBL:C07412 comes from this gene	400	47.015
4226	X99583	Homo sapiens CHL1 protein	229	67.308
4227	AJ007583	Homo sapiens acetylglucosaminyltransferase-like protein	1044	67.757
4228	AF132552	Drosophila melanogaster BcDNA.GM01838	1600	65.395
4229	L05779	Homo sapiens cytosolic epoxide hydrolase	159	100.000
4230	X97818	Mus musculus samaphorin G	188	96.296
4231	U38252	Mus musculus fractionated X-irradiation-induced 29 thymoma	469	97.333
4232	X74794	Homo sapiens P1 Cdc21 protein	5616	99.770

4233	X98259	Homo sapiens M-phase phosphoprotein 8	454	100.000
4234	D83043	Homo sapiens allele A*2711	312	90.000
4235	AL080150	Homo sapiens hypothetical protein	5789	99.542
4236	AC004594	Homo sapiens Ca ²⁺ dependent activator protein for secretion; similar to D86214 (NID:g1398903)	2026	98.418
4237	AF117897	Bos taurus rab11 binding protein	278	88.000
4238	D31888	Homo sapiens KIAA0071	410	67.347
4239	AF160934	Drosophila melanogaster BcDNA.LD14189	204	64.286
4240	Z75330	Homo sapiens nuclear protein SA-1	3665	99.819
4241	AB007918	Homo sapiens KIAA0449 protein	745	69.565
4242	AB030644	Rattus norvegicus tudor repeat associator with PCTAIRE 2	3647	89.474
4243	AB030502	Xenopus laevis XDRP1	435	72.000
4244	Z24725	Homo sapiens mitogen inducible gene mig-2	1993	52.783
4245	Z67961	Schizosaccharomyces pombe hypothetical protein	440	33.188
4246	AB002326	Homo sapiens KIAA0328	11013	100.000
4247	M63180	Homo sapiens threonyl-tRNA synthetase	1846	59.111
4248	AF093097	Homo sapiens putative RNA-binding protein Q99	264	90.476
4249	AL080158	Homo sapiens hypothetical protein	801	35.698
4250	U23502	Plasmodium chabaudi chabaudi POM1	487	46.012
4251	Y17392	Homo sapiens prefoldin subunit 1	705	98.291
4252	Z69634	Unknown cDNA EST EMBL:C11678 comes from this gene; cDNA EST EMBL:C13926 comes from this gene; cDNA	704	34.375
4253	U22387	Homo sapiens immunoglobulin heavy chain	198	64.583
4254	AL050163	Homo sapiens hypothetical protein	735	100.000
4255	AB007945	Homo sapiens KIAA0476 protein	9511	99.711
4256	Z37166	Homo sapiens nuclear RNA helicase (DEAD family)	1864	100.000
4257	X06764	Homo sapiens Ig(k) L-chain precursor	696	84.328
4258	AF048731	Homo sapiens cyclin T2a	4386	100.000
4259	M28732	Mus musculus beta-tubulin	281	66.154
4260	Y10392	Human endogenous retrovirus K protease	452	49.206
4261	AC003682	Homo sapiens R27945_2	1686	100.000
4262	AF044033	Marmota marmota olfactory receptor	267	92.857
4263	L07924	Mus musculus guanine nucleotide dissociation stimulator	3514	84.968
4264	X75931	Bos taurus Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit	1686	99.222
4265	AC006264	Arabidopsis thaliana unknown protein	278	41.573
4266	X84101	Streptomyces clavuligerus Proclavaminic acid amidino hydrolase	631	38.340
4267	AF108420	Fugu rubripes 1-aminocyclopropane-carboxilate synthase	1001	59.149
4268	AC009325	Arabidopsis thaliana putative phosphate/phosphoenolpyruvate translocator	197	38.571
4269	Z74201	Saccharomyces cerevisiae ORF YDL153c	215	30.380
4270	AL110193	Homo sapiens hypothetical protein	2638	99.229
4271	AF187318	Homo sapiens F-box protein Fbx2	444	55.263
4272	Z77655	Caenorhabditis elegans predicted using Genefinder; similar to EF hand (2 domains)	644	34.184
4273	AF124511	Gallus gallus BVES	339	36.757
4274	AF056035	Rattus norvegicus s-nexilin	3148	85.841
4275	AJ005621	Mus musculus skeletal and cardiac muscle-specific gene	1791	95.139
4276	X58288	Homo sapiens protein-tyrosine phosphatase	4182	99.836

4277	M74495	Mus musculus adenylosuccinate synthetase	1924	92.233
4278	M26460	Homo sapiens retinoblastoma 1	155	36.667
4279	M83679	Rattus norvegicus RAB15	368	96.491
4280	AL021106	Unknown /prediction=(method:"genscan", version:"1.0", score:"113.71"); /prediction=(method:	747	50.215
4281	X05806	Acetabularia mediterranea put. ORF	189	71.429
4282	AB007900	Homo sapiens HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440.	774	40.389
4283	M95762	Rattus norvegicus GABA transporter	507	81.395
4284	Z99118	Bacillus subtilis aspartyl-tRNA synthetase	1374	43.667
4285	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	1749	67.385
4286	M55176	Rhizomucor racemosus MRAS2 gene product	207	32.990
4287	Z70310	Caenorhabditis elegans similar to Glutathione S-transferases.; cDNA EST yk536e7.3 comes from this gene	763	44.565
4288	AB020676	Homo sapiens KIAA0869 protein	814	42.338
4289	AJ006054	Homo sapiens UDP glucuronosyltransferase	345	76.923
4290	U80223	Drosophila melanogaster eukaryotic initiation factor eIF-2 alpha kinase; DGCN2	783	29.412
4291	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	432	39.205
4292	AB007925	Homo sapiens KIAA0456 protein	235	45.122
4293	AF095150	Homo sapiens protein O-mannosyl-transferase 1	2731	100.000
4294	D87433	Homo sapiens KIAA0246	727	38.323
4295	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	1377	51.768
4296	AF151811	Homo sapiens CGI-53 protein	2164	99.096
4297	AB011399	Homo sapiens AF-6	515	100.000
4298	AL080123	Homo sapiens hypothetical protein	4248	99.832
4299	AF134726	Homo sapiens NG22	2967	97.821
4300	AB011084	Homo sapiens KIAA0512 protein	347	30.342
4301	AF092094	Homo sapiens AP-4 adaptor complex beta4 subunit	3564	99.441
4302	L14745	Caenorhabditis elegans homology with GTP binding protein; putative	546	51.592
4303	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3931	100.000
4304	AF132484	Mus musculus unknown	523	51.266
4305	AL050393	Homo sapiens hypothetical protein	420	51.261
4306	D88158	Sus scrofa cytochrome b561	433	50.350
4307	D86964	Homo sapiens similar to a human major CRK- binding protein DOCK180.	12180	100.000
4308	AL110151	Homo sapiens hypothetical protein	2418	99.721
4309	AF140690	Homo sapiens melusin	307	47.778
4310	AC002396	Arabidopsis thaliana Hypothetical protein	1347	51.157
4311	AF068718	Caenorhabditis elegans No definition line found	514	32.394
4312	AB023157	Homo sapiens KIAA0940 protein	1944	91.391
4313	AF059569	Homo sapiens actin binding protein MAYVEN	404	28.421
4314	AB028981	Homo sapiens KIAA1058 protein	1609	68.946
4315	AF133123	Homo sapiens transcription factor IIIC102	4090	100.000
4316	X78927	Homo sapiens zinc finger protein	3146	99.307
4317	AF028722	Mus musculus fetal globin inducing factor	490	83.908
4318	M55542	Homo sapiens guanylate binding protein isoform	1774	64.678

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4319	AB029015	Homo sapiens KIAA1092 protein	7731	100.000
4320	AB014548	Homo sapiens KIAA0648 protein	5548	100.000
4321	Z68753	Unknown predicted using Genefinder; Similarity to Glucose-repressible alcohol dehydrogenase transc	420	46.875
4322	U70855	Caenorhabditis elegans similar to the RAS gene family	552	35.039
4323	Y00649	Homo sapiens CR2 receptor	217	27.933
4324	D88315	Mus musculus tetracycline transporter-like protein	2647	98.768
4325	Z68215	Caenorhabditis elegans C53B4.4c	156	24.370
4326	AJ009698	Rattus norvegicus embigin protein	535	80.392
4327	AB001488	Bacillus subtilis FUNCTION UNKNOWN.	182	36.364
4328	D63877	Homo sapiens KIAA0157 gene product is novel.	208	28.972
4329	M14949	Homo sapiens R-ras	1443	100.000
4330	D42041	Homo sapiens The ha1225 gene product is related to human alpha-glucosidase.	6494	99.787
4331	AJ001015	Homo sapiens RAMP2	574	98.824
4332	AF186461	Rattus norvegicus ring finger protein Fxy	295	25.075
4333	AF064255	Homo sapiens very long-chain acyl-CoA synthetase homolog 2; VLCS-H2	1347	100.000
4334	AC004955	Homo sapiens supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan	1096	100.000
4335	Z46676	Unknown weak similarity to microtubule associated proteins; cDNA EST EMBL:T01154 comes from this ge	443	35.514
4336	U40029	Caenorhabditis elegans No definition line found	1552	47.647
4337	AL032626	Unknown cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this gene; cDN	957	48.000
4338	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	1875	99.296
4339	X78998	Homo sapiens endosomal protein	372	24.702
4340	AF153208	Homo sapiens GC-rich sequence DNA-binding factor candidate	588	81.667
4341	U00050	Caenorhabditis elegans No definition line found	362	32.512
4342	Z81586	Caenorhabditis elegans cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene; cDNA EST yk656d4.3 comes from this gene	624	31.796
4343	AJ388555	Canis familiaris hypothetical protein	915	43.021
4344	U79776	Mus musculus ajuba; jub	431	82.090
4345	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase precursor	2134	67.550
4346	AB011097	Homo sapiens KIAA0525 protein	1360	44.270
4347	AF124512	Homo sapiens BVES	907	100.000
4348	A47122	unidentified unnamed protein product	1067	100.000
4349	AC006593	Arabidopsis thaliana putative transmembrane protein	490	30.350
4350	M23159	Cricetus cricetus DHFR-coamplified protein	496	85.542
4351	D87515	Rattus norvegicus aminopeptidase-B	2615	92.593
4352	AF090136	Rattus norvegicus lin-7-C	322	100.000

4353	D79998	Homo sapiens KIAA0176	511	70.370
4354	AF098993	Caenorhabditis elegans No definition line found	296	25.000
4355	AF087826	Mus musculus claudin-8	646	79.310
4356	AL023704	Schizosaccharomyces pombe weak similarity to B.subtilis spore outgrowth f actor B	1525	56.585
4357	AJ223301	Bos taurus aralkyl acyl-CoA:amino acid N-acyltransferase	694	38.806
4358	AC004908	Homo sapiens zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333)	1961	100.000
4359	AF099032	Homo sapiens embryonic ectoderm development protein short isoform	173	96.154
4360	AF133670	Mus musculus ARL-6 interacting protein-2	620	96.939
4361	M98502	Mus musculus pMLZ-4	1035	59.535
4362	M97204	Drosophila melanogaster goliath protein	305	67.273
4363	U47924	Homo sapiens C9	905	100.000
4364	AL080144	Homo sapiens hypothetical protein	4653	99.866
4365	AJ222798	Lycopersicon esculentum tDET1 protein	277	37.607
4366	AF024497	Caenorhabditis elegans weak similarity to drosophila tyrosine kinase (GB:G455391)	333	29.515
4367	Z82083	Caenorhabditis elegans ZK1010.2	407	28.621
4368	AB020626	Homo sapiens KIAA0819 protein	330	40.972
4369	D26488	Homo sapiens This sequence is almost identical to HUMRSC433, D13632.	4588	100.000
4370	AL031387	Homo sapiens dJ596C15.1.1 (novel protein) (isoform 1)	1083	100.000
4371	AL049699	Homo sapiens dJ747H23.2 (novel protein)	1297	100.000
4372	D90916	Synechocystis sp. hypothetical protein	522	52.695
4373	AC006530	Homo sapiens unknown	681	55.758
4374	AB018323	Homo sapiens KIAA0780 protein	866	98.473
4375	AC004020	Homo sapiens Unknown gene product	958	97.351
4376	AL023518	Schizosaccharomyces pombe conserved hypothetical protein	667	52.857
4377	AF151799	Homo sapiens CGI-40 protein	424	71.605
4378	AF070637	Homo sapiens unknown	1278	100.000
4379	S60885	Mus sp. LYAR=cell growth regulating nucleolar protein	536	67.797
4380	Z93244	Homo sapiens bK116F5.1 (unknown PUTATIVE protein)	448	53.600
4381	Z95619	Caenorhabditis elegans H21P03.2	201	29.060
4382	U29154	Caenorhabditis elegans T07F12.1 gene product	426	33.617
4383	AF162680	Homo sapiens TRIF	922	99.270
4384	D87433	Homo sapiens KIAA0246	15929	99.955
4385	AF129812	Homo sapiens candidate tumor suppressor protein NOC2	668	97.895
4386	AB002347	Homo sapiens KIAA0349	8658	99.843
4387	Z68166	Schizosaccharomyces pombe unknown	373	35.176
4388	Z35641	Caenorhabditis elegans cDNA EST yk273d8.5 comes from this gene	280	32.402
4389	D79994	Homo sapiens similar to ankyrin of Chromatium vinosum.	1049	46.667
4390	U40420	Caenorhabditis elegans weak similarity to procollagen alpha chain 1(V) chain	537	50.000
4391	AL023828	Caenorhabditis elegans cDNA EST yk289g5.5 comes from this gene; cDNA EST yk391h4.5 comes from	1017	41.943

		this gene; cDNA EST EMBL:C09408 comes from this gene; cDNA EST yk332h9.5 comes from this gene		
4392	U49056	Rattus norvegicus rA1	1640	94.779
4393	X78801	Gallus gallus ovomacroglobulin, ovostatin	515	47.159
4394	AB014590	Homo sapiens KIAA0690 protein	1584	99.580
4395	AB000216	Rattus norvegicus CCA3	338	73.239
4396	Z81515	Caenorhabditis elegans F26H11.3c	516	39.444
4397	X02488	Homo sapiens collagen N-prepropeptide (aa -22 to 72)	132	41.379
4398	AF067172	Homo sapiens RNA cyclase homolog	1142	97.790
4399	AF181623	Drosophila melanogaster BcDNA.GH02974	223	44.737
4400	Z75543	Caenorhabditis elegans cDNA EST EMBL:M89063 comes from this gene; cDNA EST yk384f1.3 comes from this gene; cDNA EST yk384f1.5 comes from this gene	295	39.091
4401	A27266	Homo sapiens TGR-CL7	790	100.000
4402	AF041377	Mus musculus cell death activator CIDE-B	218	63.793
4403	X64600	Rattus norvegicus trans golgi network (TGN) specific integral membrane protein TGN38	198	27.317
4404	AF061555	Mus musculus ubiquitin-protein ligase E3-alpha	1751	94.141
4405	AF117723	Glycine max seed maturation protein PM27	231	29.189
4406	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	1167	41.606
4407	AL117518	Homo sapiens hypothetical protein	9043	99.925
4408	U22376	Homo sapiens alternatively spliced product using exon 13A	396	64.286
4409	AL050018	Homo sapiens hypothetical protein	2489	99.478
4410	AL049943	Homo sapiens hypothetical protein	2268	99.682
4411	Y08991	Homo sapiens adaptor protein	2325	100.000
4412	AB004538	Schizosaccharomyces pombe HYPOTHETICAL 59.2KD PROTEIN IN PFK26-SGA1 INTERGENIC REGION	267	43.434
4413	U73820	Mus musculus polypeptide GalNAc transferase-T1	246	28.090
4414	AL121804	Drosophila melanogaster BACR7C10.a	541	52.381
4415	X83973	Homo sapiens transcription factor	1246	100.000
4416	M96860	Homo sapiens dipeptidyl aminopeptidase like protein	493	47.436
4417	AF024691	Drosophila ananassae putative inorganic phosphate cotransporter	523	45.614
4418	A38809	Homo sapiens unnamed protein product	564	98.824
4419	U89336	Homo sapiens unknown	197	30.702
4420	U41543	Unknown Similar to Rat trg gene product; coded for by C. elegans cDNA yk31e7.5; coded for by C. ele	898	46.795
4421	AF017418	Homo sapiens homeobox protein MEIS2	859	99.194
4422	Z47075	Unknown similar to Yeast DEG-1 protein (Swiss Prot accession number P31115); cDNA EST EMBL:D70252 c	558	32.000
4423	AJ011812	Homo sapiens transcription factor NRF	2606	100.000
4424	AB007883	Homo sapiens KIAA0423	330	49.495
4425	U76759	Mus musculus nuclear protein NIP45	1207	81.140
4426	AL117499	Homo sapiens hypothetical protein	1109	100.000
4427	AJ132192	Mus musculus HS1 binding protein 3	781	67.568
4428	AL022018	Unknown /prediction=(method:"genscan", version:"1.0", score:"133.82");	423	35.156

		/prediction=(method:		
4429	AB018345	Homo sapiens KIAA0802 protein	9178	100.000
4430	AL050095	Homo sapiens hypothetical protein	4235	100.000
4431	AF151363	Mus musculus Cdc42 GTPase-activating protein	276	60.938
4432	AF060153	Homo sapiens METH2 protein	6295	99.888
4433	AF186115	Mus musculus putative secreted protein SIG9	243	45.000
4434	AJ222636	Homo sapiens hypothetical protein	219	45.370
4435	AB028980	Homo sapiens KIAA1057 protein	6539	99.795
4436	D83206	Mus musculus P24 protein	184	46.429
4437	AF132946	Homo sapiens CGI-12 protein	2097	99.388
4438	AB028985	Homo sapiens KIAA1062 protein	10207	100.000
4439	Z93386	Unknown Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes fr	1110	48.036
4440	U41107	Caenorhabditis elegans No definition line found	680	40.071
4441	U64601	Caenorhabditis elegans Gene probably begins in the next cosmid	289	51.765
4442	AL117204	Caenorhabditis elegans predicted using Genefinder	299	35.616
4443	L32372	Mus musculus AMPA selective glutamate receptor	332	94.545
4444	M63180	Homo sapiens threonyl-tRNA synthetase	2594	76.170
4445	U89529	Rattus norvegicus fatty acid transport protein	289	84.000
4446	X93357	Mus musculus homolog of human SYT	2215	95.652
4447	AB014565	Homo sapiens KIAA0665 protein	323	58.824
4448	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	5398	99.497
4449	AF131826	Homo sapiens Unknown	763	52.804
4450	AF038007	Homo sapiens FIC1	742	49.780
4451	Z12840	Oryctolagus cuniculus protein of unknown function	831	33.014
4452	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase	925	81.595
4453	U40800	Caenorhabditis elegans similar to thymidine diphosphoglucose 4,6-dehydratase	1647	67.341
4454	AL117233	Homo sapiens hypothetical protein	3180	99.792
4455	D17629	Homo sapiens GALNS	3665	100.000
4456	Z82053	Unknown predicted using Genefinder; similar to MUTT protein like; cDNA EST EMBL:C07418 comes from t	286	56.757
4457	U71205	Mus musculus rit	358	34.906
4458	AF112481	Homo sapiens RAD54B protein	2357	100.000
4459	Z81137	Unknown Similarity to Yeast YIP1 protein (SW:P53039); cDNA EST EMBL:T01608 comes from this gene; cD	643	50.256
4460	D83146	Mus musculus Six5	306	92.308
4461	AJ133768	Homo sapiens ZASP protein	3315	99.787
4462	Z99277	Caenorhabditis elegans cDNA EST CEMSA26F comes from this gene; cDNA EST yk575g11.3 comes from this gene	410	31.206
4463	AB020629	Homo sapiens KIAA0822 protein	1959	69.784
4464	AF074086	Homo sapiens envelope	1469	62.121
4465	Z83123	Caenorhabditis elegans predicted using Genefinder	300	37.956
4466	AB007828	Homo sapiens necdin	407	52.679
4467	AF101361	Drosophila melanogaster Abnormal X segregation	310	31.963
4468	AL021106	Unknown /prediction=(method:"genscan",	228	29.114

		version:"1.0"); /prediction=(method:"genefinder", ve		
4469	AC003672	Arabidopsis thaliana putative zinc finger protein	506	30.164
4470	D29766	Rattus norvegicus Crk-associated substrate, p130	3067	91.339
4471	X86779	Homo sapiens FAST kinase	162	27.119
4472	U20286	Rattus norvegicus lamina associated polypeptide 1C	1622	74.775
4473	M76720	Xenopus laevis egg-specific protein	149	35.185
4474	AL035086	Homo sapiens dJ44A20.2 (novel protein)	1717	100.000
4475	AF056116	Fugu rubripes unknown	1570	71.976
4476	Z29115	Unknown similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice;	1917	64.027
4477	AF115435	Rattus norvegicus syntaxin 17	629	95.098
4478	AF025424	Rattus norvegicus RNA polymerase I 127 kDa subunit	1970	95.302
4479	Z54328	Schizosaccharomyces pombe hypothetical protein	289	34.266
4480	U15765	Rattus norvegicus nonmuscle myosin heavy chain-B	256	89.744
4481	AF003140	Caenorhabditis elegans No definition line found	432	31.229
4482	AJ224306	Arabidopsis thaliana PRT1	218	34.000
4483	AB002584	Rattus norvegicus beta-alanine-pyruvate aminotransferase	2102	85.515
4484	AL117204	Caenorhabditis elegans predicted using Genefinder	253	26.250
4485	Z11502	Homo sapiens intestine-specific annexin	1581	98.814
4486	AF111713	Homo sapiens junctional adhesion molecule	504	38.565
4487	AF151968	Gallus gallus RGS protein RGS-17	480	91.250
4488	Z69944	Schizosaccharomyces pombe hypothetical protein	490	28.615
4489	Z69637	Caenorhabditis elegans predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene	309	63.291
4490	Z79754	Caenorhabditis elegans Similarity to some phosphatases and kinases; cDNA EST EMBL:Z14643 comes from this gene; cDNA EST yk531b4.3 comes from this gene; cDNA EST yk642e5.3 comes from this gene	502	30.508
4491	L41816	Homo sapiens cam kinase I	1106	85.484
4492	AF120102	Homo sapiens calsenilin	630	80.531
4493	AL110300	Homo sapiens hypothetical protein	2338	98.352
4494	U28412	Caenorhabditis elegans similar to polyposis locus protein 1 (SP:DP1 HUMAN, Q00765)	362	51.429
4495	L12147	Mus musculus early B-cell factor	1671	99.609
4496	D86964	Homo sapiens similar to a human major CRK-binding protein DOCK180.	1450	99.563
4497	AB020690	Homo sapiens KIAA0883 protein	479	41.176
4498	AC004780	Homo sapiens F17127 1	2136	94.253
4499	AF057365	Canis familiaris UDP N-acetylglucosamine transporter	254	32.639
4500	AF099186	Mus musculus EH domain-containing protein EHD1	952	67.347
4501	U27838	Mus musculus glycosyl-phosphatidyl-inositol-anchored protein homolog	460	40.693

4502	AF128625	Homo sapiens CDC42-binding protein kinase beta	426	100.000
4503	X69489	Rattus norvegicus beta-chimaerin	290	34.711
4504	AB012933	Rattus norvegicus acyl-CoA synthetase 5	2880	78.571
4505	U53366	Oncorhynchus mykiss terminal deoxynucleotidyl transferase	550	51.099
4506	AF095741	Rattus norvegicus unknown	1198	58.123
4507	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	10968	100.000
4508	U62906	Mus musculus zinc finger protein 94	1328	69.231
4509	AF109377	Mus musculus ldlBp	782	84.138
4510	AF151799	Homo sapiens CGI-40 protein	3487	95.963
4511	X16262	Rattus norvegicus myosin heavy chain 21 (AA 621)	199	24.437
4512	U43607	Mus musculus transcription factor-like protein 4 beta	1481	87.732
4513	AF135421	Homo sapiens GDP-mannose pyrophosphorylase B	2421	100.000
4514	AL031427	Homo sapiens dJ167A19.4 (novel protein)	146	92.000
4515	Z99129	Homo sapiens dJ425C14.2 (Placental protein DIFF33 LIKE)	884	52.893
4516	Y08135	Mus musculus acid sphingomyelinase-like phosphodiesterase	2365	81.995
4517	AL023286	Schizosaccharomyces pombe probable atp-dependent rna helicase	215	32.374
4518	AL031667	Homo sapiens dJ620E11.1e (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	1028	99.342
4519	D63850	Mus musculus hepatoma-derived growth factor	1444	74.441
4520	AC004523	Homo sapiens F22329 1	214	84.615
4521	M60706	Homo sapiens topoisomerase I	2869	68.243
4522	AF019236	Dictyostelium discoideum TipD	691	37.459
4523	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST E	192	28.125
4524	U22376	Homo sapiens alternatively spliced product using exon 13A	363	67.500
4525	L13977	Homo sapiens prolylcarboxypeptidase	453	37.297
4526	D78572	Mus musculus membrane glycoprotein	4177	81.630
4527	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	386	27.046
4528	AB029005	Homo sapiens KIAA1082 protein	1769	52.795
4529	Z70307	Caenorhabditis elegans Similarity to B.subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene; cDNA EST yk619c11.3 comes from this gene	384	35.135
4530	Y16008	Mus musculus neuronal-STOP protein	914	57.692
4531	U80931	Caenorhabditis elegans strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases	1001	48.377
4532	AF039023	Homo sapiens Ran-GTP binding protein; RanBP6	1209	97.861
4533	AF051945	Mus musculus Xin	492	51.515
4534	AF005856	Drosophila yakuba anon2A5	499	34.454
4535	AF105374	Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-2	2512	99.455

4536	AC004472	Homo sapiens P1.11659 3	1465	75.078
4537	Z66519	Caenorhabditis elegans similar to phytoene synthase precursor; cDNA EST yk340f7.3 comes from this gene; cDNA EST yk340f7.5 comes from this gene; cDNA EST yk565e5.3 comes from this gene	351	30.769
4538	L12018	Caenorhabditis elegans putative	229	39.669
4539	Z78201	Unknown Similarity to E.coli 2-oxoglutarate dehydrogenase (SW:ODO1_ECOLI); cDNA EST EMBL:D32590 com	1681	52.665
4540	Y17833	Human endogenous retrovirus K pol protein	741	80.597
4541	AC003673	Arabidopsis thaliana unknown protein	383	27.596
4542	U20861	Caenorhabditis elegans similar to yeast antiviral protein SKI2 and ATP-dependent DNA-helicases	278	24.416
4543	Z69384	Caenorhabditis elegans Similarity to Salmonella regulatory protein UHPC (SW:UHPC SALTY)	345	54.023
4544	AC004890	Homo sapiens similar to zinc finger proteins; similar to AAC01956 (PID:g2843171)	2856	100.000
4545	AC005532	Homo sapiens supported by GENSCAN prediction and spliced EST; similar to Z35641 (PID:g3874821) and AI059600 (NID:g3333377)	1394	100.000
4546	M27508	Homo sapiens beta-galactosidase related protein precursor	966	49.379
4547	AB023176	Homo sapiens KIAA0959 protein	5305	99.026
4548	L17337	Caenorhabditis elegans coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative	647	46.445
4549	AJ011523	Caenorhabditis elegans CHE-2 protein	532	37.811
4550	U53475	Rattus norvegicus GTPase Rab8b	245	97.436
4551	U74297	Oryctolagus cuniculus PiUS	218	96.774
4552	AL117434	Homo sapiens hypothetical protein	4171	99.685
4553	AL021492	Caenorhabditis elegans Y45F10D.11	518	33.158
4554	D14336	Mus musculus RNA polymerase I associated factor (PAF53)	1494	77.700
4555	AF040965	Homo sapiens unknown protein IT12	5694	99.771
4556	AC005053	Homo sapiens match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112)	2522	100.000
4557	AF099742	Rattus norvegicus putative short-chain dehydrogenase/reductase	448	63.158
4558	U39648	Caenorhabditis elegans T13C5.6 gene product	497	51.250
4559	AL031027	Unknown /prediction=(method:""genefinder"", version:""084"", score:""67.72""); /prediction=(metho	754	56.614
4560	AF132164	Drosophila melanogaster unknown	278	35.762
4561	AB020669	Homo sapiens KIAA0862 protein	200	36.585
4562	AL117430	Homo sapiens hypothetical protein	1227	100.000
4563	U21324	Caenorhabditis elegans No definition line found	166	48.936
4564	AF098633	Mus musculus GLUT4 vesicle protein	411	47.656
4565	AF053630	Homo sapiens monocyte/neutrophil elastase inhibitor	1490	100.000
4566	J05499	Rattus norvegicus L-glutamine amidohydrolase	462	92.208
4567	AF068749	Mus musculus sphingosine kinase	1716	81.908
4568	Z48804	Homo sapiens OA1	1258	100.000
4569	X85030	Homo sapiens calpain	1541	100.000

4570	AL079349	Arabidopsis thaliana putative protein	289	30.962
4571	AF155110	Homo sapiens NY-REN-45 antigen	5381	99.877
4572	AB002301	Homo sapiens KIAA0303	14352	99.953
4573	AC002400	Homo sapiens Acyl carrier protein, Mitochondrial (ACP) (5'partial)	1000	100.000
4574	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase precursor	2320	59.331
4575	S45663	Rattus sp. SC2=synaptic glycoprotein	722	50.538
4576	AB025411	Mus musculus Ten-m2	4766	98.476
4577	Z46381	Unknown Weak similarity with the Ysy6 protein (Yeast) (PIR accession number JQ0912); cDNA EST EMBL:	550	42.157
4578	AF151863	Homo sapiens CGI-105 protein	187	93.333
4579	AB014564	Homo sapiens KIAA0664 protein	7558	100.000
4580	X98494	Homo sapiens M phase phosphoprotein 10	4243	98.960
4581	AL008635	Homo sapiens dJ510H16.1	844	54.412
4582	AF041206	Homo sapiens midline 1 cerebellar isoform 1	460	26.515
4583	AC006416	Arabidopsis thaliana Similar to	530	43.750
4584	AF123653	Homo sapiens FEZ1	362	41.341
4585	AF000195	Caenorhabditis elegans similar to oxysterol-binding proteins	490	42.246
4586	U93569	Homo sapiens p40	167	54.545
4587	X94313	Mus musculus p68 RNA helicase	153	95.455
4588	D87438	Homo sapiens Similar to a C.elegans protein in cosmid C14H10	5406	99.512
4589	U61953	Caenorhabditis elegans No definition line found	764	49.798
4590	U93569	Homo sapiens p40	238	37.963
4591	Z70780	Unknown similar to Zinc finger, C2H2 type; cDNA EST EMBL:D27516 comes from this gene; cDNA EST EMBL	975	40.000
4592	AB007923	Homo sapiens KIAA0454 protein	701	91.200
4593	AC002336	Arabidopsis thaliana hypothetical protein	647	33.668
4594	AB011096	Homo sapiens KIAA0524 protein	3955	100.000
4595	AL050331	Homo sapiens dJ486I3.4 (TSPY-like (testis specific protein, Y-linked like))	750	65.269
4596	AB029033	Homo sapiens KIAA1110 protein	4928	99.595
4597	AB002364	Homo sapiens KIAA0366	406	30.000
4598	AF017639	Mus musculus carboxypeptidase X2	923	90.411
4599	Y17462	Fugu rubripes cysteine conjugate beta-lyase	1613	55.904
4600	AF060173	Rattus norvegicus SV2 related protein	1828	96.140
4601	M36501	Homo sapiens alpha-2-macroglobulin	211	91.429
4602	X65964	Homo sapiens nestin	1907	95.652
4603	X03743	Homo sapiens L apoferritin (aa 126-175)	174	92.857
4604	Z69240	Schizosaccharomyces pombe putative amidohydrolase	996	52.708
4605	U73819	Mus musculus polypeptide GalNAc transferase-T4	734	39.527
4606	AF187318	Homo sapiens F-box protein Fbx2	492	43.103
4607	AF104260	Homo sapiens hiwi	1062	48.951
4608	Z46786	Drosophila melanogaster acetyl-CoA synthetase	348	61.446
4609	X76092	Homo sapiens DNA binding protein RFX3	417	100.000
4610	X68880	Homo sapiens EMX2	1076	100.000
4611	AF093097	Homo sapiens putative RNA-binding protein Q99	5782	100.000
4612	AF038960	Homo sapiens SKD1 homolog	340	97.917
4613	AB020807	Homo sapiens TLR6	1680	56.849

4614	U39546	Rattus norvegicus surface protein MCA-32	372	30.904
4615	AL031228	Homo sapiens dJ1033B10.8.1 (Ring finger protein 1 (RING1, RNF1))	1300	100.000
4616	AB015330	Homo sapiens HRIHFB2007	341	55.914
4617	U20086	Mus musculus NF2d9	297	89.796
4618	AF016417	Caenorhabditis elegans Similar to BZIP transcription factor	648	42.105
4619	L12701	Homo sapiens engrailed protein	667	100.000
4620	X55885	Homo sapiens KDEL receptor	497	100.000
4621	Y08200	Homo sapiens rab geranylgeranyl transferase	169	33.803
4622	U79260	Homo sapiens unknown	191	58.730
4623	U95973	Arabidopsis thaliana endomembrane protein EMP70 precursor isolog	1683	59.698
4624	AL034433	Schizosaccharomyces pombe ubiquitin-activating enzyme e1	456	48.538
4625	AL117404	Homo sapiens hypothetical protein	458	100.000
4626	L07765	Homo sapiens carboxylesterase	273	50.000
4627	AC003038	Homo sapiens R30923 1	482	98.611
4628	AJ010482	Homo sapiens Myopodin protein	1271	100.000
4629	AJ010305	Mus musculus mouse smoothelin, large isoform	834	54.751
4630	AF118637	Homo sapiens feline leukemia virus subgroup C receptor FLVCR	446	28.342
4631	AB029023	Homo sapiens KIAA1100 protein	1059	72.093
4632	AB014568	Homo sapiens KIAA0668 protein	4888	99.865
4633	X92857	Homo sapiens NFI /CAAT-binding transcription factor 5 (CTF5)	1014	100.000
4634	U13875	Caenorhabditis elegans No definition line found	485	43.367
4635	U34925	Drosophila melanogaster TH1	220	52.727
4636	AF031897	Meleagris gallopavo G protein coupled P2Y nucleotide receptor	563	35.632
4637	L22005	Homo sapiens ubiquitin conjugating enzyme	2038	99.664
4638	AF145615	Drosophila melanogaster BcDNA.GH03377	221	33.333
4639	Z49909	Caenorhabditis elegans weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene; cDNA EST yk549e12.3 comes from this gene; cDNA EST yk618d6.3 comes from this gene	628	36.508
4640	AF078850	Homo sapiens steroid dehydrogenase homolog	1175	98.925
4641	D88153	Homo sapiens HYA22	1155	71.429
4642	AF155739	Mus musculus axotrophin	1761	90.203
4643	AF079527	Mus musculus IER5	450	78.261
4644	AF080217	Sinorhizobium meliloti acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme	883	47.826
4645	X04823	Bos taurus cGMP phosphodiesterase (AA 1-87)	275	88.889
4646	Z95559	Caenorhabditis elegans cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene	648	56.497
4647	X80169	Mus musculus tsg24	3148	92.032
4648	X92750	Mus musculus red-1	1174	98.352
4649	J02459	bacteriophage lambda ea22 (182)	856	96.296
4650	U06631	Homo sapiens homologous to mouse gene PC326:GenBank Accession Number M95564	400	64.583

4651	L36340	Xenopus laevis importin alpha 1b	194	57.692
4652	AF135027	Homo sapiens OB binding protein-like protein	2931	89.655
4653	U22818	Cricetulus griseus mutant sterol regulatory element binding protein-2	469	63.636
4654	AB028981	Homo sapiens KIAA1058 protein	10125	100.000
4655	AL049996	Homo sapiens hypothetical protein	51	36.364
4656	D86979	Homo sapiens KIAA0226	1103	55.172
4657	U28789	Mus musculus PACT	2740	78.743
4658	X97674	Homo sapiens transcriptional intermediary factor 2	8231	100.000
4659	A58799	unidentified unnamed protein product	407	94.444
4660	AF072506	Homo sapiens envelope protein precursor	373	75.949
4661	X98374	Rattus norvegicus KIS	314	100.000
4662	Z71259	Caenorhabditis elegans Weak similarity to Yeast mitochondrial carrier protein YIL006W (SW:YIA6_YEAST); cDNA EST EMBL:C09181 comes from this gene	365	42.748
4663	AB028986	Homo sapiens KIAA1063 protein	811	80.000
4664	AL021748	Schizosaccharomyces pombe hypothetical protein	232	35.971
4665	AB002374	Homo sapiens KIAA0376	962	45.433
4666	AB023203	Homo sapiens KIAA0986 protein	242	100.000
4667	AJ010973	Homo sapiens DEDD protein	578	53.049
4668	AF116553	Drosophila melanogaster antennal-specific short-chain dehydrogenase/reductase	390	32.663
4669	X07311	Drosophila melanogaster heat shock protein	167	35.714
4670	X75042	Homo sapiens c-rel	2965	100.000
4671	X17531	Strongylocentrotus purpuratus epidermal growth factor	407	57.831
4672	AB011123	Homo sapiens KIAA0551 protein	443	87.671
4673	AB020711	Homo sapiens KIAA0904 protein	312	100.000
4674	AF000234	Homo sapiens P2x purinoceptor	216	100.000
4675	Z36715	Homo sapiens Net	2006	98.101
4676	AL109819	Arabidopsis thaliana extensin-like protein	414	24.194
4677	AJ006268	Homo sapiens ATPase	811	92.308
4678	AF132180	Drosophila melanogaster unknown	940	35.849
4679	Z72511	Unknown possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D715	228	33.333
4680	AC005053	Homo sapiens match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112)	881	49.580
4681	AE000119	Escherichia coli orf, hypothetical protein	675	100.000
4682	AB015630	Homo sapiens type II membrane protein	551	34.448
4683	AB005541	Rattus rattus PCTAIRE3	2521	91.707
4684	AF089730	Rattus norvegicus potassium channel subunit	488	94.937
4685	AB011541	Homo sapiens MEGF8	12808	99.942
4686	AF006466	Mus musculus lymphocyte specific formin related protein	2651	81.426
4687	U71273	Sus scrofa glucosidase II	179	30.488
4688	D90750	Escherichia coli Hypothetical transcriptional regulator in metG-dld intergenic region.	550	100.000
4689	M59742	Rattus norvegicus GABA transporter protein	2732	90.991
4690	AB014568	Homo sapiens KIAA0668 protein	511	37.838
4691	D29013	Homo sapiens DNA polymerase beta	512	33.333
4692	AB028972	Homo sapiens KIAA1049 protein	201	100.000

4693	AC004685	Homo sapiens Unknown gene product	287	100.000
4694	AE000799	Methanobacterium thermoautotrophicum O-linked GlcNAc transferase	193	38.776
4695	X99209	Homo sapiens arginine methyltransferase	250	34.884
4696	AL031685	Homo sapiens dJ963K23.2 (novel protein)	533	41.765
4697	AL121741	Schizosaccharomyces pombe vacuolar protein sorting-associated protein	1078	35.199
4698	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	591	86.735
4699	Z93239	Unknown predicted using Genefinder; cDNA EST EMBL:D68680 comes from this gene; cDNA EST yk212g2.5 c	1063	44.986
4700	AL078627	Schizosaccharomyces pombe actin-like protein; (2 actin domains)	403	46.043
4701	Z68318	Caenorhabditis elegans Similarity to Human Transcriptional repressor protein PRDI-BF1 (PIR Acc. No. A39564)	194	39.216
4702	AB015339	Homo sapiens HRIHFB2255	293	65.556
4703	X63692	Homo sapiens DNA (cytosine-5-)-methyltransferase	1422	99.510
4704	AF053130	Mus musculus unconventional myosin MYO15	254	97.561
4705	AF121081	Mus musculus cAMP inducible 2 protein	473	68.182
4706	AC003007	Homo sapiens Unknown gene product (partial)	1141	96.237
4707	AB014573	Homo sapiens KIAA0673 protein	8121	100.000
4708	Z68751	Unknown Similarity to Yeast hypothetical protein YKK0 (SW:YKK0_YEAST); cDNA EST EMBL:C12578 comes f	662	47.222
4709	AF111168	Homo sapiens unknown	163	55.556
4710	AF146688	Fugu rubripes kelch protein	264	31.056
4711	AB006627	Homo sapiens KIAA0289	8904	99.313
4712	AL080058	Homo sapiens hypothetical protein	2277	99.701
4713	AB001772	Ciona savignyi PEM-5	301	32.576
4714	AB020676	Homo sapiens KIAA0869 protein	5658	99.217
4715	Z73906	Caenorhabditis elegans cDNA EST EMBL:M88866 comes from this gene	298	30.290
4716	AF077032	Homo sapiens sec61 homolog	476	95.890
4717	AF064092	Homo sapiens mutant guanine nucleotide-binding protein G(s), alpha subunit	158	100.000
4718	AF030253	Rattus norvegicus vesicular GABA transporter	398	98.305
4719	U36309	Gallus gallus rhoGap protein	877	48.235
4720	AL050331	Homo sapiens dJ486I3.4 (TSPY-like (testis specific protein, Y-linked like))	1554	99.556
4721	X77681	Picea abies cdc2Pa	125	45.455
4722	U66411	Drosophila melanogaster putative type III alcohol dehydrogenase	294	54.878
4723	L07063	Mus musculus FKBP65 binding protein	2255	89.444
4724	AB007923	Homo sapiens KIAA0454 protein	292	33.790
4725	X69090	Homo sapiens 190kD protein	3235	99.393
4726	X61047	Hydra sp. mini-collagen	124	53.333
4727	AL035424	Homo sapiens dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins)	3848	100.000
4728	AF003384	Caenorhabditis elegans weak similarity to the peptidase family A2	713	34.988
4729	U43317	Mus musculus transmembrane receptor	1084	99.401

4730	AC002400	Homo sapiens Gene product with similarity to Ubiquitin binding enzyme	1378	90.870
4731	L15313	Caenorhabditis elegans homology with leucine aminopeptidase; coded for by C. elegans cDNAs CE2F12 (GenBank: Z14714) and CE15D11 (GenBank: Z14518); putative	1227	46.991
4732	AJ238706	Drosophila melanogaster monocarboxylate transporter 1 homologue	297	30.400
4733	AF072934	Homo sapiens translational release factor.1	1050	48.773
4734	AC005306	Homo sapiens R27216.1	1480	80.970
4735	AF113131	Homo sapiens host cell factor homolog LCP	276	80.000
4736	AB007926	Homo sapiens KIAA0457 protein	5616	99.763
4737	AC004500	Homo sapiens GDF-9	3109	100.000
4738	AF007170	Homo sapiens unknown	404	26.415
4739	X60152	Homo sapiens zinc finger 2.2	2795	100.000
4740	D25215	Homo sapiens KIAA0032	593	38.565
4741	AC005534	Homo sapiens supported by human ESTs AA412402 (NID:g2070990) NH44021 (NID:g1182549), mouse EST AA065933 (NID:g1562789), and genscan	1486	88.845
4742	Z83115	Caenorhabditis elegans predicted using Genefinder; Similarity to Human P619 protein (TR:Q15751)	212	48.387
4743	AF153230	Xenopus laevis allantoicase	817	56.345
4744	Y07759	Homo sapiens myosin heavy chain 12	413	61.798
4745	M98529	Homo sapiens 21 kDa protein	418	100.000
4746	U23522	Caenorhabditis elegans No definition line found	574	31.875
4747	AF070996	Monodelphis domestica lactate dehydrogenase A	767	41.534
4748	Z25420	Gallus gallus class II INCENP protein	238	26.103
4749	AF117892	Homo sapiens aspartic-like protease	3428	99.807
4750	AL050126	Homo sapiens hypothetical protein	740	73.077
4751	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	369	32.035
4752	AL031320	Homo sapiens dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)	260	97.436
4753	U34932	Rattus norvegicus Fos-related antigen	1129	82.432
4754	AF083108	Homo sapiens sirtuin type 3	2730	100.000
4755	AL049938	Homo sapiens hypothetical protein	1438	99.552
4756	AJ006470	Homo sapiens cartilage-associated protein (CASP)	1944	100.000
4757	AF000195	Caenorhabditis elegans similar to oxysterol-binding proteins	839	44.966
4758	U54638	Mus musculus rhotekin	1438	81.176
4759	Z78542	Caenorhabditis elegans similar to Mitochondrial carrier proteins; cDNA EST EMBL:T01651 comes from this gene	523	51.592
4760	X13916	Homo sapiens LDL-receptor related precursor (AA -19 to 4525)	1252	96.196
4761	AF053308	Drosophila affinis putative guanine nucleotide releasing factor	656	57.962
4762	AF167320	Mus musculus zinc finger protein ZFP113	672	67.669
4763	AF049611	Homo sapiens huntingtin interacting protein HYPE	1221	100.000
4764	AB014596	Homo sapiens KIAA0696 protein	3747	100.000
4765	AL034408	Homo sapiens dJ710L4.2 (similar to	1985	99.660

		MYOTUBULARIN-RELATED PROTEIN)		
4766	Z46787	Caenorhabditis elegans similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	1209	51.582
4767	D78359	Rattus norvegicus consensus repeat domain: nt120-174; consensus repeat domain: nt262-317; consensus repeat domain: nt57-115; transmembrane domain: nt376-413	235	32.168
4768	AF083217	Homo sapiens WD repeat protein WDR3	6181	99.788
4769	X95272	Rattus norvegicus ORF	304	25.000
4770	AL096842	Homo sapiens hypothetical protein	409	95.385
4771	AF061817	Rattus norvegicus DNA-binding protein PREB	1471	92.373
4772	AL021481	Unknown similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168	1138	44.089
4773	Z92832	Caenorhabditis elegans F31D4.2	578	42.273
4774	X52022	Homo sapiens collagen type VI, alpha 3 chain	4690	99.582
4775	U70854	Caenorhabditis elegans No definition line found	985	39.231
4776	X76116	Caenorhabditis elegans carrier protein (c2)	693	50.877
4777	U06713	Rattus norvegicus SM-20	993	61.860
4778	Z46373	Saccharomyces cerevisiae orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum	945	44.142
4779	Z46354	Homo sapiens hexokinase II	200	70.732
4780	Z93239	Unknown predicted using Genefinder; cDNA EST EMBL:D68680 comes from this gene; cDNA EST yk212g2.5 c	593	37.917
4781	AB023233	Homo sapiens KIAA1016 protein	4916	99.185
4782	U49954	Caenorhabditis elegans coded for by C. elegans cDNA CEESG19F; short region of weak similarity to Thermomonospora protein kinase (GB:U23820)	281	27.759
4783	M17099	Oryctolagus cuniculus progesterone-induced protein	1158	91.623
4784	AL117482	Homo sapiens hypothetical protein	2001	100.000
4785	Z29094	Caenorhabditis elegans similar to Na/Ca, K antiporter	234	33.884
4786	D49473	Mus musculus truncated form of Sox17	1402	78.400
4787	L31349	Drosophila melanogaster out at first protein	644	41.228
4788	U66088	Homo sapiens sodium iodide symporter	186	33.654
4789	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	325	39.344
4790	AF038957	Homo sapiens translation initiation factor 4e	169	100.000
4791	AF002196	Caenorhabditis elegans No definition line found	227	38.462
4792	U21324	Caenorhabditis elegans similar to entire S. cerevisiae ABC1 protein (Swiss-Prot Acc: P27697)	420	50.862
4793	AL050102	Homo sapiens hypothetical protein	3182	99.798
4794	AF097887	Rattus norvegicus Chp	1135	98.810
4795	L34581	Mus musculus tyrosine phosphatase	200	33.708
4796	L15313	Caenorhabditis elegans homology with leucine aminopeptidase; coded for by C. elegans cDNAs CE2F12 (GenBank: Z14714) and CE15D11 (GenBank: Z14518); putative	1227	46.991
4797	L43631	Homo sapiens scaffold attachment factor B	377	44.937

4798	AF083389	Homo sapiens putative WHSC1 protein	3574	100.000
4799	AC004473	Arabidopsis thaliana T13D8.31	630	36.901
4800	AJ238097	Homo sapiens Lsm5 protein	24	60.000
4801	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	363	67.568
4802	Z75552	Unknown predicted using Genefinder; Similarity to Prototheca mitochondiral ribosomal protein S11 (382	43.704
4803	X92763	Homo sapiens tafazzins	2043	100.000
4804	Z75170	Saccharomyces cerevisiae ORF YOR262w	727	44.939
4805	Z48583	Unknown similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623	1246	59.868
4806	AF104919	Unknown Arabidopsis thaliana ABC1 protein (GB:AJ001158)	819	45.946
4807	X13320	Homo sapiens keratin	340	98.214
4808	AF145649	Drosophila melanogaster BcDNA.GH08388	907	38.362
4809	U58652	Oryctolagus cuniculus ubiquitin-conjugating enzyme E2-32k	1413	99.515
4810	X76013	Homo sapiens glutamyl-tRNA synthetase	4012	100.000
4811	AF047659	Caenorhabditis elegans No definition line found	1162	46.731
4812	AL080214	Homo sapiens hypothetical protein	693	100.000
4813	AB031292	Mus musculus proteolipid protein 2	192	30.208
4814	AF069291	Homo sapiens hT41	925	44.970
4815	AL109832	Schizosaccharomyces pombe hypothetical protein	175	32.632
4816	AF070470	Mus musculus SPARC-related protein	1583	58.530
4817	U22376	Homo sapiens alternatively spliced product using exon 13A	402	62.245
4818	D50086	Mus musculus neuropilin	248	37.500
4819	L20319	Rattus norvegicus developmentally regulated protein	221	55.172
4820	M81088	Rattus norvegicus EF-1-alpha	165	96.667
4821	U82982	Cavia porcellus GEC-3	544	47.399
4822	AF000195	Caenorhabditis elegans similar to oxysterol-binding proteins	1346	47.899
4823	AC004912	Homo sapiens similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070)	1309	99.459
4824	D87973	Mus musculus Impact	396	86.765
4825	X75756	Homo sapiens protein kinase C mu	675	99.020
4826	AF070614	Homo sapiens unknown	2568	100.000
4827	L08069	Homo sapiens DNAJ homologue-2	1329	68.613
4828	AL117525	Homo sapiens hypothetical protein	172	96.000
4829	U22376	Homo sapiens alternatively spliced product using exon 13A	425	73.626
4830	M11437	Homo sapiens kininogen	2074	100.000
4831	AB005142	Homo sapiens klotho	576	37.097
4832	Y18208	Rattus norvegicus serine-threonine specific protein phosphatase, glycogen-binding (GL) subunit	873	90.226
4833	U63840	Rattus norvegicus nucleoporin p54	1155	96.257
4834	AL031588	Homo sapiens dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases) (isoform 1)	892	97.744
4835	AF116509	Homo sapiens Ets transcription factor TEL-2b	2415	100.000

4836	AB011168	Homo sapiens KIAA0596 protein	8110	99.836
4837	X66357	Homo sapiens serine/threonine protein kinase	1667	99.595
4838	X86682	Mus musculus HNP36 protein	275	34.320
4839	AF055666	Mus musculus kinesin light chain 2	2075	73.884
4840	AF100657	Caenorhabditis elegans Contains similarity to Pfam domain: PF00614 (PLDc), Score=13.8, E-value=0.2, N=1	217	38.400
4841	AL031447	Homo sapiens dJ126A5.2.1 (novel protein) (isoform 1)	1670	100.000
4842	AB002319	Homo sapiens KIAA0321	10277	100.000
4843	AL096768	Homo sapiens dJ858B16.2 (novel protein similar to hamster PSSC (Phosphatidylserine Decarboxylase Proenzyme, EC 4.1.1.65)	2108	99.670
4844	U86074	Homo sapiens tesmin	206	54.386
4845	AB023136	Homo sapiens KIAA0919 protein	4673	100.000
4846	X87237	Homo sapiens a-glucosidase I	4405	97.869
4847	AF016421	Caenorhabditis elegans Similar to nitrophenylphosphatase; coded for by C. elegans cDNA yk312h2.5; coded for by C. elegans cDNA yk267e8.5; coded for by C. elegans cDNA yk312h2.3	344	37.013
4848	Z29121	Caenorhabditis elegans ZK757.1	734	39.858
4849	AB020702	Homo sapiens KIAA0895 protein	834	64.324
4850	U55021	Saccharomyces cerevisiae O3635p	138	33.333
4851	AB029000	Homo sapiens KIAA1077 protein	5570	99.750
4852	AB029035	Homo sapiens KIAA1112 protein	3399	95.131
4853	AF074603	Streptomyces griseus subsp. griseus NonF	265	38.571
4854	AF081249	Homo sapiens JAW1-related protein MRVI1A long isoform	5849	99.215
4855	AL031786	Schizosaccharomyces pombe hypothetical protein	209	33.628
4856	D87908	Mus musculus nuclear protein np95	512	46.286
4857	AC007178	Arabidopsis thaliana hypothetical protein	680	32.326
4858	X70804	Mus musculus rab17	304	90.000
4859	M34054	Cavia porcellus complement C3 protein (GPC3) precursor	436	39.773
4860	M25579	Bos taurus adenyl cyclase Type I	5713	91.300
4861	AL031644	Schizosaccharomyces pombe hypothetical protein	292	28.319
4862	Y17832	Human endogenous retrovirus K pol protein	175	48.000
4863	M76411	Escherichia coli cadA	590	100.000
4864	AB011177	Homo sapiens KIAA0605 protein	457	36.574
4865	AF080171	Homo sapiens zinc finger protein ZNF232	1962	100.000
4866	AL117462	Homo sapiens hypothetical protein	308	46.457
4867	X64878	Homo sapiens oxytocin receptor	902	100.000
4868	M92843	Homo sapiens zinc finger transcriptional regulator	261	100.000
4869	AF059569	Homo sapiens actin binding protein MAYVEN	305	50.000
4870	AB023216	Homo sapiens KIAA0999 protein	7456	99.728
4871	AF026794	Mus musculus galectin-6	201	28.877
4872	AL117478	Homo sapiens hypothetical protein	4882	99.713
4873	J04605	Homo sapiens prolidase	301	91.837
4874	AF019236	Dictyostelium discoideum TipD	746	39.869
4875	AB001451	Homo sapiens Sck	992	100.000
4876	X85019	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase	902	48.029
4877	U86074	Homo sapiens tesmin	2133	100.000

4878	D86980	Homo sapiens KIAA0227	501	45.312
4879	D86979	Homo sapiens KIAA0226	234	43.662
4880	Z92809	Caenorhabditis elegans predicted using Genefinder; similar to Thrombospondin type 1 domain	414	30.126
4881	Z37139	Unknown similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; c	1556	64.756
4882	AF095286	Homo sapiens guanine deaminase GDA	793	100.000
4883	AF126162	Homo sapiens HERV-H LTR associating protein 2	160	100.000
4884	AB002331	Homo sapiens KIAA0333	6685	100.000
4885	X85545	Homo sapiens protein kinase	427	86.957
4886	AF149045	Homo sapiens Sex comb on midleg homolog 1 isoform 1	1784	92.568
4887	U13149	Pennisetum ciliare possible apospory-associated protein	189	45.588
4888	U23172	Caenorhabditis elegans No definition line found	619	37.631
4889	AB002304	Homo sapiens KIAA0306	9825	99.724
4890	M32512	Sus scrofa Na ⁺ , K ⁺ -ATPase alpha subunit	167	92.308
4891	D10923	Homo sapiens HM74	530	45.226
4892	AL049944	Homo sapiens hypothetical protein	193	51.613
4893	AF089745	Homo sapiens FK506-binding protein	264	80.851
4894	M16538	Homo sapiens G protein beta subunit	745	91.964
4895	U00063	Caenorhabditis elegans No definition line found	140	20.792
4896	AF077831	Homo sapiens tumor-related protein	3255	100.000
4897	M16141	Gallus gallus ovoidinhibitor	184	37.681
4898	Z81030	Caenorhabditis elegans similar to citrate lyase beta chain; cDNA EST yk302b4.5 comes from this gene	602	54.023
4899	J04621	Homo sapiens heparan sulfate proteoglycan core protein	2591	99.748
4900	AJ003125	Homo sapiens procollagen I N-proteinase	444	33.508
4901	AF053367	Mus musculus carboxyl terminal LIM domain protein	433	45.578
4902	AF002668	Homo sapiens MLD	634	72.034
4903	Z82266	Caenorhabditis elegans predicted using Genefinder; similar to WD domain, G-beta repeats	959	39.118
4904	M28821	Mus musculus Tcte-1 peptide	202	30.769
4905	AF076957	Homo sapiens SDP1 protein	526	98.824
4906	U76638	Homo sapiens BRCA1-associated RING domain protein	419	40.957
4907	U22376	Homo sapiens alternatively spliced product using exon 13A	390	72.727
4908	AF060152	Homo sapiens METH1 protein	6696	100.000
4909	AF117892	Homo sapiens aspartic-like protease	1132	47.965
4910	U32394	Mus musculus Max-interacting transcriptional repressor	280	80.000
4911	D21205	Homo sapiens estrogen responsive finger protein (efp)	294	37.857
4912	AL034381	Schizosaccharomyces pombe conserved hypothetical PFAM UPF0031 containing protein	298	40.708
4913	X63692	Homo sapiens DNA (cytosine-5-)-methyltransferase	5745	99.880
4914	Z75526	Caenorhabditis elegans Weak similarity to	692	48.485

		Staphylococcus autolysin gene (TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene		
4915	AF000198	Caenorhabditis elegans weak similarity to HSP90	594	30.952
4916	AB020721	Homo sapiens KIAA0914 protein	666	56.716
4917	AF083246	Homo sapiens HSPC028	1540	100.000
4918	AF001434	Homo sapiens Hpast	1630	84.698
4919	U36340	Mus musculus BKLF	956	99.242
4920	AF126484	Homo sapiens CARD4	424	44.944
4921	AF186469	Rattus norvegicus TM6P1	951	90.385
4922	AC007071	Arabidopsis thaliana hypothetical protein	221	26.400
4923	AC003093	Homo sapiens OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	503	53.731
4924	AF067660	Mus musculus Bcl-2 homolog	407	47.368
4925	AF145204	Homo sapiens E2a-Pbx1-associated protein	1458	79.333
4926	X69089	Homo sapiens 165kD protein	815	96.875
4927	AF022080	Homo sapiens R-ras3	302	100.000
4928	AC006585	Arabidopsis thaliana hypothetical protein	212	25.108
4929	D42047	Homo sapiens The ha3662 gene product is related to mouse glycerophosphate dehydrogenase.	2715	100.000
4930	AB028998	Homo sapiens KIAA1075 protein	9734	99.427
4931	AF051162	Drosophila melanogaster SLOB	443	39.574
4932	AF001533	Mus musculus mitogen-induced	497	98.750
4933	Z72604	Saccharomyces cerevisiae ORF YGL082w	230	27.500
4934	Z70780	Caenorhabditis elegans cDNA EST yk465d10.3 comes from this gene; cDNA EST yk465d10.5 comes from this gene; cDNA EST yk481d9.5 comes from this gene	548	49.032
4935	AB007948	Homo sapiens KIAA0479 protein	2327	100.000
4936	AF187318	Homo sapiens F-box protein Fbx2	873	48.289
4937	Y17048	Rattus norvegicus caldendrin	1274	94.500
4938	AB020626	Homo sapiens KIAA0819 protein	349	39.583
4939	L06237	Homo sapiens microtubule-associated protein 1B	671	35.782
4940	U81491	Mus musculus polyhomeotic 2	197	44.776
4941	AF007787	Enterococcus faecalis orfC	309	44.444
4942	AF058919	Arabidopsis thaliana regions of weak similarity to l-asparaginase	267	45.556
4943	AF051155	Rattus norvegicus G beta-like protein GBL	1280	94.388
4944	X57108	Homo sapiens cerebroside sulfate activator	338	100.000
4945	AL117589	Homo sapiens hypothetical protein	1787	100.000
4946	U22376	Homo sapiens alternatively spliced product using exon 13A	185	88.571
4947	AL050157	Homo sapiens hypothetical protein	747	100.000
4948	AF090133	Rattus norvegicus lin-7-A	860	96.350
4949	U37150	Bos taurus peptide methionine sulfoxide reductase	1402	89.238
4950	AF025441	Homo sapiens Opa-interacting protein OIP5	1557	100.000
4951	Z69240	Schizosaccharomyces pombe putative amidohydrolase	996	52.708
4952	U21309	Caenorhabditis elegans No definition line found	307	39.157
4953	AB018188	Bos taurus myocilin	323	35.583
4954	AL035424	Homo sapiens dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins)	382	66.667

4955	AL031261	Schizosaccharomyces pombe conserved hypothetical protein	400	35.519
4956	U55376	Caenorhabditis elegans coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	515	35.350
4957	X78933	Homo sapiens zinc finger protein	1012	74.731
4958	AF007139	Homo sapiens unknown	1597	98.780
4959	D83327	Homo sapiens DCRR1	390	23.862
4960	Z81052	Caenorhabditis elegans Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene	613	42.326
4961	AF118274	Homo sapiens DNb-5	1759	100.000
4962	AL050197	Homo sapiens hypothetical protein	496	48.529
4963	AL031393	Homo sapiens dJ733D15.1 (Zinc-finger protein)	3520	100.000
4964	L07780	Bos taurus UDP-GalNAc:polypeptide, N-acetylgalactosaminyltransferase	663	34.713
4965	AF155117	Homo sapiens NY-REN-62 antigen	505	49.708
4966	X80903	Mus musculus DELTA-like 1	716	40.240
4967	AB002323	Homo sapiens KIAA0325	13746	100.000
4968	AB014520	Homo sapiens KIAA0620 protein	13395	99.950
4969	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	390	71.622
4970	AF154671	Homo sapiens CRB1	9674	99.626
4971	U29096	Caenorhabditis elegans coded for by C. elegans cDNA yk44f2.5; similar to P59 protein (HSP binding immunophilin) and to TPR domain	527	38.000
4972	AF125188	Homo sapiens adenosine deaminase acting on tRNA 1	301	91.667
4973	D26549	Bos taurus bovine adseverin	4422	90.795
4974	AJ007798	Homo sapiens nuclear protein SA3	481	92.000
4975	AF068749	Mus musculus sphingosine kinase	175	41.791
4976	AL031685	Homo sapiens dJ963K23.2 (novel protein)	1621	100.000
4977	AF187552	Homo sapiens ezrin	201	90.909
4978	U95098	Xenopus laevis mitotic phosphoprotein 44	611	71.774
4979	X77383	Homo sapiens cathepsin O	1878	100.000
4980	Z49967	Unknown cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA	535	32.240
4981	Z78542	Caenorhabditis elegans similar to Mitochondrial carrier proteins; cDNA EST EMBL:T01651 comes from this gene	250	54.412
4982	D87757	Mus musculus ECF-L precursor	762	68.919
4983	L20319	Rattus norvegicus developmentally regulated protein	670	83.636
4984	U49057	Rattus norvegicus rA9	1098	70.472
4985	AC007504	Arabidopsis thaliana Hypothetical Protein	1211	35.835
4986	X61047	Hydra sp. mini-collagen	197	39.759
4987	U85969	Xenopus laevis middle molecular weight neurofilament protein NF-M(1)	259	29.102
4988	AL022238	Homo sapiens dJ1042K10.4 (novel protein)	793	51.029
4989	AC006128	Homo sapiens Human homolog of Mus musculus wizS protein	382	100.000
4990	U90880	Fugu rubripes zinc finger protein	1285	75.336
4991	U23175	Caenorhabditis elegans similar to anion	1184	46.250

		exchange protein		
4992	AL031788	Schizosaccharomyces pombe putative mitochondrial inner membrane protease subunit 2	203	55.000
4993	U96113	Homo sapiens WWP1	4692	99.853
4994	X57228	Rattus norvegicus beta COP	4867	98.830
4995	U35776	Rattus norvegicus ADP-ribosylation factor 1-directed GTPase activating protein	1453	80.505
4996	AF040944	Mus musculus P140	454	33.158
4997	AC007858	Oryza sativa Similar to gb U43629 integral membrane protein from Beta vulgaris and is a member of the sugar transporter family PF 00083. ES	677	37.243
4998	AL117654	Homo sapiens hypothetical protein	2059	100.000
4999	AB006629	Homo sapiens KIAA0291	6027	99.895
5000	L04673	Saccharomyces cerevisiae phosphatase	198	30.000
5001	AF047659	Caenorhabditis elegans No definition line found	291	51.020
5002	U29378	Caenorhabditis elegans No definition line found	910	53.462
5003	U23515	Caenorhabditis elegans weakly similar to gastrula zinc finger protein	375	40.000
5004	D64001	Synechocystis sp. hypothetical protein	396	39.888
5005	AL035416	Homo sapiens dJ782L23.1 (HOOK1)	475	60.294
5006	S66407	Homo sapiens receptor tyrosine kinase isoform FLT4 long, FLT41 {C-terminal}	498	100.000
5007	AB015630	Homo sapiens type II membrane protein	388	48.819
5008	Z70269	Unknown predicted using Genefinder; Similarity to Yeast hypothetical protein YHG1 (SW:YHG1 YEAST);	1526	44.857
5009	AF105228	Bos taurus tuftelin	711	94.915
5010	U23169	Caenorhabditis elegans No definition line found	329	51.923
5011	AB020637	Homo sapiens KIAA0830 protein	3451	100.000
5012	M31013	Homo sapiens nonmuscle myosin heavy chain (NMHC)	7708	99.840
5013	AF125158	Homo sapiens zinc finger DNA binding protein 99	635	100.000
5014	AE001719	Thermotoga maritima NADH oxidase, putative	221	26.126
5015	U82163	Oryctolagus cuniculus No definition line found	364	53.571
5016	AB006013	Rattus norvegicus RGS8	214	49.180
5017	L26955	Streptomyces verticillus beta-hydroxylase	313	51.579
5018	AF140501	Homo sapiens RAD30B	4689	99.441
5019	X98374	Rattus norvegicus KIS	963	98.621
5020	AF172849	Homo sapiens AIM-1 protein	3564	100.000
5021	Z72795	Saccharomyces cerevisiae ORF YGR010w	655	41.538
5022	AB020682	Homo sapiens KIAA0875 protein	4162	98.885
5023	U90908	Homo sapiens unknown	352	41.007
5024	Z70034	Unknown similarity to 35.1KD hypothetical yeast protein (Swiss Prot accession number P38805); cDNA	1020	51.678
5025	AB000280	Rattus norvegicus peptide/histidine transporter	3185	87.057
5026	AB029010	Homo sapiens KIAA1087 protein	6354	100.000
5027	AC005620	Homo sapiens R33590 1	2089	100.000
5028	M38222	Trypanosoma brucei procyclic acidic repetitive	182	88.462

		protein		
5029	AB029018	Homo sapiens KIAA1095 protein	7344	99.454
5030	AB018299	Homo sapiens KIAA0756 protein	5678	99.761
5031	AB019280	Mus musculus sprouty-4	1559	95.853
5032	AB007948	Homo sapiens KIAA0479 protein	519	36.634
5033	U22376	Homo sapiens alternatively spliced product using exon 13A	202	69.565
5034	U21317	Caenorhabditis elegans similar to SP:YR40_BACSU (P37512) hypothetical 78.8 kD protein in TETB-EXOA intergenic region	566	31.268
5035	AB018324	Homo sapiens KIAA0781 protein	4316	100.000
5036	AL031525	Schizosaccharomyces pombe ubiquitin carboxyl-terminal hydrolase	987	42.147
5037	D63477	Homo sapiens The KIAA0143 gene product is related to a putative C.elegans gene encoded on cosmid C32D5.	496	62.500
5038	U50193	Caenorhabditis elegans weak similarity to SP:YAD5_CLOAB (P33746) hypothetical protein and to PIR:C48583 stress-inducible protein STI1	706	35.135
5039	Z74031	Unknown Similarity to Yeast D-lactate dehydrogenase (SW:DLD1_YEAST); cDNA EST EMBL:C12235 comes fro	701	50.495
5040	AB009593	Tetragenococcus halophilus xylose transporter	169	35.294
5041	U97107	Mus musculus membrane glycoprotein CIG30	651	48.901
5042	AF055084	Homo sapiens very large G-protein coupled receptor-1	689	100.000
5043	X55019	Homo sapiens acetylcholine receptor delta subunit	1138	99.408
5044	X70223	Rattus norvegicus peroxisomal membrane protein	882	76.829
5045	M29015	Mus musculus ribosomal protein L7	689	43.983
5046	Z99124	Bacillus subtilis urocanase	414	33.772
5047	AC004010	Homo sapiens similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	474	39.819
5048	AF087940	Homo sapiens basic helix-loop-helix transcription factor HAND2	433	98.529
5049	M19441	Mus musculus Kruppel-related protein	767	87.500
5050	AC006017	Homo sapiens similar to ALR; similar to AAC51735 (PID:g2358287)	2363	98.596
5051	AF145613	Drosophila melanogaster BcDNA.GH03108	498	30.278
5052	AL117435	Homo sapiens hypothetical protein	681	49.315
5053	AL117578	Homo sapiens hypothetical protein	1812	100.000
5054	U22376	Homo sapiens alternatively spliced product using exon 13A	333	65.909
5055	AJ010901	Homo sapiens MUC4	8100	99.654
5056	X14549	Chlamydomonas reinhardtii spoke protein	565	49.412
5057	AC009322	Arabidopsis thaliana Hypothetical protein	235	24.460
5058	X74798	Homo sapiens TRGV10	669	99.057
5059	Z93323	Bos taurus butyrophilin	115	31.343
5060	AC005587	Homo sapiens similar to meningioma-expressed antigen 6 (MEA6); similar to U94780 (PID:g2231999)	1868	99.612
5061	U27486	Pseudorabies virus EP0	109	38.806
5062	AF041106	Rattus norvegicus tulip 1	729	60.571

5063	AF077032	Homo sapiens sec61 homolog	971	96.026
5064	AL117435	Homo sapiens hypothetical protein	6181	99.891
5065	U83660	Homo sapiens multidrug resistance-associated protein homolog	158	66.667
5066	AF017369	Mus musculus faciogenital dysplasia protein 3	878	61.765
5067	AF005775	Homo sapiens caspase-like apoptosis regulatory protein 2	242	90.698
5068	U02098	Mus musculus Pur-alpha	209	50.769
5069	AF027826	Homo sapiens putative seven pass transmembrane protein	333	38.994
5070	Z22181	Caenorhabditis elegans ZK632.11	299	36.527
5071	AF058445	Gallus gallus histone macroH2A1.1	193	27.326
5072	AC007228	Homo sapiens BC37295_2 (partial)	575	58.915
5073	Z12173	Homo sapiens N-acetylglucosamine-6-sulphatase	1861	100.000
5074	AL110217	Homo sapiens hypothetical protein	5031	100.000
5075	U23514	Caenorhabditis elegans similar to S. cerevisiae SSD1 protein (SP:SSD1 YEAST, P24276) and to E. coli VACB and Ribonuclease II genes	1365	45.591
5076	AF167319	Mus musculus zinc finger protein ZFP112	834	87.121
5077	AF119711	Homo sapiens cysLT1 LTD4 receptor	2233	99.703
5078	AF143171	Mus musculus high affinity immunoglobulin gamma Fc receptor I	364	47.692
5079	U43194	Mus musculus rhophilin	214	47.297
5080	AC003003	Homo sapiens Homolog of rat B/K protein product	169	50.000
5081	AF039390	Homo sapiens vascular endothelial cell growth inhibitor	1165	100.000
5082	AF027514	Homo sapiens zinc finger protein	661	100.000
5083	AL035478	Streptomyces coelicolor putative transferase	187	32.479
5084	AB014531	Homo sapiens KIAA0631 protein	348	47.664
5085	AB028980	Homo sapiens KIAA1057 protein	241	100.000
5086	AL110124	Homo sapiens hypothetical protein	285	30.622
5087	AF116910	Homo sapiens putative ribonuclease III	3237	100.000
5088	AF072758	Mus musculus fatty acid transport protein 3; FATP3	1219	87.864
5089	AC002561	Arabidopsis thaliana hypothetical protein	271	25.123
5090	AC005238	Homo sapiens PSGIIA-c	235	30.114
5091	AL078579	Arabidopsis thaliana putative protein	191	27.215
5092	Z47811	Unknown similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes f	523	43.000
5093	AJ242976	Homo sapiens p241 protein	2120	90.490
5094	AC004077	Arabidopsis thaliana putative end13 protein	957	56.274
5095	X14968	Homo sapiens RII-alpha subunit (AA 1-404)	623	90.741
5096	AF118562	Rattus norvegicus evectin-1	605	70.803
5097	AF096771	Homo sapiens smooth muscle/nonmuscle myosin light chain kinase	268	40.741
5098	AB028955	Homo sapiens KIAA1032 protein	6551	100.000
5099	AL117537	Homo sapiens hypothetical protein	1799	100.000
5100	U95044	Homo sapiens zinc finger protein	975	76.571
5101	U14372	Rana catesbeiana myosin I alpha	183	96.552
5102	X95073	Homo sapiens Translin associated protein X	437	100.000
5103	U16800	Xenopus laevis ribonucleoprotein	510	89.157
5104	AF100421	Rattus norvegicus p80	1617	82.524

5105	Y17267	Mus musculus ubiquitin-conjugating enzyme	4532	93.690
5106	AB028949	Homo sapiens KIAA1026 protein	3428	100.000
5107	AB011126	Homo sapiens KIAA0554 protein	1560	48.527
5108	AL034491	Schizosaccharomyces pombe conserved hypothetical protein	280	46.392
5109	AF061025	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1	1521	98.413
5110	AF083340	Homo sapiens double-stranded RNA-binding zinc finger protein JAZ	1996	100.000
5111	AF042001	Homo sapiens zinc finger protein slug	832	77.536
5112	AB008548	Mus musculus type 1 procollagen C-proteinase enhancer protein	1091	41.176
5113	U70854	Caenorhabditis elegans similar to Enterococcus faecalis TRAB (GI:388268)	865	45.070
5114	AB023419	Mus musculus mSox7	631	91.176
5115	Z70270	Caenorhabditis elegans predicted using Genefinder; Similarity to Mouse angiotensin II receptor (SW:AG2R MOUSE)	187	35.106
5116	Z83230	Caenorhabditis elegans cDNA EST yk355g3.5 comes from this gene; cDNA EST yk645c2.3 comes from this gene	210	41.096
5117	AL021748	Schizosaccharomyces pombe hypothetical protein	140	22.826
5118	U88308	Caenorhabditis elegans No definition line found	807	60.185
5119	AF149413	Arabidopsis thaliana contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1	234	58.730
5120	Z99129	Homo sapiens dJ425C14.2 (Placental protein DIFF33 LIKE)	2021	100.000
5121	U66496	Homo sapiens leptin receptor	233	82.051
5122	L37380	Rattus norvegicus apical endosomal glycoprotein	860	72.626
5123	X74946	Gallus gallus alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase	1329	67.153
5124	AB011536	Homo sapiens MEGF2	9438	99.927
5125	U22376	Homo sapiens alternatively spliced product using exon 13A	428	70.103
5126	L07045	Strongylocentrotus purpuratus fibropellin c	1007	45.455
5127	AB014531	Homo sapiens KIAA0631 protein	4250	99.842
5128	AL050100	Homo sapiens hypothetical protein	1137	100.000
5129	AC004770	Homo sapiens BC269730 2	3002	99.765
5130	AF097518	Homo sapiens liver-specific transporter	927	100.000
5131	AB007876	Homo sapiens KIAA0416	318	28.497
5132	AF069442	Arabidopsis thaliana putative ribonucleoprotein	161	30.973
5133	U78978	Homo sapiens putative ATPase	2177	97.626
5134	Z46241	Unknown carboxyl terminus of the predicted protein shows similarity to chimaerin; cDNA EST EMBL:Z14	475	43.716
5135	AL117444	Homo sapiens hypothetical protein	2760	100.000
5136	AB014532	Homo sapiens KIAA0632 protein	4861	100.000
5137	AC002398	Homo sapiens F25965 1	702	96.117
5138	AF152361	Drosophila melanogaster Kua protein	909	64.706
5139	AB021179	Homo sapiens HEXIM1 protein	365	47.586
5140	U92010	Rattus norvegicus lin-10 protein homolog	2248	96.997

5141	J04695	Mus musculus alpha-2 type IV collagen	4422	87.816
5142	AL009196	Unknown /prediction=(method:"genefinder", version:"084"); /prediction=(method:"genscan", ve	1136	48.092
5143	AE001394	Plasmodium falciparum predicted integral membrane protein	111	59.259
5144	AF065389	Homo sapiens tetraspan NET-4	490	47.794
5145	AB012886	Mus musculus mac25	470	37.561
5146	AJ006692	Homo sapiens ultra high sulfur keratin	756	88.776
5147	AB030502	Xenopus laevis XDRP1	174	60.345
5148	AB023143	Homo sapiens KIAA0926 protein	328	53.125
5149	X99140	Homo sapiens type II intermediate filament of hair keratin	1885	100.000
5150	AB013607	Mus musculus c29	1331	77.985
5151	AC006053	Arabidopsis thaliana putative potassium transport protein	149	36.905
5152	AF176838	Homo sapiens N-acetylglucosamine 6-O-sulfotransferase	620	100.000
5153	U14417	Homo sapiens Ral guanine nucleotide dissociation stimulator	382	34.400
5154	U55208	Homo sapiens myosin VIIa	458	71.111
5155	AF188634	Drosophila melanogaster F protein	766	51.373
5156	Z70203	Caenorhabditis elegans cDNA EST yk414c9.3 comes from this gene; cDNA EST yk414c9.5 comes from this gene	631	32.099
5157	AB021981	Homo sapiens UDP-N-acetylglucosamine transporter	292	30.396
5158	AB014527	Homo sapiens KIAA0627 protein	259	97.500
5159	AL021571	Caenorhabditis elegans predicted using Genefinder	282	48.837
5160	U10861	Rattus norvegicus calpain small subunit	220	31.897
5161	X07715	Homo sapiens protein Po (partial) (217 is 2nd base in codon)	1909	98.551
5162	X85992	Mus musculus semaphorin C	1542	80.645
5163	U00050	Caenorhabditis elegans similarity across entire gene to DNA-directed RNA polymerase	474	71.111
5164	U46569	Homo sapiens aquaporin-5	1693	99.623
5165	AF125955	Caenorhabditis elegans contains similarity to AMP-binding domains (Pfam: PF00501, Score=82.1, E=1.1e-20, n=1); similar to long-chain-fatty-acid--CoA ligases	1244	43.875
5166	U41548	Caenorhabditis elegans weak similarity to hemolysins	202	48.333
5167	X69490	Homo sapiens titin	838	99.231
5168	Z80220	Unknown Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene;	774	56.944
5169	AB011109	Homo sapiens KIAA0537 protein	511	42.810
5170	J04204	Bos taurus 32 kd accessory protein	962	69.951
5171	AF095193	Homo sapiens BAG-family molecular chaperone regulator-3; BAG-3	3926	99.304
5172	U50927	Rattus norvegicus zinc transporter ZnT-2	1420	86.166
5173	AC004472	Homo sapiens P1.11659 5	397	54.867
5174	M62972	Drosophila melanogaster RP140-upstream	161	31.111
5175	Z71180	Caenorhabditis elegans similar to BPTI/KUNITZ	442	41.146

		inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene		
5176	X53556	Bos taurus type X collagen	657	42.963
5177	AB018295	Homo sapiens KIAA0752 protein	1265	84.426
5178	AE001079	Archaeoglobus fulgidus acetyl-CoA synthetase (acs-2)	563	39.919
5179	AF097707	Bos taurus serine protease	395	80.263
5180	X68011	Homo sapiens ZNF81	1180	64.800
5181	M13536	Homo sapiens ceruloplasmin	263	100.000
5182	Z36531	Homo sapiens fibrinogen-like protein	500	38.462
5183	X59372	Homo sapiens homeobox protein	2336	98.538
5184	AF030558	Rattus norvegicus phosphatidylinositol 5-phosphate 4-kinase gamma	695	85.600
5185	L27479	Homo sapiens X123	1629	97.959
5186	AC005005	Homo sapiens similar to smoothelin; similar to PID:g4128006	3446	99.811
5187	AC005328	Homo sapiens R26660 1, partial CDS	521	97.436
5188	X52140	Rattus norvegicus precursor polypeptide (AA - 28 to 1152)	2566	83.084
5189	AF151977	Homo sapiens orphan neurotransmitter transporter NTT5	996	96.667
5190	AL035461	Homo sapiens dJ967N21.5 (novel MCM2/3/5 family member)	2110	99.699
5191	AF064553	Mus musculus NSD1 protein	3648	80.606
5192	S67156	Homo sapiens aspartoacylase, ASP	669	44.131
5193	AJ000522	Homo sapiens axonemal dynein heavy chain	528	98.780
5194	U22376	Homo sapiens alternatively spliced product using exon 13A	199	76.190
5195	AJ010901	Homo sapiens MUC4	429	81.159
5196	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	500	52.143
5197	AC006014	Homo sapiens similar to KIAA0618 and nuclear envelope protein POM 121; similar to PID:g3327050 and P52591 (PID:g1709213)	921	94.702
5198	U47924	Homo sapiens C9	445	50.382
5199	D25215	Homo sapiens KIAA0032	597	38.813
5200	M26217	Gallus gallus prolyl 4-hydroxylase, alpha subunit (EC 1.14.11.2)	233	30.500
5201	U80736	Homo sapiens CAGF9	197	78.947
5202	AC005328	Homo sapiens R26660 1, partial CDS	321	80.357
5203	Z71181	Caenorhabditis elegans similar to hydrolase	213	39.785
5204	D83777	Homo sapiens expressed ubiquitously with strong expression in brain	778	49.351
5205	AF164623	Homo sapiens trypsin-like serine protease	171	58.974
5206	AF117064	Homo sapiens transitional epithelia response protein	1016	100.000
5207	AL080318	Arabidopsis thaliana stress-induced protein stil-like protein	215	27.451
5208	AB023155	Homo sapiens KIAA0938 protein	658	68.939
5209	L15313	Caenorhabditis elegans homology with leucine aminopeptidase; coded for by C. elegans cDNAs CE2F12 (GenBank: Z14714) and CE15D11 (GenBank: Z14518); putative	1227	46.991

5210	AC006841	Arabidopsis thaliana hypothetical protein	308	24.903
5211	AF169963	Homo sapiens WNT16 protein	2594	100.000
5212	AB007877	Homo sapiens KIAA0417	173	54.167
5213	Z73974	Caenorhabditis elegans cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene; cDNA EST yk638b3.3 comes from this gene	202	28.090
5214	U33630	Mus musculus myeloid ecotropic viral integration site-1b	664	94.681
5215	X75314	Homo sapiens SEB4D	1491	97.817
5216	X98625	Mus musculus sialic acid-specific 9-O-acetylcysteine	742	74.306
5217	U22376	Homo sapiens alternatively spliced product using exon 13A	451	69.072
5218	AF101361	Drosophila melanogaster Abnormal X segregation	731	37.931
5219	AC006539	Homo sapiens BC39498 3	217	100.000
5220	AF131826	Homo sapiens Unknown	564	56.944
5221	AJ248283	Pyrococcus abyssi hypothetical protein	163	20.747
5222	Z73102	Caenorhabditis elegans Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene	735	40.312
5223	K03202	Homo sapiens salivary proline-rich protein precursor	146	50.000
5224	AF136715	Homo sapiens taxol resistant associated protein	394	80.519
5225	AF082556	Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase	1843	79.940
5226	AF149046	Homo sapiens Sex comb on midleg homolog 1 isoform 2	427	61.404
5227	AL035601	Arabidopsis thaliana putative protein	237	32.667
5228	AB020683	Homo sapiens KIAA0876 protein	5650	100.000
5229	X73113	Homo sapiens fast MyBP-C	2418	99.722
5230	U49046	Mus musculus Zfp64	1027	83.237
5231	M20638	Bos taurus phospholipase C-III	1335	54.271
5232	AF015043	Homo sapiens EH-binding protein	248	100.000
5233	AF006264	Homo sapiens hHR21spB	3712	100.000
5234	AF027955	Mus musculus G protein-coupled receptor	910	94.203
5235	S76975	Mus sp. cerebellin 2, Cbln2	429	100.000
5236	AB023138	Homo sapiens KIAA0921 protein	9710	100.000
5237	X91856	Fugu rubripes valyl-tRNA synthetase	621	36.278
5238	D43949	Homo sapiens This gene is novel.	1073	100.000
5239	U32575	Rattus norvegicus similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author	3968	94.255
5240	AC005970	Arabidopsis thaliana putative translation initiation factor eIF-2B, alpha subunit	700	67.066
5241	U63420	Homo sapiens Spl40 protein	760	61.798
5242	AC006017	Homo sapiens N-acetylgalactosaminyltransferase; similar to Q10473 (PID:g1709559)	4206	99.836
5243	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	841	96.947
5244	Y08026	Mus musculus immune associated protein 38	590	56.000

5245	AB014540	Homo sapiens KIAA0640 protein	411	35.885
5246	AF093098	Homo sapiens transcription factor TBLYM; T-box transcription factor family member	3821	100.000
5247	X05908	Homo sapiens lipocortin (AA 1-346)	200	86.486
5248	AF163254	Homo sapiens adaptor protein DAPP1	1099	100.000
5249	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	390	71.622
5250	U97006	Caenorhabditis elegans No definition line found	395	26.075
5251	Z75550	Caenorhabditis elegans Similarity with Schizosaccharomyces hypothetical gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from this gene	179	28.814
5252	AE001727	Thermotoga maritima conserved hypothetical protein	374	35.233
5253	L07294	Homo sapiens T-cell receptor beta	1919	93.204
5254	AB014460	Homo sapiens tuberin	255	100.000
5255	AF094508	Homo sapiens dentin phosphoryn	214	22.532
5256	AL022718	Homo sapiens dJ1052M9.3 (mouse DOC4 LIKE protein)	8523	100.000
5257	Z33879	Sus scrofa G-beta like protein	1978	100.000
5258	AF060244	Mus musculus zinc finger protein 106	2094	94.969
5259	AL050331	Homo sapiens dJ486I3.2 (KIAA0721 (NAP (Nucleosome Assembly Protein) domain containg protein))	3136	100.000
5260	X63436	Bos taurus poly(A) polymerase	525	93.258
5261	AB001684	Chlorella vulgaris ORF49b	77	60.000
5262	X97668	Homo sapiens XLRP3	170	96.000
5263	AL117390	Schizosaccharomyces pombe putative nuclear pore protein	254	24.194
5264	U41060	Homo sapiens LIV-1 protein	483	49.324
5265	AC002131	Arabidopsis thaliana Contains similarity to hypothetical protein C18b11.05 gb Z50728 from S. pombe. EST gb H76601 comes from this gene.	267	30.612
5266	AL032646	Caenorhabditis elegans cDNA EST yk330e11.3 comes from this gene; cDNA EST yk330e11.5 comes from this gene	561	41.294
5267	AL049474	Schizosaccharomyces pombe hypothetical protein	179	35.165
5268	X99142	Homo sapiens type II intermediate filament of hair keratin	397	100.000
5269	Z67999	Schizosaccharomyces pombe hypothetical protein	397	32.090
5270	X86019	Homo sapiens SH3-domain interacting protein	157	35.507
5271	AB013452	Homo sapiens ATPaseII	443	54.135
5272	AB023207	Homo sapiens KIAA0990 protein	663	35.621
5273	Z74866	Saccharomyces cerevisiae ORF YOL124c	671	36.420
5274	X60465	Gallus gallus delta-9 desaturase	935	69.730
5275	AF037364	Homo sapiens paraneoplastic neuronal antigen MA1	1148	54.655
5276	X66286	Gallus gallus tensin	819	71.676
5277	L16559	Caenorhabditis elegans homology with ATP-dependent RNA helicase; putative	409	38.272
5278	AF064447	Mus musculus sex-determination protein homolog Femla	1023	90.303
5279	AF096870	Homo sapiens estrogen-responsive B box protein	266	32.727
5280	AF151816	Homo sapiens CGI-58 protein	482	49.624
5281	X80343	Homo sapiens regulatory partner for cdk5	1759	100.000

		kinase		
5282	AC006577	Arabidopsis thaliana Contains similarity to gb U45880 X-linked inhibitor of apoptosis protein from Homo sapiens and contains PF 00097 Zinc finger C3HC4 (Ring finger) domain.	248	24.895
5283	U42580	Paramecium bursaria Chlorella virus 1 contains 10 ankyrin-like repeats; similar to human ankyrin, corresponds to Swiss-Prot Accession Number P16157	360	38.217
5284	X13255	Homo sapiens dopamine beta-hydroxylase preprotein (AA -25 to 578)	972	99.281
5285	Z99262	Schizosaccharomyces pombe threonine synthase	821	35.135
5286	U04380	Naegleria gruberi calcineurin B	223	30.882
5287	AC004475	Homo sapiens F23858 1	4072	99.671
5288	AC004890	Homo sapiens similar to zinc finger proteins; similar to BAA24380	227	53.125
5289	D31887	Homo sapiens KIAA0062	3500	99.623
5290	S79463	Mus sp. semaphorin homolog=M-Sema F	1051	95.541
5291	M57465	Neurospora crassa phytoene dehydrogenase	182	23.874
5292	AB014558	Homo sapiens KIAA0658 protein	4074	100.000
5293	AL080092	Homo sapiens hypothetical protein	922	100.000
5294	X91655	Bacillus subtilis lepA	735	54.167
5295	AF095741	Rattus norvegicus unknown	575	81.443
5296	AF053130	Mus musculus unconventional myosin MYO15	860	35.211
5297	U13019	Caenorhabditis elegans No definition line found	1315	50.272
5298	AC006978	Homo sapiens supported by human and rodent ESTs; match to AA454028 (NID:g2167697), similar to AA9255224 (NID:g4236415) and AA023712 (NID:g1487627)	537	78.824
5299	U56965	Caenorhabditis elegans No definition line found	819	39.077
5300	AE000887	Methanobacterium thermoautotrophicum N2,N2-dimethylguanosine tRNA methyltransferase	323	27.554
5301	M13212	Gallus gallus cartilage link protein	1090	60.417
5302	AF132479	Mus musculus Ese2L protein	2132	94.611
5303	AF019082	Borrelia burgdorferi virulent strain associated lipoprotein	219	24.603
5304	AB014543	Homo sapiens KIAA0643 protein	1370	99.535
5305	AF081497	Homo sapiens tumor-related protein	3235	100.000
5306	AF098505	Caenorhabditis elegans similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891)	482	31.604
5307	AF116865	Mus musculus hedgehog-interacting protein	4485	93.899
5308	AB014566	Homo sapiens KIAA0666 protein	3117	98.008
5309	AL034374	Homo sapiens dJ483K16.2 (novel protein)	914	100.000
5310	AJ225124	Mus musculus hyperpolarization-activated cation channel, HAC3	255	84.091
5311	AF140538	Homo sapiens histamine H3 receptor	1396	98.985
5312	U17989	Homo sapiens GS2NA	1756	52.000
5313	X80930	Saccharomyces cerevisiae RHC18	687	22.506
5314	AF125102	Homo sapiens HSPC041 protein	398	82.192
5315	AC004076	Homo sapiens R30217 1	4916	100.000
5316	U22015	Mus musculus retinoid X receptor interacting protein	1343	65.257

5317	U66561	Homo sapiens kruppel-related zinc finger protein	305	30.000
5318	AB002405	Homo sapiens LAK-4p	514	38.693
5319	D14572	Mus musculus 'PEBP2b1 protein'	1230	98.889
5320	U79298	Homo sapiens unknown	396	56.881
5321	D86640	Homo sapiens stac	554	54.194
5322	AB011084	Homo sapiens KIAA0512 protein	767	45.907
5323	AC004490	Homo sapiens R29381 1	301	59.223
5324	AF036696	Caenorhabditis elegans contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632)	591	41.150
5325	U02082	Homo sapiens guanine nucleotide regulatory protein	976	54.027
5326	D26018	Homo sapiens KIAA0039	3182	100.000
5327	AF077738	Mus musculus metallocarboxypeptidase CPX-1	3977	87.790
5328	AF062006	Homo sapiens orphan G protein-coupled receptor HG38	1523	45.941
5329	AB007936	Homo sapiens KIAA0467 protein	636	100.000
5330	AL049689	Homo sapiens hypothetical protein	8803	100.000
5331	Z14016	Nicotiana tabacum pistil extensin like protein, partial CDS	179	33.673
5332	X70804	Mus musculus rab17	271	65.714
5333	U75329	Homo sapiens serine protease	843	52.521
5334	Y18620	Arabidopsis thaliana DsPTP1 protein	316	41.791
5335	AL023854	Caenorhabditis elegans similar to Regulator of chromosome condensation (RCC1); cDNA EST yk246c2.5 comes from this gene	421	35.981
5336	Z73944	Lotus japonicus RAB8A	253	34.400
5337	U04379	Mus musculus ZAP-70	3112	92.323
5338	AL110261	Homo sapiens hypothetical protein	1579	100.000
5339	AF106062	Homo sapiens Wiskott-Aldrich syndrome protein interacting protein	361	47.287
5340	U46068	Mus musculus von Ebner minor salivary gland protein	494	63.710
5341	D14478	Rattus norvegicus calpain	516	80.435
5342	Z68297	Unknown Similarity to Yeast TAT-binding homolog 7 (SW:TBP7_YEAST); cDNA EST EMBL:D37124 comes from	330	22.820
5343	AC006014	Homo sapiens similar to RFP transforming protein; similar to P14373 (PID:g132517)	425	94.118
5344	S67247	Homo sapiens smooth muscle myosin heavy chain isoform SMemb	202	28.834
5345	Z93385	Caenorhabditis elegans predicted using Genefinder; Similarity to B.subtilis GTP-binding protein (SW:P20964); cDNA EST yk457c2.5 comes from this gene	687	50.213
5346	AF175967	Mus musculus Lemna coiled-coil protein variant 1	683	58.173
5347	AB029001	Homo sapiens KIAA1078 protein	990	49.858
5348	D83785	Homo sapiens expressed ubiquitously; product similar to D.melanogaster mam protein.	450	30.812
5349	M37884	Homo sapiens muscle beta spectrin	404	100.000
5350	AF156884	Homo sapiens RIP-like kinase	2130	100.000
5351	AF091035	Homo sapiens GTP-binding protein RAB21	1496	100.000

5352	D10523	Homo sapiens 2-oxoglutarate dehydrogenase precursor	1043	71.649
5353	AL021768	Arabidopsis thaliana ATP binding protein-like	650	58.491
5354	X16934	Homo sapiens B23 nucleophosmin (280 AA)	990	100.000
5355	U09284	Homo sapiens PINCH protein	343	86.538
5356	X96770	Saccharomyces cerevisiae P2558 protein	232	27.451
5357	D79998	Homo sapiens KIAA0176	1078	83.333
5358	AL117664	Homo sapiens hypothetical protein	215	96.774
5359	Z69725	Schizosaccharomyces pombe hypothetical protein	293	35.838
5360	U93305	Homo sapiens triple LIM domain protein	244	65.116
5361	AC005757	Homo sapiens R32611.1	600	98.837
5362	AF159567	Homo sapiens C2H2 (Kruppel-type) zinc finger protein	2768	100.000
5363	Y08139	Rattus norvegicus dermo-1 protein	903	99.281
5364	X87852	Homo sapiens SEX protein	11260	99.821
5365	X91619	Rattus norvegicus scal	359	39.645
5366	L42612	Homo sapiens keratin type II	981	63.052
5367	X07695	Homo sapiens cytokeratin 4 (408 AA)	2515	99.755
5368	AL031583	Unknown /prediction=(method:"genefinder", version:"084", score:"124.90"); /prediction=(meth	690	33.735
5369	AF106518	Homo sapiens sialomucin CD164	212	32.258
5370	D83596	Mus musculus unnamed protein product	2350	91.645
5371	U43194	Mus musculus rhophilin	727	67.722
5372	AB005549	Rattus norvegicus atypical PKC specific binding protein	712	81.955
5373	AJ011855	Homo sapiens PAK4 protein	966	74.737
5374	U70369	Mus musculus hematopoietic-specific IL-2 deubiquitinating enzyme	757	49.282
5375	J05065	Bos taurus calpain II regulatory subunit (EC 3.4.22.17)	751	78.676
5376	Z75542	Unknown cDNA EST EMBL:D34386 comes from this gene; cDNA EST EMBL:D37434 comes from this gene; cDNA	343	21.836
5377	AB013607	Mus musculus c29	1351	89.916
5378	AF135440	Mus musculus huntington yeast partner C	4056	94.977
5379	AF132297	Homo sapiens cytokine-inducible SH2-containing protein	2466	99.723
5380	D45913	Mus musculus leucine-rich-repeat protein	1243	95.960
5381	AL022018	Unknown /prediction=(method:"genefinder", version:"084", score:"165.48"); /prediction=(meth	1242	38.814
5382	AB023207	Homo sapiens KIAA0990 protein	1092	66.977
5383	U88167	Caenorhabditis elegans No definition line found	395	23.502
5384	U05340	Homo sapiens p55CDC	904	92.361
5385	AF064604	Homo sapiens KE03 protein	173	96.154
5386	AF043725	Homo sapiens PHD-finger protein	5849	96.544
5387	AJ003147	Homo sapiens marenostarin	654	57.055
5388	AF124435	Danio rerio p55-related MAGUK protein DLG3	629	43.636
5389	AC003989	Homo sapiens argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	1100	100.000
5390	AF155108	Homo sapiens NY-REN-41 antigen	559	77.778

5391	Z27116	Saccharomyces cerevisiae ORF YKR407	191	33.333
5392	AB018349	Homo sapiens KIAA0806 protein	1588	62.916
5393	U41534	Caenorhabditis elegans Contains similarity to Pfam domain: PF00096 (zf-C2H2), Score=17.4, E-value=0.11, N=3	531	36.255
5394	AF075461	Mus musculus ADP-ribosylation factor-directed GTPase activating protein isoform a	2124	91.916
5395	AB023207	Homo sapiens KIAA0990 protein	216	42.857
5396	AF098505	Caenorhabditis elegans similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891)	637	34.783
5397	AF151857	Homo sapiens CGI-99 protein	212	89.189
5398	D87077	Homo sapiens KIAA0240	6429	99.898
5399	AF153362	Dictyostelium discoideum adenylyl cyclase	417	45.890
5400	D87449	Homo sapiens Similar to a C.elegans protein encoded in cosmid C52E12 (U50135)	2444	100.000
5401	Z77666	Unknown cDNA EST EMBL:T01059 comes from this gene; cDNA EST EMBL:D71534 comes from this gene; cDNA	502	37.500
5402	AB020527	Homo sapiens Na/PO4 cotransporter homolog	306	95.833
5403	AL079314	Homo sapiens hypothetical protein, similar to (U06944) PRAJA1	169	100.000
5404	AB023212	Homo sapiens KIAA0995 protein	6648	100.000
5405	U22321	Rattus norvegicus casein kinase 1 gamma 3 isoform	701	61.749
5406	AF144573	Mesocricetus auratus Mx-interacting protein kinase PKM	615	93.000
5407	AE000209	Escherichia coli orf, hypothetical protein	569	100.000
5408	AF009603	Rattus norvegicus SH3p4	223	26.829
5409	X98614	Homo sapiens cytokeratin	199	61.017
5410	M76665	Homo sapiens 11-beta-hydroxysteroid dehydrogenase	1075	100.000
5411	AF183961	Homo sapiens carbon catabolite repression 4 protein homolog	2962	99.768
5412	AB018302	Homo sapiens KIAA0759 protein	954	45.506
5413	X85237	Homo sapiens human splicing factor	4766	100.000
5414	U51032	Saccharomyces cerevisiae Ydr341cp	1366	39.226
5415	D63476	Homo sapiens The KIAA0142 gene is related to human KIAA0006 gene.	220	100.000
5416	AB004538	Schizosaccharomyces pombe HYPOTHETICAL 59.2KD PROTEIN IN PFK26-SGA1 INTERGENIC REGION	157	34.483
5417	AL080159	Homo sapiens hypothetical protein	610	64.336
5418	AF141884	Homo sapiens oligophrenin-1-like protein	5117	100.000
5419	AB011370	Mus musculus Ankhzn	1396	94.836
5420	U50193	Caenorhabditis elegans ZK328.4 gene product	398	37.748
5421	AC005943	Homo sapiens methyl-CpG binding protein MBD3	1947	99.656
5422	AF132149	Drosophila melanogaster unknown	1024	60.474
5423	AL049481	Arabidopsis thaliana putative protein	497	51.948
5424	AF105365	Homo sapiens K-C1 cotransporter KCC4	1856	100.000
5425	AF033566	Mus musculus cdc2/CDC28-like protein kinase 4	1590	98.283
5426	AL031685	Homo sapiens dJ963K23.2 (novel protein)	378	30.811
5427	AF083955	Homo sapiens G protein-coupled receptor	994	100.000
5428	Y18101	Mus musculus macrophage actin-associated-tyrosine-phosphorylated protein	1327	84.211
5429	AF134149	Homo sapiens 2-pore K+ channel subunit TOSS	2053	100.000
5430	AF117888	Homo sapiens myosin-IXa	2539	100.000

5431	M55532	Rattus norvegicus carbohydrate-binding receptor	468	47.407
5432	AF031939	Mus musculus RalBP1-associated EH domain protein Repl1	1393	91.304
5433	AL021816	Schizosaccharomyces pombe SPBC24E9.03c, unknown, len:251aa	201	44.737
5434	M95046	Mycoplasma fermentans translation initiation factor IF3	427	47.917
5435	AF071777	Mus musculus IRE1	2248	85.979
5436	AF030131	Mus musculus Plenty of SH3s; POSH	178	85.714
5437	U40410	Caenorhabditis elegans C54G7.2 gene product	520	36.400
5438	AC004381	Homo sapiens SA gene	2023	60.832
5439	U78597	Plectonema boryanum kinesin light chain	526	42.793
5440	M58297	Homo sapiens zinc finger protein 42	914	51.131
5441	U80955	Caenorhabditis elegans contains a domain found in band 4.1, ezrin, moesin, radixin and talin	708	50.000
5442	AC006234	Arabidopsis thaliana hypothetical protein	269	36.607
5443	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	424	77.632
5444	AB019438	Homo sapiens immunoglobulin heavy chain variable region	715	90.598
5445	U57053	Homo sapiens myosin-ID	426	74.227
5446	AF040652	Caenorhabditis elegans Contains similarity to Pfam domain: PF00400 (G-beta), Score=62.3, E-value=3.5e-15, N=3	311	36.957
5447	V00638	bacteriophage lambda reading frame gam	776	99.138
5448	Z98762	Schizosaccharomyces pombe SPAC4A8.15c, cdc3; profilin, len:127aa, identical to PROF_SCHPO, P39825, (127aa), similar eg. to PROF_YEAST, P07274, profilin, (126aa), fasta scores,opt:479, E():0, (52.8 % identity in 127 aa overlap)	238	37.168
5449	M85227	Escherichia coli activator protein	1001	100.000
5450	L27153	Mus musculus kinesin heavy chain	220	21.689
5451	U03416	Rattus norvegicus neuronal olfactomedin-related ER localized protein	473	28.198
5452	L06443	Mus musculus growth factor	906	79.375
5453	D90716	Escherichia coli MoaB protein.	1109	100.000
5454	AE000451	Escherichia coli putative 2-component regulator	406	100.000
5455	AF039034	Caenorhabditis elegans contains similarity to G-coupled protein receptors	367	27.734
5456	AB014604	Homo sapiens KIAA0704 protein	1680	68.902
5457	AF132961	Homo sapiens CGI-27 protein	2018	100.000
5458	S63848	Bos taurus G-protein coupled receptor type B, GCR type B {clone PPR1}	708	86.777
5459	AF189817	Mus musculus evectin-2	296	97.778
5460	AL022721	Homo sapiens dJ109F14.1.1 (Transcriptional Enhancer Factor TEF-5) (isoform 1)	420	100.000
5461	U73960	Homo sapiens ADP-ribosylation factor-like protein 4	155	100.000
5462	AB014601	Homo sapiens KIAA0701 protein	4013	99.683
5463	D37979	Rattus norvegicus AIR carboxylase-SAICAR synthetase	157	74.194
5464	AC007292	Homo sapiens R31167 1, partial protein	2907	99.302
5465	Z46787	Unknown similar to leucyl-tRNA synthetase; cDNA EST EMBL:D64208 comes from this gene;	1396	45.766

		cDNA EST EMBL		
5466	AB020672	Homo sapiens KIAA0865 protein	7122	100.000
5467	Y15521	Homo sapiens start position 1	2663	98.025
5468	AB008184	Bos taurus ganglioside sialidase	354	30.992
5469	AF144731	Rattus norvegicus putative splicing factor YT521-B	3563	93.285
5470	U41548	Caenorhabditis elegans weak similarity to hemolysins	291	47.475
5471	AB020715	Homo sapiens KIAA0908 protein	689	39.803
5472	A18007	Penicillium chrysogenum FacA	228	46.575
5473	AC005525	Homo sapiens F22162 1	718	87.879
5474	AL031588	Homo sapiens dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEGF2)	403	100.000
5475	AB023178	Homo sapiens KIAA0961 protein	958	83.019
5476	AF055636	Homo sapiens leucine-rich glioma-inactivated protein precursor	387	50.505
5477	AB029029	Homo sapiens KIAA1106 protein	6832	99.705
5478	U95740	Homo sapiens Unknown gene product	722	64.677
5479	AF049344	Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5	2978	90.260
5480	U43959	Homo sapiens beta 4 adducin	203	100.000
5481	AF005654	Homo sapiens actin-binding double-zinc-finger protein	3272	99.584
5482	AL021481	Unknown similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168	1095	50.456
5483	D10627	Mus musculus zinc finger protein	876	47.368
5484	AB014575	Homo sapiens KIAA0675 protein	664	100.000
5485	X07037	Escherichia coli ORF A	669	100.000
5486	D90728	Escherichia coli Hypothetical protein HI1265	298	100.000
5487	U70214	Escherichia coli gamma-glutamyl phosphate reductase	998	99.367
5488	D90705	Escherichia coli Apolipoprotein n-acyltransferase (EC 2.3.1.-) (alp n-acyltransferase) (copper homeostasis protein cute).	222	96.970
5489	M87049	Escherichia coli guanosine pentaphosphatase	646	88.889
5490	D90811	Escherichia coli ORF ID:o320#13; similar to	761	99.130
5491	AE000451	Escherichia coli glucose-inhibited division; chromosome replication?	735	100.000
5492	D90732	Escherichia coli Hypothetical protein M	571	90.722
5493	U00007	Escherichia coli yehV	555	100.000
5494	U14003	Escherichia coli ORF f254	804	100.000
5495	U00007	Escherichia coli yehP	801	100.000
5496	D90702	Escherichia coli Citrate lyase beta chain (acyl lyase subunit) (citE) homolog	592	92.157
5497	D85081	Escherichia coli unnamed protein product	1101	99.398
5498	D64044	Escherichia coli YFHH-ECOLI protein similarity	573	88.679
5499	U28377	Escherichia coli ORF o183	427	78.889
5500	AE000401	Escherichia coli putative enzyme	674	99.020
5501	D90701	Escherichia coli ORF ID:o166#7	651	95.370
5502	AE000390	Escherichia coli orf, hypothetical protein	656	100.000
5503	D90715	Escherichia coli Molybdenum transport ATP-	944	98.621

		binding protein ModC.		
5504	U29579	Escherichia coli ORF o191	381	100.000
5505	D14054	Escherichia coli partial ORF	164	89.655
5506	U00006	Escherichia coli No definition line found	794	100.000
5507	X52227	Escherichia coli fh1A gene product (AA 1-692)	1486	97.107
5508	U09177	Escherichia coli hydrogenase-2 large subunit	248	100.000
5509	D28595	Escherichia coli transcriptional activator protein from homology search	650	100.000
5510	D83194	Shewanella sp. RNA polymerase alpha subunit	437	100.000
5511	M94248	Escherichia coli acriflavine resistance protein	265	100.000
5512	D90704	Escherichia coli ORF ID:o169#14	622	100.000
5513	M60916	Escherichia coli cytidine deaminase	615	97.895
5514	Y07802	Escherichia coli membrane protein	263	95.122
5515	AE000324	Escherichia coli orf, hypothetical protein	1012	98.026
5516	D90820	Escherichia coli Synaptic vesicle protein 2 (SV2).	459	98.649
5517	U14003	Escherichia coli soluble lytic transglycosylase	893	100.000
5518	U82664	Escherichia coli similar to human protein that oxidizes 11-cis retinol into 11-cis retinaldehyde	384	98.333
5519	V01503	Escherichia coli mannitol permease	345	96.610
5520	AE000394	Escherichia coli orf, hypothetical protein	695	95.283
5521	M67452	Escherichia coli cadB	692	98.148
5522	D90891	Escherichia coli GLYCINE BETAINE-BINDING PERIPLASMIC PROTEIN PRECURSOR.	365	94.643
5523	D90713	Escherichia coli TolR protein	539	98.837
5524	D90789	Escherichia coli Dipeptide transport ATP-binding protein DppD.	1482	94.828
5525	D90722	Escherichia coli Hypothetical protein f410	733	95.798
5526	L27665	Escherichia coli lipoate-protein ligase A	1195	92.746
5527	AE000309	Escherichia coli ferredoxin-type protein: electron transfer	697	100.000
5528	L20915	Escherichia coli alternative putative coding sequence; GTG start codon; homology to acyl CoA dehydrogenases and isovaleryl CoA dehydrogenases	405	100.000
5529	U82664	Escherichia coli similar to H. influenzae HI1305	998	98.658
5530	D90753	Escherichia coli ORF ID:o245#1	627	100.000
5531	X01666	Escherichia coli GSH-II	1239	100.000
5532	V00279	Escherichia coli ORF 2 (AA 1-301)	1670	98.770
5533	D90827	Escherichia coli DNA-directed DNA polymerase (EC 2.7.7.7) III q chain	326	100.000
5534	U21094	Saccharomyces cerevisiae Ylr435wp	232	28.395
5535	Z70284	Caenorhabditis elegans cDNA EST EMBL:T01421 comes from this gene; cDNA EST yk413b1.5 comes from this gene	349	66.667
5536	D42054	Homo sapiens KIAA0092 gene product is distantly related to smooth muscle myosin.	234	33.621
5537	AB028968	Homo sapiens KIAA1045 protein	424	100.000
5538	AF026565	Mus musculus ring finger protein	462	32.326
5539	U90946	Dictyostelium discoideum myosin heavy chain kinase B	540	35.165

5540	AL109739	Schizosaccharomyces pombe trp-asp repeat protein	699	36.544
5541	Z69240	Schizosaccharomyces pombe putative amidohydrolase	996	52.708
5542	AL024499	Caenorhabditis elegans cDNA EST EMBL:C08541 comes from this gene; cDNA EST EMBL:C07241 comes from this gene; cDNA EST yk562a6.3 comes from this gene	718	45.374
5543	AL117483	Homo sapiens hypothetical protein	2477	100.000
5544	AF131220	Homo sapiens HEMK homolog	272	94.737
5545	AF062740	Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1	1142	96.023
5546	AL110295	Schizosaccharomyces pombe conserved hypothetical protein	1198	35.494
5547	AF111168	Homo sapiens unknown	922	100.000
5548	U60269	Homo sapiens putative polymerase; orf similar to the integrase domain of Type A and Type B retroviruses and to class II HERVs	663	100.000
5549	AB020690	Homo sapiens KIAA0883 protein	258	43.396
5550	U53225	Homo sapiens sorting nexin 1	3359	99.808
5551	AF132963	Homo sapiens CGI-29 protein	1349	99.495
5552	U96963	Mus musculus p140mDia	439	30.605
5553	AC002131	Arabidopsis thaliana Similar to seryl-tRNA synthetase gb U10400 from S cerevisiae. EST gb N96627 comes from this gene.	374	49.573
5554	AF110647	Homo sapiens translocon-associated protein gamma subunit	359	98.276
5555	AF127035	Homo sapiens calcium-activated chloride channel protein 2	6038	99.782
5556	AB011102	Homo sapiens KIAA0530 protein	1010 3	99.424
5557	M31423	Homo sapiens cerebellar-degeneration-related antigen (CDR34)	1162	86.283
5558	X86779	Homo sapiens FAST kinase	3652	98.548
5559	U70935	Peromyscus maniculatus reverse transcriptase	319	49.153
5560	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	183	50.000
5561	AF119231	Homo sapiens histone acetyltransferase MORF beta	1391 9	99.904
5562	X02761	Homo sapiens fibronectin precursor	1529 3	99.057
5563	AJ011679	Homo sapiens Rab6 GTPase activating protein, GAPCenA	6605	99.321
5564	Y17816	Suberites domuncula cytochrome P450	600	28.838
5565	AF117754	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240	1455 9	99.724
5566	M58511	Homo sapiens iron-responsive element-binding protein/iron regulatory protein 2	6263	99.481
5567	X63652	Homo sapiens inter-alpha-trypsin inhibitor heavy chain ITIH1	5534	95.425
5568	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	1757	82.030
5569	D87442	Homo sapiens KIAA0253	4348	96.783
5570	AF104413	Homo sapiens large tumor suppressor 1	7569	98.060
5571	D87078	Homo sapiens similar to D.melanogaster pumilio	5451	98.595

		protein (S22026): similar to human KIAA0099 protein(D43951)		
5572	X02661	Homo sapiens 2-5A synthetase fragment (229 aa)	769	80.537
5573	Z15005	Homo sapiens CENP-E	16398	99.100
5574	AF132969	Homo sapiens CGI-35 protein	1230	98.387
5575	U79260	Homo sapiens unknown	400	74.194
5576	AJ243460	Leishmania major proteophosphoglycan	222	30.502
5577	M59216	Homo sapiens gamma-aminobutyric acid receptor beta-1 subunit	3077	99.578
5578	AC006069	Arabidopsis thaliana unknown protein	334	25.829
5579	D31884	Homo sapiens KIAA0063	562	54.301
5580	AF098799	Homo sapiens RanBP7/importin 7	6699	98.460
5581	AF093250	Homo sapiens P38IP	4675	99.184
5582	AF188706	Homo sapiens g20 protein	262	35.758
5583	AB029030	Homo sapiens KIAA1107 protein	8318	99.844
5584	D87446	Homo sapiens Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	11448	98.672
5585	AF047663	Caenorhabditis elegans W09G12.7 gene product	261	29.963
5586	X52138	Homo sapiens L7a protein	1499	92.593
5587	V00488	Homo sapiens alpha globin	434	70.093
5588	AF083107	Homo sapiens sirtuin type 2	1761	82.796
5589	AF151848	Homo sapiens CGI-90 protein	1863	94.937
5590	X79440	Homo sapiens NADP+-dependent malic enzyme	3291	90.879
5591	AC002398	Homo sapiens F25965 1	1075	74.477
5592	AJ011812	Homo sapiens transcription factor NRF	320	27.083
5593	AB023215	Homo sapiens KIAA0998 protein	7978	99.674
5594	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	4350	97.896
5595	AF071070	Mus musculus protein kinase Myak-L	3927	95.556
5596	X81889	Homo sapiens p0071 protein	7433	96.478
5597	AL023828	Caenorhabditis elegans cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene	735	37.752
5598	D83781	Homo sapiens the KIAA0197 gene is expressed ubiquitously.; the KIAA0197 protein has histidine acid phosphatase signature at amino acid positions 1047-1061.	8491	98.627
5599	X99802	Homo sapiens ZYG homologue	4280	94.444
5600	AJ238248	Homo sapiens centaurin beta2	4569	94.891
5601	Y15164	Homo sapiens Cxorf5 (71-7A) protein	5882	97.544
5602	U53450	Rattus norvegicus Jun dimerization protein 1 JDP-1	257	50.000
5603	AP000060	Aeropyrum pernix 118aa long hypothetical protein	81	39.623
5604	M54788	Homo sapiens pyruvate dehydrogenase E1-beta subunit	1699	91.233
5605	AL117233	Homo sapiens hypothetical protein	4241	98.268
5606	M27826	Homo sapiens neutral protease large subunit	649	74.522
5607	AB020688	Homo sapiens KIAA0881 protein	4895	76.923
5608	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit	1471	87.153
5609	AF132938	Homo sapiens CGI-03 protein	3980	98.148
5610	AF055470	Homo sapiens ZNF258	4709	98.056
5611	Z78416	Unknown predicted using Genefinder; Similarity	787	24.825

		to S.pombe RAD18 gene (TR:E198069); cDNA EST CEESX52		
5612	U51205	Homo sapiens HCOP9	1320	90.476
5613	M99375	Borna disease virus duplicated domain within paramyxovirus and rhabdovirus polymerase proteins, complete cds., gene product	724	39.402
5614	AL035307	Homo sapiens hypothetical protein	1068	55.220
5615	AF056929	Homo sapiens sarcosin	3750	98.325
5616	AF159164	Homo sapiens ankyrin repeat-containing protein ASB-2	3163	96.360
5617	AL117629	Homo sapiens hypothetical protein	496	42.471
5618	X89750	Homo sapiens TGIF protein	1520	93.116
5619	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	411	41.558
5620	AB020694	Homo sapiens KIAA0887 protein	2821	99.099
5621	AC003114	Arabidopsis thaliana T12M4.6	485	30.652
5622	AB029025	Homo sapiens KIAA1102 protein	5385	98.585
5623	AL080156	Homo sapiens hypothetical protein	575	35.714
5624	AB018289	Homo sapiens KIAA0746 protein	6654	96.609
5625	D38549	Homo sapiens ha1025 is new	8361	96.796
5626	L77968	Ovis aries type II small proline-rich protein	100	32.468
5627	AB018276	Homo sapiens KIAA0733 protein	3382	87.960
5628	AL031534	Schizosaccharomyces pombe putative asparagine synthase	798	31.357
5629	AF131766	Homo sapiens Similar to Ena-VASP like protein	2266	98.898
5630	AL117665	Homo sapiens hypothetical protein	7681	95.211
5631	AF098066	Homo sapiens squamous cell carcinoma antigen recognized by T cell	6387	99.269
5632	AC007842	Homo sapiens BC331191_1	2054	49.922
5633	X05472	Rattus norvegicus ORF 2	159	39.394
5634	X70040	Homo sapiens tyrosine kinase	9361	99.572
5635	AC004983	Homo sapiens similar to PID:g3877944	2354	83.811
5636	Z83838	Homo sapiens GTPASE-ACTIVATING PROTEIN	1369	87.967
5637	X60036	Homo sapiens phosphate carrier protein	2195	78.431
5638	X89633	Saccharomyces cerevisiae tRNA isopentenyltransferase	710	34.813
5639	X06272	Homo sapiens docking protein	3891	97.488
5640	AJ238248	Homo sapiens centaurin beta2	4565	94.757
5641	AB007929	Homo sapiens KIAA0460 protein	6025	98.453
5642	AJ233591	Mus musculus reverse transcriptase	232	49.515
5643	Z81039	Unknown predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3	258	34.706
5644	X89602	Homo sapiens rTSbeta	2599	94.313
5645	AL110218	Homo sapiens hypothetical protein	1038 5	99.249
5646	Z34278	Homo sapiens mucin	222	24.749
5647	AL117530	Homo sapiens hypothetical protein	814	37.594
5648	AJ243797	Homo sapiens deoxyribonuclease III (DNase III)	1940	97.368
5649	AF051325	Homo sapiens SH3 domain containing adaptor protein	225	26.603
5650	X73902	Homo sapiens nicein	8104	98.996
5651	AF019413	Homo sapiens complement component C4	1147 4	99.599
5652	X55777	Homo sapiens put. ORF	248	53.247
5653	X75888	Mus musculus cyclin E	2381	73.428

5654	AF055985	Onchocerca volvulus pyrrolidone-rich antigen	166	42.857
5655	X59512	Homo sapiens integrin alpha6 subunit	6161	94.161
5656	X78931	Homo sapiens zinc finger protein	1085	93.023
5657	AF093593	Homo sapiens snRNA activating protein complex 19kDa subunit	463	65.772
5658	X57527	Homo sapiens alpha 1(VIII) collagen	5463	98.925
5659	AF061939	Homo sapiens staufen protein	1273	46.346
5660	X61585	Bos taurus polynucleotide adenylyltransferase	4357	93.883
5661	AF083068	Homo sapiens NAD+ ADP-ribosyltransferase 2	3354	96.834
5662	X92485	Plasmodium vivax pval	329	58.889
5663	AB018308	Homo sapiens KIAA0765 protein	3935	98.658
5664	U58658	Homo sapiens unknown	267	58.537
5665	U39849	Caenorhabditis elegans similar to leucine-rich repeat regions of L. monocytogenes internalin and S. pombe SDS22	320	37.931
5666	AF151875	Homo sapiens CGI-117 protein	953	94.972
5667	U88180	Caenorhabditis elegans similar to molybdenum cofactor biosynthesis protein E	239	26.033
5668	U97553	murine herpesvirus 68 unknown	100	30.682
5669	M13100	Rattus norvegicus unknown protein	288	38.922
5670	L22030	Glycine max hydroxyproline-rich glycoprotein	196	34.314
5671	AB021660	Homo sapiens carbonic anhydrase VB	573	42.547
5672	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	5228	98.936
5673	X60957	Homo sapiens receptor tyrosine kinase	7637	98.599
5674	AB020706	Homo sapiens KIAA0899 protein	5914	99.355
5675	X70764	Mus musculus serine/threonine protein kinase	683	51.149
5676	U43360	Peromyscus maniculatus reverse transcriptase	419	46.907
5677	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	145	47.170
5678	U52426	Homo sapiens GOK	1892	50.635
5679	AB005618	Gallus gallus chromobox protein (CHCB2)	381	72.340
5680	AE001448	Helicobacter pylori J99 THREONINE SYNTHASE	747	34.591
5681	AB018272	Homo sapiens KIAA0729 protein	7947	99.749
5682	Y18314	Homo sapiens paraplegin-like protein	5116	97.872
5683	AF072508	Homo sapiens envelope protein	272	34.483
5684	U76714	Rattus norvegicus cell adhesion regulator	2354	87.624
5685	X98259	Homo sapiens M-phase phosphoprotein 8	1232	75.735
5686	AL022316	Homo sapiens bK126B4.1 (novel protein)	268	60.759
5687	X86779	Homo sapiens FAST kinase	3431	95.848
5688	AL049848	Homo sapiens hypothetical protein	250	31.304
5689	AC006284	Arabidopsis thaliana putative ankyrin	267	39.189
5690	Z37139	Unknown similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; c	431	33.469
5691	X61048	Hydra sp. mini-collagen	189	34.815
5692	AL032654	Caenorhabditis elegans similar to Heme-binding domain in cytochrome b5 and oxidoreductases	698	31.870
5693	X55686	Lycopersicon esculentum extensin (class II)	74	27.711
5694	AF036977	Homo sapiens unknown	2126	94.706
5695	U26743	Homo sapiens similar to the 87 kDa Torpedo acetylcholine receptor-associated protein; similar to human dystrophin-related protein, PIR Accession Number S03966	207	52.000
5696	AL050131	Homo sapiens hypothetical protein	265	39.548

5697	M12140	Homo sapiens envelope protein	2012	57.143
5698	U93567	Homo sapiens p40	404	33.115
5699	AF108843	Homo sapiens env protein	992	37.115
5700	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	352	52.308
5701	AC003979	Arabidopsis thaliana ESTs gb Z34075, gb Z34835 and gb AA404888 come from this gene.	613	41.045
5702	L06505	Homo sapiens ribosomal protein L12	586	71.429
5703	U79260	Homo sapiens unknown	347	66.327
5704	X07704	Homo sapiens Po protein	267	31.707
5705	M63835	Homo sapiens IgG Fc receptor I	2307	98.667
5706	K01075	synthetic construct circumsporozoite (CS) fusion prot (partial)	135	25.210
5707	M11902	Mus musculus proline-rich salivary protein	216	30.126
5708	AF126164	Homo sapiens alternative HHLA3 protein	432	69.091
5709	AF111106	Homo sapiens protein serine/threonine phosphatase 4 regulatory subunit 1	5431	92.596
5710	AF083107	Homo sapiens sirtuin type 2	1642	79.679
5711	U22818	Cricetulus griseus mutant sterol regulatory element binding protein-2	601	46.512
5712	AF069781	Drosophila melanogaster Bem46-like protein	820	42.284
5713	AL080119	Homo sapiens hypothetical protein	2454	96.203
5714	L27104	Bos sp. muscarinic receptor, M4 subtype	99	31.034
5715	Y14690	Homo sapiens procollagen alpha 2(V)	1081 7	97.933
5716	L34001	Homo sapiens ORF; putative	348	87.500
5717	U58755	Caenorhabditis elegans C34D4.11 gene product	156	36.207
5718	X82157	Homo sapiens hevjin	3929	95.075
5719	U95098	Xenopus laevis mitotic phosphoprotein 44	1439	68.085
5720	X70944	Homo sapiens PTB-associated splicing factor	3439	83.062
5721	U66796	Homo sapiens laminin alpha 2 chain	2132 4	99.165
5722	M84379	Homo sapiens lymphocyte antigen	2011	84.946
5723	X65165	Volvox carteri extensin	352	33.852
5724	AF129085	Homo sapiens carboxy terminus of Hsp70-interacting protein	1864	96.066
5725	AP000060	Aeropyrum pernix 143aa long hypothetical protein	178	35.256
5726	X07881	Homo sapiens proline-rich protein G1	284	33.754
5727	U80848	Caenorhabditis elegans No definition line found	338	36.076
5728	AC002544	Homo sapiens Unknown gene product splice form-1	667	54.430
5729	Y09615	Homo sapiens mTERF	498	30.357
5730	AL050071	Homo sapiens hypothetical protein	2272	88.278
5731	AB018331	Homo sapiens KIAA0788 protein	7248	92.485
5732	Z98974	Schizosaccharomyces pombe putative vacuolar protein sorting-associated protein	244	42.708
5733	U37351	Mus musculus Paneth cell enhanced expression PCEE	777	77.005
5734	AJ249732	Homo sapiens G8 protein	792	90.000
5735	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	416	61.165
5736	X57110	Homo sapiens c-cbl protein	6141	98.677
5737	X86779	Homo sapiens FAST kinase	3487	96.926
5738	AL080318	Arabidopsis thaliana putative protein	757	40.456
5739	AF019413	Homo sapiens complement component C2	4106	93.054

5740	AF123881	multiple sclerosis associated retrovirus element gag polyprotein	256	37.129
5741	X55777	Homo sapiens put. ORF	243	52.326
5742	AF127142	Homo sapiens NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2,6-sialyltransferase alpha2,6-sialyltransferase	1633	87.742
5743	AF072506	Homo sapiens envelope protein precursor	3502	97.774
5744	X83413	Human herpesvirus 6 U88	555	43.719
5745	AJ010099	Homo sapiens NKp44RG1	230	29.500
5746	Y13374	Homo sapiens putative prenylated protein	1201	79.426
5747	U58658	Homo sapiens unknown	266	64.935
5748	D00189	Rattus norvegicus Na ⁺ ,K ⁺ -ATPase alpha-subunit	6543	98.422
5749	U10185	Xenopus laevis XPMC2 protein	1322	50.463
5750	U00043	Caenorhabditis elegans similar to beta-mannosyltransferase	682	45.627
5751	S62929	Homo sapiens PRB1L precursor protein=basic proline rich proteins (Ps, PmF, PmS, and Pe) precursor {C-terminal}	167	26.203
5752	Y16610	Homo sapiens paraplegin	5001	98.745
5753	AJ243460	Leishmania major proteophosphoglycan	173	26.923
5754	AC004473	Arabidopsis thaliana EST gb N37577 comes from this gene.	167	37.391
5755	K03208	Homo sapiens salivary proline-rich protein precursor	312	31.502
5756	M13100	Rattus norvegicus unknown protein	279	44.737
5757	AJ252550	Homo sapiens glycerol kinase	3363	97.744
5758	U09407	Rattus norvegicus putative protein kinase C inhibitor	500	57.353
5759	D87450	Homo sapiens Similar to D.melanogaster parallel sister chromatids protein	8232	96.243
5760	AL096753	Homo sapiens hypothetical protein	780	43.450
5761	X84909	Homo sapiens phosphorylase kinase	6934	93.910
5762	X52851	Homo sapiens peptidylprolyl isomerase	709	74.847
5763	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	509	42.484
5764	X94912	Homo sapiens Pr22	292	62.179
5765	Z25535	Homo sapiens nuclear pore complex protein hnup153	9276	97.427
5766	X57766	Homo sapiens stromelysin-3 precursor	3138	96.349
5767	AL117610	Homo sapiens hypothetical protein	3606	96.970
5768	X15311	Woolly monkey sarcoma virus reverse transcriptase (476 AA)	507	48.000
5769	AF023261	Human endogenous retrovirus K pol-env	628	48.469
5770	U78312	Mus musculus zinc finger protein	632	35.955
5771	X13293	Homo sapiens B-myb protein (AA 1-700)	4641	99.144
5772	Z96047	Caenorhabditis elegans DY3.6	491	28.718
5773	AB002363	Homo sapiens KIAA0365	5491	96.931
5774	M74027	Homo sapiens mucin	364	27.138
5775	D87469	Homo sapiens Similar to D.melanogaster cadherin-related tumor suppressor	1625 0	99.295
5776	AF145732	Homo sapiens endoplasmic reticulum alpha-mannosidase I	4511	99.397
5777	U48251	Homo sapiens protein kinase C-binding protein RACK7	3002	94.414
5778	M12240	human herpesvirus 1 infected cell protein	195	29.288
5779	X74764	Homo sapiens protein-tyrosine kinase	5477	96.636

5780	AF169346	Cavia porcellus pro-alpha-1 type 1 collagen	122	29.091
5781	X55686	Lycopersicon esculentum extensin (class II)	143	34.091
5782	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	222	28.814
5783	U04706	Bos taurus 50 kDa protein	2579	83.476
5784	AF092207	Rattus norvegicus unknown	1179	78.648
5785	X59892	Homo sapiens 471 aa polypeptide (gamma2)	2145	86.694
5786	AF065391	Homo sapiens ZIS1	627	81.618
5787	X55777	Homo sapiens put. ORF	241	61.194
5788	U29380	Caenorhabditis elegans No definition line found	343	33.654
5789	AJ245553	Homo sapiens AP4 protein	3145	84.722
5790	AF177203	Homo sapiens cerebral cell adhesion molecule	3328	96.731
5791	AF134726	Homo sapiens G9A	6856	99.800
5792	AF064205	Homo sapiens dynactin 1 p150 isoform	7889	98.753
5793	U21317	Caenorhabditis elegans No definition line found	184	46.835
5794	AF131743	Homo sapiens Unknown	515	67.153
5795	AF111178	Homo sapiens glypican-6	1733	93.357
5796	U97553	murine herpesvirus 68 unknown	141	37.736
5797	D87076	Homo sapiens similar to human bromodomain protein BR140(JC2069)	2835	89.876
5798	M73491	Mus musculus N-acetylglucosaminyltransferase I	499	37.193
5799	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	2058	81.028
5800	AF109126	Homo sapiens stromal cell-derived receptor-1 beta	2474	97.250
5801	U43360	Peromyscus maniculatus reverse transcriptase	246	37.714
5802	AF027826	Homo sapiens putative seven pass transmembrane protein	487	46.691
5803	M63438	Homo sapiens , gene product	1629	79.834
5804	U00059	Saccharomyces cerevisiae Yhr121wp	42	24.176
5805	AF090867	Rattus norvegicus guanosine monophosphate reductase	1749	70.694
5806	AF070588	Homo sapiens unknown	2218	95.122
5807	AF022985	Caenorhabditis elegans No definition line found	580	40.179
5808	AC004544	Homo sapiens cytochrome C oxidase; match to P14406 (PID:g117121)	547	88.119
5809	AF132937	Homo sapiens CGI-02 protein	4002	98.875
5810	Z37997	Saccharomyces cerevisiae orf, len: 360, CAI: 0.13, some similarity to gag polyproteins	278	23.711
5811	AJ011497	Homo sapiens Claudin-7	997	92.958
5812	X63563	Homo sapiens RNA polymerase II 140 kDa subunit	6432	91.221
5813	AF151825	Homo sapiens CGI-67 protein	1516	89.726
5814	AF067226	Homo sapiens cGMP phosphodiesterase A4	2920	94.553
5815	X62677	Oryctolagus cuniculus retrovirus related reverse transcriptase	238	54.622
5816	X89718	Sus scrofa 26S protease subunit	1472	67.981
5817	AF136587	Homo sapiens retinoic acid-induced protein	3449	98.120
5818	AL031187	Arabidopsis thaliana kinesin-related protein kata (fragment)	191	21.923
5819	AF062249	Homo sapiens immunoglobulin heavy chain variable region	627	84.167
5820	AF042386	Homo sapiens cyclophilin-33B	452	44.976

5821	D30747	Acropora donei mini-collagen	209	37.975
5822	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	746	43.987
5823	M30023	orf virus ORF4	186	37.736
5824	AJ243459	Leishmania major proteophosphoglycan	219	27.864
5825	L01042	Homo sapiens TATA element modulatory factor	6749	99.543
5826	Y00064	Homo sapiens precursor polypeptide (AA -20 to 657)	4510	99.409
5827	AJ223830	Rattus norvegicus ARE1	4156	93.689
5828	U17000	Gallus gallus TOP AP	461	33.333
5829	AC004077	Arabidopsis thaliana hypothetical protein	397	31.907
5830	AL021726	Unknown /match=(desc:""CK00326.5prime CK Drosophila melanogaster embryo BlueScript Drosophila mel	200	39.823
5831	U40061	Caenorhabditis elegans ZK563.5 gene product	330	30.526
5832	U92820	Homo sapiens unnamed HERV-H protein	378	85.075
5833	AF064782	Mus musculus unknown	2158	81.884
5834	AB022694	Homo sapiens MOK protein kinase	2049	82.339
5835	AF117653	Homo sapiens double homeobox protein	813	65.044
5836	AF000412	Plasmodium berghei merozoite surface protein-1	151	36.364
5837	X56010	Sorghum bicolor hydroxyproline-rich glycoprotein	186	29.197
5838	U47856	Araneus diadematus fibroin-4	227	30.769
5839	AL050261	Homo sapiens hypothetical protein	1084	93.237
5840	U80931	Caenorhabditis elegans strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases	1331	46.256
5841	U10281	Sus scrofa gastric mucin	264	22.283
5842	D87684	Homo sapiens similar to a C.elegans ZK353.8 protein (S44655)	3356	98.507
5843	X52479	Homo sapiens protein kinase C alpha (AA 1-672)	4426	97.926
5844	AF140507	Homo sapiens Ca2+/calmodulin-dependent protein kinase kinase beta	3443	91.709
5845	V00572	Homo sapiens coding sequence	2389	92.723
5846	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	243	27.253
5847	Z83227	Caenorhabditis elegans predicted using Genefinder; Weak similarity to high-sulphur keratins.; cDNA EST yk663a1.3 comes from this gene	270	29.297
5848	X14850	Homo sapiens histone H2A.X	424	75.694
5849	K03208	Homo sapiens salivary proline-rich protein precursor	226	27.645
5850	AF022729	Rattus norvegicus HNK-1 sulfotransferase	438	33.010
5851	X51394	Xenopus laevis APEG precursor protein	304	30.124
5852	M12100	Mus musculus proline-rich protein MP-3	296	26.667
5853	S83364	Homo sapiens putative Rab5-interacting protein {clone L1-57}	676	86.777
5854	X55683	Lycopersicon esculentum extensin (class I)	168	41.892
5855	AJ007666	Cryptosporidium parvum unnamed protein product	163	43.750
5856	U70935	Peromyscus maniculatus reverse transcriptase	265	37.500
5857	Z97184	Homo sapiens HKE2	388	48.430
5858	Z83227	Caenorhabditis elegans predicted using Genefinder; Weak similarity to high-sulphur	243	32.857

		keratins.; cDNA EST yk663a1.3 comes from this gene		
5859	AF111784	Homo sapiens myosin heavy chain IIa	1084 1	93.496
5860	D00723	Homo sapiens hydrogen carrier protein precursor	627	67.630
5861	D49387	Homo sapiens NADP dependent leukotriene b4 12-hydroxydehydrogenase	1935	89.275
5862	U84371	Homo sapiens adenylate kinase 2A	876	64.664
5863	D83206	Mus musculus P24 protein	367	42.143
5864	AL050022	Homo sapiens hypothetical protein	649	33.555
5865	AL050267	Homo sapiens hypothetical protein	3956	96.825
5866	AF072506	Homo sapiens envelope protein precursor	3502	97.774
5867	U33460	Homo sapiens DNA-directed RNA polymerase I, largest subunit	1126 3	99.477
5868	X54326	Homo sapiens glutaminyl-tRNA synthetase	9593	99.722
5869	S74562	Human T-cell lymphotropic virus type 1 Gag	267	24.924
5870	AF004107	Mus musculus unknown	1215	64.839
5871	AB030503	Mus musculus UBE-1a	518	36.728
5872	U58658	Homo sapiens unknown	210	52.381
5873	Z21487	Saccharomyces cerevisiae internal membrane protein	680	39.198
5874	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	209	59.155
5875	X12966	Homo sapiens 3-oxoacyl-CoA thiolase propeptide (424 AA)	2434	92.056
5876	AF070660	Homo sapiens HSPC004	917	72.851
5877	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	334	26.977
5878	U59453	Macaca mulatta flavin-containing monooxygenase form 2	3483	96.449
5879	Z11773	Homo sapiens SRE-ZBP	2703	97.567
5880	X94754	Homo sapiens yeast methionyl-tRNA synthetase homolog	5178	95.710
5881	X63755	Homo sapiens high-sulphur keratin	178	30.481
5882	X61280	Oryza sativa hydroxyproline-rich glycoprotein	217	29.000
5883	M19419	Mus musculus proline-rich salivary protein	206	35.862
5884	J04670	Haemonchus contortus collagen 2c	143	31.690
5885	J03244	Bos taurus H+ ATPase 31kDa subunit (EC 3.6.1.3)	1006	75.664
5886	X95518	Mus musculus neuronal tyrosine threonine phosphatase 1	1647	46.696
5887	AB001322	Gallus gallus aminopeptidase H	1918	70.194
5888	X79510	Homo sapiens protein-tyrosine-phosphatase	7567	97.447
5889	AB000468	Homo sapiens zinc finger protein	550	52.198
5890	Z14016	Nicotiana tabacum pistil extensin like protein, partial CDS	180	32.787
5891	AF082302	Arabidopsis thaliana arabinogalactan-protein	164	37.778
5892	Z96047	Caenorhabditis elegans DY3.6	509	30.691
5893	AB008227	Adiantum capillus-veneris Extensin	201	36.000
5894	M36912	Zea mays cell wall protein (put.); putative	287	37.173
5895	Z66523	Caenorhabditis elegans similar to gamma-butyrobetaine,2-oxoglutarate dioxygenase	670	34.540
5896	L32610	Homo sapiens ribonucleoprotein	1734	94.757
5897	X55681	Lycopersicon esculentum extensin (class I)	202	31.250

5898	AL117615	Homo sapiens hypothetical protein	3855	96.082
5899	L17318	Rattus norvegicus proline-rich proteoglycan	264	30.137
5900	Y15228	Homo sapiens Leu2	415	84.444
5901	X60155	Homo sapiens zinc finger 41	5499	99.362
5902	AF098499	Caenorhabditis elegans No definition line found	291	37.500
5903	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	294	72.059
5904	A06669	synthetic construct preTGF-beta1	2248	95.929
5905	AF159164	Homo sapiens ankyrin repeat-containing protein ASB-2	3173	96.176
5906	Z98265	Homo sapiens plakophilin 3	4869	97.878
5907	AF140598	Homo sapiens ring-box protein 1	479	69.444
5908	X07881	Homo sapiens proline-rich protein G1	229	31.718
5909	AB030234	Canis familiaris D4 dopamine receptor	133	35.789
5910	Y15918	Homo sapiens COL1A1 and PDGFB fusion transcript	134	37.168
5911	J05592	Rattus norvegicus protein phosphatase inhibitor-1 protein	303	37.805
5912	M29297	Transposon Tn4556 unknown protein	225	36.000
5913	Y07867	Homo sapiens pirin	1552	93.197
5914	X59720	Saccharomyces cerevisiae YCL054w, len:841	1680	35.862
5915	X16899	Mus musculus SAP	671	52.821
5916	U06944	Mus musculus PRAJA1	1944	78.068
5917	AP000060	Aeropyrum pernix 143aa long hypothetical protein	166	34.167
5918	AE000789	Borrelia burgdorferi B. burgdorferi predicted coding region BBI16	250	26.259
5919	X03145	Homo sapiens pot. ORF V	210	37.864
5920	X63005	Mus musculus proline-rich protein	170	26.389
5921	AF072880	Homo sapiens SOCS box-containing WD protein SWiP-1	1942	47.826
5922	M36914	Zea mays cell wall protein (put.); putative	145	31.356
5923	AP000062	Aeropyrum pernix 141aa long hypothetical protein	151	38.843
5924	U79413	Bos taurus BSP30	520	37.849
5925	AF144477	Homo sapiens myotilin	3240	98.798
5926	U89336	Homo sapiens unknown	127	27.083
5927	X75042	Homo sapiens c-rel	3919	98.546
5928	AF036906	Homo sapiens LAT	188	33.621
5929	AB015630	Homo sapiens type II membrane protein	774	40.777
5930	AF181659	Drosophila melanogaster BcDNA.GM05306	1965	52.914
5931	X57812	Homo sapiens immunoglobulin lambda light chain	956	83.682
5932	Z49068	Unknown similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D2	1048	40.373
5933	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	28.169
5934	U87408	Homo sapiens unknown	2156	85.144
5935	M15530	Homo sapiens B-cell growth factor	140	60.000
5936	M80596	Saccharomyces cerevisiae VAC1	231	24.918
5937	M19338	Oryctolagus cuniculus protein kinase delta	4637	96.011
5938	X55687	Lycopersicon esculentum extensin (class II)	128	37.179
5939	AF131851	Homo sapiens Unknown	365	38.235
5940	AJ133352	Homo sapiens ZNF237 protein	1644	70.681
5941	X97675	Homo sapiens plakophilin 2b	5249	96.288

5942	AC008075	Arabidopsis thaliana F24J5.4	178	29.714
5943	AC005581	Homo sapiens R31237 1, partial CDS	2485	80.235
5944	Y13141	Bromheadia finlaysoniana extensin	94	37.500
5945	AB002320	Homo sapiens KIAA0322	1006 5	98.403
5946	Z83128	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk433e5.3 comes from this gene; cDNA EST yk433e5.5 comes from this gene; cDNA EST yk469e11.5 comes from this gene	250	23.929
5947	U79260	Homo sapiens unknown	361	74.684
5948	AL117481	Homo sapiens hypothetical protein	165	24.125
5949	X77055	Homo sapiens gp70 region of endogenous retro virus erv-10	242	37.500
5950	X85134	Homo sapiens RB protein binding protein	3538	98.887
5951	M30023	orf virus ORF2	193	35.135
5952	U16360	Homo sapiens caudal-type homeobox protein	172	34.127
5953	L36120	Medicago sativa proline rich protein	135	27.338
5954	AF061741	Homo sapiens retinal short-chain dehydrogenase/reductase retSDR1	1336	81.132
5955	AF000198	Caenorhabditis elegans Similar to cuticular collagen	229	32.843
5956	M17236	Homo sapiens MHC HLA-DQ alpha precursor	1375	94.186
5957	AF099505	Homo sapiens colon carcinoma related protein	2279	94.416
5958	AL021366	Homo sapiens cICK0721Q.5 (polypeptide from patented cDNA EMBL:E06811)	687	84.932
5959	X59656	Homo sapiens CRKL	2048	99.670
5960	X91012	Mus musculus alpha 3 type IX collagen	212	36.552
5961	D42044	Homo sapiens The ha3523 gene product is related to S.cerevisiae gene product located in chromosome III.	5690	99.449
5962	Z75166	Saccharomyces cerevisiae ORF YOR258w	195	28.505
5963	AL035453	Homo sapiens CB42E1.1 (PUTATIVE novel protein similar to various different known and predicted proteins)	163	29.839
5964	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	405	34.091
5965	Y13618	Homo sapiens abundant transcript	1718 3	99.727
5966	X69090	Homo sapiens 190kD protein	9483	99.243
5967	AL078468	Arabidopsis thaliana putative protein	821	37.681
5968	M28515	Mus musculus zinc finger protein mfg3 mRNA (put.); putative	308	28.030
5969	Z98046	Homo sapiens dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE)	3060	92.869
5970	U31089	Homo sapiens Abl binding protein 3	2562	96.939
5971	AF044924	Homo sapiens hook2 protein	4561	96.496
5972	X12451	Homo sapiens pro- (cathepsin L)	1757	90.029
5973	D45371	Homo sapiens a novel adipose specific collagen-like factor, apM1 (adipose most abundant gene transcript 1)	327	31.818
5974	Y18046	Homo sapiens FGFR1 oncogene partner (FOP)	2466	98.030
5975	AF123320	Homo sapiens lymphocyte activation-associated protein	312	26.437
5976	L41270	Homo sapiens natural killer associated transcript 4	2781	89.451
5977	M11902	Mus musculus proline-rich salivary protein	333	36.986

5978	M12140	Homo sapiens pol gene protein; Xxx	184	55.714
5979	U79267	Homo sapiens unknown	360	43.713
5980	X56681	Homo sapiens junD protein	1750	88.701
5981	X97477	Rattus norvegicus NKR-P1B protein	303	33.663
5982	U41557	Caenorhabditis elegans proline and glycine-rich	345	28.816
5983	M19441	Mus musculus Kruppel-related protein	255	36.986
5984	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	738	29.891
5985	AF009666	multiple sclerosis associated retrovirus protease	179	35.294
5986	M82829	Homo sapiens fusion protein	4919	95.495
5987	Y14737	Homo sapiens immunoglobulin lambda heavy chain	2919	90.985
5988	AB023151	Homo sapiens KIAA0934 protein	9056	99.852
5989	Y00345	Homo sapiens polyA binding protein (AA 1-633)	554	54.106
5990	AF055985	Onchocerca volvulus pyrrolidone-rich antigen	102	34.247
5991	AF181640	Drosophila melanogaster BcDNA.GH09817	753	41.692
5992	X78929	Homo sapiens zinc finger protein	61	28.758
5993	AP000062	Aeropyrum pernix 141aa long hypothetical protein	151	38.843
5994	X79389	Homo sapiens glutathione transferase T1	1334	96.234
5995	U43701	Homo sapiens ribosomal protein L23a	793	84.516
5996	M99578	Homo sapiens 550 amino acids MW=61kDa, glycosylated=75 kDa; expressed on endothelium, activated lymphocytes and syncytiotrophoblast, contains leucine zipper and basic region homologous to myc; 721P	3531	95.130
5997	M12140	Homo sapiens envelope protein	1454	44.621
5998	AL117608	Homo sapiens hypothetical protein	331	42.400
5999	AE000446	Escherichia coli regulator protein for dgo operon	673	87.395
6000	X95677	Homo sapiens argBP1B	224	30.137
6001	Z67990	Caenorhabditis elegans similar to cuticle collagen	220	32.000
6002	M31013	Homo sapiens nonmuscle myosin heavy chain (NMHC)	4764	67.062
6003	AF083391	Homo sapiens putative WHSC1 protein	645	31.078
6004	U09848	Homo sapiens zinc finger protein	2109	99.689
6005	U00051	Caenorhabditis elegans coded for by C. elegans cDNA yk50b2.5; coded for by C. elegans cDNA CEESV26F; similar to lipases over a short region	903	29.872
6006	X07173	Homo sapiens trypsin inhibitor	6197	100.000
6007	AF061739	Homo sapiens unknown	1123	98.870
6008	AB016237	Oryctolagus cuniculus lectin-like oxidized LDL receptor	273	26.549
6009	X67156	Rattus norvegicus (S)-2-hydroxy-acid oxidase	1627	72.521
6010	U85481	Bos taurus glyceraldehyde-3-phosphate dehydrogenase like-17 protein	396	71.028
6011	AB011179	Homo sapiens KIAA0607 protein	4804	99.726
6012	Z29481	Homo sapiens 3-hydroxyanthranilic acid dioxygenase	1805	97.232
6013	AJ005566	Mus musculus SPR2H protein	161	38.667
6014	U28131	Homo sapiens novel transcript; similar to transcription factors activation domains;	171	49.206

		linked at 5' end to AT hook motif of HMGI-C; Method: conceptual translation supplied by author		
6015	AB001452	Rattus rattus Sck	2805	86.920
6016	Y00644	Homo sapiens precursor polypeptide (AA -34 to 287)	1929	98.428
6017	AF151848	Homo sapiens CGI-90 protein	410	34.498
6018	AF095791	Homo sapiens TACC2 protein	4105	98.930
6019	M63274	Plasmodium falciparum malaria antigen	186	44.578
6020	S80864	Homo sapiens cytochrome c-like polypeptide	970	85.340
6021	AF161081	Homo sapiens activatory receptor PIRIbeta	199	74.000
6022	AF151800	Homo sapiens CGI-41 protein	2945	99.115
6023	AL117496	Homo sapiens hypothetical protein	1092 1	99.046
6024	AJ011779	Homo sapiens SEC63 protein	4827	99.212
6025	X78933	Homo sapiens zinc finger protein	3469	99.590
6026	X01655	Homo sapiens type III procollagen (aa 892- 1023)	170	34.400
6027	AF105332	Homo sapiens vitamin D3 receptor interacting protein	9085	99.345
6028	AF155113	Homo sapiens NY-REN-55 antigen	4902	96.370
6029	AL032821	Homo sapiens dJ55C23.1 (vanin 1)	3411	100.000
6030	X06562	Homo sapiens growth hormone receptor (AA 1- 638)	4282	99.843
6031	M69181	Homo sapiens non-muscle myosin B	1235 8	99.545
6032	X61046	Hydra sp. mini-collagen	215	41.176
6033	X51798	Homo sapiens precursor	900	98.000
6034	AF084256	Homo sapiens beta glucuronidase isoform d	145	60.465
6035	AF152307	Homo sapiens protocadherin alpha 11	5459	89.053
6036	Y12711	Homo sapiens putative progesterone binding protein	939	90.955
6037	AB002330	Homo sapiens KIAA0332	6743	99.415
6038	AF106681	Homo sapiens ras-related GTP-binding protein	838	87.864
6039	AF083419	Homo sapiens calcium/calmodulin-dependent protein kinase II beta e subunit	3294	96.731
6040	AB020649	Homo sapiens KIAA0842 protein	6812	99.510
6041	AF123880	multiple sclerosis associated retrovirus element unknown protein U5/1	297	75.758
6042	AB002306	Homo sapiens KIAA0308	8346	99.692
6043	X06745	Homo sapiens DNA polymerase alpha-subunit (AA 1 - 1462)	9630	99.183
6044	AF028827	Homo sapiens Tax interaction protein 40	1520	99.567
6045	X71428	Homo sapiens FUS glycine rich protein	3601	95.336
6046	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	3034	99.580
6047	AF151877	Homo sapiens CGI-119 protein	1545	99.598
6048	AF165124	Homo sapiens gamma-aminobutyric acid A receptor gamma 2	3150	99.786
6049	AF110267	Rattus norvegicus golgi stacking protein homolog GRASP55	2305	85.092
6050	AF084530	Homo sapiens cyclin-D binding Myb-like protein	4818	99.213
6051	U82319	Homo sapiens novel ORF	382	92.754
6052	AB007922	Homo sapiens KIAA0453 protein	6946	99.905
6053	Y00816	Homo sapiens CR1 precursor protein	1472	99.461

			2	
6054	X52053	Homo sapiens HP-1 (AA 1-94)	244	86.842
6055	AJ238764	Homo sapiens UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase	4603	98.483
6056	L10908	Mus musculus Gcap1 gene product	167	34.568
6057	AB002312	Homo sapiens KIAA0314	8357	99.919
6058	X51798	Homo sapiens precursor	900	98.000
6059	AF123534	Homo sapiens nucleolar protein NOP5/NOP58	3278	100.000
6060	AJ223948	Homo sapiens RNA helicase	8270	99.523
6061	X66276	Homo sapiens C protein	7583	99.824
6062	X67055	Homo sapiens inter-alpha-trypsin inhibitor heavy chain H3	5715	99.774
6063	Y08612	Homo sapiens 88kDa nuclear pore complex protein	4897	99.595
6064	M13442	Mus musculus alpha-tubulin isotype M-alpha-6	2922	98.667
6065	X59864	Rattus rattus ORF	467	57.407
6066	AB014597	Homo sapiens KIAA0697 protein	6439	99.897
6067	AF129756	Homo sapiens BAT4	2409	99.719
6068	AF131775	Homo sapiens Unknown	2239	98.387
6069	AL109701	Homo sapiens PTD014	1228	100.000
6070	AF187305	Myxine glutinosa calmodulin	396	45.270
6071	X52966	Homo sapiens ribosomal protein L35a (AA 1-110)	485	75.000
6072	X15954	Homo sapiens mannose binding protein	1597	100.000
6073	X78990	Mus musculus testin	2504	91.582
6074	AB011139	Homo sapiens KIAA0567 protein	6325	99.080
6075	AF153606	Homo sapiens angiopoietin-related protein	2754	100.000
6076	Z98885	Homo sapiens dJ522J7.2 (Peregrin (BR140) LIKE protein)	7051	99.623
6077	L76571	Homo sapiens nuclear hormone receptor	1750	99.609
6078	AF036145	Homo sapiens meningioma-expressed antigen 5	5242	99.748
6079	D87685	Homo sapiens similar to human transcription factor TFIIS (S34159).	1137 2	99.942
6080	D80007	Homo sapiens similar to hypothetical protein YM9959.11C of S.cerevisiae.	1210 9	99.893
6081	D88769	Mus musculus latexin	1275	84.685
6082	X56807	Homo sapiens desmocollin type 2a	5633	99.650
6083	X78710	Homo sapiens metal-regulatory transcription factor	5075	100.000
6084	AL050258	Homo sapiens hypothetical protein	5719	100.000
6085	AF141289	Homo sapiens bo,+ amino acid transporter; bo,+AT	3107	100.000
6086	X15512	Rattus norvegicus apolipoprotein CI, preprotein	147	45.349
6087	AC002464	Homo sapiens organic cation transporter; 50% similarity to JC4884 (PID:g2143892)	2977	99.344
6088	AL050272	Homo sapiens hypothetical protein	854	95.522
6089	AB023147	Homo sapiens KIAA0930 protein	2197	99.425
6090	X15652	Cricetulus longicaudatus N-ethylmaleimide sensitive fusion protein	4788	97.872
6091	AL022329	Homo sapiens bK407F11.2 (adrenergic, beta, receptor kinase 2)	4647	99.855
6092	AF087438	Homo sapiens protein phosphatase 2 subunit A isoform beta	3799	99.834
6093	L11702	Homo sapiens phospholipase D	5659	99.881
6094	AL110160	Homo sapiens hypothetical protein	1460	100.000

6095	X95586	Homo sapiens proteasome	1730	100.000
6096	AB011149	Homo sapiens KIAA0577 protein	6750	99.904
6097	M34449	Homo sapiens complement receptor 1	859	78.882
6098	X63564	Homo sapiens RNA polymerase II largest subunit	13138	99.493
6099	AJ006984	Capsicum annuum proline-rich protein	199	35.052
6100	AF111162	Homo sapiens guanine nucleotide exchange factor	12066	99.568
6101	AJ245600	Homo sapiens hypothetical protein	3243	100.000
6102	X95762	Homo sapiens Aminopeptidase P-like	4163	99.839
6103	AL110469	Schizosaccharomyces pombe hypothetical protein	872	45.833
6104	L36531	Homo sapiens integrin alpha 8 subunit	6712	98.254
6105	X98296	Homo sapiens ubiquitin hydrolase	17093	99.451
6106	Z97074	Homo sapiens p40	2279	93.651
6107	M16973	Homo sapiens complement protein C8 beta subunit precursor	4125	100.000
6108	AL117646	Homo sapiens hypothetical protein	1877	100.000
6109	X82200	Homo sapiens gpStaf50	2904	98.655
6110	AB011139	Homo sapiens KIAA0567 protein	6345	99.080
6111	AL117496	Homo sapiens hypothetical protein	10921	99.046
6112	AL110219	Homo sapiens hypothetical protein	3897	99.180
6113	X97065	Homo sapiens Sec23 protein	5155	99.739
6114	X80909	Homo sapiens Nascent polypeptide associated complex alpha subunit	1267	97.727
6115	M64982	Homo sapiens fibrinogen alpha-E chain	5694	98.274
6116	X66363	Homo sapiens serine/threonine protein kinase	3213	98.413
6117	Z83067	Homo sapiens FAA	9638	99.794
6118	U19617	Mus musculus Elf-1	3289	87.279
6119	D14531	Homo sapiens 'human homologue of rat ribosomal protein L9'	1110	93.814
6120	X15875	Homo sapiens cAMP response element binding protein (AA 1-505)	3213	99.802
6121	Y13115	Homo sapiens serine/threonine protein kinase	6264	99.794
6122	AF132947	Homo sapiens CGI-13 protein	2822	96.368
6123	D29810	Homo sapiens unknown	2011	94.022
6124	AF141289	Homo sapiens bo,+ amino acid transporter; bo,+AT	3107	100.000
6125	AB018319	Homo sapiens KIAA0776 protein	5036	100.000
6126	AL034452	Homo sapiens dJ682J15.1 (novel Collagen triple helix repeat containing protein)	2539	100.000
6127	X99270	Homo sapiens unknown	1922	98.294
6128	Y14494	Homo sapiens aralar1	4330	98.818
6129	X80695	Homo sapiens OXA1Hs	2894	99.087
6130	AF126963	Gallus gallus osteoglycin	1246	64.214
6131	AF132968	Homo sapiens CGI-34 protein	1321	98.624
6132	Y18483	Homo sapiens SLC7A8 protein	3463	99.065
6133	A58799	unidentified unnamed protein product	3900	99.644
6134	X91879	Homo sapiens sperm specific protein	4810	100.000
6135	U66140	Canis familiaris forssman synthetase	1948	82.421
6136	AB023065	Rattus norvegicus O-sialoglycoprotease	2017	94.410
6137	AB018350	Homo sapiens KIAA0807 protein	8370	99.921
6138	AF140690	Homo sapiens melusin	2317	97.994
6139	AF045646	Caenorhabditis elegans No definition line	293	30.726

		found		
6140	AF151859	Homo sapiens CGI-101 protein	1408	100.000
6141	AB011125	Homo sapiens KIAA0553 protein	7326	99.543
6142	AF146531	Homo sapiens bridging integrator-2	3583	99.823
6143	AF171877	Homo sapiens cleavage and polyadenylation specificity factor 73 kDa subunit	4362	99.701
6144	AJ010346	Homo sapiens RING-H2	4510	100.000
6145	AB020656	Homo sapiens KIAA0849 protein	3286	97.244
6146	D25217	Homo sapiens KIAA0027	2894	99.543
6147	X59543	Homo sapiens M1 subunit of ribonucleotide reductase	5217	100.000
6148	X85786	Homo sapiens binding regulatory factor	4103	99.838
6149	Y08319	Homo sapiens kinesin-2	4277	99.558
6150	AF135422	Homo sapiens GDP-mannose pyrophosphorylase A	2707	99.749
6151	Z47362	Homo sapiens T cell factor 1 splice form E	2423	93.947
6152	AF151820	Homo sapiens CGI-62 protein	2193	98.466
6153	X85133	Homo sapiens RB protein binding protein	6231	99.052
6154	AB023139	Homo sapiens KIAA0922 protein	5160	98.108
6155	L08240	Homo sapiens located at OATL1	4361	98.618
6156	U24078	Homo sapiens p58 natural killer cell receptor precursor	2346	99.713
6157	AB020663	Homo sapiens KIAA0856 protein	6983	99.254
6158	X92689	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	4198	99.211
6159	X77395	Saccharomyces cerevisiae N2040	536	34.259
6160	AB029334	Halocynthia roretzi HRPET-1	727	32.808
6161	AL050114	Homo sapiens hypothetical protein	1699	98.168
6162	AF156098	Homo sapiens RNA binding motif protein 7	357	58.824
6163	AF100749	Homo sapiens Sec22 homolog	1842	99.291
6164	AB020705	Homo sapiens KIAA0898 protein	6464	99.694
6165	M74089	Homo sapiens TB1	2874	100.000
6166	AL117455	Homo sapiens hypothetical protein	5936	100.000
6167	Y00062	Homo sapiens precursor polypeptide (AA -23 to 1120)	7496	98.339
6168	X80821	Homo sapiens ribosomal protein L18a homologue	493	67.097
6169	AF009243	Homo sapiens proline-rich Gla protein 2	1235	96.078
6170	D90912	Synechocystis sp. melibiose carrier protein	446	25.094
6171	AF132948	Homo sapiens CGI-14 protein	2371	93.659
6172	AB007941	Homo sapiens KIAA0472 protein	2468	100.000
6173	X98248	Homo sapiens sortilin	5527	99.040
6174	AL031320	Homo sapiens dJ20N2.5 (novel protein similar to fucosidase, alpha-L-1, tissue (EC 3.2.1.51, alpha-L-fucosidase fucosylhydrolase))	3276	100.000
6175	AJ132637	Homo sapiens ATP-dependent metalloprotease YME1L	4546	98.884
6176	AL121742	Homo sapiens hypothetical protein	3861	98.795
6177	AF176903	Mus musculus sprouty 1	1900	83.072
6178	AJ243310	Homo sapiens C14orf3 protein	449	34.451
6179	L00073	Homo sapiens renin	2525	96.078
6180	X17459	Mus musculus J kappa RS-binding protein	3205	94.626
6181	X78669	Homo sapiens EF-hand protein	2116	100.000
6182	AF129112	Homo sapiens vanilloid receptor-like protein 1	5045	99.869
6183	D80010	Homo sapiens KIAA0188	5933	99.889
6184	X98411	Homo sapiens myosin-IE	5014	96.561
6185	AF036718	Homo sapiens FGFR signalling adaptor SNT-2	3454	99.593

6186	AF106934	Homo sapiens vitamin D receptor-interacting protein	5502	97.605
6187	AF078164	Homo sapiens Ku70-binding protein	1939	99.303
6188	AJ005801	Homo sapiens PP2C	3041	98.337
6189	X59244	Homo sapiens ZNF43	5421	96.766
6190	X61100	Homo sapiens 75 kDa subunit NADH dehydrogenase precursor	4727	99.450
6191	X06026	Homo sapiens T-cell receptor T3 gamma chain	1012	92.432
6192	D63480	Homo sapiens The KIAA0146 gene product is novel.	6100	99.673
6193	AB014543	Homo sapiens KIAA0643 protein	2336	99.505
6194	S58544	Homo sapiens 75 kda infertility-related sperm protein	3192	98.603
6195	AF117888	Homo sapiens myosin-IXa	1667 8	99.804
6196	AL110265	Homo sapiens hypothetical protein	941	100.000
6197	X14968	Homo sapiens RII-alpha subunit (AA 1-404)	2607	99.753
6198	AL050283	Homo sapiens hypothetical protein	2476	100.000
6199	U49082	Homo sapiens transporter protein	1229	50.256
6200	D00596	Homo sapiens thymidylate synthase	412	88.000
6201	AF151830	Homo sapiens CGI-72 protein	2621	96.706
6202	AF090990	Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 beta; putative GAP protein beta	1186 5	99.945
6203	U96113	Homo sapiens WWP1	4660	99.706
6204	X63547	Homo sapiens oncogene	7209	95.133
6205	AJ011863	Homo sapiens homeobox protein LSX	4739	97.775
6206	AF151905	Homo sapiens CGI-147 protein	1124	100.000
6207	D50912	Homo sapiens The KIAA0122 gene product is novel.	6658	99.604
6208	X92493	Homo sapiens STM-7	3389	99.630
6209	L29218	Homo sapiens clk2; putative	3071	92.885
6210	X63465	Homo sapiens smg GDS	3435	99.641
6211	D42043	Homo sapiens The ha2022 gene product is novel.	4308	100.000
6212	U40739	Homo sapiens cyclin C	2031	99.670
6213	AF140360	Homo sapiens histone acetyltransferase	3989	99.673
6214	U44803	Rattus norvegicus ovarian-specific protein	1337	78.431
6215	Y09723	Homo sapiens Miz-1 protein	5439	99.751
6216	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	2127	82.292
6217	AL096880	Homo sapiens hypothetical protein	4132	99.190
6218	AF078853	Homo sapiens NPD001	871	100.000
6219	AB011167	Homo sapiens KIAA0595 protein	9955	99.932
6220	AF053628	Mus musculus D3Mm3e	1919	87.463
6221	D13744	Holotrichia diomphalia holotricin 3	111	46.939
6222	AF143815	Bos taurus ribosomal protein	1431	98.605
6223	X98507	Homo sapiens myosin I beta	6636	98.444
6224	AF132962	Homo sapiens CGI-28 protein	2087	99.678
6225	AF151891	Homo sapiens CGI-133 protein	924	99.338
6226	U39205	Saccharomyces cerevisiae Lpe10p	352	26.934
6227	AF155099	Homo sapiens NY-REN-18 antigen	3935	100.000
6228	AF092137	Homo sapiens FK506-binding protein	1478	99.099
6229	AL035297	Homo sapiens hypothetical protein	666	61.310
6230	AJ225089	Homo sapiens 2'-5' oligoadenylate synthetase (p59OAS)	3192	98.641
6231	K01747	Homo sapiens actin prepeptide	2143	98.788

6232	L48211	Homo sapiens angiotensin II receptor	451	98.592
6233	Z81326	Homo sapiens neuroserpin	2615	100.000
6234	X66357	Homo sapiens serine/threonine protein kinase	1975	99.016
6235	Y09561	Homo sapiens ATP receptor	4140	99.832
6236	AB007864	Homo sapiens KIAA0404	1318 4	99.796
6237	X93996	Homo sapiens AFX	3338	99.002
6238	AB004884	Homo sapiens PKU-alpha	4563	98.194
6239	AL022326	Homo sapiens dJ333H23.2.3 (Synaptogyrin 1C (SYNGR1C))	1088	89.552
6240	D87682	Homo sapiens similar to a C.elegans protein encoded in cosmid T26A5.	3297	99.808
6241	AF144237	Homo sapiens LOMP protein	5228	99.875
6242	AF099149	Homo sapiens TRIAD1 type I	3454	98.008
6243	AL050331	Homo sapiens dJ486I3.1 (novel protein)	1856	99.640
6244	M14660	Homo sapiens ISG-K54	3067	99.788
6245	X06661	Homo sapiens calbindin (AA 1-261)	1697	100.000
6246	AJ001306	Homo sapiens PDZ domain protein	9914	100.000
6247	X98657	Homo sapiens lipopolysaccharide binding protein	3070	99.792
6248	AL117637	Homo sapiens hypothetical protein	2838	100.000
6249	AF094609	Rattus norvegicus fertility related protein WMP1	2042	63.553
6250	Z99109	Bacillus subtilis similar to glycerophosphodiester phosphodiesterase	121	23.529
6251	AF151894	Homo sapiens CGI-136 protein	679	82.000
6252	AB014527	Homo sapiens KIAA0627 protein	8132	99.153
6253	X96618	Mus musculus novel stromal cell protein	975	78.109
6254	X76104	Homo sapiens DAP-kinase	9494	99.651
6255	AC008044	Homo sapiens ABH	2629	100.000
6256	X86691	Homo sapiens Mi-2 protein	1266 3	99.582
6257	AF177346	Mus musculus PLIC-2	3513	86.427
6258	AB020315	Homo sapiens homologue of mouse dkk-1 gene:Acc# AF030433	1876	100.000
6259	AF045459	Homo sapiens Etk/Bmx cytosolic tyrosine kinase	4549	97.714
6260	U67934	Homo sapiens 44.9 kDa protein C18B11 homolog	1200	98.942
6261	AB023173	Homo sapiens KIAA0956 protein	4409	100.000
6262	AF011359	Bos taurus regulator of G-protein signaling 7	3129	99.147
6263	AB011150	Homo sapiens KIAA0578 protein	8781	98.113
6264	AB018327	Homo sapiens KIAA0784 protein	7154	99.720
6265	AB018314	Homo sapiens KIAA0771 protein	6199	99.473
6266	AB002318	Homo sapiens KIAA0320	5828	99.684
6267	AL050024	Homo sapiens hypothetical protein	699	91.176
6268	X90840	Homo sapiens axonal transporter of synaptic vesicles	1111 4	99.645
6269	AJ001684	Homo sapiens NKG2C	1518	99.134
6270	X14766	Homo sapiens GABA-A receptor alpha 1 subunit	2924	98.906
6271	AB023177	Homo sapiens KIAA0960 protein	9381	99.922
6272	AL110222	Homo sapiens hypothetical protein	6397	99.687
6273	AF186273	Homo sapiens leucine-rich repeats containing F-box protein FBL3	2834	100.000
6274	AF007155	Homo sapiens unknown	683	99.010
6275	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	393	77.500
6276	Z34975	Homo sapiens ldlCp	4634	99.053

6277	AF151886	Homo sapiens CGI-128 protein	938	95.732
6278	AB001452	Rattus rattus Sch	2805	86.920
6279	AF053630	Homo sapiens monocyte/neutrophil elastase inhibitor	2405	99.736
6280	AF000145	Homo sapiens germinal center kinase related protein kinase	5840	99.320
6281	AL050306	Homo sapiens dJ475B7.2 (novel protein)	4521	97.087
6282	Z83067	Homo sapiens FAA	9645	99.931
6283	U83194	Homo sapiens TRAF4-associated factor 2	1500	60.407
6284	M94043	Rattus norvegicus rab-related GTP-binding protein	1368	96.190
6285	U18982	Rattus norvegicus fos-related antigen 2	1099	65.244
6286	AJ237672	Homo sapiens methylenetetrahydrofolate reductase	4524	98.370
6287	AF118394	Homo sapiens putative nucleotide binding protein	1164	75.277
6288	AB014566	Homo sapiens KIAA0666 protein	7077	99.724
6289	U88309	Caenorhabditis elegans No definition line found	211	31.694
6290	AL050390	Homo sapiens hypothetical protein	2503	99.474
6291	Z75330	Homo sapiens nuclear protein SA-1	8199	99.841
6292	AB018353	Homo sapiens KIAA0810 protein	5464	99.272
6293	AB020504	Rattus norvegicus PMF31	381	80.247
6294	Z21966	Homo sapiens mPOU homeobox protein	1911	99.003
6295	AF151860	Homo sapiens CGI-102 protein	1464	99.545
6296	AL110499	Caenorhabditis elegans cDNA EST yk512b10.3 comes from this gene; cDNA EST yk512b10.5 comes from this gene; cDNA EST EMBL:T01004 comes from this gene	322	26.259
6297	AJ223351	Homo sapiens HIRA-interacting protein 3	3527	98.741
6298	AL117401	Homo sapiens hypothetical protein	3212	92.322
6299	AL022395	Homo sapiens dJ273N12.1 (PUTATIVE protein based on EST matches)	3999	97.760
6300	M69181	Homo sapiens non-muscle myosin B	1235 8	99.545
6301	Z46389	Homo sapiens vasodilator-stimulated phosphoprotein (VASP)	2545	99.737
6302	X59841	Homo sapiens homeobox protein	2389	94.292
6303	X92896	Homo sapiens ITBA2	719	98.095
6304	X16707	Homo sapiens fra-1 gene product (AA 1-271)	1809	99.631
6305	Y14391	Homo sapiens GTP-binding protein	2778	99.548
6306	Y07704	Rattus norvegicus hypothetical protein	1798	82.369
6307	AF091242	Homo sapiens ATP sulfurylase/APS kinase 2	4122	99.674
6308	AB028974	Homo sapiens KIAA1051 protein	2302	100.000
6309	AB023231	Homo sapiens KIAA1014 protein	4722	99.323
6310	AB011139	Homo sapiens KIAA0567 protein	6345	99.080
6311	AF168418	Homo sapiens activating signal cointegrator 1	3862	99.139
6312	AL096713	Homo sapiens hypothetical protein	9330	98.535
6313	X69151	Homo sapiens vacuolar proton-ATPase	2356	97.396
6314	U20239	Mus musculus fibrosin	399	80.000
6315	AF124251	Homo sapiens SH2-containing protein Nsp3	4516	99.276
6316	M13755	Homo sapiens 17-kDa protein	1018	98.182
6317	X05562	Homo sapiens alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon)	7809	99.617
6318	U58337	Mus musculus ligatin	2997	80.070

6319	X54131	Homo sapiens protein-tyrosine phosphatase	1313 6	99.650
6320	AF153612	Homo sapiens peroxisomal D3,D2-enoyl-CoA isomerase	2137	97.778
6321	AF072441	Homo sapiens calcineurin binding protein cabin 1	1476 7	100.000
6322	AL049487	Arabidopsis thaliana hypothetical protein	253	31.364
6323	AP000367	Oryza sativa ESTs AU070372(S13446),AU075541(S0353) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana BAC genomic sequence. (AC002292)	395	37.981
6324	D42046	Homo sapiens The ha3631 gene product is related to S.cerevisiae protein encoded in chromosome VIII.	6997	99.443
6325	D50926	Homo sapiens The KIAA0136 gene product is novel.	6073	99.685
6326	AF125188	Homo sapiens adenosine deaminase acting on tRNA 1	3363	99.402
6327	U03416	Rattus norvegicus neuronal olfactomedin-related ER localized protein	2446	96.401
6328	AB011178	Homo sapiens KIAA0606 protein	5699	99.884
6329	AF134726	Homo sapiens G7A	8155	97.792
6330	L22031	Glycine max hydroxyproline-rich glycoprotein	188	36.697
6331	AC004142	Homo sapiens similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906)	4613	99.858
6332	X86018	Homo sapiens mufl	4040	99.673
6333	U13070	Caenorhabditis elegans No definition line found	610	44.749
6334	AB018271	Homo sapiens KIAA0728 protein	6896	100.000
6335	AF176039	Homo sapiens high mobility group protein-R	1254	89.055
6336	X80590	Homo sapiens phosphorylase kinase	2503	100.000
6337	AB002318	Homo sapiens KIAA0320	5828	99.684
6338	AL050258	Homo sapiens hypothetical protein	5719	100.000
6339	AF070598	Homo sapiens ABC transporter	3208	98.047
6340	AL021396	Homo sapiens dJ971N18.2	1679	100.000
6341	S72462	Homo sapiens beta-glucuronidase	255	64.615
6342	U04520	Homo sapiens type IV collagen a5 chain	1283 0	100.000
6343	AF160728	Homo sapiens sex comb on midleg-like-1 protein	1391	100.000
6344	AF031588	Homo sapiens WASP interacting protein	3688	99.801
6345	AF006751	Homo sapiens ES/130	6050	99.898
6346	X52127	Mus musculus domesticus testis-specific protein, clone 46	975	38.173
6347	AL031259	Homo sapiens PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG)	2442	100.000
6348	AJ224945	Xenopus laevis groucho protein	4757	96.229
6349	A47490	unidentified HUMAN OBF-1	1698	98.828
6350	AC005757	Homo sapiens R32611_1	3469	99.265
6351	S61069	Homo sapiens reverse transcriptase homolog=pol {retroviral element}	491	84.000
6352	AC004079	Homo sapiens 40% similar to yeast high mobility group-like nuclear protein, P32495	684	90.435

		(PID:g417360)		
6353	AF084521	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2	11344	99.539
6354	X13988	Homo sapiens embryonic myosin heavy chain (AA 1 - 1940)	12133	99.690
6355	AJ006215	Mus musculus CMP-N-acetylneuraminic acid synthetase	2644	93.911
6356	U04241	Homo sapiens homologous to Swiss-Prot accession number P16371	715	88.832
6357	U64033	Mus musculus Tera	975	88.158
6358	AF106862	Homo sapiens zinc finger homeobox protein ZHX1	5679	100.000
6359	AF083208	Homo sapiens Che-1	3499	98.743
6360	AF035178	Oryctolagus cuniculus elongation factor 1 A2	3013	99.784
6361	U26162	Homo sapiens myosin regulatory light chain	1104	99.422
6362	X99404	Homo sapiens Berg36	2117	98.750
6363	U64601	Caenorhabditis elegans Gene probably begins in the next cosmid	531	50.336
6364	AL080065	Homo sapiens hypothetical protein	2287	98.880
6365	Y17999	Homo sapiens Dyrk1B protein kinase	4307	99.841
6366	AF152961	Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit	6721	99.618
6367	L31783	Mus musculus uridine kinase	982	70.155
6368	AL117462	Homo sapiens hypothetical protein	849	49.841
6369	AB020710	Homo sapiens KIAA0903 protein	6183	99.480
6370	AF151870	Homo sapiens CGI-112 protein	1355	96.602
6371	AF143321	Homo sapiens unknown	829	65.789
6372	X06256	Homo sapiens integrin alpha 5 subunit precursor	7083	99.905
6373	AF051151	Homo sapiens Toll/interleukin-1 receptor-like protein 3	5659	99.650
6374	Y13620	Homo sapiens BCL9	9699	99.498
6375	Z73102	Caenorhabditis elegans Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene	884	40.943
6376	AB018257	Homo sapiens KIAA0714 protein	7325	99.820
6377	AJ224741	Homo sapiens matrilin-3	3300	100.000
6378	U65416	Homo sapiens MHC class I molecule	2560	99.215
6379	AF004876	Homo sapiens 54TmP	1031	56.803
6380	AL021878	Homo sapiens dJ257I20.4	205	72.000
6381	D90734	Escherichia coli ORF ID:o223#11	785	100.000
6382	X86779	Homo sapiens FAST kinase	3626	99.637
6383	AJ005890	Homo sapiens JM1	3931	99.518
6384	AF069762	Homo sapiens map kinase phosphatase-like protein MK-STYX	2111	100.000
6385	AF131826	Homo sapiens Unknown	1980	99.664
6386	AF157600	Mus musculus pleckstrin 2	2055	92.918
6387	X83425	Homo sapiens Lutheran blood group glycoprotein	4087	98.722
6388	AL096749	Homo sapiens DKFZp434G153	3100	99.360
6389	AF036130	Homo sapiens collagen type IX alpha I chain, long form	6706	99.457
6390	AF151814	Homo sapiens CGI-56 protein	1900	99.051
6391	AB020662	Homo sapiens KIAA0855 protein	4070	97.372
6392	M58378	Homo sapiens synapsin I	4798	99.008
6393	AF151846	Homo sapiens CGI-88 protein	1351	99.000
6394	X03528	Homo sapiens lambda L-chain C region	588	87.736

6395	AF039697	Homo sapiens antigen NY-CO-31	1580	97.414
6396	AF093543	Homo sapiens transforming acidic coiled-coil containing protein 3	5319	99.404
6397	AF096160	Homo sapiens protein phosphatase 2A BR gamma subunit	2686	99.294
6398	AJ222801	Homo sapiens neutral sphingomyelinase	2675	97.887
6399	L39061	Homo sapiens transcription factor SL1	3745	99.639
6400	AB002293	Homo sapiens KIAA0295	6494	99.898
6401	AC004774	Homo sapiens Dlx-5	1950	100.000
6402	AF151863	Homo sapiens CGI-105 protein	2052	97.771
6403	AF065215	Homo sapiens cytosolic phospholipase A2 beta	6677	99.306
6404	AJ005892	Homo sapiens JM23	2079	95.482
6405	U47634	Homo sapiens beta-tubulin	2892	97.517
6406	M13442	Mus musculus alpha-tubulin isotype M-alpha-6	2942	98.667
6407	AB014574	Homo sapiens KIAA0674 protein	7874	99.354
6408	AF030001	Mus musculus unknown	1499	71.510
6409	X75621	Homo sapiens tuberin	1155 1	99.006
6410	AF169548	Homo sapiens gamma-synergin	8623	99.924
6411	X90530	Homo sapiens ragB	2426	99.465
6412	AF104923	Homo sapiens putative transcription factor	5936	96.013
6413	AF151896	Homo sapiens CGI-138 protein	1000	99.346
6414	AF151873	Homo sapiens CGI-115 protein	1628	100.000
6415	AL050276	Homo sapiens hypothetical protein	4457	99.850
6416	AL080157	Homo sapiens hypothetical protein	2850	99.533
6417	AF077033	Homo sapiens putative ATP-dependent RNA helicase ROK1	3791	99.165
6418	Z99707	Arabidopsis thaliana methionyl aminopeptidase-like protein	904	53.069
6419	Z48570	Homo sapiens Sp17	961	100.000
6420	Z81053	Unknown predicted using Genefinder; Similarity to Yeast mitochondrial ribosomal protein S5 (SW:RT05)	455	33.129
6421	X15306	Homo sapiens heavy neurofilament subunit	6271	98.150
6422	AB007884	Homo sapiens KIAA0424	3501	99.806
6423	AB018323	Homo sapiens KIAA0780 protein	7519	99.909
6424	Z97992	Schizosaccharomyces pombe conserved hypothetical protein	403	33.096
6425	AF132950	Homo sapiens CGI-16 protein	2625	99.750
6426	AF042713	Rattus norvegicus neurexophilin 3	1675	95.635
6427	U53366	Oncorhynchus mykiss terminal deoxynucleotidyl transferase	620	43.866
6428	AB018303	Homo sapiens KIAA0760 protein	8254	99.503
6429	X83573	Homo sapiens ARSE	4104	99.321
6430	AJ243274	Homo sapiens AP-2rep protein	2454	94.828
6431	AF151838	Homo sapiens CGI-80 protein	2128	100.000
6432	AL035608	Homo sapiens dJ479J7.1 (similar to CHONDROMODULIN-1)	1791	100.000
6433	AF051240	Picea mariana probable ubiquitin-conjugating enzyme E2	680	48.598
6434	AF153606	Homo sapiens angiopoietin-related protein	2754	100.000
6435	AF151904	Homo sapiens CGI-146 protein	778	74.869
6436	X83973	Homo sapiens transcription factor	5570	99.548
6437	AL080169	Homo sapiens hypothetical protein	1135	94.536
6438	AF130367	Mus musculus Fas-apoptosis inhibitory molecule	1029	90.395

6439	M63193	Homo sapiens endothelial cell growth factor	801	72.917
6440	AF151810	Homo sapiens CGI-52 protein	2256	99.721
6441	AL022237	Homo sapiens bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1)	1620	75.819
6442	Z67743	Homo sapiens CLC-7 chloride channel protein	5148	99.620
6443	L14610	Rattus norvegicus transcription factor	3065	96.281
6444	AF006264	Homo sapiens hHR21spB	3324	98.543
6445	Z92825	Unknown predicted using Genefinder; Similarity to Yeast low-afinity glucose transporter HXT4 (PS:32	1178	42.576
6446	AJ006266	Homo sapiens AND-1 protein	7551	100.000
6447	AF151908	Homo sapiens CGI-150 protein	3180	99.405
6448	AF093744	Homo sapiens unknown	293	100.000
6449	AF180919	Homo sapiens RNA lariat debranching enzyme	3611	99.816
6450	AF100750	Homo sapiens SLAP-2 homolog	2697	91.616
6451	S41204	Mus sp. H beta 58=essential for embryogenesis	1141	58.537
6452	Z83844	Homo sapiens dJ37E16.4 (similar to mouse p116Rip protein)	1515	98.062
6453	X83378	Homo sapiens putative chloride channel	5711	99.541
6454	AL110240	Homo sapiens hypothetical protein	916	98.571
6455	A69608	unidentified unnamed protein product	3965	99.353
6456	AF153192	Homo sapiens ras-related protein	1827	100.000
6457	AB029031	Homo sapiens KIAA1108 protein	4913	99.737
6458	D79994	Homo sapiens similar to ankyrin of Chromatium vinosum.	8478	99.847
6459	AL050149	Homo sapiens hypothetical protein	3634	98.599
6460	AB018301	Homo sapiens KIAA0758 protein	6455	99.595
6461	AB008376	Sus scrofa 17-kDa PKC-potentiated inhibitory protein of PP1	798	87.248
6462	AB028991	Homo sapiens KIAA1068 protein	2343	100.000
6463	U58658	Homo sapiens unknown	275	60.227
6464	AB023190	Homo sapiens KIAA0973 protein	1044 6	99.369
6465	AB018295	Homo sapiens KIAA0752 protein	2139	100.000
6466	AL050015	Homo sapiens hypothetical protein	1245	100.000
6467	AF124512	Homo sapiens BVES	259	39.130
6468	AC004531	Homo sapiens Gene with similaity to DEAD box helicases	3400	99.076
6469	A12142	synthetic construct IFN-pseudo-omega 2	987	99.351
6470	AF065215	Homo sapiens cytosolic phospholipase A2 beta	6677	99.306
6471	U31629	Mus musculus unknown	1855	94.257
6472	Z82268	Caenorhabditis elegans cDNA EST yk478b4.5 comes from this gene; cDNA EST EMBL:D74716 comes from this gene; cDNA EST yk456b12.5 comes from this gene; cDNA EST EMBL:T00892 comes from this gene	393	26.519
6473	M32317	Homo sapiens HLA protein allele B7	2284	97.245
6474	X07384	Homo sapiens GLI protein (AA 1-1106)	7827	99.910
6475	AJ000327	Homo sapiens adrenoleukodystrophy related protein	4340	99.112
6476	AL031228	Homo sapiens dJ1033B10.10 (membrane protein with histidine rich charge clusters (HKE4, RING5))	544	38.973
6477	Y11395	Homo sapiens seventransmembrane-domain protein	2638	99.250

6478	L24444	Homo sapiens DNA repair protein	175	35.294
6479	AB020630	Homo sapiens KIAA0823 protein	2479	96.154
6480	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	5466	92.705
6481	AF035178	Oryctolagus cuniculus elongation factor 1 A2	3013	99.784
6482	L10244	Mus musculus spermidine/spermine N1-acetyltransferase	548	47.059
6483	AL031228	Homo sapiens dJ1033B10.3 (GalT3 (beta3-Galactosyltransferase))	2521	99.208
6484	AC003965	Homo sapiens SP001LA	456	33.740
6485	AF151821	Homo sapiens CGI-63 protein	2425	99.464
6486	Z24680	Homo sapiens garp	4207	100.000
6487	AL117429	Homo sapiens hypothetical protein	1320	100.000
6488	U73585	Bos taurus Fanconi anemia group C protein	2586	73.488
6489	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	404	100.000
6490	AF078165	Homo sapiens conductin	5558	98.935
6491	AF038844	Homo sapiens MKP-1 like protein tyrosine phosphatase	205	56.061
6492	U69127	Homo sapiens FUSE binding protein 3	3989	99.497
6493	U79304	Homo sapiens unknown	2190	96.953
6494	X17094	Homo sapiens furin (AA 1-794)	5413	99.874
6495	AF100745	Homo sapiens PTD016 protein	1286	99.497
6496	AF073344	Homo sapiens ubiquitin-specific protease 3	3533	99.616
6497	AB007918	Homo sapiens KIAA0449 protein	4931	99.735
6498	X68561	Homo sapiens SPR-1	5000	99.745
6499	AF056116	Fugu rubripes unknown	1934	66.596
6500	AB014547	Homo sapiens KIAA0647 protein	7086	99.902
6501	AB002360	Homo sapiens KIAA0362	7335	99.278
6502	X81788	Homo sapiens ICT1 protein	1320	99.034
6503	AL023839	Caenorhabditis elegans similar to HECT-domain (ubiquitin-transferase).; cDNA EST yk480d10.5 comes from this gene; cDNA EST yk531b3.3 comes from this gene; cDNA EST yk196d10.5 comes from this gene	2005	36.396
6504	AB014593	Homo sapiens KIAA0693 protein	2598	96.543
6505	S70011	Rattus sp. tricarboxylate carrier	1156	55.732
6506	Z99709	Caenorhabditis elegans C47B2.2b	670	51.961
6507	X97065	Homo sapiens Sec23 protein	5155	99.739
6508	AF107834	Homo sapiens aminopeptidase	2968	98.943
6509	L38709	Mesocricetus auratus orf	1847	71.968
6510	AB018318	Homo sapiens KIAA0775 protein	191	26.935
6511	D12816	Bos taurus actin2	2597	90.670
6512	AF072733	Homo sapiens putative secreted protein	1550	80.831
6513	AL080141	Homo sapiens hypothetical protein	6209	99.891
6514	L29554	Rattus norvegicus alpha 2,6-sialyltransferase	745	42.629
6515	AJ011654	Homo sapiens triple LIM domain protein	4277	98.703
6516	X03528	Homo sapiens lambda L-chain C region	588	87.736
6517	AF151819	Homo sapiens CGI-61 protein	2063	94.022
6518	AB011148	Homo sapiens KIAA0576 protein	7231	99.349
6519	K02882	Homo sapiens immunoglobulin delta-chain	2480	98.695
6520	U88567	Mus musculus secreted frizzled related protein sFRP-2	1911	97.627
6521	X07979	Homo sapiens integrin beta 1 subunit precursor	5368	97.378
6522	L76200	Homo sapiens guanylate kinase	1202	95.610

6523	AB017332	Homo sapiens Aurora/Ipl1-related kinase 3	1924	99.655
6524	AB007902	Homo sapiens HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442.	8176	99.659
6525	X59727	Homo sapiens 63kDa protein kinase	3602	98.925
6526	Y00291	Homo sapiens hap protein	2971	99.777
6527	AB024057	Homo sapiens vascular Rab-GAP/TBC-containing protein	5910	99.666
6528	AJ228139	Homo sapiens LEKTI precursor	7301	99.436
6529	A16794	Homo sapiens cDNA isolated for this protein using a monoclonal antibody directed against the p27k prosomal protein	1740	100.000
6530	X78873	Homo sapiens inhibitor 2	1304	99.512
6531	AJ005895	Homo sapiens protein translocase	1033	97.110
6532	AJ224819	Homo sapiens tumor suppressor	2561	97.066
6533	D29958	Homo sapiens KIAA0116	1252	88.255
6534	AB011154	Homo sapiens KIAA0582 protein	3020	99.782
6535	X51985	Homo sapiens LAG-3 protein precursor	3603	99.619
6536	Y07595	Homo sapiens transcription factor TFIIH	2845	98.491
6537	AB002631	Homo sapiens collectin 34	933	50.598
6538	AC007017	Arabidopsis thaliana putative RNA helicase A	2366	42.857
6539	AF052052	Homo sapiens unknown	812	82.209
6540	AJ245738	Homo sapiens claudin-15	1447	98.673
6541	AF159092	Homo sapiens syld709613 protein	2333	96.226
6542	AL109652	Schizosaccharomyces pombe hypothetical protein	773	44.884
6543	D14480	Rattus norvegicus calpain	2325	86.856
6544	M23197	Homo sapiens differentiation antigen	1130	60.197
6545	AL022398	Homo sapiens dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7 intergenic region)	4915	99.735
6546	X79882	Homo sapiens lrp	5825	100.000
6547	L08237	Homo sapiens located at OATL1	191	46.903
6548	AF187318	Homo sapiens F-box protein Fbx2	1950	98.986
6549	AF036702	Caenorhabditis elegans contains weak similarity to HIV P17 matrix protein (GB:L35970)	285	26.335
6550	AB018290	Homo sapiens KIAA0747 protein	7076	99.907
6551	AL050369	Homo sapiens hypothetical protein	3085	98.031
6552	AC005917	Arabidopsis thaliana putative WD-40 repeat protein	1145	42.472
6553	D26311	Gallus gallus unknown protein	1318	58.537
6554	AF091083	Homo sapiens unknown	1871	99.650
6555	M29581	Homo sapiens zinc finger protein 8 (ZFP8)	3533	96.324
6556	AL096879	Homo sapiens hypothetical protein	616	37.631
6557	AF139682	Homo sapiens putative N6-DNA-methyltransferase; N6AMT1	1383	100.000
6558	X16135	Homo sapiens L protein (AA 1-558)	1847	56.098
6559	AF156777	Homo sapiens ASB-1 protein	2245	99.110
6560	Z19555	Caenorhabditis elegans cDNA EST yk425a6.3 comes from this gene; cDNA EST yk406e6.3 comes from this gene; cDNA EST yk425a6.5 comes from this gene; cDNA EST yk480c6.5 comes from this gene; cDNA EST yk406e6.5 comes from this gene	347	25.818
6561	AL032623	Unknown cDNA EST yk331e12.5 comes from this	200	35.338

		gene; cDNA EST EMBL:D69131 comes from this gene; cDNA		
6562	AF069954	Mus musculus unknown	2305	84.235
6563	AB011139	Homo sapiens KIAA0567 protein	6357	99.183
6564	AF003151	Caenorhabditis elegans No definition line found	481	28.231
6565	X55684	Lycopersicon esculentum extensin (class I)	98	32.143
6566	AB028968	Homo sapiens KIAA1045 protein	2622	96.471
6567	D63484	Homo sapiens The KIAA0150 gene product is novel.	6425	100.000
6568	Z82215	Homo sapiens dJ6802.2	1232 4	99.796
6569	Y13492	Homo sapiens smoothelin-B	5831	99.346
6570	AL096768	Homo sapiens dJ858B16.2 (novel protein similar to hamster PSSC (Phosphatidylserine Decarboxylase Proenzyme, EC 4.1.1.65)	2574	99.733
6571	AF125099	Homo sapiens HSPC038 protein	466	89.412
6572	AF132964	Homo sapiens CGI-30 protein	1764	94.949
6573	AB029012	Homo sapiens KIAA1089 protein	6572	99.899
6574	X15218	Homo sapiens ski protein (AA 1 - 728)	4677	100.000
6575	AL035461	Homo sapiens dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	1936	99.007
6576	U45998	Onchocerca volvulus mitochondrial solute carrier	705	47.489
6577	AF091080	Homo sapiens unknown	2120	100.000
6578	Y08200	Homo sapiens rab geranylgeranyl transferase	3709	98.604
6579	AF151868	Homo sapiens CGI-110 protein	813	100.000
6580	X74142	Homo sapiens transcription factor	3301	99.161
6581	AJ132545	Homo sapiens protein kinase	3757	99.820
6582	M60165	Homo sapiens guanine nucleotide-binding regulatory protein 1	2297	99.435
6583	AF151522	Homo sapiens hairy and enhancer of split related-1	1989	100.000
6584	AJ243460	Leishmania major proteophosphoglycan	182	25.909
6585	AL117664	Homo sapiens hypothetical protein	889	49.508
6586	AF106685	Homo sapiens myelin gene expression factor 2	3579	97.441
6587	AF124490	Homo sapiens ARF GTPase-activating protein GIT1	4971	99.081
6588	AC004131	Homo sapiens Unknown gene product	2567	98.020
6589	L77967	Ovis aries small proline-rich protein with paired repeat	111	46.667
6590	AB011129	Homo sapiens KIAA0557 protein	3444	100.000
6591	AB018310	Homo sapiens KIAA0767 protein	3775	100.000
6592	AB018338	Homo sapiens KIAA0795 protein	2834	94.872
6593	AF079098	Homo sapiens arginine-tRNA-protein transferase 1-1p; ATE1-1p	3506	99.611
6594	AJ010119	Homo sapiens Ribosomal protein kinase B (RSK-B)	4956	98.448
6595	AF017777	Drosophila melanogaster helicase	1530	48.423
6596	U96724	Mus musculus putative phosphoinositide 5-phosphatase type II	2343	74.145
6597	U71363	Homo sapiens zinc finger protein zfp6	3057	98.144
6598	Z35227	Homo sapiens small G protein	1247	100.000
6599	AJ133115	Homo sapiens TSC-22-like protein	2583	97.727
6600	AC004798	Homo sapiens R31546 1	4899	99.863

6601	AJ005559	Mus musculus SPR2A protein	158	41.333
6602	X83572	Homo sapiens ARSD	4046	99.157
6603	AF121859	Homo sapiens sorting nexin 9	3985	99.832
6604	AF102166	Homo sapiens intracellular chloride channel CLIC3	1115	91.905
6605	X68277	Homo sapiens protein-tyrosine phosphatase	2292	97.568
6606	AL117491	Homo sapiens hypothetical protein	9306	100.000
6607	AL117634	Homo sapiens hypothetical protein	1366	100.000
6608	X74226	Rattus norvegicus putative	4435	86.380
6609	U71601	Homo sapiens zinc finger protein zfp47	2291	97.598
6610	X63368	Homo sapiens HSJ1b	2325	99.715
6611	X90530	Homo sapiens ragB	2426	99.465
6612	AB020724	Homo sapiens KIAA0917 protein	3802	95.156
6613	Z29067	Homo sapiens protein kinase	3051	99.564
6614	AB011135	Homo sapiens KIAA0563 protein	5824	99.310
6615	AF061025	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1	4406	100.000
6616	L00352	Homo sapiens low density lipoprotein receptor	6091	99.767
6617	AF042831	Homo sapiens forkhead-related transcription factor FREAC-10	776	100.000
6618	X65873	Homo sapiens kinesin heavy chain	6033	99.274
6619	M62362	Mus musculus CCAAT/enhancer binding protein	2382	91.479
6620	Y14488	Homo sapiens 14 kDa protein	831	96.124
6621	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	221	65.000
6622	AJ224997	Rattus norvegicus huntingtin	87	48.276
6623	AB029016	Homo sapiens KIAA1093 protein	8451	99.668
6624	AB027013	Homo sapiens Nucleosome Assembly Protein 1-like 2	3028	99.565
6625	X98258	Homo sapiens M-phase phosphoprotein 9	1112	99.457
6626	U97191	Caenorhabditis elegans strong similarity to the YPT1 sub-family of RAS proteins	1199	85.185
6627	AB006624	Homo sapiens KIAA0286	2841	99.767
6628	AF151805	Homo sapiens CGI-47 protein	2625	100.000
6629	AF106858	Homo sapiens G-protein-coupled receptor	4558	99.134
6630	X76057	Homo sapiens phosphomannose isomerase	2719	99.522
6631	AL049746	Arabidopsis thaliana putative protein	287	19.729
6632	X97064	Homo sapiens Sec23 protein	5093	99.869
6633	L09634	Caenorhabditis elegans putative	205	26.974
6634	AJ005642	Rattus rattus serine protease	930	47.535
6635	AL079310	Homo sapiens hypothetical protein	2994	96.768
6636	X79563	Homo sapiens 8.2 kDa differentiation factor	606	96.907
6637	Z66520	Caenorhabditis elegans similar to ERG-3 like protein	709	38.971
6638	M19529	Sus scrofa follistatin A	2420	98.246
6639	AF060154	Homo sapiens activated B-cell factor-1	1453	99.541
6640	U79260	Homo sapiens unknown	284	58.416
6641	AJ249457	Trichomonas vaginalis centrin, putative	193	29.787
6642	AF078850	Homo sapiens steroid dehydrogenase homolog	1967	99.679
6643	AF128625	Homo sapiens CDC42-binding protein kinase beta 4	1118	99.416
6644	AC004410	Homo sapiens fos39554 1	2699	100.000
6645	AL035541	Homo sapiens dJ718J7.1 (PUTATIVE novel protein similar to Tr:O15168)	1407	100.000
6646	AC004537	Homo sapiens similar to tumor suppressor	2611	99.265

		p33ING1; similar to AF044076 (PID:g2829208)		
6647	X03528	Homo sapiens lambda L-chain C region	588	87.736
6648	D12768	Rattus norvegicus Sp1	4713	93.932
6649	AF132944	Homo sapiens CGI-10 protein	2956	98.718
6650	AB011136	Homo sapiens KIAA0564 protein	9414	99.584
6651	AB011138	Homo sapiens KIAA0566 protein	7537	99.312
6652	Z92825	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene; cDNA EST yk605b12.3 comes from this gene	655	43.359
6653	AB010491	Homo sapiens natriuretic peptide A type receptor	7000	100.000
6654	D79205	Homo sapiens ribosomal protein L39	238	76.471
6655	D83782	Homo sapiens the KIAA0199 gene is expressed ubiquitously.; the KIAA0199 protein shows similarity to sea urchin hydroxymethylglutaryl-CoA reductase, and retains 8 hydrophobic domains.	8679	100.000
6656	AF016903	Homo sapiens agrin precursor	1433 0	99.557
6657	Z22181	Unknown similar to PH (pleckstrin homology) domain; cDNA EST EMBL:C07493 comes from this gene; cDN	747	50.000
6658	X61045	Hydra sp. mini-collagen	200	36.036
6659	AF019926	Mus musculus protein kinase	2099	89.944
6660	AB020715	Homo sapiens KIAA0908 protein	3301	99.802
6661	AF118838	Homo sapiens citrin; adult-onset type II citrullinemia protein	4359	100.000
6662	U30831	Rattus norvegicus B/K protein	3068	96.835
6663	M26312	Oryctolagus cuniculus unknown protein	162	42.466
6664	L32162	Homo sapiens transcription factor	1758	99.265
6665	X02585	Xenopus laevis unidentified open reading frame 2	350	62.766
6666	D87930	Homo sapiens myosin phosphatase target subunit 1	6441	99.903
6667	AF036717	Homo sapiens FGFR signalling adaptor SNT-1	3373	99.803
6668	AL050060	Homo sapiens hypothetical protein	2185	99.692
6669	U07151	Homo sapiens ARL3	230	32.090
6670	AL110245	Homo sapiens hypothetical protein	931	64.259
6671	Z72497	Gallus gallus CEPU-1	1817	78.632
6672	AB014590	Homo sapiens KIAA0690 protein	7783	99.013
6673	AF041377	Mus musculus cell death activator CIDE-B	1214	84.793
6674	X79237	Mustela vison ribosomal protein S26	128	57.500
6675	AB007914	Homo sapiens KIAA0445 protein	7847	98.477
6676	X03528	Homo sapiens lambda L-chain C region	588	87.736
6677	AF002223	Homo sapiens myotubularin related 1	4423	99.698
6678	Y10812	Homo sapiens fructose-1,6-bisphosphatase	2073	100.000
6679	AF055000	Homo sapiens unknown	2557	98.297
6680	AF165217	Homo sapiens tropomodulin	2229	99.710
6681	L32162	Homo sapiens transcription factor	532	94.681
6682	AF135028	Homo sapiens kallikrein-like protein 2 KLK-L2	2010	98.639
6683	AL031541	Streptomyces coelicolor putative dehydrogenase	481	37.308
6684	AF084256	Homo sapiens beta glucuronidase isoform d	182	68.182
6685	U38934	Gallus gallus histone H2A	758	98.400
6686	AF065215	Homo sapiens cytosolic phospholipase A2 beta	6677	99.306

6687	U76374	Mus musculus skm-BOP2	765	31.808
6688	X71623	Homo sapiens zinc finger	4073	99.825
6689	X68362	Mus musculus Oct-1A protein	3938	88.472
6690	AF132856	Homo sapiens suppressor of G2 allele of skp1 homolog	2164	99.701
6691	Y09501	Homo sapiens NADH-cytochrome-b5 reductase	2015	100.000
6692	J04628	Rattus norvegicus 3-hydroxyisobutyrate dehydrogenase	2053	90.909
6693	AB023139	Homo sapiens KIAA0922 protein	5160	98.108
6694	X01655	Homo sapiens type III procollagen (aa 892-1023)	119	37.190
6695	Y15521	Homo sapiens start position 1	4126	99.524
6696	AL117496	Homo sapiens hypothetical protein	1090 1	99.046
6697	X76538	Homo sapiens hMpv17	1172	97.207
6698	AF131826	Homo sapiens Unknown	277	27.667
6699	AL049176	Homo sapiens dAl41H5.1 (C-terminal part of a Chordin LIKE protein with von Willebrand factor type C domains)	1786	100.000
6700	AJ133421	Homo sapiens vacuolar protein sorting	3543	99.649
6701	AF125807	Homo sapiens DNA 5'-kinase/3'-phosphatase	3468	99.616
6702	AC004923	Homo sapiens similar to UNC-93; similar to U89424 (PID:g3642687)	2082	97.619
6703	AF151867	Homo sapiens CGI-109 protein	1166	94.608
6704	AF009624	Homo sapiens KIF3-related motor protein	1518	99.160
6705	X92475	Homo sapiens ITBA1	1761	98.855
6706	AL031716	Homo sapiens c360B4.1 (PUTATIVE novel protein similar to predicted bacterial and worm proteins)	1133	87.143
6707	AF077205	Homo sapiens HSPC019	816	100.000
6708	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	3383	99.426
6709	AJ010482	Homo sapiens Myopodin protein	5470	100.000
6710	AL049955	Homo sapiens hypothetical protein	1061	81.905
6711	Y16752	Homo sapiens secretagoin	1786	98.913
6712	AB004678	Homo sapiens dihydropyrimidinase	1990	58.382
6713	X51416	Homo sapiens hormone receptor hERR1 (AA 1-521)	3447	99.040
6714	D50911	Homo sapiens The KIAA0121 gene product is novel.	1365	98.571
6715	X99459	Homo sapiens sigma 3 protein	1243	100.000
6716	AJ006591	Homo sapiens cysteine-rich protein	2295	100.000
6717	AL080155	Homo sapiens hypothetical protein	2563	94.771
6718	Z97653	Homo sapiens c380A1.2.1 (novel protein (isoform 1))	644	45.324
6719	X54232	Homo sapiens glypican	3531	98.571
6720	U17989	Homo sapiens GS2NA	2343	54.331
6721	AF176642	Homo sapiens ubiquitin-specific protease ISG43	2499	99.464
6722	AF117336	Aplysia californica mollusk-derived growth factor; MDGF	1229	38.833
6723	AL050003	Homo sapiens hypothetical protein	1970	100.000
6724	AJ223324	Homo sapiens MAX.3 cell surface antigen	414	32.797
6725	A08695	Homo sapiens rap2	943	93.478
6726	Z12173	Homo sapiens N-acetylglucosamine-6-sulphatase	3750	99.819
6727	AF151814	Homo sapiens CGI-56 protein	703	42.405
6728	M37030	Mus musculus ORF	2258	94.823

6729	D13744	Holotrichia diomphalia holotricin 3	108	59.375
6730	AB007930	Homo sapiens KIAA0461 peroteine	8939	96.028
6731	U32575	Rattus norvegicus similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author	4586	94.430
6732	D38491	Homo sapiens KIAA0117	1018	78.829
6733	AJ012590	Homo sapiens glucose 1-dehydrogenase	5158	98.235
6734	Z83869	Rattus norvegicus serine/threonine kinase	4210	89.529
6735	X74331	Homo sapiens DNA primase (p58 subunit)	3328	98.821
6736	X68362	Mus musculus Oct-1A protein	3938	88.472
6737	AL080133	Homo sapiens hypothetical protein	7089	99.543
6738	M84725	Rattus norvegicus neuronal protein	1386	96.347
6739	X75316	Mus musculus SEB4	971	64.591
6740	AF151833	Homo sapiens CGI-75 protein	2042	93.017
6741	A58331	Homo sapiens unnamed protein product	2759	98.529
6742	AF153686	Homo sapiens calcium binding protein precursor	1604	97.638
6743	AL008583	Homo sapiens dJ327J16.2 (human ortholog of rat Neuronal Pentraxin Receptor)	3295	99.600
6744	AF151888	Homo sapiens CGI-130 protein	976	81.250
6745	AB017112	Mus musculus mCAC	493	34.185
6746	AL080121	Homo sapiens hypothetical protein	1573	100.000
6747	X04434	Homo sapiens IGF-I receptor	9297	99.854
6748	AJ224538	Homo sapiens AMP-activated protein kinase beta 2 subunit	1812	99.632
6749	AF151829	Homo sapiens CGI-71 protein	2052	99.691
6750	M17466	Homo sapiens coagulation factor XII	4464	100.000
6751	AF106473	Mus musculus leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1	526	70.714
6752	M25826	Kluyveromyces lactis actin	1891	81.432
6753	U92819	Homo sapiens unnamed HERV-H protein	324	69.512
6754	AF061262	Mus musculus semaF cytoplasmic domain associated protein 2	1644	83.387
6755	AF108831	Homo sapiens K:Cl cotransporter 3	7183	99.909
6756	AF151806	Homo sapiens CGI-48 protein	3348	99.423
6757	AJ004832	Homo sapiens neuropathy target esterase	8691	99.623
6758	AF097439	Mus musculus brain expressed X-linked protein 2	629	71.318
6759	AJ005562	Mus musculus SPR2D protein	99	35.556
6760	AF132600	Homo sapiens B-lymphocyte stimulator	1827	100.000
6761	AL079292	Homo sapiens hypothetical protein, similar to (AC007017) putative RNA helicase A	5094	99.752
6762	X07876	Homo sapiens Irp protein (AA 1-360)	2511	99.446
6763	D14592	Rattus norvegicus MAP kinase kinase-related protein	2462	93.216
6764	A65892	unidentified MURINE PSA-99	5941	97.177
6765	Z22819	Mus musculus Rab24 protein	1232	85.470
6766	U79260	Homo sapiens unknown	384	73.626
6767	AL035656	Arabidopsis thaliana putative protein	1383	58.127
6768	Z97029	Homo sapiens ribonuclease HI large subunit	1798	98.333
6769	AC006042	Homo sapiens supported by human ESTs AI681256.1 (NID:g4891438), N32168.1 (NID:g1152567), and genscan	854	45.278
6770	AL033514	Caenorhabditis elegans predicted using	991	53.160

		Genefinder; cDNA EST EMBL:D71127 comes from this gene; cDNA EST EMBL:D73731 comes from this gene; cDNA EST yk527c3.3 comes from this gene; cDNA EST yk645b5.3 comes from this gene		
6771	A63340	unidentified unnamed protein product	2823	98.081
6772	X67325	Homo sapiens p27	415	87.097
6773	AF133911	Mus musculus ARL-6 interacting protein-4	300	79.688
6774	AF010258	Homo sapiens homeodomain protein	1862	99.632
6775	A37078	Homo sapiens NUCLEOTIDE WITH CORRESPONDING PROTEIN	271	81.132
6776	AF003145	Caenorhabditis elegans No definition line found	690	26.910
6777	AJ005564	Mus musculus SPR2F protein	103	34.694
6778	X85237	Homo sapiens human splicing factor	5383	100.000
6779	AL117496	Homo sapiens hypothetical protein	1092 1	99.046
6780	AB007447	Homo sapiens Fln29	3992	99.656
6781	X53427	Rattus norvegicus glycogen synthase kinase 3 alpha (AA 1 - 483)	3040	96.488
6782	AC007055	Homo sapiens unknown	2053	100.000
6783	AF184969	Homo sapiens cytokine homolog CYT07	1263	100.000
6784	AF077038	Homo sapiens unc-50 related protein homolog	1705	97.368
6785	AC004382	Homo sapiens Unknown gene product	1799	81.471
6786	AF045584	Homo sapiens PB39	653	30.114
6787	AF173380	Mus musculus angiotensin II AT2 receptor-interacting protein	2334	86.395
6788	X68596	Homo sapiens parathyroid hormone receptor	4020	100.000
6789	U13021	Homo sapiens ICH-1L	2837	95.302
6790	AB014585	Homo sapiens KIAA0685 protein	5753	95.503
6791	M95178	Homo sapiens alpha-actinin	5377	97.213
6792	U26401	Homo sapiens galactokinase	2454	97.970
6793	D89141	Schizosaccharomyces pombe similar to Saccharomyces cerevisiae hypothetical 27.6KD protein in chromosome VII, SWISS-PROT Accession Number P46948	564	43.802
6794	AF151836	Homo sapiens CGI-77 protein	1798	100.000
6795	AF042800	Homo sapiens suppressor of white apricot homolog 2	4277	99.545
6796	Z46973	Homo sapiens phosphatidylinositol 3-kinase	5722	97.750
6797	AL030996	Homo sapiens dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)	7299	99.731
6798	AB015331	Homo sapiens HRIHFB2017	1301	99.539
6799	AF042752	Gorilla gorilla cytochrome c oxidase subunit IV	551	59.712
6800	U18468	Homo sapiens pregnancy-specific beta 1-glycoprotein 4 precursor	2625	97.837
6801	Z14954	Homo sapiens codes for a 184 aminoacid peptide (BCM)	1211	100.000
6802	AF093543	Homo sapiens transforming acidic coiled-coil containing protein 3	5399	99.404
6803	AF073920	Homo sapiens regulator of G-protein signaling 6	3721	98.239
6804	M99487	Homo sapiens prostate- specific membrane antigen	5005	98.800

6805	AF070663	Homo sapiens HSPC007	1127	99.465
6806	U08377	Homo sapiens similar to the Drosophila splicing regulator, suppressor-of-white-apricot: Swiss-Prot Accession Number P12297	6185	99.579
6807	AB025905	Homo sapiens neighbor of A-kinase anchoring protein 95	4088	98.609
6808	Z29067	Homo sapiens protein kinase	3051	99.564
6809	AL035295	Homo sapiens hypothetical protein	751	94.215
6810	AF157562	Homo sapiens unknown	1057	99.387
6811	AC006023	Homo sapiens similar to KIAA0904; similar to AAA58424 (PID:g180492)	4923	99.862
6812	AF073770	Homo sapiens carnitine octanoyltransferase	3986	99.668
6813	AF105369	Homo sapiens actin-associated protein 2E4/kaptein	3055	95.591
6814	A14656	synthetic construct protein antigen	1882	99.647
6815	U15370	Pseudomonas aeruginosa similar to E. coli protein PolB/DinA, Swiss-Prot Accession Number P21189	130	45.946
6816	AB020636	Homo sapiens KIAA0829 protein	7599	99.915
6817	Z35278	Homo sapiens Runt domain containing protein	2668	98.795
6818	X03528	Homo sapiens lambda L-chain C region	588	87.736
6819	AC007087	Arabidopsis thaliana unknown protein	246	23.589
6820	Y12781	Homo sapiens transducin (beta) like 1 protein	3607	99.449
6821	AF030227	Homo sapiens vav protein	5649	99.764
6822	X66899	Homo sapiens RNA binding protein	4687	100.000
6823	V00638	bacteriophage lambda reading frame ea10	799	99.180
6824	AE000406	Escherichia coli putative DNA topoisomerase	1219	100.000
6825	AF049103	Homo sapiens Huntingtin interacting protein	1153	99.435
6826	AF086608	Rattus norvegicus neurestin beta	296	32.738
6827	M55593	Homo sapiens type IV collagenase	4683	100.000
6828	D85884	Homo sapiens glutamate transporter	3642	99.652
6829	U40978	Homo sapiens DNA mismatch repair protein homolog	4779	99.603
6830	D31765	Homo sapiens KIAA0061	6234	100.000
6831	AL009191	Unknown /prediction=(method:"genefinder", version:"084"); /prediction=(method:"genscan", ve	456	30.056
6832	AF109719	Mus musculus unknown	1430	75.850
6833	U71075	Homo sapiens protein tyrosine phosphatase receptor omicron	9516	97.524
6834	AL096768	Homo sapiens dJ858B16.2 (novel protein similar to hamster PSSC (Phosphatidylserine Decarboxylase Proenzyme, EC 4.1.1.65)	2528	98.408
6835	X57351	Homo sapiens 1-8D	819	96.970
6836	U06632	Homo sapiens p80-coilin	3729	99.307
6837	AC005594	Homo sapiens R26984_1	3433	98.641
6838	L49054	Homo sapiens t(3;5)(q25.1;p34) fusion gene	1712	98.885
6839	Z26317	Homo sapiens desmoglein 2	7096	99.015
6840	S72869	Homo sapiens putative cytoskeletal protein-H4 (D10S170)	3805	99.316
6841	AF044195	Homo sapiens IkappaB kinase complex associated protein; IKAP	8837	99.775
6842	M62415	Pseudopleuronectes americanus HPLC6	114	39.623
6843	X73113	Homo sapiens fast MyBP-C	7378	98.953
6844	AF083249	Homo sapiens Rb binding protein homolog	4573	98.670

6845	M64934	Homo sapiens kell blood group protein	4481	96.744
6846	AJ005162	Homo sapiens UDP-glucuronosyltransferase	3555	99.811
6847	AB011097	Homo sapiens KIAA0525 protein	5680	99.654
6848	M55614	Homo sapiens TK14 protein	5498	99.757
6849	U15155	Gallus gallus trypsinogen	459	37.500
6850	AB018320	Homo sapiens KIAA0777 protein	7314	98.268
6851	AF018956	Homo sapiens neuropilin	6334	99.783
6852	X00776	Escherichia coli lipoprotein signal peptidase	1071	99.390
6853	AE000236	Escherichia coli putative enzyme	1457	94.902
6854	D86974	Homo sapiens KIAA0220	3648	99.458
6855	X07936	Homo sapiens epoxide hydrolase (AA 1-455)	2732	98.253
6856	Z11518	Homo sapiens histidyl-tRNA synthetase	3185	98.232
6857	M84725	Rattus norvegicus neuronal protein	1386	96.347
6858	AF097025	Homo sapiens cysteine desulfurase	2961	98.687
6859	AL117424	Homo sapiens hypothetical protein	1640	100.000
6860	AJ236885	Homo sapiens ZBP-89 protein	5179	99.748
6861	M74002	Homo sapiens arginine-rich nuclear protein	467	34.495
6862	U05812	Herpetomonas muscarum 3'-end	115	31.325
6863	L06505	Homo sapiens ribosomal protein L12	627	66.460
6864	Y08769	Rattus norvegicus microvascular endothelial differentiation gene 2	151	47.761
6865	X82260	Homo sapiens RanGAP1	3708	99.830
6866	Y13186	Homo sapiens dystrophin	142	71.429
6867	M15386	Homo sapiens gamma-globin	522	70.175
6868	U79260	Homo sapiens unknown	203	50.794
6869	AB023179	Homo sapiens KIAA0962 protein	4135	99.049
6870	Y08162	Homo sapiens heptahelix receptor	316	25.364
6871	U18745	Homo sapiens corticostatin/defensin HP-4 precursor	330	56.522
6872	X55777	Homo sapiens put. ORF	360	62.921
6873	L01664	Homo sapiens lysophospholipase	441	47.143
6874	AF081110	Mus musculus domesticus ORF2	194	47.761
6875	U23452	Caenorhabditis elegans No definition line found	631	33.758
6876	M19419	Mus musculus proline-rich salivary protein	207	36.496
6877	AL031907	Schizosaccharomyces pombe hypothetical protein	275	26.531
6878	AF033664	Mus musculus cbp146	1197	83.491
6879	AB023167	Homo sapiens KIAA0950 protein	982	48.071
6880	Z72946	Saccharomyces cerevisiae ORF YGR159c	236	44.660
6881	AF000060	Aeropyrum pernix 108aa long hypothetical protein	144	31.731
6882	AF064604	Homo sapiens KE03 protein	459	51.634
6883	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	351	67.500
6884	M15530	Homo sapiens B-cell growth factor	162	41.758
6885	AC002294	Arabidopsis thaliana Unknown protein	721	50.000
6886	AJ243460	Leishmania major proteophosphoglycan	173	28.319
6887	J04076	Homo sapiens early growth response 2 protein	167	24.468
6888	M17294	Human herpesvirus 4 unknown protein	172	33.161
6889	AF138957	Bos taurus type II collagen cyanogen bromide fragment CB8	154	32.061
6890	AB023201	Homo sapiens KIAA0984 protein	4765	98.072
6891	U41557	Caenorhabditis elegans glycine-rich	134	46.429
6892	AB030237	Canis familiaris D4 dopamine receptor	126	36.667
6893	U58658	Homo sapiens unknown	296	65.385

6894	M97662	Rattus norvegicus beta-alanine synthase	2276	83.206
6895	AB028972	Homo sapiens KIAA1049 protein	3676	98.919
6896	X64897	Bos taurus MLRQ subunit of the NADH: ubiquinone oxidoreductase complex	343	64.935
6897	AF172328	Homo sapiens unknown	679	97.895
6898	U26358	Rattus norvegicus S100A1 gene product	420	55.556
6899	AF174394	Homo sapiens apoptotic-related protein PCAR	66	36.957
6900	Z35093	Homo sapiens SURF-1	1818	92.593
6901	AL096725	Homo sapiens hypothetical protein	1120	97.576
6902	AF044923	Homo sapiens hook1 protein	4543	93.565
6903	Z99494	Mycobacterium leprae hypothetical protein MLCB57.05c	110	33.684
6904	Z79695	Unknown Similarity to Yeast hypothetical protein YOR316OW (TR:E217727); cDNA EST EMBL:T00498 comes	1020	47.500
6905	L78671	Homo sapiens CoxII/D-loop DNA fusion protein	513	91.358
6906	AF174481	Typhlonectes natans gonadotropin-releasing hormone receptor	405	45.033
6907	Z95620	Schizosaccharomyces pombe putative dna binding protein	267	36.364
6908	S85655	Homo sapiens prohibitin	273	64.706
6909	L08816	Hepatitis E virus poly-proline hinge	80	33.333
6910	AF072508	Homo sapiens envelope protein	178	44.776
6911	X17400	Mus sp. TIS7 protein (AA 1-449)	2606	93.381
6912	X54518	Gossypium hirsutum late embryogenesis abundant protein	109	32.000
6913	AF041060	Mus musculus co-chaperone mt-GrpE#2 precursor	1228	83.929
6914	Z74029	Unknown Similarity to C.elegans alcohol dehydrogenase (WP:C17G10.8); cDNA EST EMBL:D66106 comes fro	778	66.484
6915	AB018423	Mus musculus SH2 domain-containing protein	1772	76.453
6916	U49973	Homo sapiens ORF1; MER37; putative transposase similar to pogo element	230	30.147
6917	Z73497	Homo sapiens cU240C2.1 (Core histone H2A/H2B/H3/H4)	738	83.803
6918	U63542	Homo sapiens FAP protein	217	70.455
6919	U97553	murine herpesvirus 68 unknown	144	39.189
6920	AF125569	Homo sapiens tumor suppressing STF cDNA 6	961	97.203
6921	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	91	41.667
6922	X72963	Nicotiana tabacum pAP8 product	149	33.333
6923	Z83246	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:M79771 comes from this gene	1147	59.524
6924	J01055	Chironomus tentans giant secretory protein	138	29.078
6925	X55777	Homo sapiens put. ORF	365	63.218
6926	U61947	Caenorhabditis elegans No definition line found	124	32.051
6927	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	110	34.483
6928	X98485	Plasmodium vivax putative	112	30.208
6929	X16282	Homo sapiens zinc finger protein (217 AA) (1 is 2nd base in codon)	1420	97.512
6930	U88368	Sus scrofa inositol(1,3,4,5)tetrakisphosphate receptor	1054	59.919

6931	Z92539	Mycobacterium tuberculosis pth	396	35.450
6932	AL008730	Homo sapiens dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1)	3980	99.127
6933	U28131	Homo sapiens novel transcript; similar to transcription factors activation domains; linked at 5' end to AT hook motif of HMGI-C; Method: conceptual translation supplied by author	197	49.351
6934	AF169346	Cavia porcellus pro-alpha-1 type 1 collagen	197	34.043
6935	M62324	Homo sapiens modulator recognition factor I	4210	99.186
6936	X68600	Hordeum vulgare pZE40	157	35.780
6937	X55777	Homo sapiens put. ORF	319	54.639
6938	Z99113	Bacillus subtilis similar to long-chain acyl-CoA synthetase	750	49.074
6939	X55777	Homo sapiens put. ORF	346	66.667
6940	AB030483	Mus musculus B9	294	27.083
6941	X01655	Homo sapiens type III procollagen (aa 892-1023)	176	38.393
6942	U43200	Boreogadus saida antifreeze glycopeptide AFGP polyprotein precursor	183	25.110
6943	U37150	Bos taurus peptide methionine sulfoxide reductase	1220	83.412
6944	X92109	Homo sapiens hcgIX	69	42.424
6945	AL117555	Homo sapiens hypothetical protein	984	98.496
6946	AC005328	Homo sapiens R26660 2, partial CDS	1226	86.667
6947	Z68752	Caenorhabditis elegans T12G3.5	179	32.203
6948	X63508	Mycobacterium tuberculosis predicted ORF	145	29.091
6949	L34807	Musca domestica transposase	261	18.375
6950	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	61.538
6951	M24543	Homo sapiens prostate-specific antigen	480	85.185
6952	AB020719	Homo sapiens KIAA0912 protein	8368	99.769
6953	S68106	Ascaris suum, Peptide Partial, 100 aa type IV collagen alpha 2 chain, alpha 2 (IV) {alternatively spliced}	120	32.530
6954	AF151832	Homo sapiens CGI-74 protein	725	52.652
6955	AF095737	Homo sapiens unknown	344	67.416
6956	AF076607	Mus musculus prediabetic NOD sera-reactive autoantigen	3374	94.727
6957	AJ010100	Homo sapiens NKp44RG2	191	27.632
6958	AJ011736	Homo sapiens growth factor receptor binding protein (GRBLG)	701	82.812
6959	AF022985	Caenorhabditis elegans No definition line found	239	24.609
6960	AL022018	Unknown /prediction=(method:"genscan", version:"1.0", score:"133.82"); /prediction=(method:	808	38.623
6961	AC007067	Arabidopsis thaliana T10024.21	577	29.653
6962	AJ006692	Homo sapiens ultra high sulfur keratin	1011	66.162
6963	U23037	Oryctolagus cuniculus eIF-2Bepsilon	4335	90.390
6964	U05313	Trypanosoma brucei CR3	73	29.412
6965	Y08250	Homo sapiens immunoglobulin kappa light chain	100	39.062
6966	AF061812	Homo sapiens keratin 16	2994	98.943
6967	AF151899	Homo sapiens CGI-141 protein	535	56.835
6968	AF057489	Mycobacterium thermoresistibile RNA polymerase	129	30.476

		beta		
6969	AF005654	Homo sapiens actin-binding double-zinc-finger protein	611	31.570
6970	Y07604	Homo sapiens nucleoside-diphosphate kinase	1063	89.730
6971	U01849	Trypanosoma brucei ORF2	165	30.435
6972	X02585	Xenopus laevis unidentified open reading frame 2	241	58.462
6973	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006), AA823760 (NID:g2893628), AA215791 (NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)	3418	98.450
6974	AB029034	Homo sapiens KIAA1111 protein	7038	99.060
6975	AJ009761	Homo sapiens putative dimethyladenosine transferase	252	76.923
6976	L10326	Rattus norvegicus GTP-binding protein alpha-s subunit	281	93.182
6977	X66403	Homo sapiens acetylcholine receptor epsilon subunit CHRNE	2897	78.069
6978	U63332	Homo sapiens super cysteine rich protein; SCRP	288	67.442
6979	X02585	Xenopus laevis unidentified open reading frame 2	203	32.192
6980	AF108138	Homo sapiens DNA helicase homolog	2348	95.968
6981	M26460	Homo sapiens retinoblastoma 1	145	37.879
6982	U58658	Homo sapiens unknown	248	60.938
6983	AF151800	Homo sapiens CGI-41 protein	317	33.607
6984	AF086709	Homo sapiens NAG-7 protein	653	98.936
6985	AF151866	Homo sapiens CGI-108 protein	1276	99.487
6986	X61045	Hydra sp. mini-collagen	165	70.833
6987	AL022117	Schizosaccharomyces pombe hypothetical protein	422	39.535
6988	AF166262	Arabidopsis thaliana HAL3A protein	611	49.490
6989	M61745	Bos taurus phosphatidylinositol 3-kinase	4634	96.409
6990	AF119121	Homo sapiens putative RNA binding protein	3749	99.480
6991	AL035523	Arabidopsis thaliana hypothetical protein	216	21.782
6992	AF123880	multiple sclerosis associated retrovirus element unknown protein U5/1	45	50.000
6993	X98709	Homo sapiens COL1A1 and PDGFB fusion transcript	119	37.143
6994	X13354	Homo sapiens T-cell receptor gamma-chain	485	94.937
6995	X84194	Homo sapiens acylphosphatase	201	64.151
6996	Z93785	Unknown predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain)	500	31.492
6997	AF160909	Drosophila melanogaster BcDNA.LD03471	1277	53.959
6998	AL035700	Homo sapiens dJ75K24.1 (novel protein similar to SH3BGR (SH3 domain binding glutamic acid-rich protein) and SH3BGRL)	202	41.053
6999	M15530	Homo sapiens B-cell growth factor	157	54.545
7000	AF067219	Caenorhabditis elegans No definition line found	82	36.207
7001	AC005587	Homo sapiens similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	1450	71.382
7002	AB011154	Homo sapiens KIAA0582 protein	373	87.879
7003	X63797	Gallus gallus decorin	342	32.547
7004	AF064597	Homo sapiens LINE-1 like protein	157	49.153

7005	AB002354	Homo sapiens KIAA0356	6204	98.920
7006	X67703	Drosophila melanogaster Mst84Db	88	33.871
7007	A61971	unidentified MCSP	1516 7	99.738
7008	AC004450	Arabidopsis thaliana hypothetical protein	262	27.018
7009	X68600	Hordeum vulgare pZE40	161	35.185
7010	Z67873	Pisum sativum proline- and leucine-rich protein	127	43.333
7011	V00662	Homo sapiens ATPase 6	1301	94.690
7012	Y11709	Homo sapiens collagen type XIV	723	89.167
7013	U92819	Homo sapiens unnamed HERV-H protein	313	53.982
7014	AF003999	Mus musculus GS15	468	83.146
7015	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	99	39.130
7016	AB011542	Homo sapiens MEGF9	2648	99.200
7017	M22332	Homo sapiens unknown protein	292	53.488
7018	AB012933	Rattus norvegicus acyl-CoA synthetase 5	3914	81.113
7019	AF026198	Fugu rubripes putative protein 2	677	62.195
7020	AJ242724	Homo sapiens putative mitogen-activated protein kinase kinase kinase	1683	82.524
7021	AL117567	Homo sapiens hypothetical protein	2042	99.385
7022	U18237	Homo sapiens ATP-binding cassette protein	470	98.701
7023	AL021366	Homo sapiens cICK0721Q.3 (Kinesin related protein)	4347	99.110
7024	D00173	Homo sapiens cytochrome P-450	3275	100.000
7025	X68061	Mus musculus HCNGP	1902	95.130
7026	AF035940	Homo sapiens similar to mago nashi	968	100.000
7027	AC005783	Homo sapiens R33083 1	2526	99.467
7028	AB014599	Homo sapiens KIAA0699 protein	5341	100.000
7029	AL050069	Homo sapiens hypothetical protein	1751	98.496
7030	AF132963	Homo sapiens CGI-29 protein	1681	99.174
7031	AF134983	Mus musculus energy-dependent regulator of proteolysis	3936	95.110
7032	AF100753	Homo sapiens ancient ubiquitous 46 kDa protein AUP1	2748	100.000
7033	AB015982	Homo sapiens serine/threonine kinase	6054	100.000
7034	M64229	Homo sapiens type I collagen	181	96.429
7035	Z81037	Caenorhabditis elegans predicted using Genefinder; Weak similarity in N-terminus to UNC-42 (WP:F58E6.1); cDNA EST EMBL:Z14323 comes from this gene	308	29.834
7036	M35522	Canis familiaris GTP-binding protein (rab7)	449	49.624
7037	U40952	Caenorhabditis elegans C03B1.10 gene product	200	65.000
7038	AJ131395	Mus musculus collagen type XIV	128	34.211
7039	AB023210	Homo sapiens KIAA0993 protein	2577	100.000
7040	M64983	Homo sapiens fibrinogen beta chain	3373	99.793
7041	D88010	Homo sapiens ribosomal protein S13	978	100.000
7042	L25314	Drosophila melanogaster actin-related protein	1269	47.328
7043	M83104	Bos taurus cytochrome b-5 reductase	1278	64.260
7044	AC005614	Homo sapiens F23269 2	4179	96.546
7045	U90549	Homo sapiens non-histone chromosomal protein	601	100.000
7046	AB018288	Homo sapiens KIAA0745 protein	5822	98.472
7047	AF132960	Homo sapiens CGI-26 protein	2162	99.107
7048	S42658	Homo sapiens S3 ribosomal protein	1589	100.000
7049	U09813	Homo sapiens mitochondrial ATP synthase	896	100.000

		subunit 9 precursor		
7050	X12517	Homo sapiens C protein (AA 1-159)	1226	100.000
7051	AL079277	Homo sapiens hypothetical protein, similar to (U32865) linotte protein	1776	100.000
7052	AF006087	Homo sapiens p20-Arc	1059	100.000
7053	AF125101	Homo sapiens HSPC040 protein	744	100.000
7054	X52425	Homo sapiens interleukin 4 receptor	5823	99.758
7055	AF067730	Homo sapiens TLS-associated protein TASR-2	815	55.597
7056	X60489	Homo sapiens elongation factor-1-beta	1483	100.000
7057	AF186264	Homo sapiens brain specific membrane-anchored protein BSMAP	2360	100.000
7058	AB007876	Homo sapiens KIAA0416	3504	100.000
7059	X54938	Homo sapiens inositol 1,4,5-triphosphate 3-kinase	3126	100.000
7060	U27831	Homo sapiens striatum-enriched phosphatase	3656	98.324
7061	AF001533	Mus musculus mitogen-induced	2474	97.911
7062	D16181	Homo sapiens peripheral myelin protein 2 (PMP2)	838	100.000
7063	Z50053	Homo sapiens alpha2i-subunit of soluble guanylyl cyclase	5086	100.000
7064	L26288	Rattus norvegicus CaM-like protein kinase	1803	82.663
7065	Y15060	Homo sapiens GalT2 protein	2925	100.000
7066	AB023223	Homo sapiens KIAA1006 protein	8196	99.918
7067	AL032684	Schizosaccharomyces pombe hypothetical protein	392	37.126
7068	X76199	Bos taurus synaptobrevin	747	99.138
7069	AJ005585	Homo sapiens unnamed protein product	1795	99.617
7070	AF077045	Homo sapiens ATP synthase epsilon chain	321	100.000
7071	AL050028	Homo sapiens hypothetical protein	901	99.275
7072	X78444	Rattus norvegicus ribosomal protein L22	565	69.291
7073	U27838	Mus musculus glycosyl-phosphatidyl-inositol-anchored protein homolog	4246	96.189
7074	U25034	Homo sapiens neuronatin beta	205	72.340
7075	X03484	Homo sapiens raf protein (aa 1-648)	4370	100.000
7076	AC004539	Homo sapiens unknown function; similar to Y09105 (PID:g1666171)	962	99.231
7077	X60188	Homo sapiens protein serine/threonine kinase	2534	99.736
7078	AF132961	Homo sapiens CGI-27 protein	2018	100.000
7079	AJ001258	Homo sapiens NIPSNAP1 protein	1967	99.648
7080	AL031266	Caenorhabditis elegans VM106R.1	290	42.593
7081	AF151898	Homo sapiens CGI-140 protein	754	100.000
7082	AF044953	Homo sapiens NADH:ubiquinone oxidoreductase PGIV subunit	1240	100.000
7083	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	1219	100.000
7084	L00354	Homo sapiens cholecystokinin	775	100.000
7085	AC004381	Homo sapiens Unknown gene product	1570	100.000
7086	Y13276	Homo sapiens Tailless protein	2557	100.000
7087	AF159055	Homo sapiens leucine zipper-like protein	139	81.481
7088	AJ010793	Triturus carnifex Newt Ovary Ribozyme-Associated protein	1446	60.050
7089	AF181685	Mus musculus membrane protein TMS-2	2988	95.806
7090	S65091	Rattus sp. cyclic AMP-regulated phosphoprotein, ARPP-21	443	82.759
7091	U41315	Homo sapiens ZNF127-Xp	2663	82.099
7092	AF067937	Caenorhabditis elegans contains similarity to	417	40.698

		E. coli cation transport protein (GB:L28709)		
7093	Z12830	Homo sapiens SSR alpha subunit	1856	99.650
7094	AL049548	Homo sapiens dJ398G3.1 (ortholog of rat CPG2)	4426	99.856
7095	X55954	Homo sapiens HL23 ribosomal protein	915	100.000
7096	AL023653	Homo sapiens dJ753P9.2 (novel protein)	2517	100.000
7097	U01317	Homo sapiens delta-globin	987	100.000
7098	A18921	synthetic construct tissue-specific secretory protein	1025	100.000
7099	Z28407	Homo sapiens ribosomal protein L8	1732	100.000
7100	X57346	Homo sapiens HS1	1568	100.000
7101	AF140598	Homo sapiens ring-box protein 1	797	100.000
7102	AC006389	Homo sapiens similar to Schizosaccharomyces pombe splicing factor; similar to PID:3395591	593	100.000
7103	X04327	Homo sapiens 2,3 biphosphoglycerated mutase (AA 1 - 259)	1747	100.000
7104	U00043	Caenorhabditis elegans similar to D. melanogaster trithorax protein	519	40.359
7105	Z22968	Homo sapiens M130 antigen	8047	100.000
7106	AF189817	Mus musculus evectin-2	1417	87.391
7107	X60367	Mus musculus cellular retinol binding protein I	553	55.970
7108	Z93388	Unknown predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452	911	61.966
7109	AL050225	Homo sapiens hypothetical protein	1788	98.885
7110	AJ011007	Homo sapiens 6.2 kd protein	365	98.182
7111	AC002343	Arabidopsis thaliana Ser/Thr protein kinase isolog	511	33.431
7112	X14329	Homo sapiens carboxypeptidase N precursor (AA -20 to 438)	3148	99.782
7113	A23031	Homo sapiens trophoblast membrane expressed protein	2903	99.766
7114	Y17392	Homo sapiens prefoldin subunit 1	669	98.198
7115	X75500	Homo sapiens microsomal triglyceride transfer protein, 97kDa subunit	5680	100.000
7116	AF111713	Homo sapiens junctional adhesion molecule	1950	100.000
7117	X08055	Homo sapiens preglycophorin B	537	100.000
7118	AL050254	Homo sapiens hypothetical protein	3548	99.808
7119	Z46522	Drosophila subobscura bcn92	310	55.422
7120	Z48334	Caenorhabditis elegans F10B5.8	2274	68.113
7121	AL021546	Homo sapiens Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	762	100.000
7122	X13923	Homo sapiens cytochrome c oxidase subunit VIb (AA 1-86)	424	67.059
7123	Y08915	Homo sapiens alpha 4 protein	2215	100.000
7124	AL050101	Homo sapiens hypothetical protein	3605	100.000
7125	X04494	Homo sapiens precursor polypeptide	2437	100.000
7126	L02956	Xenopus laevis ribonucleoprotein	2120	85.286
7127	AF082526	Mus musculus MEK binding partner 1	759	97.581
7128	AJ223352	Homo sapiens Histone H2B	787	100.000
7129	AF100761	Homo sapiens PTD017	1820	100.000
7130	L31783	Mus musculus uridine kinase	1619	92.692
7131	AL117608	Homo sapiens hypothetical protein	541	92.473
7132	AF084259	Mus musculus bromodomain-containing protein BP75	3884	88.000

7133	Z81108	Unknown similar to Ubiquitin-conjugating enzymes; cDNA EST EMBL:T01737 comes from this gene; cDNA E	567	53.459
7134	AF134772	Mus musculus LIM protein	2134	99.286
7135	AF132952	Homo sapiens CGI-18 protein	2008	88.483
7136	X63692	Homo sapiens DNA (cytosine-5)-methyltransferase	11017	100.000
7137	X63527	Homo sapiens ribosomal protein L19	1259	100.000
7138	U39402	Homo sapiens ORF; Method: conceptual translation supplied by author.	2084	100.000
7139	AF083110	Homo sapiens sirtuin type 5	2134	100.000
7140	AF151884	Homo sapiens CGI-126 protein	1165	100.000
7141	AF092134	Homo sapiens PTD013	1548	99.588
7142	AL117629	Homo sapiens hypothetical protein	796	73.545
7143	M37679	Mus musculus Ig heavy chain precursor	133	72.727
7144	Z49068	Caenorhabditis elegans mitochondrial carrier protein	674	41.176
7145	Z94160	Homo sapiens dJ63G5.1 (human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein)	2319	100.000
7146	X04085	Homo sapiens catalase	3642	100.000
7147	Z28339	Homo sapiens delta 4-3-oxosteroid 5 beta-reductase	2207	100.000
7148	X55656	Homo sapiens gamma-G globin	1047	100.000
7149	AL050273	Homo sapiens hypothetical protein	677	100.000
7150	M61832	Homo sapiens S-adenosylhomocysteine hydrolase	2890	100.000
7151	U40952	Caenorhabditis elegans C03B1.10 gene product	164	94.737
7152	U01317	Homo sapiens beta-globin	991	100.000
7153	U31449	Homo sapiens tetraspan membrane protein	1471	100.000
7154	Y14769	Gallus gallus paralemmin	474	36.525
7155	L42374	Homo sapiens protein phosphatase 2A B56-beta	3317	100.000
7156	AF118108	Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1	2059	98.758
7157	AB003103	Homo sapiens 26S proteasome subunit p55	2902	100.000
7158	L05093	Homo sapiens ribosomal protein L18a	1222	100.000
7159	AF043254	Homo sapiens heat shock protein 75	4094	98.773
7160	D13630	Homo sapiens KIAA0005	2051	72.596
7161	AF035262	Homo sapiens BAF57	2702	100.000
7162	U28413	Homo sapiens CSA protein	2691	100.000
7163	Z69904	Caenorhabditis elegans cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene; cDNA EST yk537a3.3 comes from this gene; cDNA EST yk621h11.3 comes from this gene	400	29.694
7164	K03020	Homo sapiens phenylalanine hydroxylase	1452	98.636
7165	X00129	Homo sapiens precursor RBP	1339	97.512
7166	D78134	Homo sapiens CIRP	1159	100.000
7167	AF076191	Trichosurus vulpecula gamma-actin	2491	100.000
7168	X00910	Homo sapiens IGF-II precursor	1245	100.000
7169	Y07593	Homo sapiens coxsackie and adenovirus receptor protein	408	29.167
7170	X61118	Homo sapiens TTG-2a/RBTN-2a	1142	100.000
7171	Y12860	Homo sapiens peroxisomal integral membrane protein	1967	100.000
7172	M10014	Homo sapiens fibrinogen gamma chain	3008	99.771

7173	Y11435	Homo sapiens b4 integrin interactor	1593	100.000
7174	AF070666	Homo sapiens Kruppel-associated box protein	596	98.936
7175	AJ131057	Homo sapiens immunoglobulin gamma chain (BAB3-L)	215	96.875
7176	AF077207	Homo sapiens HSPC021	3772	100.000
7177	AF126531	Homo sapiens putative DNA-directed RNA polymerase III C11 subunit	805	100.000
7178	L23767	Homo sapiens a2,3 sialyltransferase	2182	100.000
7179	V00488	Homo sapiens alpha globin	925	100.000
7180	X04429	Homo sapiens precursor polypeptide	2633	99.751
7181	D17793	Homo sapiens KIAA0119	2172	100.000
7182	M26759	Rattus norvegicus thymosin beta-4 precursor	179	55.357
7183	AF072832	Homo sapiens UbCH 7-binding protein	4001	99.820
7184	M62831	Homo sapiens ETR101	1474	99.103
7185	M63109	Leishmania major glycoprotein 96-92	187	27.128
7186	D28915	Homo sapiens hepatitis C-associated microtubular aggregate protein p44	2923	99.550
7187	M92383	Homo sapiens thymosin beta-10	313	100.000
7188	AL031673	Homo sapiens dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	5240	99.865
7189	Y11652	Homo sapiens phosphate cyclase	229	84.091
7190	AF155095	Homo sapiens NY-REN-2 antigen	3897	100.000
7191	AB020648	Homo sapiens KIAA0841 protein	4253	100.000
7192	AF151880	Homo sapiens CGI-122 protein	1224	100.000
7193	A06977	Homo sapiens albumin	4118	100.000
7194	AF052432	Homo sapiens katanin p80 subunit	4366	99.542
7195	U64028	Homo sapiens NADPH:ubiquinone oxidoreductase subunit B13	772	100.000
7196	X79805	Homo sapiens PC4, p15	823	100.000
7197	U75467	Drosophila melanogaster Atu	1197	36.667
7198	X17042	Homo sapiens hematopoietic proteoglycan core protein (AA 1 - 158)	991	99.324
7199	X99209	Homo sapiens arginine methyltransferase	2976	100.000
7200	AJ007509	Homo sapiens E1B-55kDa-associated protein	5996	98.383
7201	AF132965	Homo sapiens CGI-31 protein	1978	100.000
7202	AF173868	Homo sapiens DNA binding protein p96PIF	3609	99.822
7203	AL031427	Homo sapiens dJ167A19.1 (novel protein)	2037	99.673
7204	AF054174	Homo sapiens histone macroH2A1.2	1631	68.464
7205	AJ133769	Homo sapiens nuclear transport receptor	6151	100.000
7206	AF151832	Homo sapiens CGI-74 protein	2573	98.992
7207	X52142	Homo sapiens CTP synthetase (AA 1-591)	3979	99.662
7208	AL021331	Homo sapiens dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1365	99.524
7209	X14608	Homo sapiens propionyl-CoA carboxylase	4559	100.000
7210	AL110249	Homo sapiens hypothetical protein	5725	99.769
7211	X95648	Homo sapiens alfa subunit	1931	100.000
7212	X64177	Homo sapiens metallothionein	513	100.000
7213	AB028942	Homo sapiens KIAA1019 protein	1198	99.839
7214	X56932	Homo sapiens 23 kD highly basic protein	1329	100.000
7215	AF134404	Homo sapiens delta-6 fatty acid desaturase	3152	100.000
7216	AC004982	Homo sapiens similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461)	2616	100.000
7217	AL049548	Homo sapiens dJ398G3.2 (novel protein)	987	100.000

7218	AF114263	Homo sapiens unknown	1295	100.000
7219	Z68220	Homo sapiens Similarity to Human ADP/ATP carrier protein (SW:ADT1_HUMAN); cDNA EST EMBL:D71893 comes fro	566	43.519
7220	AJ002308	Homo sapiens synaptogyrin 2	1524	100.000
7221	Z49130	Caenorhabditis elegans cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene; cDNA EST yk615b1.3 comes from this gene; cDNA EST yk626c2.3 comes from this gene	169	26.364
7222	AL021937	Homo sapiens dJ149A16.6 (novel protein, human ortholog of worm F16A11.2 and bacterial and archea-bacterial predicted proteins)	3381	100.000
7223	Y16241	Homo sapiens nebullette	6605	100.000
7224	X97544	Homo sapiens preprotein translocase	1169	100.000
7225	X15949	Homo sapiens interferon regulatory factor-2 (AA 1-349)	2323	99.427
7226	AF095927	Rattus norvegicus protein phosphatase 2C	2475	95.153
7227	AF151895	Homo sapiens CGI-137 protein	1164	100.000
7228	AC005757	Homo sapiens R32611.2	1065	100.000
7229	L41254	Rattus norvegicus transmembrane protein	336	62.637
7230	AF106583	Caenorhabditis elegans contains similarity to BC-2 protein (GB:AF042384)	727	56.923
7231	AF106580	Caenorhabditis elegans No definition line found	382	50.442
7232	X13227	Homo sapiens D-amino acid oxidase (AA 1 - 347)	2389	99.135
7233	Z84395	Mycobacterium tuberculosis hypothetical protein Rv0712	723	39.933
7234	Z66511	Unknown similar to ribokinase; cDNA EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 come	657	43.651
7235	X93498	Homo sapiens 21-Glutamic Acid-Rich Protein	1596	99.582
7236	Y11651	Homo sapiens phosphate cyclase	2397	100.000
7237	X79417	Sus scrofa 40S ribosomal protein S12	880	100.000
7238	AL078579	Arabidopsis thaliana putative acyl-CoA binding protein	531	38.077
7239	AF095737	Homo sapiens unknown	366	68.085
7240	AB023203	Homo sapiens KIAA0986 protein	9554	100.000
7241	AL117463	Homo sapiens hypothetical protein	1293	100.000
7242	U34350	Gallus gallus cThy28kD	1025	66.525
7243	D78592	Rattus norvegicus glucose-6-phosphatase catalytic subunit	767	37.537
7244	AF073298	Homo sapiens small EDRK-rich factor 2	378	100.000
7245	U53155	Caenorhabditis elegans No definition line found	893	39.071
7246	X90858	Homo sapiens uridine phosphorylase	1878	99.677
7247	AB014589	Homo sapiens KIAA0689 protein	3783	100.000
7248	X72755	Homo sapiens Humig	806	100.000
7249	Z74167	Saccharomyces cerevisiae ORF YDL119c	433	32.107
7250	AL117662	Homo sapiens hypothetical protein	1393	99.517
7251	AC005058	Homo sapiens similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519)	2532	100.000
7252	AB029020	Homo sapiens KIAA1097 protein	6718	100.000
7253	X01410	Homo sapiens T-cell receptor beta chain	1311	99.492

7254	AB014540	Homo sapiens KIAA0640 protein	3964	100.000
7255	AF020313	Mus musculus proline-rich protein 48	1266	84.052
7256	U79260	Homo sapiens unknown	256	61.765
7257	X66171	Homo sapiens CMRF-35 antigen	1539	99.554
7258	Z14093	Homo sapiens branched chain decarboxylase alpha subunit	3018	100.000
7259	AB011123	Homo sapiens KIAA0551 protein	8838	99.925
7260	Y10936	Homo sapiens hypothetical protein	1441	97.525
7261	AB028946	Homo sapiens KIAA1023 protein	3583	99.819
7262	U72245	Homo sapiens phospholemman chloride channel	252	51.220
7263	X53280	Homo sapiens general transcription factor	1334	100.000
7264	X72964	Homo sapiens caltractin	1087	100.000
7265	AL080178	Homo sapiens hypothetical protein	739	100.000
7266	AB007863	Homo sapiens KIAA0403	2738	100.000
7267	Z99106	Bacillus subtilis similar to hypothetical proteins	464	32.540
7268	U67536	Methanococcus jannaschii conserved hypothetical protein	268	26.609
7269	U21855	Mus musculus mCAF1 protein	1914	99.649
7270	Z75331	Homo sapiens nuclear protein SA-2	7581	99.656
7271	Z75134	Canis familiaris rod transducin	2322	100.000
7272	AB014601	Homo sapiens KIAA0701 protein	4008	99.524
7273	AB007889	Homo sapiens KIAA0429	2432	100.000
7274	Y09615	Homo sapiens mTERF	2584	100.000
7275	AL117635	Homo sapiens hypothetical protein	1169	99.454
7276	Z14136	Homo sapiens spermidine/spermine N1-acetyltransferase	242	57.627
7277	X16663	Homo sapiens haematopoietic lineage cell protein (AA 1-486)	3310	100.000
7278	X70476	Homo sapiens subunit of coatomer complex	6038	100.000
7279	M55531	Homo sapiens GLUT5 protein	1457	45.895
7280	AF078849	Homo sapiens dynein light chain-A	3463	99.426
7281	AF099935	Homo sapiens MDC-3.13 isoform 2	672	55.000
7282	X81804	Bos taurus ozf	2147	95.223
7283	AL117573	Homo sapiens hypothetical protein	3714	99.824
7284	X95648	Homo sapiens alfa subunit	1931	100.000
7285	AF083930	Homo sapiens ES18	1411	98.165
7286	AF151839	Homo sapiens CGI-81 protein	1890	98.940
7287	U59240	Rattus norvegicus N-tropomodulin	1748	77.557
7288	Z49213	Saccharomyces cerevisiae Imp2p	378	43.333
7289	AL080177	Homo sapiens hypothetical protein	785	100.000
7290	X76534	Homo sapiens NMB	3859	99.821
7291	Z68493	Caenorhabditis elegans predicted using Genefinder	466	41.379
7292	AF125101	Homo sapiens HSPC040 protein	744	100.000
7293	Z99281	Unknown similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMB	1100	84.865
7294	U29488	Caenorhabditis elegans No definition line found	706	52.155
7295	AF103731	Homo sapiens putative glycolipid transfer protein	2466	98.210
7296	AF150100	Homo sapiens small zinc finger-like protein	597	100.000
7297	AL050277	Homo sapiens hypothetical protein	655	100.000
7298	AJ238098	Homo sapiens Lsm6 protein	521	100.000

7299	AF023611	Homo sapiens Dimlp homolog	263	39.583
7300	AB011115	Homo sapiens KIAA0543 protein	7541	100.000
7301	AE001724	Thermotoga maritima conserved hypothetical protein	479	36.032
7302	X76013	Homo sapiens glutaminyl-tRNA synthetase	5223	99.871
7303	L34041	Homo sapiens L-glycerol-3-phosphate:NAD oxidoreductase	2316	99.713
7304	AP000364	Oryza sativa Similar to sequence of BAC F7G19 from Arabidopsis thaliana. (AC000106)	194	41.667
7305	AF073839	Rattus norvegicus bithoraxoid-like protein	562	93.750
7306	U51999	Caenorhabditis elegans C43H6.7 gene product	411	27.645
7307	AF102850	Homo sapiens dolichyl-phosphate beta-glucosyltransferase	2142	100.000
7308	AL031228	Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	4111	100.000
7309	AF160934	Drosophila melanogaster BcDNA.LD14189	1140	61.508
7310	AL117629	Homo sapiens hypothetical protein	796	73.545
7311	AF151826	Homo sapiens CGI-68 protein	2240	99.401
7312	AL110295	Schizosaccharomyces pombe conserved hypothetical protein	1455	36.475
7313	AF016441	Caenorhabditis elegans No definition line found	851	41.892
7314	X58141	Homo sapiens erythrocyte alpha adducin	4876	99.457
7315	AF056490	Homo sapiens cAMP-specific phosphodiesterase 8A	4713	99.719
7316	Z93382	Caenorhabditis elegans F45G2.9	545	41.935
7317	X91817	Homo sapiens transketolase	3532	96.948
7318	Z69727	Schizosaccharomyces pombe putative peroxisomal membrane protein	248	30.769
7319	AL117576	Homo sapiens hypothetical protein	2984	99.566
7320	AJ237946	Homo sapiens DEAD Box Protein 5	3108	100.000
7321	X69480	Saccharomyces cerevisiae uORF1	665	53.552
7322	AF050641	Homo sapiens NADH-ubiquinone oxidoreductase 39kDa subunit	2527	100.000
7323	U47924	Homo sapiens C10	809	100.000
7324	AF054986	Homo sapiens putative transmembrane GTPase	2387	100.000
7325	AF146018	Homo sapiens hydroxypyruvate reductase	1100	99.401
7326	Z97184	Homo sapiens HKE2	794	100.000
7327	AF077044	Homo sapiens RNA polymerase I 16 kDa subunit	874	100.000
7328	AJ131389	Homo sapiens PEX3 protein	2410	100.000
7329	L54057	Homo sapiens deduced protein product shows significant homology to coactosin from Dictyostelium discoideum	922	100.000
7330	X73478	Homo sapiens phosphotyrosyl phosphatase activator	2196	99.690
7331	U51032	Saccharomyces cerevisiae Ydr341cp	1365	41.556
7332	AF026198	Fugu rubripes putative protein 2	855	66.146
7333	M83104	Bos taurus cytochrome b-5 reductase	1198	56.757
7334	AJ245587	Homo sapiens Kruppel-type zinc finger	2460	100.000
7335	D87453	Homo sapiens KIAA0264	2704	100.000
7336	AL031666	Homo sapiens dJ569M23.1 (similar to BS69 protein)	2168	100.000
7337	Z22820	Canis familiaris Rab22a protein	1272	98.454
7338	AF151841	Homo sapiens CGI-83 protein	1915	100.000

7339	AF019082	Borrelia burgdorferi virulent strain associated lipoprotein	209	22.458
7340	AF112968	Homo sapiens ornithine transporter	1991	100.000
7341	AF141882	Homo sapiens APMCF1	315	100.000
7342	X58022	Homo sapiens corticotropin releasing factor-binding protein	2195	99.068
7343	AF118023	Homo sapiens SH3 domain-binding protein SNP70	4484	99.844
7344	L04733	Homo sapiens kinesin light chain	2521	70.107
7345	U47618	Drosophila melanogaster ovary2	195	27.152
7346	AF143676	Homo sapiens multispinning nuclear envelope membrane protein nurim	1747	100.000
7347	AF001160	Homo sapiens G-protein gamma subunit	448	100.000
7348	U62940	Rattus norvegicus mt-GrpE#1 precursor	1267	88.479
7349	X14046	Homo sapiens CD37 (AA 1-244)	1891	99.644
7350	X78606	Rattus norvegicus ras-homologous GTPase rab28	1417	96.380
7351	AB002348	Homo sapiens KIAA0350	6010	99.891
7352	M32486	Mus musculus 19.5 protein	1300	64.364
7353	X72879	Homo sapiens ORF	149	88.462
7354	AF085481	Homo sapiens serum deprivation response	2664	100.000
7355	AB020681	Homo sapiens KIAA0874 protein	3936	100.000
7356	AJ242015	Homo sapiens eMDC II protein	5433	100.000
7357	AF026816	Homo sapiens putative oncogene protein	1101	100.000
7358	AF015913	Homo sapiens SkblHs	4349	99.686
7359	L34734	Homo sapiens T-cell receptor beta	2042	96.835
7360	AF117065	Homo sapiens male-specific lethal-3 homolog 1	3240	99.590
7361	Y13736	Homo sapiens Protein Enriched in Diabetes	829	100.000
7362	AJ223353	Homo sapiens Histone H2B	787	100.000
7363	M55542	Homo sapiens guanylate binding protein isoform I	3356	87.372
7364	AB014550	Homo sapiens KIAA0650 protein	5623	100.000
7365	U41857	Xenopus laevis WD-40 motifs; up-regulated by thyroid hormone in tadpoles	1285	51.105
7366	Y10319	Homo sapiens carnitine carrier	2052	100.000
7367	U66059	Homo sapiens V segment translation product	794	100.000
7368	A68104	unidentified unnamed protein product	130	28.455
7369	U71598	Homo sapiens zinc finger protein zfp2	1096	100.000
7370	X68505	Homo sapiens myocyte-specific enhancer factor 2 (MEF2)	3397	100.000
7371	AJ242975	Homo sapiens p38 protein	2583	100.000
7372	AL034488	Caenorhabditis elegans predicted using Genefinder	925	35.118
7373	AF044671	Homo sapiens MM46	698	87.069
7374	AF171099	Xenopus laevis Mi-2 histone deacetylase complex protein 66	871	48.396
7375	AB011182	Homo sapiens KIAA0610 protein	4424	100.000
7376	X83218	Homo sapiens ATP synthase, oligomycin sensitivity conferring protein	1310	100.000
7377	U41558	Caenorhabditis elegans No definition line found	537	31.474
7378	AF039692	Homo sapiens antigen NY-CO-10	2397	99.462
7379	X56389	Canis familiaris rab4b	1395	100.000
7380	X06820	Homo sapiens rhoB	1324	100.000
7381	AJ243721	Homo sapiens dTDP-4-keto-6-deoxy-D-glucose 4-reductase	2124	99.682
7382	X77953	Rattus norvegicus ribosomal protein S15a	860	100.000

7383	Z46676	Caenorhabditis elegans cDNA EST yk484g1.3 comes from this gene; cDNA EST yk484g1.5 comes from this gene	401	40.690
7384	J01163	Oxytricha fallax actin	381	27.083
7385	AF156098	Homo sapiens RNA binding motif protein 7	1820	100.000
7386	AF157028	Homo sapiens protein phosphatase methylesterase-1	2599	100.000
7387	L24804	Homo sapiens p23	423	46.094
7388	AF151876	Homo sapiens CGI-118 protein	1336	100.000
7389	Z97210	Schizosaccharomyces pombe hypothetical protein	201	40.196
7390	X95592	Homo sapiens C1D protein	901	100.000
7391	AE000984	Archaeoglobus fulgidus dinitrogenase reductase activating glycohydrolase (draG)	294	26.608
7392	Z98979	Schizosaccharomyces pombe hypothetical protein	348	40.157
7393	D50807	Bos taurus synaphin	194	33.088
7394	X56667	Homo sapiens calretinin	1793	99.631
7395	M23159	Cricetus cricetus DHFR-coamplified protein	194	28.761
7396	D64000	Synechocystis sp. hypothetical protein	220	33.803
7397	AB020684	Homo sapiens KIAA0877 protein	3836	99.310
7398	U22229	Felis catus ribosomal protein L41	170	100.000
7399	AJ010392	Rattus norvegicus Bdeight protein	1427	92.340
7400	AF093673	Cricetulus griseus layilin	2179	84.182
7401	X74801	Homo sapiens gamma subunit of CCT chaperonin	3492	99.632
7402	Z97630	Homo sapiens dJ466N1.2 (2-amino-3-ketobutyrate-CoA ligase mRNA, nuclear gene encoding mitochondrial protein)	2785	99.761
7403	AC002301	Homo sapiens Homolog of rat Zymogen granule membrane protein	270	37.594
7404	AF147717	Homo sapiens ubiquitin C-terminal hydrolase UCH37	2165	100.000
7405	AL096779	Homo sapiens hypothetical protein	1978	100.000
7406	AF069442	Arabidopsis thaliana putative WD-repeat protein	1130	42.721
7407	AF020262	Bos taurus general protein transport factor p16	776	100.000
7408	AF097439	Mus musculus brain expressed X-linked protein 2	648	72.868
7409	U97001	Caenorhabditis elegans similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (GB:X62722, NID:g5005)	767	51.969
7410	X71978	Mus musculus Fif	1923	95.904
7411	AL117526	Homo sapiens hypothetical protein	5576	99.883
7412	AC002550	Homo sapiens Unknown gene product	1104	99.379
7413	U81002	Homo sapiens TRAF4 associated factor 1	1710	99.267
7414	AF151900	Homo sapiens CGI-142 protein	1167	100.000
7415	AB011145	Homo sapiens KIAA0573 protein	3074	100.000
7416	AF059569	Homo sapiens actin binding protein MAYVEN	3881	99.658
7417	AL031765	Unknown /prediction=(method:""genefinder"", version:""084"", score:""31.96""); /prediction=(metho	473	34.348
7418	U80447	Caenorhabditis elegans similar to the beta transducin family	742	32.767
7419	AL080186	Homo sapiens hypothetical protein	1860	99.664
7420	AL049758	Homo sapiens dJ437M21.2 (novel putative GTP-	1415	100.000

		ase activating protein for Arf similar to worm F07F6.4)		
7421	AL023780	Schizosaccharomyces pombe zinc finger protein	359	31.606
7422	AJ224326	Homo sapiens ribulose-5-phosphate-epimerase	1179	100.000
7423	AB023191	Homo sapiens KIAA0974 protein	3780	100.000
7424	Z35663	Caenorhabditis elegans Weak similarity with non-histone chromosomal protein HMG-1 (human). Glutamate rich carboxyl terminus; cDNA EST EMBL:D74688 comes from this gene; cDNA EST EMBL:D71938 comes from this gene	211	27.184
7425	X16901	Homo sapiens 30kb subunit of RAB30 /74	1623	100.000
7426	D14696	Homo sapiens KIAA0108	703	44.395
7427	AB014581	Homo sapiens KIAA0681 protein	659	36.336
7428	AF000423	Rattus norvegicus synaptotagmin XI	2699	94.896
7429	U90313	Homo sapiens glutathione-S-transferase homolog	1044	64.069
7430	AB015345	Homo sapiens HRIHFB2216	3300	99.588
7431	L02241	Mus musculus protein kinase inhibitor	354	74.359
7432	AL021068	Homo sapiens dJ206D15.3	3310	99.607
7433	U40628	Rattus norvegicus unknown	181	50.000
7434	AC003028	Arabidopsis thaliana unknown protein	172	43.137
7435	X65724	Homo sapiens ORF2	1092	100.000
7436	Z97341	Arabidopsis thaliana hypothetical protein	292	36.424
7437	D88157	Ovis aries cytochrome b561	591	45.238
7438	AF133207	Homo sapiens protein kinase	1362	99.490
7439	AJ235271	Rickettsia prowazekii unknown	458	30.638
7440	AF094583	Homo sapiens putative HIV-1 infection related protein	627	98.925
7441	J04970	Homo sapiens carboxypeptidase M precursor	3050	100.000
7442	AC006978	Homo sapiens supported by human and rodent ESTs; match to AA454028 (NID:g2167697), similar to AA9255224 (NID:g4236415) and AA023712 (NID:g1487627)	1048	99.315
7443	AL021683	Homo sapiens unnamed protein product	1820	100.000
7444	A68112	unidentified unnamed protein product	175	28.926
7445	U41515	Homo sapiens Method: conceptual translation supplied by author	494	100.000
7446	X57351	Homo sapiens 1-8D	873	99.242
7447	AB018325	Homo sapiens KIAA0782 protein	7932	100.000
7448	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	1630	99.608
7449	X66901	Mus musculus En-2/lacZ fusion protein	307	90.196
7450	AF129756	Homo sapiens NG33	808	100.000
7451	J00911	Gallus gallus alpha-tropomyosin (partial)	164	96.296
7452	Z80220	Unknown Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene;	774	56.944
7453	X67325	Homo sapiens p27	318	67.500
7454	AL117530	Homo sapiens hypothetical protein	3104	99.554
7455	AF151857	Homo sapiens CGI-99 protein	1611	100.000
7456	AL035301	Homo sapiens hypothetical protein	275	100.000
7457	U19142	Homo sapiens GAGE-1 protein	327	51.351
7458	Z49858	Rattus norvegicus plasmolipin	435	45.062
7459	AL050147	Homo sapiens hypothetical protein	3647	100.000
7460	Z82096	Caenorhabditis elegans predicted using Genefinder; Similarity to E.coli guanosine-3',	419	56.410

		5'-bis(diphosphate)-pyrophosphohydrolase (SW:P17580)		
7461	AF143956	Mus musculus coronin-2	3101	94.262
7462	AB007836	Homo sapiens Hic-5	3323	100.000
7463	AC008263	Arabidopsis thaliana Contains similarity to gb Z95637 acyl-CoA:1-acylglycerol-3-phosphate acyltransferase from Brassica napus.	495	28.981
7464	AF117210	Homo sapiens host cell factor 2	5379	100.000
7465	J03801	Homo sapiens lysozyme precursor (EC 3.2.1.17)	1033	100.000
7466	AF149720	Danio rerio unknown	165	41.379
7467	AL022724	Homo sapiens dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1716	100.000
7468	AF151844	Homo sapiens CGI-86 protein	2246	100.000
7469	X77631	Cricetulus griseus intermediate filament associated protein	100	37.500
7470	X78686	Homo sapiens ENA-78	741	100.000
7471	AL049610	Homo sapiens dJ1055C14.1 (transcription elongation factor A (SII)-like 1)	181	37.097
7472	AL008637	Homo sapiens NCF4	2221	100.000
7473	Z81108	Unknown similar to Ubiquitin-conjugating enzymes; cDNA EST EMBL:T01737 comes from this gene; cDNA E	567	53.459
7474	M10942	Homo sapiens human metallothionein-Ie	512	100.000
7475	AF077034	Homo sapiens HSPC010	611	100.000
7476	K01383	Homo sapiens MT1A	508	98.361
7477	X90999	Homo sapiens glyoxalase II	1757	100.000
7478	M74161	Homo sapiens inositol polyphosphate 5-phosphatase	6355	99.894
7479	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	536	27.381
7480	AF181685	Mus musculus membrane protein TMS-2	2988	95.806
7481	AF145615	Drosophila melanogaster BcDNA.GH03377	1057	46.133
7482	U09410	Homo sapiens zinc finger protein ZNF131	3134	99.366
7483	AF047431	Homo sapiens AAPT1-like protein	1580	98.340
7484	AF176012	Homo sapiens J domain containing protein 1 isoform a	1335	100.000
7485	X94917	Drosophila melanogaster head-elevated expression in 0.9 kb	194	33.000
7486	U54807	Rattus norvegicus GTP-binding protein	1483	97.357
7487	AF058807	Bos taurus GTP-binding protein rah	1248	85.106
7488	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase	1578	82.500
7489	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	108	34.375
7490	AF072864	Homo sapiens peroxisomal membrane protein PMP 24	1406	99.528
7491	AL050269	Homo sapiens hypothetical protein	1339	99.034
7492	AF078850	Homo sapiens steroid dehydrogenase homolog	739	40.065
7493	Z97204	Schizosaccharomyces pombe hypothetical protein	410	38.021
7494	U23484	Caenorhabditis elegans No definition line found	627	52.660
7495	X63679	Homo sapiens TRAM protein	2432	100.000
7496	X57352	Homo sapiens 1-8U	883	98.496
7497	Z81097	Caenorhabditis elegans cDNA EST EMBL:D69071	190	31.858

		comes from this gene		
7498	AL035419	Homo sapiens dJ1100H13.1 (putative novel protein)	1440	100.000
7499	Z37166	Homo sapiens nuclear RNA helicase (DEAD family)	2817	100.000
7500	Z66515	Unknown cDNA EST EMBL:C07816 comes from this gene; cDNA EST EMBL:C09328 comes from this gene; cDNA	411	35.135
7501	AF131220	Homo sapiens HEMK homolog	2311	99.704
7502	Z49128	Unknown similar to cAMP-dependant protein kinase; cDNA EST EMBL:T00719 comes from this gene; cDNA E	1098	44.759
7503	AJ223980	Homo sapiens BCL7C	1487	99.078
7504	X61381	Rattus rattus interferon-induced protein	238	43.023
7505	U16697	Torpedo marmorata 14 kDa transmembrane protein	113	32.692
7506	Z82214	Homo sapiens dJ526I14.3a (fragment of novel CUB and EGF-like domain protein)	1387	80.995
7507	AL008583	Homo sapiens dJ327J16.1 (human ortholog of mouse outer arm Dynein light chain 4)	716	100.000
7508	D38169	Homo sapiens inositol 1,4,5-trisphosphate 3-kinase isoenzyme	4207	99.834
7509	D90053	Sus scrofa destrin	1109	100.000
7510	AF016685	Caenorhabditis elegans similar to short chain-type dehydrogenases	776	42.073
7511	U23484	Caenorhabditis elegans No definition line found	517	33.133
7512	X52509	Homo sapiens tyrosine aminotransferase	3098	100.000
7513	X13923	Homo sapiens cytochrome c oxidase subunit VIb (AA 1-86)	206	52.941
7514	Z70208	Caenorhabditis elegans predicted using Genefinder; similar to Zinc finger, C3HC4 type (RING finger)	272	28.141
7515	AE000715	Aquifex aeolicus ribosomal protein L20	270	41.053
7516	AL031432	Homo sapiens dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	1476	99.558
7517	AL035588	Homo sapiens dJ696P19.1 (TFEB)	3221	98.975
7518	U79275	Homo sapiens unknown	918	100.000
7519	AJ011306	Homo sapiens guanine nucleotide exchange factor (long isoform)	2716	99.523
7520	AE001788	Thermotoga maritima ribosomal protein S15	178	37.037
7521	AE001070	Archaeoglobus fulgidus ribonuclease PH (rph)	328	33.937
7522	X87176	Homo sapiens 17beta-hydroxysteroid dehydrogenase	4839	100.000
7523	AC005189	Homo sapiens match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773)	976	100.000
7524	AL049802	Homo sapiens hypothetical protein	4303	100.000
7525	AF067219	Caenorhabditis elegans No definition line found	117	41.860
7526	AF060568	Homo sapiens promyelocytic leukemia zinc finger protein; kruppel-like zinc finger protein; PLZF	4578	99.554
7527	AL031670	Homo sapiens similar to Zinc finger, C3HC4 type (RING finger); match PFAM PF00097; similar to SW:GOLI_DROME Q06003 GOLIATH PROTEIN	1054	100.000

7528	AF140501	Homo sapiens RAD30B	4696	99.720
7529	AF116827	Homo sapiens unknown	3851	100.000
7530	U28282	Homo sapiens zinc finger protein	2382	99.443
7531	AF180920	Homo sapiens cyclin ania-6a	2016	100.000
7532	AL031121	Homo sapiens dJ495010.2 (novel protein similar to worm E04F6.2	343	100.000
7533	AB031292	Mus musculus proteolipid protein 2	195	31.746
7534	AL117562	Homo sapiens hypothetical protein	2411	99.425
7535	U25801	Homo sapiens Tax1 binding protein	801	98.374
7536	X94910	Homo sapiens ERp28	1682	99.234
7537	X15722	Homo sapiens glutathione reductase (AA 1-479)	3163	100.000
7538	Z70213	Caenorhabditis elegans predicted using Genefinder; Weak similarity to Sea Urchin myosin heavy chain (PIR Acc. No. A37352)	296	28.910
7539	AF151818	Homo sapiens CGI-60 protein	2142	97.605
7540	AF144700	Homo sapiens small zinc finger-like protein	654	100.000
7541	U46690	Mus musculus ATP-dependent RNA helicase	2643	85.000
7542	L14331	Caenorhabditis elegans coded for by C. elegans cDNAs GenBank: CE5D1 (Z14791), CEL01F1 (M88817), CEL04B5 (M88849), and CEL04C1 (M75812); putative	938	44.407
7543	AF139461	Homo sapiens hypothetical protein SBBI31	976	100.000
7544	AL031775	Homo sapiens dJ30M3.2 (novel protein)	599	100.000
7545	AF049523	Homo sapiens huntingtin-interacting protein HYPA/FBP11	2775	99.764
7546	AC005521	Homo sapiens similar to yeast SSU72; similar to P53538 (PID:g1711532)	964	69.543
7547	AJ005894	Homo sapiens JM27	703	100.000
7548	AL035464	Homo sapiens dJ1043E3.1 (novel protein)	1211	100.000
7549	AF153605	Homo sapiens androgen induced protein	1625	99.580
7550	U43701	Homo sapiens ribosomal protein L23a	999	100.000
7551	X07523	Homo sapiens complement factor H	3307	100.000
7552	AF028823	Homo sapiens Tax interaction protein 1	744	100.000
7553	X67155	Homo sapiens mitotic kinase-like protein-1	6116	98.857
7554	AL034353	Schizosaccharomyces pombe putative 60s ribosomal protein	282	41.071
7555	AF143889	Homo sapiens unknown	1190	99.465
7556	X08055	Homo sapiens preglycophorin B	537	100.000
7557	Z93783	Homo sapiens dJ377F16.1 (PUTATIVE novel protein)	975	100.000
7558	AF151845	Homo sapiens CGI-87 protein	2474	99.472
7559	AJ000414	Homo sapiens Cdc42-interacting protein 4	3628	100.000
7560	Z36531	Homo sapiens fibrinogen-like protein	3024	100.000
7561	M29458	Homo sapiens carbonic anhydrase III	1852	100.000
7562	X95384	Homo sapiens 14.5 kDa translational inhibitor protein, p14.5	854	100.000
7563	AF132971	Homo sapiens CGI-37 protein	1192	100.000
7564	AF132484	Mus musculus unknown	897	80.864
7565	X54941	Homo sapiens Cks1 protein homologue	561	100.000
7566	AL035369	Homo sapiens hypothetical protein	2450	100.000
7567	U94991	Xenopus laevis transcription factor XLMO1	1051	97.973
7568	AF017096	Drosophila melanogaster similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c	634	61.379
7569	S73775	Homo sapiens calmitine; calsequestrine	2557	99.231
7570	AL049522	Schizosaccharomyces pombe hypothetical protein	859	51.464

7571	Y13141	Bromheadia finlaysoniana extensin	122	44.118
7572	U85431	Homo sapiens unknown protein	159	70.000
7573	AF151882	Homo sapiens CGI-124 protein	1153	100.000
7574	AF022913	Homo sapiens GPI transamidase	2640	100.000
7575	Z35604	Unknown cDNA EST EMBL:Z14593 comes from this gene; cDNA EST EMBL:T01764 comes from this gene; cDNA	1003	37.168
7576	X77635	Drosophila melanogaster lethal(2)essential for life	179	35.000
7577	X65020	Bos taurus PSST subunit of the NADH: ubiquinone oxidoreductase complex	1249	88.725
7578	Z93382	Caenorhabditis elegans F45G2.10	440	57.377
7579	AF079317	Sphingomonas aromaticivorans unknown	777	39.763
7580	Z99278	Caenorhabditis elegans cDNA EST EMBL:D75703 comes from this gene; cDNA EST yk513g5.3 comes from this gene; cDNA EST yk528b10.3 comes from this gene	817	52.964
7581	AF152583	Homo sapiens unknown	377	100.000
7582	Z30093	Homo sapiens basic transcription factor 2, 35 kD subunit	2025	99.669
7583	D43636	Homo sapiens KIAA0096 gene product is related to a protein kinase.	3491	100.000
7584	AF177758	Homo sapiens ubiquitin specific protease 16	3900	100.000
7585	X16166	Homo sapiens cytokine 21	624	98.913
7586	U73522	Homo sapiens AMSH	2818	100.000
7587	Y17454	Homo sapiens LSFR1 protein	892	98.496
7588	Y07968	Homo sapiens TFG	2711	99.501
7589	AB023222	Homo sapiens KIAA1005 protein	6867	100.000
7590	U88167	Caenorhabditis elegans No definition line found	124	30.208
7591	AF117657	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80	4754	99.860
7592	U46754	Aphrodite aculeata nerve myoglobin	186	30.496
7593	X91809	Homo sapiens GAIP	1523	100.000
7594	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	102	57.143
7595	X76228	Homo sapiens vacuolar H+ ATPase E subunit	1427	100.000
7596	X80333	Mus musculus rab18	1344	99.029
7597	AL022238	Homo sapiens dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3) (isoform 1)	5195	99.871
7598	AJ224875	Homo sapiens glucosyltransferase	3557	99.060
7599	AB020680	Homo sapiens KIAA0873 protein	3012	99.785
7600	Z37986	Homo sapiens phenylalkylamine binding protein	1611	100.000
7601	D43949	Homo sapiens This gene is novel.	4103	100.000
7602	Y07923	Homo sapiens GTP-binding protein	1530	99.138
7603	Z32683	Caenorhabditis elegans similar to RNA binding protein; cDNA EST EMBL:D73574 comes from this gene; cDNA EST yk613f4.3 comes from this gene	229	41.379
7604	AB007893	Homo sapiens KIAA0433	8170	98.956
7605	A58552	unidentified unnamed protein product	720	100.000
7606	AF055016	Homo sapiens unknown	1511	99.539
7607	AF078848	Homo sapiens BUP	1272	100.000
7608	U28168	Mus musculus GP106	760	60.819
7609	AL117237	Homo sapiens hypothetical protein	6229	99.783

7610	AJ010277	Homo sapiens TBX19 protein	3093	100.000
7611	X95190	Homo sapiens branched chain acyl-CoA oxidase	4547	100.000
7612	K01075	synthetic construct circumsporozoite (CS) fusion prot (partial)	141	26.271
7613	AL023859	Unknown SPBC19C7.07c, putative tRNA splicing endonuclease ga mma subunit, len:284aa, similar eg.	281	25.436
7614	AF100748	Homo sapiens HSPC035 protein	2389	99.410
7615	S75997	Rattus sp. nucleoporin p62 homolog	227	36.184
7616	X66295	Mus musculus Clq C chain	1273	73.171
7617	U72680	Mus musculus ion channel homolog RIC	437	48.913
7618	AB028962	Homo sapiens KIAA1039 protein	2901	99.097
7619	AF132966	Homo sapiens CGI-32 protein	1750	99.267
7620	AF042284	Homo sapiens unknown	2991	100.000
7621	AB002377	Homo sapiens KIAA0379	5874	100.000
7622	X55681	Lycopersicon esculentum extensin (class I)	173	34.524
7623	AC005023	Homo sapiens match to EST AA361117 (NID:g2013436)	1021	100.000
7624	X78925	Homo sapiens zinc finger protein	5133	99.727
7625	AF044956	Homo sapiens NADH:ubiquinone oxidoreductase B22 subunit	1311	100.000
7626	X03084	Homo sapiens Clq B-chain precursor	1598	100.000
7627	AF064257	Homo sapiens Dhml-like protein	6589	98.947
7628	AC007055	Homo sapiens unknown	1337	100.000
7629	AC005253	Homo sapiens R26445 1	1191	100.000
7630	AL031179	Schizosaccharomyces pombe hypothetical protein	192	29.577
7631	X03077	Homo sapiens lactate dehydrogenase-A	2167	100.000
7632	M16424	Homo sapiens beta-hexosaminidase alpha chain	3651	100.000
7633	Z77667	Caenorhabditis elegans cDNA EST EMBL:C08125 comes from this gene; cDNA EST EMBL:C09753 comes from this gene	1034	38.673
7634	X02544	Homo sapiens alpha-acid glycoprotein	1338	99.502
7635	AC004000	Homo sapiens match to EST AA085966 (NID:g1629547)	491	100.000
7636	U47924	Homo sapiens B-cell receptor associated protein	1872	100.000
7637	X17025	Homo sapiens homologue of yeast IPP isomerase	1537	100.000
7638	AF129131	Xenopus laevis putative Zic3 binding protein; CBP3 protein homolog	1094	75.000
7639	M57424	Homo sapiens adenine nucleotide translocator-2	1876	92.905
7640	U57344	Mus musculus Meis3	2357	89.153
7641	U57344	Mus musculus Meis3	2067	81.266
7642	AF033120	Homo sapiens p53 regulated PA26-T2 nuclear protein	1765	58.439
7643	AF052193	Gallus gallus translation repressor	506	100.000
7644	U27838	Mus musculus glycosyl-phosphatidyl-inositol-anchored protein homolog	4246	96.189
7645	AB008549	Homo sapiens type 1 procollagen C-proteinase enhancer protein	3096	100.000
7646	D79990	Homo sapiens KIAA0168	1147	58.567
7647	L14429	Caenorhabditis elegans putative	497	88.235
7648	AL023496	Streptomyces coelicolor hypothetical protein	202	34.483
7649	AF098669	Emericella nidulans pantothenate kinase	608	36.943
7650	AF151869	Homo sapiens CGI-111 protein	1256	98.492
7651	U79258	Homo sapiens unknown	797	100.000

7652	U77327	Homo sapiens Ki-1/57 intracellular antigen	2064	98.997
7653	X51466	Homo sapiens elongation factor 2	5711	100.000
7654	X83618	Homo sapiens hydroxymethylglutaryl-CoA synthase	3368	99.803
7655	X02544	Homo sapiens alpha1-acid glycoprotein	1338	99.502
7656	D50646	Mus musculus SDF2	905	65.482
7657	AF102805	Drosophila melanogaster Peter Pan	976	35.745
7658	AL031431	Homo sapiens dJ462023.2 (novel protein)	2614	100.000
7659	X83300	Homo sapiens SMA4	993	99.286
7660	K03207	Homo sapiens salivary proline-rich protein precursor	1712	89.879
7661	AJ000342	Homo sapiens DMBT1/6kb.1 protein	1281 5	99.888
7662	X54134	Homo sapiens protein-tyrosine phosphatase	4739	100.000
7663	AL031709	Homo sapiens c316G12.3 (novel protein)	2093	100.000
7664	S45367	Canis familiaris contractin	2488	100.000
7665	M27444	Bos taurus phosphoprotein	1218	90.196
7666	AF007889	Symbiodinium microadriaticum calmodulin	845	91.304
7667	X97324	Homo sapiens adipophilin	2740	99.542
7668	X14479	Canis familiaris calcyphosin (AA 1-189)	726	55.738
7669	Z38113	Saccharomyces cerevisiae orf, len: 99, CAI=0.21	262	42.424
7670	M65066	Homo sapiens cAMP-dependent protein kinase RI-beta regulatory subunit	2497	99.737
7671	AJ001340	Homo sapiens U3 snoRNP associated 55 kDa protein	3168	100.000
7672	U88573	Homo sapiens NBR2	419	95.082
7673	AF077030	Homo sapiens hypothetical 43.2 kDa protein	581	32.283
7674	Z32840	Unknown similar to TCP-1 like chaperonin; cDNA EST EMBL:Z14945 comes from this gene; cDNA EST EMBL:	2514	68.470
7675	U40060	Caenorhabditis elegans weakly similar to E. nidulans bimA gene product (SP:P17885)	1086	39.367
7676	AL080125	Homo sapiens hypothetical protein	3827	100.000
7677	D80002	Homo sapiens KIAA0180	2380	100.000
7678	Z49878	Homo sapiens guanidinoacetate N-methyltransferase	1640	100.000
7679	AF092092	Homo sapiens AP-3 adaptor complex mu3A subunit	2760	100.000
7680	X95073	Homo sapiens Translin associated protein X	1890	100.000
7681	Z68218	Caenorhabditis elegans K01H12.1	348	67.143
7682	Y12065	Homo sapiens hNop56	3730	98.833
7683	AF110956	Homo sapiens SUMO-1 activating enzyme subunit 1	2280	100.000
7684	AL022476	Homo sapiens dJ323M22.2.1 (novel protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase) (isoform 1)	2864	100.000
7685	AL050373	Homo sapiens hypothetical protein	2230	100.000
7686	AF151879	Homo sapiens CGI-121 protein	1092	100.000
7687	AF093680	Homo sapiens transcription factor IIB	1281	100.000
7688	AL080125	Homo sapiens hypothetical protein	4064	100.000
7689	X57814	Homo sapiens immunoglobulin lambda light chain	1483	96.203
7690	AF153609	Homo sapiens serine/threonine protein kinase sgk	1878	67.561
7691	AF056617	Homo sapiens BWSCR2 associated zinc-finger protein BAZ1	4365	100.000

7692	S70312	Homo sapiens alpha-adducin {IT10C2, alternatively spliced}	209	97.059
7693	AL031228	Homo sapiens dJ1033B10.8.1 (Ring finger protein 1 (RING1, RNF1))	2607	100.000
7694	AL031324	Schizosaccharomyces pombe very hypothetical protein	210	40.909
7695	X83543	Homo sapiens APXL	1102 2	100.000
7696	AL035307	Homo sapiens hypothetical protein	1985	89.736
7697	AF067136	Homo sapiens protein phosphatase-1 regulatory subunit 7 alpha2	288	42.958
7698	AJ012008	Homo sapiens DDAH protein	1901	100.000
7699	AL117428	Homo sapiens hypothetical protein	3990	100.000
7700	AF084259	Mus musculus bromodomain-containing protein BP75	1137	36.013
7701	U71383	Homo sapiens OB binding protein-2	3754	99.819
7702	AF067406	Homo sapiens vascular adhesion protein-1; semicarbazide sensitive amine oxidase; copper-containing amine oxidase homolog	5178	97.772
7703	X74837	Homo sapiens Man9-mannosidase	4199	99.840
7704	X04494	Homo sapiens precursor polypeptide	2437	100.000
7705	AF135157	Homo sapiens complement C1q A chain precursor	1718	100.000
7706	AB009282	Homo sapiens cytochrome b5	968	99.315
7707	U91541	Homo sapiens human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end	928	100.000
7708	AF151893	Homo sapiens CGI-135 protein	947	98.684
7709	Y00752	Rattus norvegicus serine dehydratase (AA 1 - 327)	1281	61.562
7710	AF159133	Oryza sativa subsp. indica SIR2-like protein	523	40.984
7711	M94065	Homo sapiens dihydroorotate dehydrogenase	2551	99.241
7712	AJ006973	Homo sapiens TOM1	3225	100.000
7713	AC004528	Homo sapiens R32184_1	2891	99.304
7714	L11702	Homo sapiens phospholipase D	5653	99.761
7715	AL050280	Homo sapiens hypothetical protein	2481	100.000
7716	U28412	Caenorhabditis elegans similar to polyposis locus protein 1 (SP:DP1_HUMAN, Q00765)	558	52.174
7717	AE001044	Archaeoglobus fulgidus carboxylesterase (est-1)	258	25.726
7718	Z71316	Saccharomyces cerevisiae ORF YNL040w	513	28.029
7719	AF132954	Homo sapiens CGI-20 protein	1824	99.638
7720	X71129	Homo sapiens electron transfer flavoprotein beta subunit	1613	99.608
7721	AL035602	Arabidopsis thaliana putative protein	840	37.845
7722	AJ133534	Homo sapiens prenylated Rab acceptor 1 (PRA1)	1224	99.459
7723	X67250	Rattus norvegicus n-chimaerin	2184	97.006
7724	Z77654	Caenorhabditis elegans predicted using Genefinder; Similarity to Drosophila RNA binding protein squid (SW:SQD_DROME); cDNA EST yk638a1.3 comes from this gene	225	31.356
7725	S82637	Homo sapiens Ig lambda-like gene/beta-glucuronidase exon 11 homolog	317	100.000
7726	Y07847	Homo sapiens RRP22 protein	1420	100.000
7727	X82224	Homo sapiens glutamine--phenylpyruvate aminotransferase	2906	100.000

7728	AL049989	Homo sapiens hypothetical protein	2730	99.045
7729	U05784	Rattus norvegicus light chain 3 subunit of microtubule-associated proteins 1A and 1B	777	96.000
7730	AF056184	Homo sapiens WS basic-helix-loop-helix leucine zipper protein	1499	99.142
7731	U82381	Homo sapiens proline dehydrogenase/proline oxidase	3335	99.802
7732	Y16346	Homo sapiens COL1A1 and PDGFB fusion transcript	99	37.500
7733	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	343	44.800
7734	AF118240	Homo sapiens peroxisomal biogenesis factor 16	2218	99.405
7735	AF060862	Homo sapiens unknown	547	96.296
7736	AC005917	Arabidopsis thaliana putative transmembrane transport protein	657	29.472
7737	Z47356	Caenorhabditis elegans similar to DNAJ	1348	58.892
7738	AC003028	Arabidopsis thaliana unknown protein	150	29.825
7739	AC002550	Homo sapiens Unknown gene product	1244	100.000
7740	AF095927	Rattus norvegicus protein phosphatase 2C	2475	95.153
7741	U14003	Escherichia coli Kenn Rudd identifies as gpmB	199	35.156
7742	AJ224639	Homo sapiens Surf5b	1290	99.500
7743	AB004534	Schizosaccharomyces pombe pi015	246	25.105
7744	AB002368	Homo sapiens KIAA0370	5083	100.000
7745	X64002	Homo sapiens RAP74	3384	99.807
7746	AF070572	Homo sapiens unknown	4096	100.000
7747	Z96932	Homo sapiens nuclear autoantigen fo 14 kDa	735	99.160
7748	AL117458	Homo sapiens hypothetical protein	2341	100.000
7749	X69910	Homo sapiens P63 protein	3775	99.336
7750	U80736	Homo sapiens CAGF9	2129	99.091
7751	AC005609	Homo sapiens KIAA0345-like 4	5346	99.279
7752	Z99112	Bacillus subtilis similar to hypothetical proteins	506	34.127
7753	AB014514	Homo sapiens KIAA0614 protein	1073 6	100.000
7754	AF097518	Homo sapiens liver-specific transporter	3611	100.000
7755	U47101	Homo sapiens NifU-like protein	779	100.000
7756	AJ005897	Homo sapiens JM5	2429	100.000
7757	AC004997	Unknown match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and	3045	100.000
7758	Y16790	Homo sapiens keratin type I	2592	99.239
7759	AF091621	Catharanthus roseus ubiquitin-conjugating enzyme E2	513	51.370
7760	Z98981	Schizosaccharomyces pombe hypothetical protein	225	39.450
7761	V00148	Caenorhabditis elegans unnamed protein product	164	39.024
7762	AL022729	Homo sapiens hypothetical protein	1200	98.925
7763	AF091087	Homo sapiens unknown	309	100.000
7764	AL049746	Arabidopsis thaliana putative protein	862	65.746
7765	AJ222969	Mus musculus S-periaxin	156	27.835
7766	AB014525	Homo sapiens KIAA0625 protein	5286	99.874
7767	AC002342	Arabidopsis thaliana Dreg-2 like protein	348	32.075
7768	AF151855	Homo sapiens CGI-97 protein	1538	96.400
7769	U41559	Caenorhabditis elegans No definition line found	311	26.724
7770	AF025459	Caenorhabditis elegans No definition line	261	28.326

		found		
7771	M74555	Mus musculus house-keeping protein	1452	53.061
7772	Z50194	Homo sapiens PQ-rich protein	2794	96.750
7773	X79888	Homo sapiens AU-binding protein/Enoyl-CoA hydratase	514	59.504
7774	U37251	Homo sapiens Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between the KRAB box and the zinc finger region; Method: conceptual translation supplied by author	254	43.689
7775	D42084	Homo sapiens KIAA0094 gene product is related to S.cerevisiae methionine aminopeptidase.	2745	100.000
7776	AL022117	Schizosaccharomyces pombe hypothetical protein	413	41.379
7777	AF173378	Homo sapiens 60S acidic ribosomal protein PO	1567	99.582
7778	Z25821	Homo sapiens dodecenoyl-CoA delta-isomerase	1966	100.000
7779	AC007231	Arabidopsis thaliana putative disease resistance protein	825	39.640
7780	AF110643	Homo sapiens UMP-CMP kinase	1296	100.000
7781	U88173	Caenorhabditis elegans weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	418	80.822
7782	X95826	Homo sapiens mono-ADP-ribosyltransferase	1768	99.251
7783	M12098	Rattus norvegicus myosin heavy chain	164	24.458
7784	AF151899	Homo sapiens CGI-141 protein	848	94.286
7785	AF177862	Homo sapiens HN1 protein	1030	100.000
7786	M97589	Homo sapiens prostatic acid phosphatase	311	27.295
7787	X54352	Mus musculus domesticus ORF MD6	2778	97.852
7788	AF049090	Homo sapiens casein kinase I gamma 3L	3101	99.560
7789	U69263	Homo sapiens matrillin-2 precursor	625	82.787
7790	AF053356	Homo sapiens ORF3, splicevariant b	1599	100.000
7791	X54162	Homo sapiens 64 Kd autoantigen	3694	99.301
7792	AF184939	Homo sapiens LDL induced EC protein	575	52.023
7793	X75593	Homo sapiens rab 13	1320	100.000
7794	AF118670	Homo sapiens orphan G protein-coupled receptor	2496	100.000
7795	AL117639	Homo sapiens hypothetical protein	1718	99.621
7796	U29463	Homo sapiens cytochrome b561	1643	98.805
7797	AL110479	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	916	47.535
7798	AB024984	Mus musculus Sid329p	2524	98.649
7799	AJ005273	Homo sapiens Kin17	2556	100.000
7800	AF152463	Homo sapiens RAB14 protein	1417	99.535
7801	M81231	Rattus norvegicus primary translation product of SP-D	639	35.738
7802	X02530	Homo sapiens early response precursor polypeptide (aa-21 to 77)	631	98.980
7803	AF121860	Homo sapiens sorting nexin 10	1341	98.507
7804	AC006233	Arabidopsis thaliana hypothetical protein	156	46.429
7805	AF100740	Homo sapiens ARF-family of Ras related GTPases	1187	100.000
7806	X86030	Vigna unguiculata extensin-like protein	218	31.405
7807	AJ243972	Homo sapiens 6-phosphogluconolactonase	1694	99.612
7808	AF058953	Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit	2741	100.000
7809	Z82192	Homo sapiens dJ18601.1	820	100.000
7810	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	272	66.667

7811	AF139658	Homo sapiens origin recognition complex subunit 6	965	100.000
7812	J04204	Bos taurus 32 kd accessory protein	2213	100.000
7813	L37877	Filobasidiella neoformans ribosomal protein L27	241	45.349
7814	AF116865	Mus musculus hedgehog-interacting protein	4208	93.858
7815	X66975	Homo sapiens nuclear ribonucleoprotein	3362	95.332
7816	AF151864	Homo sapiens CGI-106 protein	1431	100.000
7817	X99906	Homo sapiens alpha endosulfine	798	100.000
7818	AF110520	Mus musculus NG29	968	56.884
7819	AB015339	Homo sapiens HRIHFB2255	868	55.556
7820	AC006233	Arabidopsis thaliana hypothetical protein	147	48.000
7821	AF111856	Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b	4595	99.855
7822	AF151835	Homo sapiens CGI-78 protein	973	59.167
7823	AF092094	Homo sapiens AP-4 adaptor complex beta4 subunit	4916	99.865
7824	D13208	Mus musculus 8hs20 protein precursor	514	65.487
7825	X94355	Cowpox virus D17L	261	29.412
7826	AC002388	Arabidopsis thaliana 60S ribosomal protein L30 isolog	628	60.140
7827	U28412	Caenorhabditis elegans similar to polyposis locus protein 1 (SP:DP1 HUMAN, Q00765)	515	47.134
7828	X93036	Homo sapiens MAT8 protein	608	100.000
7829	AF060862	Homo sapiens unknown	302	85.417
7830	AB020630	Homo sapiens KIAA0823 protein	977	43.765
7831	AJ001874	Homo sapiens orf	524	98.701
7832	Z78542	Unknown predicted using Genefinder; cDNA EST EMBL:Z14514 comes from this gene; cDNA EST EMBL:D71033	261	35.156
7833	AJ002309	Homo sapiens synaptogyrin 3	1471	100.000
7834	AB021866	Homo sapiens CIB	50	38.095
7835	AC005067	Homo sapiens Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan	2465	100.000
7836	D86971	Homo sapiens no similarities to reported gene products	4509	99.851
7837	X91504	Homo sapiens GTPase	1339	100.000
7838	X99584	Homo sapiens SMT3A protein	669	98.058
7839	AL031778	Homo sapiens dJ34B21.3 (PUTATIVE novel protein)	539	100.000
7840	X66295	Mus musculus Clq C chain	1273	73.171
7841	M96264	Homo sapiens galactose-1-phosphate uridyl transferase	2668	100.000
7842	X77307	Homo sapiens 5-HT2B serotonin receptor	3109	100.000
7843	AC004625	Arabidopsis thaliana unknown protein	244	44.660
7844	Z49968	Caenorhabditis elegans weak similarity to the yeast SSM4 protein (Swiss Prot accession number P40318)	200	40.909
7845	AF001602	Homo sapiens paraoxonase	154	100.000
7846	Y11411	Homo sapiens pristanoyl-CoA oxidase	4620	99.000
7847	AJ235270	Rickettsia prowazekii GLUTAMYL-tRNA AMIDOTRANSFERASE SUBUNIT A (gata)	1206	40.562
7848	AF181856	Rattus norvegicus tRNA selenocysteine associated protein	1941	99.303

7849	AL035398	Homo sapiens dJ796I17.2 (CGI-51)	3174	99.787
7850	X53064	Homo sapiens small proline-rich protein	628	100.000
7851	X04366	Homo sapiens CANP, large subunit (aa 1-714)	4816	100.000
7852	AF151834	Homo sapiens CGI-76 protein	2156	99.077
7853	U89649	Chlamydomonas reinhardtii Mr19,000 outer arm dynein light chain	319	34.454
7854	AL050008	Homo sapiens hypothetical protein	761	56.923
7855	J05019	Mus musculus high affinity IgE receptor beta subunit	229	28.641
7856	AJ009985	Homo sapiens annexin 31 (annexin XXXI)	2147	100.000
7857	AF115345	Homo sapiens calcium-regulated heat stable protein CRHSP-24	1017	99.320
7858	Z29328	Homo sapiens Ubiquitin-conjugating enzyme UbcH2	1228	100.000
7859	AF125175	Homo sapiens angiopoietin-related protein-2	3433	100.000
7860	U29488	Caenorhabditis elegans No definition line found	729	55.349
7861	AJ002030	Homo sapiens progesterone binding protein	1492	100.000
7862	AL080097	Homo sapiens hypothetical protein	1835	100.000
7863	AJ249248	Homo sapiens putative G protein-coupled Receptor	2270	100.000
7864	X07743	Homo sapiens pleckstrin (AA 1-350)	2360	99.714
7865	X57158	Gallus gallus CHOX M product	907	78.736
7866	X70649	Homo sapiens member of DEAD box protein family	5029	100.000
7867	AF141309	Homo sapiens polyamine modulated factor-1	1072	98.788
7868	AF072128	Mus musculus claudin-2	1404	91.304
7869	AF093204	Gallus gallus unknown	452	62.626
7870	AC005162	Homo sapiens probable carboxypeptidase precursor; 64% similar to P42660 (PID:g1718107)	2014	100.000
7871	Z72576	Saccharomyces cerevisiae ORF YGL054c	357	42.446
7872	AF020797	Homo sapiens AP-mu chain family member mu1B	2730	99.764
7873	AF145316	Homo sapiens vacuolar proton pump delta polypeptide	1515	100.000
7874	X63417	Homo sapiens IRLB	1331	100.000
7875	AC004472	Homo sapiens P1.11659_4	2107	95.798
7876	J00287	Homo sapiens pepsinogen	2579	99.742
7877	AL022020	Mycobacterium tuberculosis hypothetical protein Rv1920	254	33.835
7878	AB006628	Homo sapiens KIAA0290	6072	100.000
7879	AF159063	Homo sapiens SKD1-homolog	2872	100.000
7880	Y09333	Rattus norvegicus mitochondrial very-long-chain acyl-CoA thioesterase	2285	74.066
7881	M59488	Homo sapiens S100 protein beta subunit	606	100.000
7882	X98506	Solanum tuberosum acetyl-CoA synthetase	2624	59.685
7883	AC005545	Homo sapiens R26660_2, partial CDS	199	100.000
7884	AF022977	Caenorhabditis elegans contains similarity to leucine-rich repeats (LRR)	227	36.885
7885	S62904	Homo sapiens thiopurine methyltransferase, TPMT {EC 2.1.1.67}	1692	100.000
7886	AC006153	Homo sapiens similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	1283	88.793
7887	AJ001016	Homo sapiens RAMP3	1044	100.000
7888	AL031633	Caenorhabditis elegans cDNA EST yk404d1.5	530	43.243

		comes from this gene; cDNA EST yk404d1.3 comes from this gene; cDNA EST yk672a9.3 comes from this gene		
7889	AE001023	Archaeoglobus fulgidus A. fulgidus predicted coding region AF1178	206	35.000
7890	D00763	Homo sapiens proteasome subunit C9	1682	100.000
7891	AL050040	Homo sapiens hypothetical protein	2713	100.000
7892	X53799	Homo sapiens macrophage inflammatory protein-2alpha precursor	682	100.000
7893	AF151853	Homo sapiens CGI-95 protein	1546	100.000
7894	X57802	Homo sapiens immunoglobulin lambda light chain	1439	92.704
7895	X75208	Homo sapiens protein tyrosine kinase-receptor	6755	100.000
7896	AL021453	Homo sapiens dJ821D11.1 (PUTATIVE protein)	335	100.000
7897	AF110645	Homo sapiens candidate tumor suppressor p33 ING1 homolog	1683	100.000
7898	Y08565	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	4280	99.839
7899	AF043350	Homo sapiens lymphocyte-specific protein 1	293	100.000
7900	AF061023	Gallus gallus CHT1	180	20.879
7901	U28412	Caenorhabditis elegans similar to polyposis locus protein 1 (SP:DP1 HUMAN, Q00765)	543	49.080
7902	AF186772	Homo sapiens surfeit 6 protein	2301	99.446
7903	L16991	Homo sapiens thymidylate kinase	1376	98.585
7904	Y13835	Homo sapiens farnesylated-proteins converting enzyme 2	2269	100.000
7905	Z22555	Homo sapiens CLA-1	3422	99.607
7906	AL035521	Arabidopsis thaliana putative protein	417	41.772
7907	AF026246	Homo sapiens HERV-E integrase	498	86.250
7908	AL117473	Homo sapiens hypothetical protein	2778	100.000
7909	AL109736	Schizosaccharomyces pombe WD repeat protein	822	41.319
7910	AL110477	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk551g5.3 comes from this gene	1000	39.484
7911	AL049946	Homo sapiens hypothetical protein	3936	99.486
7912	AF115384	Homo sapiens LR8	1747	98.519
7913	X98253	Homo sapiens ZNF183	2392	100.000
7914	AF151816	Homo sapiens CGI-58 protein	2412	99.713
7915	L19684	Homo sapiens kallistatin	1128	43.972
7916	AJ238979	Homo sapiens annexin A10 protein	2198	99.074
7917	D87470	Homo sapiens KIAA0280	1989	100.000
7918	AF045606	Homo sapiens C21orf4	1091	99.367
7919	AF119297	Homo sapiens neuroendocrine-specific protein-like protein 1	1482	99.576
7920	AF151906	Homo sapiens CGI-148 protein	1184	98.324
7921	AL121733	Homo sapiens hypothetical protein	414	36.946
7922	AF094516	Homo sapiens E1-like protein	4764	100.000
7923	AL117183	Schizosaccharomyces pombe very hypothetical protein	191	33.113
7924	Z50028	Caenorhabditis elegans cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene; cDNA EST yk360f12.5 comes from this gene	776	33.915
7925	U16307	Homo sapiens glioma pathogenesis-related protein	437	38.953

7926	Y10696	Homo sapiens INE1	370	98.039
7927	X13956	Homo sapiens 9kD protein (AA 1-82)	243	91.667
7928	Z46789	Bos taurus cylicin II	202	24.590
7929	AL050137	Homo sapiens hypothetical protein	2921	99.769
7930	Z66521	Caenorhabditis elegans similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene	1012	51.333
7931	AL117540	Homo sapiens hypothetical protein	856	96.875
7932	AB028954	Homo sapiens KIAA1031 protein	6512	100.000
7933	X55740	Homo sapiens 5'-nucleotidase	3833	99.826
7934	AF132174	Drosophila melanogaster unknown	361	29.310
7935	A01046	Homo sapiens lipase	2717	100.000
7936	X68274	Homo sapiens TAG-1/axonin-1	6974	99.519
7937	AF018034	Homo sapiens endothelin converting enzyme-1	147	36.364
7938	U69172	Mus musculus unknown	1142	66.192
7939	AB001684	Chlorella vulgaris ORF54d	105	53.125
7940	L08069	Homo sapiens DNAJ homologue-2	2030	73.618
7941	X82895	Homo sapiens DLG2	3799	99.826
7942	Y14768	Homo sapiens V-ATPase G-subunit like protein	753	100.000
7943	AB013721	Oryctolagus cuniculus mitsugumin 23	1374	88.477
7944	U72970	Sus scrofa calcium/calmodulin-dependent protein kinase II isoform gamma-B	3487	100.000
7945	AL110235	Homo sapiens hypothetical protein	1099	99.387
7946	L13291	Homo sapiens ADP-ribosylarginine hydrolase	1035	45.915
7947	AF125096	Homo sapiens HSPC042 protein	697	100.000
7948	D50917	Homo sapiens The KIAA0127 gene product is novel.	244	26.923
7949	AF085361	Homo sapiens HSPC032	2043	100.000
7950	M20030	Homo sapiens small proline rich protein	126	39.623
7951	U00032	Caenorhabditis elegans No definition line found	383	43.333
7952	X92814	Homo sapiens homologous to rat HREV107 (ACC.NO. X76453)	1065	99.383
7953	Z50026	Bos taurus phosphatidylcholine transfer protein	1217	81.132
7954	AF059531	Homo sapiens protein arginine N-methyltransferase 3	3391	99.805
7955	AF009242	Homo sapiens proline-rich Gla protein 1	1493	100.000
7956	U94586	Homo sapiens NADH:ubiquinone oxidoreductase MLRQ subunit	567	100.000
7957	AL050352	Arabidopsis thaliana putative protein	212	41.333
7958	AL050100	Homo sapiens hypothetical protein	211	53.968
7959	AL050253	Homo sapiens hypothetical protein	5426	100.000
7960	AL034562	Homo sapiens dJ684024.2 (prodynorphin (Beta-Neoendorphin-Dynorphin precursor, Proenkephalin B precursor))	1709	100.000
7961	AL117444	Homo sapiens hypothetical protein	2760	100.000
7962	AF144638	Homo sapiens sphingosine-1-phosphate lyase	3786	99.824
7963	Y15286	Homo sapiens vacuolar proton-ATPase subunit M9.2	444	71.250
7964	AF071062	Homo sapiens disabled-1	3689	99.457
7965	X83006	Homo sapiens neutrophil gelatinase associated lipocalin	276	40.367
7966	U34973	Mus musculus protein tyrosine phosphatase-like	1449	95.964
7967	X78627	Homo sapiens translin	1452	100.000

7968	AF150087	Homo sapiens small zinc finger-like protein	557	100.000
7969	AJ011895	Homo sapiens Naf1 alpha protein	4210	100.000
7970	M27071	Mus musculus protein phosphatase 1	2177	99.682
7971	M23234	Homo sapiens P-glycoprotein	8147	99.609
7972	AJ132445	Homo sapiens claudin-14	1487	99.103
7973	U47924	Homo sapiens B-cell receptor associated protein	1872	100.000
7974	U66411	Drosophila melanogaster putative type III alcohol dehydrogenase	1307	49.403
7975	AF151863	Homo sapiens CGI-105 protein	2122	99.682
7976	M36803	Homo sapiens hemopexin	3365	100.000
7977	X63629	Homo sapiens p-cadherin	5547	99.759
7978	Y10376	Homo sapiens SIRP-beta1	2636	99.497
7979	M86510	Schistosoma mansoni glutathione peroxidase	431	43.125
7980	AJ238096	Homo sapiens Lsm4 protein	973	100.000
7981	AF092128	Homo sapiens putative transmembrane protein E3-16	1798	100.000
7982	X89969	Bos taurus polyA binding protein II	2062	99.346
7983	AL110239	Homo sapiens hypothetical protein	1579	99.578
7984	AF007170	Homo sapiens unknown	3714	99.645
7985	AF176116	Homo sapiens Down Syndrome candidate region 1-like protein 2	1617	100.000
7986	AE000850	Methanobacterium thermoautotrophicum transcriptional regulator	541	55.303
7987	AF098284	Cloning vector pERV3 retinoic acid receptor RXR	3127	99.784
7988	AL023592	Schizosaccharomyces pombe hypothetical protein	241	28.934
7989	AL035496	Homo sapiens dJ437022.1 (novel VHS domain containing protein similar to predicted worm and human proteins)	438	100.000
7990	AF058448	Homo sapiens herpesvirus entry protein B	3219	100.000
7991	Z48795	Unknown similarity to a thioredoxin-like protein from Bacillus subtilis (Swiss Prot accession numbe	322	37.255
7992	AJ005866	Homo sapiens Sqv-7-like protein	1669	99.617
7993	AL049929	Homo sapiens hypothetical protein	2118	99.697
7994	AL049699	Homo sapiens dJ747H23.2 (novel protein)	577	35.069
7995	AB007952	Homo sapiens KIAA0483 protein	1917	100.000
7996	Y13323	Homo sapiens disintegrin-protease	3182	100.000
7997	X15393	Homo sapiens motinlin	734	100.000
7998	X61615	Homo sapiens leukemia inhibitory factor receptor	7398	99.544
7999	AB015330	Homo sapiens HRIHFB2007	1194	98.844
8000	X04325	Homo sapiens gap junction protein (aa 1-283)	1909	99.647
8001	U08215	Mus musculus NST-1	2986	90.215
8002	X74504	Mus musculus T10	412	83.784
8003	AL110244	Homo sapiens hypothetical protein	369	29.204
8004	AB029004	Homo sapiens KIAA1081 protein	3233	100.000
8005	Z50022	Homo sapiens putative surface glycoprotein	1269	100.000
8006	L31649	Saccharomyces cerevisiae cdc91	616	27.873
8007	AL117629	Homo sapiens hypothetical protein	796	73.545
8008	AF156957	Homo sapiens NTF2-related export protein NXT1	935	100.000
8009	U05321	Homo sapiens X-linked PEST-containing transporter	4196	100.000
8010	U42580	Paramecium bursaria Chlorella virus 1 Pro- and	188	37.975

		Glu-rich, PENPEV (10x); similar to Streptococcus B antigen, corresponds to Swiss-Prot Accession Number P27951		
8011	X53390	Homo sapiens upstream binding factor (AA 1-764)	5104	100.000
8012	AB018268	Homo sapiens KIAA0725 protein	3843	99.825
8013	AF105201	Homo sapiens G-protein alpha subunit 14	2329	100.000
8014	AL117587	Homo sapiens hypothetical protein	1151	100.000
8015	AL031010	Homo sapiens dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)	336	100.000
8016	U28016	Mus musculus parathion hydrolase (phosphotriesterase)-related protein	2065	87.679
8017	AC004918	Homo sapiens structure confirmed by Genscan, human EST AA447021 (NID:g2159686) and mouse EST AA119040 (NID:g1676735)	1219	100.000
8018	AC004839	Homo sapiens similar to IgD B-cell receptor-associated protein (BAP); similar to S46997 (PID:g1085495)	1540	100.000
8019	AL034488	Caenorhabditis elegans predicted using Genefinder	430	69.512
8020	AB018260	Homo sapiens KIAA0717 protein	4288	99.841
8021	AB001568	Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase-like protein	432	40.244
8022	U56965	Caenorhabditis elegans No definition line found	664	43.182
8023	AB029334	Halocynthia roretzi HrPET-1	849	37.903
8024	AJ006291	Homo sapiens leucine rich protein	1934	100.000
8025	AL035304	Homo sapiens hypothetical protein	860	100.000
8026	AF137386	Homo sapiens plasmolipin	1190	100.000
8027	AL035678	Arabidopsis thaliana putative protein	2214	63.916
8028	AF155114	Homo sapiens NY-REN-57 antigen	2932	100.000
8029	AF155196	Rattus norvegicus mindin precursor	1951	85.843
8030	AL109831	Schizosaccharomyces pombe conserved hypothetical protein	399	24.664
8031	L27421	Rattus norvegicus neuronal calcium sensor	1257	100.000
8032	Y12735	Homo sapiens Dyrk3 protein	3726	99.636
8033	M16279	Homo sapiens antigen	251	36.788
8034	AC002985	Homo sapiens R27090 2	3158	100.000
8035	AF007791	Homo sapiens secreted cement gland protein XAG-2 homolog	1131	100.000
8036	AF092878	Homo sapiens zinc RING finger protein SAG	850	100.000
8037	A64586	unidentified unnamed protein product	4352	100.000
8038	AF045644	Caenorhabditis elegans No definition line found	364	39.623
8039	AF161081	Homo sapiens activatory receptor PIRIIBeta	1524	100.000
8040	X64588	Cricetulus longicaudatus cyclin B	2435	87.097
8041	AF132967	Homo sapiens CGI-33 protein	1483	97.826
8042	AL049758	Homo sapiens dJ437M21.2 (novel putative GTP-ase activating protein for Arf similar to worm F07F6.4)	900	63.592
8043	AF070657	Homo sapiens glutathione S-transferase subunit 13 homolog	1522	100.000
8044	AF151848	Homo sapiens CGI-90 protein	299	32.143
8045	L40357	Homo sapiens thyroid receptor interactor	692	93.750

8046	Y18503	Homo sapiens XAP-5-like protein	2142	100.000
8047	Z97340	Arabidopsis thaliana isomerase like protein	780	53.241
8048	AL080076	Homo sapiens hypothetical protein	2598	97.297
8049	M33141	Bos taurus GTP-binding protein (smg p21B)	1200	100.000
8050	X03475	Rattus norvegicus ribosomal protein L35a (aa 1-110)	731	99.091
8051	AL049688	Homo sapiens hypothetical protein	3230	100.000
8052	Z11804	Dictyostelium discoideum ras protein	519	50.303
8053	AF120102	Homo sapiens calsenilin	1713	100.000
8054	AF132951	Homo sapiens CGI-17 protein	2475	98.961
8055	AF151842	Homo sapiens CGI-84 protein	1310	100.000
8056	AL117661	Homo sapiens hypothetical protein	4447	99.558
8057	AF159055	Homo sapiens leucine zipper-like protein	139	81.481
8058	AF143859	Mus musculus DEBT-91	1860	96.622
8059	AL117195	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	525	34.746
8060	AF039568	Homo sapiens vesicle trafficking protein	142	73.913
8061	AL022316	Homo sapiens bK126B4.3 (novel protein)	1869	100.000
8062	AJ245709	Homo sapiens Akt-3 protein	3181	98.330
8063	U82382	Homo sapiens PIN1 peptidyl-prolyl cis/trans isomerase-like	124	55.882
8064	Z14122	Xenopus laevis XLCL2	585	77.885
8065	U70855	Caenorhabditis elegans similar to the RAS gene family	1684	44.302
8066	AF152498	Homo sapiens protocadherin beta 5	5120	99.245
8067	Y13647	Homo sapiens stearyl CoA desaturase	2458	99.443
8068	AF151835	Homo sapiens CGI-78 protein	1573	98.780
8069	X67712	Psychrobacter immobilis triacylglycerol lipase	339	27.799
8070	X55764	Homo sapiens 11beta-hydrolase precursor	3358	99.602
8071	AF134726	Homo sapiens NG36	1215	100.000
8072	AF070637	Homo sapiens unknown	537	37.549
8073	AF084457	Homo sapiens beta-cop homolog	6071	99.265
8074	AL050190	Homo sapiens hypothetical protein	1996	99.675
8075	AF131746	Homo sapiens Unknown	873	100.000
8076	A18411	Homo sapiens PIGF	1055	100.000
8077	U97006	Caenorhabditis elegans No definition line found	173	39.189
8078	AJ000217	Homo sapiens CLIC2	1636	99.588
8079	AB030505	Mus musculus UBE-1c2	1365	78.707
8080	AB007191	Homo sapiens AMY-1	649	99.029
8081	AC004472	Homo sapiens TERA HUMAN	5315	100.000
8082	AF077200	Homo sapiens HSPO14	917	100.000
8083	Z81035	Caenorhabditis elegans predicted using Genefinder; Similarity to Yeast DNA-directed RNA polymerase I 13.7 KD polypeptide (SW:P32529)	270	41.964
8084	AL080118	Homo sapiens hypothetical protein	945	94.521
8085	L40410	Homo sapiens thyroid receptor interactor	1040	100.000
8086	X63422	Homo sapiens H(+)-transporting ATP synthase	1035	100.000
8087	AB024713	Mus musculus Supl15h	173	26.455
8088	AP000559	Oryza sativa ESTs AU030008 (E50477), AU078239 (E50477) correspond to a region of the predicted gene.; Similar to peptidyl-prolyl cis-trans isomerase 10 & CELB0252 4 (P52017)	770	69.375

8089	AF155111	Homo sapiens NY-REN-49 antigen	1083	99.401
8090	AL023553	Homo sapiens dJ347H13.4 (novel protein)	711	100.000
8091	AL109978	Homo sapiens hypothetical protein	2154	100.000
8092	Z35597	Unknown Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:	770	35.825
8093	J00073	Homo sapiens alpha-cardiac actin	2508	100.000
8094	AF105365	Homo sapiens K-Cl cotransporter KCC4	7183	99.908
8095	M77172	Homo sapiens zinc finger protein	198	57.778
8096	Z50749	Homo sapiens yeast sds22 homolog	2266	100.000
8097	AB028966	Homo sapiens KIAA1043 protein	8243	99.762
8098	M17783	Homo sapiens glia-derived nexin precursor	2588	100.000
8099	AL021481	Unknown similar to WD domain, G-beta repeat (2 domains); cDNA EST yk258d4.3 comes from this gene;	948	42.308
8100	AB002380	Homo sapiens KIAA0382	4913	99.733
8101	M64749	Homo sapiens orphan receptor	2396	98.619
8102	AL117558	Homo sapiens hypothetical protein	918	99.320
8103	M62419	Mus musculus clathrin-associated protein	2778	99.291
8104	AB006191	Mus musculus cornichon-like protein	548	77.660
8105	AL050345	Homo sapiens hypothetical protein	809	100.000
8106	AB023185	Homo sapiens KIAA0968 protein	3495	97.753
8107	AF090402	Mus musculus KH domain RNA binding protein QKI-5A	2113	99.691
8108	L03303	Oryctolagus cuniculus small GTP-binding protein	1300	96.244
8109	L11317	Homo sapiens rhoG	1305	100.000
8110	U00025	Caenorhabditis elegans weak similarity to ATP synthase B chain	689	27.554
8111	AL050286	Homo sapiens hypothetical protein	657	100.000
8112	Y14768	Homo sapiens lymphotoxin-beta	1627	100.000
8113	AL049654	Homo sapiens hypothetical protein	2709	100.000
8114	AF098807	Homo sapiens lipoma HMGIC fusion partner	1430	100.000
8115	Y12473	Homo sapiens centrin	1064	99.401
8116	U77667	Mus musculus tyrosine kinase	3980	93.376
8117	Z35641	Caenorhabditis elegans cDNA EST yk273d8.5 comes from this gene	425	31.650
8118	AF102147	Homo sapiens putative dimethyladenosine transferase	2067	100.000
8119	Z69881	Homo sapiens adenosine triphosphatase, calcium	6546	100.000
8120	X80473	Mus musculus rab19	757	56.995
8121	AB023221	Homo sapiens KIAA1004 protein	3360	100.000
8122	X03884	Homo sapiens 20K polypeptide	1442	100.000
8123	AL023694	Homo sapiens dJ511E16.2 (putative protein based on ESTs)	850	100.000
8124	M91669	Homo sapiens autoantigen	1063 6	99.673
8125	AF151892	Homo sapiens CGI-134 protein	975	100.000
8126	AJ270205	Entodinium caudatum putative phosphatidylinositol-4-phosphate 5-kinase	204	39.326
8127	U09808	Drosophila melanogaster cDNA and genomic are colinear; similar to human connective tissue growth factor, GenBank Accession Number M92934	284	38.333
8128	AJ011400	Bos taurus NADH:ubiquinone oxidoreductase b17.2 subunit	132	30.000

8129	AF003999	Mus musculus GS15	619	90.741
8130	AL079349	Arabidopsis thaliana putative protein	289	30.962
8131	AB007859	Homo sapiens KIAA0399	5161	100.000
8132	Y17464	Fugu rubripes LSFR2 protein	308	84.615
8133	X96698	Homo sapiens D1075-like	1934	100.000
8134	AF078845	Homo sapiens 16.7Kd protein	1030	100.000
8135	Z99259	Schizosaccharomyces pombe hypothetical protein	148	35.000
8136	AF039698	Homo sapiens antigen NY-CO-33	4372	98.403
8137	AF116865	Mus musculus hedgehog-interacting protein	4208	93.858
8138	AL050371	Homo sapiens hypothetical protein	2726	87.447
8139	M20729	Chlamydomonas reinhardtii calmodulin	245	39.316
8140	AF129812	Homo sapiens candidate tumor suppressor protein NOC2	2202	100.000
8141	AL109665	Homo sapiens SLP-1	2575	99.744
8142	AF085355	Homo sapiens N-terminal acetyltransferase complex ardl subunit	1188	100.000
8143	Y09858	Homo sapiens unknown protein	1576	99.569
8144	AF133123	Homo sapiens transcription factor IIIC102	5780	100.000
8145	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	2751	100.000
8146	Y17849	Homo sapiens ganglioside-induced differentiation associated protein 1	2328	98.603
8147	Z93241	Homo sapiens dJ222E13.3.2 (PUTATIVE partial isoform 2)	2761	100.000
8148	AB028990	Homo sapiens KIAA1067 protein	4419	99.855
8149	X89984	Homo sapiens BCL7A	1515	100.000
8150	AB018337	Homo sapiens KIAA0794 protein	3263	99.796
8151	AB018285	Homo sapiens KIAA0742 protein	8392	100.000
8152	U53588	Homo sapiens HCG V	885	100.000
8153	AF070657	Homo sapiens glutathione S-transferase subunit 13 homolog	1522	100.000
8154	AE001014	Archaeoglobus fulgidus transcription initiation factor IIB	182	24.000
8155	D13634	Homo sapiens KIAA0009	292	29.268
8156	X62155	Homo sapiens Myf4 protein	1529	100.000
8157	X16576	Homo sapiens KUP protein	2892	99.540
8158	X07948	Homo sapiens TP1 (AA 1-55)	367	100.000
8159	AF155107	Homo sapiens NY-REN-37 antigen	1300	99.425
8160	AF059198	Homo sapiens protein kinase/endoribonulcease	6522	99.693
8161	AL031320	Homo sapiens dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)	1070	99.367
8162	Z69637	Caenorhabditis elegans predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene	313	37.949
8163	AB023167	Homo sapiens KIAA0950 protein	2290	100.000
8164	AJ222967	Homo sapiens cystinosin	2445	100.000
8165	Y15062	Homo sapiens GalT4 protein	2275	100.000
8166	AJ012376	Homo sapiens ATP-binding cassette transporter-1 (ABC-1)	1462	99.955
8167	L13977	Homo sapiens prolylcarboxypeptidase	1249	43.653
8168	X52987	Homo sapiens rap2b gene product (AA 1-183)	1185	99.454
8169	AC003002	Homo sapiens R29515 1	960	100.000
8170	AF156271	Homo sapiens RING finger protein terf	3273	100.000
8171	L77967	Ovis aries small proline-rich protein with	103	32.609

		paired repeat		
8172	AC006085	Arabidopsis thaliana Putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase	835	38.369
8173	AC004382	Homo sapiens Unknown gene product	2119	100.000
8174	AF129332	Homo sapiens MUM2	977	100.000
8175	U82267	Oryctolagus cuniculus sarcosine oxidase	2655	99.487
8176	U37026	Rattus norvegicus sodium channel beta 2 subunit	198	30.769
8177	AF050145	Homo sapiens iduronate-2-sulfatase	153	25.899
8178	AF132000	Homo sapiens TADA1 protein	1446	100.000
8179	AF131852	Homo sapiens Unknown	911	100.000
8180	Y15057	Homo sapiens STK9 protein	6901	99.903
8181	X82207	Homo sapiens beta-centracetin	2486	100.000
8182	AF033107	Grus americana B-G-like protein	317	32.642
8183	AF107885	Homo sapiens unknown	303	100.000
8184	AF112444	Lupinus luteus L-asparaginase	653	41.121
8185	AF151848	Homo sapiens CGI-90 protein	433	33.624
8186	AJ012295	Rhizobium etli apaG protein	261	40.476
8187	X94769	Rattus rattus choline dehydrogenase	2727	88.435
8188	AL049638	Arabidopsis thaliana putative protein	219	27.982
8189	Z82244	Homo sapiens bK286B10.2 (Heme Oxygenase 1 (HO-1, EC 1.14.99.3))	1882	100.000
8190	AC004955	Homo sapiens supported by EST AA160484 (NID:g1735912) and Genscan	1529	99.574
8191	AJ007590	Homo sapiens XRP2 protein	2394	100.000
8192	X99642	Mus musculus HP1-BP74 protein	1653	92.958
8193	AJ010973	Homo sapiens DEDD protein	326	36.612
8194	U40952	Caenorhabditis elegans C03B1.10 gene product	230	65.854
8195	X52011	Homo sapiens muscle determination factor	1633	100.000
8196	AF003130	Caenorhabditis elegans No definition line found	894	41.114
8197	AC004382	Homo sapiens Unknown gene product	1303	68.132
8198	Y10571	Homo sapiens dinG	2206	100.000
8199	AB002372	Homo sapiens KIAA0374	1117	43.750
8200	AL109630	Drosophila melanogaster BACR7A4.h	737	32.083
8201	X65293	Homo sapiens protein kinase C epsilon	5079	100.000
8202	AB018268	Homo sapiens KIAA0725 protein	3852	100.000
8203	U58761	Caenorhabditis elegans C01F1.6 gene product	617	34.746
8204	U23139	Caenorhabditis elegans similar to NIFS protein (nitrogen fixation)	348	41.317
8205	X99920	Homo sapiens S100 calcium-binding protein A13 (S100A13)	614	100.000
8206	AJ006276	Homo sapiens transient receptor potential protein	6153	100.000
8207	Y07707	Homo sapiens ITBA4	170	50.000
8208	AL117442	Homo sapiens hypothetical protein	1723	100.000
8209	AF040964	Homo sapiens unknown protein IT1	3774	99.008
8210	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	170	52.459
8211	AB020713	Homo sapiens KIAA0906 protein	5926	99.567
8212	M89797	Mus musculus Wnt-4	2425	98.860
8213	AF125044	Homo sapiens ubiquitin-conjugating enzyme HBUCE1	1036	100.000
8214	AJ245417	Homo sapiens G5b protein	1026	100.000
8215	AF102548	Mus musculus AT1 receptor-associated protein	804	77.019

8216	AF165429	Arabidopsis thaliana protein phosphatase 2A 62 kDa B'' regulatory subunit	430	26.562
8217	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	1665	99.588
8218	Z54271	Caenorhabditis elegans F21D5.6	220	25.000
8219	AJ238236	Rattus norvegicus ribosome associated membrane protein RAMP4	283	79.032
8220	AJ243503	Mus musculus m46 protein	660	82.906
8221	U43384	Mus musculus gp91phox	3675	93.146
8222	AF076531	Homo sapiens minK-related peptide 2; MiRP2	683	100.000
8223	U41278	Caenorhabditis elegans F33G12.3 gene product	421	27.407
8224	X58769	Homo sapiens V alpha gene segment	362	83.582
8225	AL050159	Homo sapiens hypothetical protein	1691	100.000
8226	AC003096	Arabidopsis thaliana putative protein phosphatase 2C	370	40.606
8227	AF132174	Drosophila melanogaster unknown	1119	52.308
8228	AL035306	Homo sapiens hypothetical protein	1690	100.000
8229	AF049069	Pinus radiata No definition line found	511	57.031
8230	AF039687	Homo sapiens antigen NY-CO-1	2343	100.000
8231	X76105	Homo sapiens DAP-1	724	100.000
8232	AF039716	Caenorhabditis elegans similar to ATP synthase B chain	628	55.357
8233	AJ243320	Canis familiaris hypothetical protein	294	32.278
8234	Y00757	Homo sapiens polypeptide 7B2 precursor	1461	99.057
8235	AB011106	Homo sapiens KIAA0534 protein	4833	100.000
8236	Y11711	Homo sapiens collagen type XIV	195	100.000
8237	AJ006470	Homo sapiens cartilage-associated protein (CASP)	2723	100.000
8238	AB017112	Mus musculus mCAC	508	33.227
8239	X82240	Homo sapiens T cell leukemia/lymphoma 1	800	100.000
8240	AJ130941	Homo sapiens claudin-9 protein	1442	100.000
8241	Z73906	Caenorhabditis elegans Similarity to B.subtilis YQJC protein (TR:G1303954); cDNA EST EMBL:T01187 comes from this gene	607	70.229
8242	AF094761	Mus musculus Rfxank	506	72.642
8243	X57985	Homo sapiens histone H2B	495	93.023
8244	AP000062	Aeropyrum pernix 152aa long hypothetical protein	183	30.857
8245	AF023130	Homo sapiens Ras-GRF2	8176	99.919
8246	AC002505	Arabidopsis thaliana unknown protein	803	59.239
8247	AB018352	Homo sapiens KIAA0809 protein	8351	100.000
8248	AJ223355	Rattus norvegicus mitochondrial dicarboxylate carrier	1726	89.474
8249	D29833	Homo sapiens proline rich peptide P-B	107	35.294
8250	AF072933	Homo sapiens Mad2-like protein	1398	100.000
8251	L27645	Danio rerio growth-associated protein	185	37.500
8252	AF098481	Gallus gallus cadherin	648	69.231
8253	AF141377	Mus musculus Ly-6/neurotoxin homolog	682	81.034
8254	AB011157	Homo sapiens KIAA0585 protein	2778	100.000
8255	U23169	Caenorhabditis elegans No definition line found	1107	51.724
8256	AF151901	Homo sapiens CGI-143 protein	897	99.270
8257	M93698	Oncorhynchus mykiss ependymin	249	24.752
8258	AB014562	Homo sapiens KIAA0662 protein	4279	99.398
8259	X68879	Homo sapiens EMX1	1050	99.346
8260	M92441	Bos taurus ornithine decarboxylase	1528	54.126

8261	M76424	Homo sapiens carbonic anhydrase VII	1742	99.603
8262	U88958	Rattus norvegicus neuritin	244	32.075
8263	Z99116	Bacillus subtilis similar to hypothetical proteins	223	35.537
8264	M98539	Homo sapiens prostaglandin D2 synthase	1272	100.000
8265	AF005050	Homo sapiens aspartyl aminopeptidase	3160	100.000
8266	U31332	Homo sapiens DP prostanoid receptor	1901	100.000
8267	AC002130	Arabidopsis thaliana F1N21.1	275	27.807
8268	X67098	Homo sapiens ORF1	238	97.297
8269	D83198	Homo sapiens homology to a plant EST:RICS2753A	1535	99.559
8270	U32828	Haemophilus influenzae Rd ribosomal protein S6 modification protein (rimK)	381	31.308
8271	X82027	Sus scrofa BM88 antigen	654	72.000
8272	AF154831	Rattus norvegicus PV-1	1816	60.860
8273	X54673	Homo sapiens GABA transporter	4063	99.332
8274	AF026528	Rattus norvegicus stathmin-like-protein RB3	1215	99.471
8275	U35244	Rattus norvegicus vacuolar protein sorting homolog r-vps33a	3790	96.817
8276	AJ001189	Homo sapiens oligophrenin 1	5367	100.000
8277	D28595	Escherichia coli unknown	260	24.671
8278	D78255	Mus musculus PAP-1	638	82.203
8279	AB026054	Homo sapiens brain finger protein	4323	100.000
8280	AL031394	Arabidopsis thaliana putative protein	376	60.204
8281	AF001308	Arabidopsis thaliana predicted glycosyl transferase	327	28.986
8282	X91257	Homo sapiens seryl-tRNA synthetase	3400	99.805
8283	AF125443	Caenorhabditis elegans contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	820	40.922
8284	AB002359	Homo sapiens KIAA0361	9350	99.927
8285	AF077202	Homo sapiens HSPC016	412	100.000
8286	AF132960	Homo sapiens CGI-26 protein	2162	99.107
8287	AF133422	Homo sapiens HMP19 protein	1139	100.000
8288	AB012309	Cyprinus carpio allograft inflammatory factor-1	740	78.169
8289	AC002505	Arabidopsis thaliana hypothetical protein	403	32.472
8290	AL049730	Arabidopsis thaliana putative protein	680	42.616
8291	Z78418	Unknown cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA	814	47.791
8292	AL050273	Homo sapiens hypothetical protein	603	98.947
8293	A52140	unidentified HUMAN NDR	1000	98.675
8294	AF151907	Homo sapiens CGI-149 protein	1385	100.000
8295	AL031775	Homo sapiens dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	2425	100.000
8296	AF065382	Yersinia pestis adenylate kinase	267	30.556
8297	Z30425	Homo sapiens orphan nuclear hormone receptor	2322	98.584
8298	Z33905	Homo sapiens 43kD Acetylcholine receptor-associated protein (Rapsyn)	2775	100.000
8299	Y16787	Homo sapiens keratin, type I	2786	100.000
8300	M21103	Ovis aries BIIIB4 high-sulfur keratin	648	82.653
8301	X76488	Homo sapiens sterol esterase	1680	60.957
8302	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	1099 5	99.864
8303	Z85986	Homo sapiens dJ108K11.3 (similar to yeast suppressor protein SRP40)	1461	78.161

8304	U18762	Rattus norvegicus retinol dehydrogenase type I	1148	52.581
8305	AF072467	Homo sapiens unknown	3245	100.000
8306	X63745	Homo sapiens KDEL receptor	1374	100.000
8307	AF117646	Homo sapiens long CBL-3 protein	3331	99.789
8308	AL117557	Homo sapiens hypothetical protein	1780	100.000
8309	AL117495	Homo sapiens hypothetical protein	2932	99.753
8310	AC002301	Homo sapiens Homolog of rat Zymogen granule membrane protein	1120	100.000
8311	U60024	Ovis aries BIIIA3	69	50.000
8312	AF188285	Homo sapiens bone morphogenetic protein 9	2890	100.000
8313	AF112982	Homo sapiens group IID secretory phospholipase A2	1113	100.000
8314	Z97208	Schizosaccharomyces pombe hypothetical protein	683	47.009
8315	X16560	Homo sapiens precursor polypeptide (AA -16 to 47)	420	100.000
8316	X04085	Homo sapiens catalase	3642	100.000
8317	M13444	Mus musculus alpha-tubulin isotype M-alpha-6	3047	100.000
8318	AF042276	Pseudomonas putida o251 homolog	752	45.818
8319	U88958	Rattus norvegicus neuritin	931	98.592
8320	L40806	Neurospora crassa Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126	821	33.623
8321	AC004131	Homo sapiens Unknown gene product	919	40.759
8322	U19596	Mus musculus p18 protein	207	35.115
8323	U21549	Mus musculus Ac39/physophilin	1623	68.208
8324	X79888	Homo sapiens AU-binding protein/Enoyl-CoA hydratase	2181	100.000
8325	AF036694	Caenorhabditis elegans No definition line found	237	25.478
8326	D45370	Homo sapiens unknown product specific to adipose tissue	462	100.000
8327	M88469	Rattus norvegicus f-spondin	5595	96.654
8328	X87237	Homo sapiens a-glucosidase I	5754	99.283
8329	AC007231	Arabidopsis thaliana putative disease resistance protein	632	34.393
8330	AF161181	Mus musculus P55T protein	3458	97.593
8331	AF117814	Mus musculus odd-skipped related 1 protein	1218	66.667
8332	D13126	Rattus norvegicus neural visinin-like Ca2+-binding protein type 3	264	32.593
8333	D14849	Mus musculus meiosis-specific nuclear structural protein 1	2498	77.393
8334	AB020711	Homo sapiens KIAA0904 protein	6583	99.900
8335	AL008729	Homo sapiens predicted protein dJ257A7.2	878	98.519
8336	Z72510	Unknown similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822	800	49.446
8337	Z97992	Schizosaccharomyces pombe hypothetical protein	223	47.761
8338	Y14768	Homo sapiens I Kappa B-like protein	2673	100.000
8339	AF069737	Xenopus laevis notchless	2762	82.452
8340	Z98944	Schizosaccharomyces pombe hypothetical protein	345	31.884
8341	AF144235	Homo sapiens hypothetical protein SBBI42	1103	100.000
8342	Y00796	Homo sapiens LFA-1 alpha subunit precursor (AA -25 to 1145)	7821	99.829

8343	L10910	Homo sapiens splicing factor	1526	59.773
8344	AB014589	Homo sapiens KIAA0689 protein	3783	100.000
8345	Y12653	Homo sapiens diubiquitin	1068	99.394
8346	AL034397	Homo sapiens dA159A1.1 (novel protein)	2669	100.000
8347	Z70750	Caenorhabditis elegans similar to vanadate resistance protein transmembranous domains; cDNA EST yk664g4.3 comes from this gene	1213	58.457
8348	AC002045	Homo sapiens Unknown protein product CIT987SK-A-589H1 1 splice form 1	2224	98.784
8349	AL034488	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene	734	54.502
8350	X02585	Xenopus laevis unidentified open reading frame 1 (166 aa)	169	65.000
8351	AF155100	Homo sapiens zinc finger protein NY-REN-21 antigen	2895	100.000
8352	AL035297	Homo sapiens hypothetical protein	1067	100.000
8353	J05071	Bos taurus GTP-binding regulatory protein gamma-6 subunit	454	100.000
8354	AF171060	Mus musculus RING finger protein AO7	2565	81.917
8355	X63417	Homo sapiens IRLB	649	51.042
8356	AF093680	Homo sapiens transcription factor IIB	1281	100.000
8357	AF087825	Mus musculus claudin-7	211	47.500
8358	AL021960	Arabidopsis thaliana adrenodoxin-like protein	414	51.282
8359	Y18007	Homo sapiens seven transmembrane domain protein	1412	93.304
8360	X75315	Homo sapiens SEB4B	1500	97.826
8361	AL050170	Homo sapiens hypothetical protein	935	100.000
8362	AF176784	Rattus norvegicus eps8 binding protein	897	39.446
8363	AL080071	Homo sapiens hypothetical protein	847	100.000
8364	X84003	Homo sapiens PolII transcription factor TFIID	816	100.000
8365	X64037	Homo sapiens RNA polymerase II associated protein RAP74	3388	100.000
8366	AF098798	Homo sapiens unknown	2301	99.713
8367	X04085	Homo sapiens catalase	3642	100.000
8368	AF132172	Drosophila melanogaster unknown	1053	40.705
8369	X54449	Oryza sativa Glycine-rich protein	203	46.512
8370	AL080201	Homo sapiens hypothetical protein	1079	99.383
8371	X69089	Homo sapiens 165kD protein	9811	99.795
8372	Z99130	Homo sapiens dJ83L6.1 (DNA binding Zinc finger protein ZFPA (ZXDA))	5467	98.257
8373	X92972	Homo sapiens protein phosphatase 6	2131	100.000
8374	M87307	Xenopus laevis fast skeletal muscle beta-tropomyosin	1514	87.324
8375	AF045564	Rattus norvegicus development-related protein	2200	93.182
8376	AL050297	Homo sapiens hypothetical protein	2957	98.886
8377	M11900	Mus musculus 15-kDa proline-rich salivary protein	216	36.508
8378	L22342	Homo sapiens phosphoprotein	233	97.059
8379	AF172854	Homo sapiens cardiotrophin-like cytokine CLC	1579	100.000
8380	AJ224878	Homo sapiens T-cell receptor interacting molecule (TRIM) protein	1242	100.000
8381	M84379	Homo sapiens lymphocyte antigen	2482	99.178

8382	Z99297	Homo sapiens dJ262D12.2 ((mitochondrial/chloroplast 30S ribosomal protein S14)-LIKE protein)	870	100.000
8383	AF007130	Homo sapiens unknown	1694	100.000
8384	D00099	Homo sapiens Na,K-ATPase alpha-subunit	6746	100.000
8385	X05908	Homo sapiens lipocortin (AA 1-346)	2207	100.000
8386	M27288	Homo sapiens oncostatin M	1682	99.603
8387	X97571	Mus musculus HCMV-interacting protein	563	96.809
8388	X04391	Homo sapiens put. precursor polypeptide	3463	99.798
8389	AF161080	Homo sapiens inhibitory receptor PIRIIalpha	2014	99.340
8390	AF054176	Homo sapiens angiotensin/vasopressin receptor AII/AVP	3449	99.416
8391	L08239	Homo sapiens located at OATL1	2701	100.000
8392	AF087679	Sus scrofa tropomyosin 4	1515	100.000
8393	AF121863	Homo sapiens sorting nexin 14	2498	100.000
8394	AL050101	Homo sapiens hypothetical protein	3605	100.000
8395	AL109846	Schizosaccharomyces pombe hypothetical protein	305	33.146
8396	Y18101	Mus musculus macrophage actin-associated-tyrosine-phosphorylated protein	1995	87.425
8397	Z81490	Unknown similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene	2184	62.427
8398	U25353	Gallus gallus homeodomain protein AKR	650	51.915
8399	AF081353	Homo sapiens GTP-binding protein	1461	100.000
8400	Y15286	Homo sapiens vacuolar proton-ATPase subunit M9.2	594	100.000
8401	AL031431	Homo sapiens dJ462O23.1 (novel protein)	2140	99.676
8402	D87973	Mus musculus Impact	1796	82.500
8403	AF156884	Homo sapiens RIP-like kinase	3567	99.807
8404	X91257	Homo sapiens seryl-tRNA synthetase	3400	99.805
8405	Z82062	Caenorhabditis elegans cDNA EST yk415c12.5 comes from this gene; cDNA EST yk526h3.3 comes from this gene; cDNA EST yk599b1.3 comes from this gene	545	42.941
8406	Z93386	Unknown Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes fr	1807	58.030
8407	AJ010059	Homo sapiens SIT protein	1335	100.000
8408	AF068302	Homo sapiens choline/ethanolaminephosphotransferase	2854	100.000
8409	U89432	Mus musculus unknown	656	69.799
8410	AL050107	Homo sapiens hypothetical protein	1732	100.000
8411	D86964	Homo sapiens similar to a human major CRK-binding protein DOCK180.	1218 0	100.000
8412	AL080091	Homo sapiens hypothetical protein	1755	99.225
8413	X89399	Homo sapiens Ins P4-binding protein	5564	99.520
8414	AL031775	Homo sapiens dJ30M3.1 (novel protein similar to (predicted) plant, worm, yeast and archaea bacterial proteins)	712	100.000
8415	AL021453	Homo sapiens dJ821D11.3 (PUTATIVE protein)	1256	100.000
8416	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase	1900	96.564
8417	AF127761	Homo sapiens ribonucleoprotein RBM8	1194	100.000
8418	A42942	unidentified unnamed protein product	219	34.314
8419	X71975	Drosophila melanogaster put. homologue to	861	59.740

		S.cerevisiae GAR1 gene		
8420	AF095927	Rattus norvegicus protein phosphatase 2C	2475	95.153
8421	U10414	Caenorhabditis elegans Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2	2268	50.142
8422	AL117472	Homo sapiens hypothetical protein	5442	99.877
8423	U61953	Caenorhabditis elegans No definition line found	1001	47.904
8424	AL031774	Homo sapiens dek (putative oncogene)	2390	100.000
8425	D42039	Homo sapiens The ha1009 gene product is novel.	1563	100.000
8426	Z99104	Bacillus subtilis similar to hypothetical proteins	461	32.955
8427	AJ001612	Homo sapiens L-3-phosphoserine-phosphatase homologue	507	100.000
8428	X15525	Homo sapiens acid phosphatase	2891	99.764
8429	AF025468	Caenorhabditis elegans No definition line found	815	34.286
8430	AC004874	Homo sapiens similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989)	1211	98.895
8431	AF120102	Homo sapiens calsenilin	998	69.388
8432	Y13148	Rattus norvegicus PAG608	1746	88.194
8433	X17320	Mus musculus put. brain specific antigen (AA 1-62)	161	46.296
8434	AF146738	Rattus norvegicus testis specific protein	992	83.523
8435	U83194	Homo sapiens TRAF4-associated factor 2	2612	100.000
8436	D10376	Bos taurus mitochondrial adenylate kinase isozyme 3	1405	92.511
8437	Y09305	Homo sapiens protein kinase	1640	100.000
8438	X94917	Drosophila melanogaster head-elevated expression in 0.9 kb	170	23.711
8439	AB017644	Homo sapiens ubiquitin-conjugating enzyme E2	1169	85.990
8440	AL050173	Homo sapiens hypothetical protein	1177	97.312
8441	AC006538	Homo sapiens BC41195 1	1062	78.894
8442	AJ001019	Homo sapiens ring finger protein	584	40.756
8443	AF156857	Homo sapiens actin-binding protein	3965	100.000
8444	AF133124	Homo sapiens transcription factor IIIC63	3466	98.479
8445	AJ005578	Homo sapiens 6-phosphofructo-2-kinase	3353	100.000
8446	U58884	Mus musculus SH3P7	2448	85.747
8447	AF151890	Homo sapiens CGI-132 protein	929	100.000
8448	U53148	Caenorhabditis elegans similar to protein kinase C inhibitors	271	35.461
8449	M77836	Homo sapiens pyrroline-5-carboxylate reductase	1739	84.591
8450	AB004316	Bos taurus mitochondrial methionyl-tRNA transformylase	2227	87.838
8451	Z35094	Homo sapiens SURF-2	1734	97.266
8452	AL050275	Homo sapiens hypothetical protein	3077	99.520
8453	D13308	Sus scrofa glycine N-methyltransferase	1887	93.493
8454	Z69944	Schizosaccharomyces pombe putative endonuclease	350	43.165
8455	AJ223183	Homo sapiens DORA protein	1568	99.585
8456	AC004890	Homo sapiens similar to HUB1; similar to BAA24380 (PID:g2789430)	5085	99.720
8457	U09280	Homo sapiens type XIX collagen	79	34.091
8458	AJ224442	Homo sapiens methyltransferase	1169	99.415

8459	Y14153	Homo sapiens beta-transducin repeats containing protein	3874	99.649
8460	AC006014	Homo sapiens similar to RFP transforming protein; similar to P14373 (PID:g132517)	1142	98.780
8461	AC005099	Homo sapiens match to AI222572 (NID:g3804775)	602	100.000
8462	V00507	Homo sapiens coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	1129	92.896
8463	AJ005259	Homo sapiens homologous to Bombyx mori multiprotein bridging factor (EMBL: AB001078)	948	100.000
8464	AL022605	Arabidopsis thaliana putative gamma-glutamyltransferase	845	35.217
8465	AL079281	Homo sapiens hypothetical protein, similar to (U77968) neuronal PAS domain protein 1	1258	98.000
8466	M19351	Mus musculus immunoglobulin heavy chain binding protein	188	34.021
8467	AF012652	Trypanosoma cruzi Tcrab27	233	68.000
8468	AC005594	Homo sapiens R33729 1, partial CDS	973	96.711
8469	Z81051	Caenorhabditis elegans predicted using Genefinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene; cDNA EST yk633h1.3 comes from this gene	257	29.348
8470	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	1801	56.263
8471	AF109674	Rattus norvegicus late gestation lung protein 1	1104	77.841
8472	AE000909	Methanobacterium thermoautotrophicum serine/threonine protein kinase related protein	464	30.032
8473	M80783	Homo sapiens B12 protein	672	68.750
8474	AL117511	Homo sapiens hypothetical protein	654	100.000
8475	AB027137	Homo sapiens RAB-26	959	73.404
8476	X53744	Canis familiaris 68kDA subunit of signal recognition particle	3855	97.049
8477	M20456	Homo sapiens aldehyde dehydrogenase	3452	99.807
8478	AL021728	Unknown /prediction=(method:"genefinder", version:"084"); /match=(desc:"GH08386.5prime GH Dr	743	27.794
8479	AF058954	Homo sapiens GTP-specific succinyl-CoA synthetase beta subunit	2569	99.505
8480	AL080168	Homo sapiens hypothetical protein	2238	100.000
8481	AJ001309	Homo sapiens DnaJ protein	2834	100.000
8482	Z81069	Caenorhabditis elegans cDNA EST yk552d5.3 comes from this gene	216	39.394
8483	AJ006068	Homo sapiens dTDP-D-glucose 4,6-dehydratase	2379	100.000
8484	AB021537	Homo sapiens immunoglobulin heavy chain variable region (IgM)	663	79.675
8485	AJ132270	Homo sapiens p24B protein	1435	100.000
8486	Z81592	Caenorhabditis elegans predicted using Genefinder	546	55.782
8487	AL117204	Caenorhabditis elegans predicted using Genefinder	605	37.276
8488	AC004449	Homo sapiens R33683 3	715	100.000
8489	AF061817	Rattus norvegicus DNA-binding protein PREB	2520	89.688
8490	AF117615	Homo sapiens heme-binding protein	1276	99.471

8491	S94541	Homo sapiens clone 4-3	359	97.959
8492	Z71181	Caenorhabditis elegans similar to hydrolase	784	36.391
8493	AB014589	Homo sapiens KIAA0689 protein	3783	100.000
8494	Z81105	Caenorhabditis elegans similar to alpha/beta hydrolase fold; cDNA EST EMBL:T02320 comes from this gene	588	37.681
8495	AJ242832	Homo sapiens calpain	4743	99.713
8496	S94421	Homo sapiens T cell receptor eta-exon	641	100.000
8497	AL050214	Homo sapiens hypothetical protein	1218	99.448
8498	AF135016	Homo sapiens protein phosphatase 2A 48 kDa regulatory subunit	2845	100.000
8499	AF117272	Octopus dofleini O-crystallin	319	31.176
8500	AF089106	Homo sapiens unknown	919	100.000
8501	U04968	Cricetulus griseus nucleotide excision repair protein	4897	97.628
8502	AL050131	Homo sapiens hypothetical protein	1517	100.000
8503	AL031266	Caenorhabditis elegans VM106R.1	198	33.333
8504	AF019661	Mus musculus zeta proteasome chain; PSMA5	1538	100.000
8505	AB020316	Homo sapiens dermatan/chondroitin sulfate 2-sulfotransferase	2845	100.000
8506	A40202	unidentified unnamed protein product	619	100.000
8507	AL035593	Homo sapiens dJ310J6.1 (novel protein)	1040	98.675
8508	Z82244	Homo sapiens bK286B10.1	288	61.176
8509	AL022318	Homo sapiens bK150C2.3 (PUTATIVE novel protein similar to APOBEC1 (Apolipoprotein B mRNA editing protein) and Phorbolin)	1457	100.000
8510	AF132794	Homo sapiens anaphase promoting complex subunit 10	1258	99.459
8511	X63657	Homo sapiens FVT1 gene is disrupted in a t(2;18) chromosomal translocation involving Ig kappa gene in a follicular lymphoma	2116	100.000
8512	Y14780	Homo sapiens lymphocyte function associated antigen-3, TM-linked precursor	1685	100.000
8513	Z81038	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene	359	34.562
8514	AF070594	Homo sapiens HNK-1 sulfotransferase	546	32.013
8515	AF060883	Mus musculus endomucin	639	48.302
8516	U05784	Rattus norvegicus light chain 3 subunit of microtubule-associated proteins 1A and 1B	669	82.500
8517	X56351	Homo sapiens delta- aminolevulinate synthase (housekeeping)	4284	100.000
8518	AF151889	Homo sapiens CGI-131 protein	1018	100.000
8519	D50617	Saccharomyces cerevisiae YFL046W	225	24.865
8520	AF171055	Homo sapiens thioredoxin reductase TR2	3716	99.288
8521	AF123880	multiple sclerosis associated retrovirus element unknown protein U5/2	323	82.456
8522	AL110151	Homo sapiens hypothetical protein	589	38.261
8523	AC007193	Homo sapiens PPP5 HUMAN	3358	99.800
8524	Y17282	Homo sapiens cytokeratin type II	3498	99.819
8525	X66901	Mus musculus En-2/lacZ fusion protein	117	49.123
8526	U41012	Caenorhabditis elegans C06A6.3 gene product	212	24.242
8527	X76029	Homo sapiens neuromedin U	1183	99.425
8528	X94991	Homo sapiens zyxin	4124	99.825
8529	U30521	Homo sapiens P311 HUM	326	92.157

8530	AB020967	Rattus sp. kinase	1708	72.905
8531	D87457	Homo sapiens KIAA0281	1336	79.098
8532	Z97207	Mus musculus B-IND1 protein	1212	94.737
8533	AJ001019	Homo sapiens ring finger protein	1675	99.593
8534	D42073	Homo sapiens reticulocalbin	1198	58.446
8535	X80035	Oryctolagus cuniculus cysteine rich hair keratin associated protein	805	65.385
8536	X73462	Ovis aries hair keratin cysteine rich protein	796	70.229
8537	Z99129	Homo sapiens dJ425C14.2 (Placental protein DIFF33 LIKE)	1733	54.955
8538	X99140	Homo sapiens type II intermediate filament of hair keratin	3354	100.000
8539	X90763	Homo sapiens HHA5 hair keratin type I intermediate filament	2824	99.529
8540	AL034488	Unknown predicted using Genefinder; cDNA EST yk490c1.5 comes from this gene; cDNA EST yk256e4.5 c	250	24.746
8541	L35604	Drosophila melanogaster ethanolamine kinase	921	40.921
8542	AF003388	Caenorhabditis elegans No definition line found	461	38.342
8543	M32334	Homo sapiens intercellular adhesion molecule 2 (ICAM-2)	1835	100.000
8544	AF064448	Mus musculus sex-determination protein homolog Fem1b	4097	98.884
8545	AF067855	Homo sapiens geminin	1328	100.000
8546	M34513	Homo sapiens omega protein	1408	96.714
8547	AF093419	Homo sapiens multi PDZ domain protein MUPP1	1317 0	100.000
8548	AC004876	Homo sapiens similar to predicted proteins AAB54240 (PID:g2088822) and S67138 (PID:g2132925)	995	55.144
8549	M69238	Homo sapiens Arnt	5341	100.000
8550	X12433	Homo sapiens put. ORF	2902	100.000
8551	D63880	Homo sapiens KIAA0159 gene product is related to yeast protein L8479.14.	9109	99.929
8552	M30185	Homo sapiens cholesteryl ester transfer protein precursor	3186	100.000
8553	AF102265	Homo sapiens N-acetylglucosamine-phosphate mutase	3544	100.000
8554	M19507	Homo sapiens myeloperoxidase	5048	99.732
8555	Y14318	Homo sapiens peroxisomal ABC-transporter	4000	100.000
8556	X85750	Homo sapiens expression associated with monocyte to macrophage differentiation	1662	98.739
8557	AF161703	Homo sapiens gammaS-crystallin	1237	99.419
8558	X01060	Homo sapiens put. transferrin receptor (aa 1-760)	5000	99.605
8559	U72678	Mus musculus EF-9	1014	92.857
8560	X81372	Homo sapiens biphenyl hydrolase-related protein	1890	99.635
8561	D28483	Homo sapiens SCR3	2702	99.263
8562	U66372	Bos taurus ribosomal protein S29	420	100.000
8563	D50063	Homo sapiens proteasome subunit p40 / Mov34 protein	2063	98.765
8564	J05594	Homo sapiens NAD+-dependent 15-hydroxyprostaglandin dehydrogenase	1725	99.624

8565	AC006033	Homo sapiens similar to MLN 64; similar to I38027 (PID:g2135214)	1517	100.000
8566	AF002697	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3	1285	100.000
8567	X79536	Homo sapiens hnRNPcore protein A1	2211	100.000
8568	AF012652	Trypanosoma cruzi Tcrab27	233	68.000
8569	D86438	Homo sapiens Iba1 (ionized calcium binding adapter molecule 1)	955	100.000
8570	X77639	Sus scrofa cellular retinol binding protein II	582	60.150
8571	X83441	Homo sapiens DNA ligase IV	5616	99.408
8572	AB023811	Homo sapiens TU3A	450	54.135
8573	U21855	Mus musculus mCAF1 protein	1914	99.649
8574	AF078857	Homo sapiens PTD002	1269	100.000
8575	Z73420	Homo sapiens match: protein P25325; match: DNA X59434	2072	100.000
8576	AC006929	Arabidopsis thaliana unknown protein	283	34.286
8577	AB018288	Homo sapiens KIAA0745 protein	5881	99.020
8578	AF065441	Mus musculus FGF binding protein 1	228	24.402
8579	AL031824	Schizosaccharomyces pombe conserved hypothetical protein	193	30.078
8580	AJ008112	Homo sapiens C17orf1 protein	2986	100.000
8581	AF003386	Caenorhabditis elegans No definition line found	1557	44.186
8582	D80004	Homo sapiens KIAA0182	7708	99.825
8583	AC003027	Arabidopsis thaliana lcl prt_seq No definition line found	481	40.329
8584	AB029028	Homo sapiens KIAA1105 protein	596	29.783
8585	X57802	Homo sapiens immunoglobulin lambda light chain	1513	97.835
8586	AB028996	Homo sapiens KIAA1073 protein	325	23.600
8587	AF111941	Dictyostelium discoideum development protein DG1148	304	56.962
8588	AB001993	Homo sapiens glia maturation factor homologous protein	941	100.000
8589	AF124249	Homo sapiens SH2-containing protein Nsp1	3932	99.826
8590	D25304	Homo sapiens this sequence overlaps D13631, it covers 954..4359 of this sequence.	5066	100.000
8591	AF132209	Homo sapiens prepro-major basic protein homolog	1608	100.000
8592	AJ002078	Homo sapiens syntaxin 6	1622	100.000
8593	U29488	Caenorhabditis elegans No definition line found	849	61.333
8594	M13444	Mus musculus alpha-tubulin isotype M-alpha-6	3047	100.000
8595	Z81137	Unknown Similarity to Yeast YIP1 protein (SW:P53039); cDNA EST EMBL:T01608 comes from this gene; cD	255	27.803
8596	AF151903	Homo sapiens CGI-145 protein	2479	99.482
8597	AL050405	Homo sapiens hypothetical protein	2129	99.688
8598	D87463	Homo sapiens KIAA0273	1782	76.364
8599	AF073518	Homo sapiens small EDRK-rich factor 1, short isoform	385	100.000
8600	AL117468	Homo sapiens hypothetical protein	1121	100.000
8601	L05425	Homo sapiens nucleolar GTPase	4793	100.000
8602	AL117600	Homo sapiens hypothetical protein	3670	99.458
8603	Y13936	Homo sapiens protein phosphatase 2C gamma	3621	100.000
8604	AJ249735	Homo sapiens claudin-6	1469	100.000

8605	AF175409	Homo sapiens unknown	2750	99.757
8606	AJ224677	Homo sapiens scrapie responsive protein 1	707	100.000
8607	X99656	Homo sapiens SH3-containing Grb-2-like 1	2426	100.000
8608	D90703	Escherichia coli Hypothetical 13.8 kd protein in cspE-lipA intergenic region.	819	98.413
8609	X57560	Escherichia coli pspE protein	682	100.000
8610	L37368	Homo sapiens RNA-binding protein	2011	100.000
8611	X77584	Homo sapiens ATL-derived factor/thioredoxin	705	100.000
8612	X78990	Mus musculus testin	1191	48.916
8613	AF151849	Homo sapiens CGI-91 protein	2001	100.000
8614	D87447	Homo sapiens KIAA0258	2628	100.000
8615	X77858	Human papillomavirus type 59 ORF putative E5	99	31.746
8616	M97935	Homo sapiens transcription factor ISGF-3	5010	100.000
8617	AB002294	Homo sapiens KIAA0296	1298 8	99.891
8618	AF151878	Homo sapiens CGI-120 protein	644	75.397
8619	AL035064	Schizosaccharomyces pombe queuine trna-ribosyltransferase	1535	56.743
8620	AF006088	Homo sapiens p16-Arc	685	68.831
8621	AF077042	Homo sapiens 30S ribosomal protein S7 homolog	1625	100.000
8622	U29195	Homo sapiens neuronal pentraxin II	3473	98.868
8623	AB018322	Homo sapiens KIAA0779 protein	2019	100.000
8624	X67209	Mus musculus npdcf-1	1511	75.585
8625	AF180819	Homo sapiens LAK1 protein	3537	99.806
8626	AF136382	Homo sapiens JNK MAP kinase scaffold protein JIP2	5730	100.000
8627	AJ248283	Pyrococcus abyssi methylmalonyl-CoA mutase, subunit alpha, C-terminus (mcmA2)	126	30.488
8628	Z75134	Canis familiaris rod transducin	2322	100.000
8629	AF007160	Homo sapiens unknown	915	100.000
8630	AL050007	Homo sapiens hypothetical protein	506	98.795
8631	AC009465	Arabidopsis thaliana unknown protein, contains TNFR/NGFR cysteine-rich region	375	38.519
8632	Z73277	Saccharomyces cerevisiae ORF YLR105c	256	29.240
8633	AF156102	Homo sapiens ELL complex EAP30 subunit	1678	99.612
8634	Z95114	Homo sapiens bK212A2.1 (TNF-inducible protein CG12-1)	1198	59.627
8635	U88964	Homo sapiens HEM45	249	90.909
8636	AL050143	Homo sapiens hypothetical protein	759	100.000
8637	U40953	Caenorhabditis elegans No definition line found	659	28.989
8638	AB018566	Homo sapiens Proline synthetase associated	1828	100.000
8639	D83767	Homo sapiens Rep-8	1750	100.000
8640	U36340	Mus musculus BKLF	1473	93.103
8641	U96769	Homo sapiens chondroadherin	2393	99.721
8642	U66411	Drosophila melanogaster putative type III alcohol dehydrogenase	1307	49.403
8643	X55989	Homo sapiens eosinophil cationic-related protein	1167	99.371
8644	AF177533	Homo sapiens tight junction protein ZO-2 isoform A	7916	99.328
8645	AF007151	Homo sapiens unknown	1908	100.000
8646	AB018307	Homo sapiens KIAA0764 protein	2802	100.000
8647	Z32684	Homo sapiens membrane transport protein	2964	100.000
8648	U09367	Homo sapiens zinc finger protein ZNF136	3902	99.815

8649	M89928	Oryctolagus cuniculus binding protein	736	100.000
8650	D90701	Escherichia coli Hypothetical protein 2.	464	100.000
8651	U19577	Escherichia coli galactonate dehydratase	508	94.805
8652	AP000064	Aeropyrum pernix 120aa long hypothetical protein	123	36.620
8653	D90699	Escherichia coli ORF ID:o163#3	696	98.182
8654	AL117660	Homo sapiens hypothetical protein	609	77.273
8655	AL117195	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	544	33.898
8656	U79298	Homo sapiens unknown	2465	100.000
8657	Z78542	Caenorhabditis elegans similar to Mitochondrial carrier proteins; cDNA EST EMBL:T01651 comes from this gene	697	47.191
8658	M23236	Mus musculus proline-rich protein	523	39.592
8659	AJ010063	Homo sapiens telethonin	1132	100.000
8660	AL049711	Arabidopsis thaliana hypothetical protein	283	33.032
8661	AF143235	Homo sapiens apoptosis related protein APR-1	1247	100.000
8662	J04173	Homo sapiens phosphoglycerate mutase 2	1721	100.000
8663	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	4364	99.394
8664	AF151878	Homo sapiens CGI-120 protein	1113	100.000
8665	AF044774	Homo sapiens breakpoint cluster region protein 2	3415	99.412
8666	Z68227	Caenorhabditis elegans cDNA EST EMBL:D72691 comes from this gene; cDNA EST yk566e9.3 comes from this gene	167	37.349
8667	AF034801	Homo sapiens liprin-alpha4	3274	98.031
8668	AL008729	Homo sapiens predicted protein dJ257A7.1	836	100.000
8669	Y17849	Homo sapiens ganglioside-induced differentiation associated protein 1	2328	98.603
8670	AF084458	Homo sapiens sec61 homolog	3083	100.000
8671	Y12642	Homo sapiens E48 antigen	787	100.000
8672	Z73102	Caenorhabditis elegans predicted using Genefinder; Similarity to Bacillus subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST EMBL:D74098 comes from this gene; cDNA EST EMBL:C12520 comes from this gene; cDNA EST EMBL:D71409 comes from this gene	608	38.800
8673	X78933	Homo sapiens zinc finger protein	630	49.296
8674	M17614	Homo sapiens transferrin	212	47.561
8675	X61497	Mus musculus I54 protein	198	56.098
8676	M12140	Homo sapiens envelope protein	588	31.894
8677	X57432	Rattus rattus ribosomal protein S2	694	58.547
8678	X03145	Homo sapiens pot. ORF III	235	51.923
8679	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Peptide, 370 aa p40	763	42.138
8680	U01849	Trypanosoma brucei ORF2	173	39.130
8681	D90176	Mus musculus ORF of NFI-B6	1593	93.841
8682	AF153062	Canis familiaris type I collagen pre-pro-alpha1(I) chain	230	27.186
8683	AB030237	Canis familiaris D4 dopamine receptor	173	41.000
8684	AF134825	Homo sapiens small nuclear ribonucleoprotein B	528	85.294
8685	X51394	Xenopus laevis APEG precursor protein	310	30.918
8686	AF052432	Homo sapiens katanin p80 subunit	194	31.282
8687	M13100	Rattus norvegicus unknown protein	237	41.667

8688	X03145	Homo sapiens pot. ORF II	304	56.190
8689	AB012223	Canis familiaris ORF2	226	47.500
8690	Z34802	Caenorhabditis elegans cDNA EST yk372h11.3 comes from this gene; cDNA EST yk372h11.5 comes from this gene	126	32.692
8691	S80905	Homo sapiens Con1=salivary concanavalin-A binding protein {exon 3}	168	28.239
8692	U04267	Gossypium barbadense proline-rich cell wall protein	267	34.731
8693	U67988	Homo sapiens guanylate kinase associated protein	570	78.571
8694	U73522	Homo sapiens AMSH	266	60.526
8695	AF123344	Homo sapiens Kruppel-like zinc finger transcription factor	283	56.250
8696	U71363	Homo sapiens zinc finger protein zfp6	430	51.678
8697	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	277	42.982
8698	X15804	Homo sapiens alpha-actinin (AA 1-892)	266	72.131
8699	U83303	Homo sapiens line-1 reverse transcriptase	168	46.835
8700	AF015454	Xenopus laevis ER1	829	66.667
8701	X90875	Mus musculus FXR1	521	64.844
8702	Z12172	Homo sapiens putative homeotic protein	429	76.190
8703	U72514	Homo sapiens C2f	363	57.944
8704	X56158	Homo sapiens immunoglobulin from VH4 family	534	76.923
8705	U01317	Homo sapiens G-gamma globin	217	50.602
8706	AL021396	Homo sapiens dJ971N18.2	861	85.161
8707	U49974	Homo sapiens mariner transposase	360	70.526
8708	U47924	Homo sapiens C8	490	68.966
8709	AC006233	Arabidopsis thaliana hypothetical protein	190	52.542
8710	M15386	Homo sapiens gamma-globin	466	71.698
8711	D88385	Sus scrofa A-Raf-1	396	72.414
8712	U95044	Homo sapiens zinc finger protein	221	43.382
8713	AF064553	Mus musculus NSD1 protein	223	57.895
8714	M15386	Homo sapiens gamma-globin	525	76.786
8715	M96982	Homo sapiens U2 snRNP auxiliary factor small subunit	398	39.608
8716	U49082	Homo sapiens transporter protein	950	62.172
8717	AF000422	Homo sapiens TTF-I interacting peptide 5	1802	84.091
8718	U01317	Homo sapiens G-gamma globin	215	50.000
8719	AF053356	Homo sapiens insulin receptor substrate like protein	317	39.631
8720	U58337	Mus musculus ligatin	330	63.636
8721	S61973	Rattus sp. NMDA receptor glutamate-binding subunit	2375	74.723
8722	M29622	Mus musculus open reading frame 2	120	50.000
8723	X74330	Homo sapiens DNA primase (subunit p48)	307	57.292
8724	M16550	Baboon endogenous virus pol polyprotein	660	34.990
8725	Z77655	Caenorhabditis elegans Weak similarity to Human calcium-dependent proetase (SW:CANS HUMAN)	194	48.718
8726	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	2155	65.565
8727	AL033125	Unknown 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end; 2-evidence=pred	1625	45.960
8728	U49974	Homo sapiens mariner transposase	889	66.045

8729	X55777	Homo sapiens put. ORF	240	59.211
8730	AF151887	Homo sapiens CGI-129 protein	177	75.000
8731	X03145	Homo sapiens put. ORF II	275	47.934
8732	X75042	Homo sapiens c-rel	2333	90.453
8733	AF003535	Homo sapiens ORF2-like protein	419	63.478
8734	AF000194	Caenorhabditis elegans No definition line found	356	25.364
8735	U93565	Homo sapiens putative p150	195	37.864
8736	AF003535	Homo sapiens ORF2-like protein	440	58.088
8737	X51394	Xenopus laevis APEG precursor protein	203	27.875
8738	U93565	Homo sapiens putative p150	472	52.381
8739	AC006585	Arabidopsis thaliana putative extragenic suppressor protein	1243	43.545
8740	AB002306	Homo sapiens KIAA0308	900	40.748
8741	AL031177	Homo sapiens dJ889M15.3 (novel protein)	1109	90.099
8742	L11366	Herpesvirus papio EBNA2 gene product	263	25.731
8743	AB012139	Rattus norvegicus procollagen C-proteinase 3	267	38.312
8744	M27878	Homo sapiens DNA binding protein	407	31.359
8745	X07704	Homo sapiens Po protein	304	45.912
8746	X53581	Rattus norvegicus ORF4	444	39.648
8747	AF006740	Homo sapiens No definition line found	276	41.935
8748	AC005825	Arabidopsis thaliana putative glucokinase	227	51.389
8749	L22031	Glycine max hydroxyproline-rich glycoprotein	155	41.379
8750	Z14019	Nicotiana tabacum pistil extensin like protein	197	32.540
8751	AJ243460	Leishmania major proteophosphoglycan	245	34.123
8752	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	219	53.731
8753	Z81074	Unknown Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST EMBL:M75819 co	1366	64.223
8754	AF107727	Rattus norvegicus sertolin	370	61.818
8755	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	323	29.964
8756	U97553	murine herpesvirus 68 unknown	181	28.381
8757	M26111	Anser anser beta-actin	527	82.979
8758	AC004136	Arabidopsis thaliana hypothetical protein	272	25.468
8759	AF015539	Mytilus edulis precollagen P	420	29.711
8760	AF129269	Homo sapiens DNA methyltransferase 3 beta 5	320	61.628
8761	AB012223	Canis familiaris ORF2	208	45.763
8762	AB015054	Rhizomucor pusillus Alg2	162	43.750
8763	D31763	Homo sapiens ha0946 protein is Kruppel-related.	758	38.259
8764	AF153127	Gallus gallus SAPK interacting protein	2179	72.782
8765	AF139185	Rattus norvegicus myomegalin	861	65.066
8766	U09116	Homo sapiens ORF2, encodes a reverse transcriptase homolog	346	44.056
8767	M74002	Homo sapiens arginine-rich nuclear protein	692	79.605
8768	AF055904	Myxococcus xanthus unknown	294	33.438
8769	AL110249	Homo sapiens hypothetical protein	183	36.449
8770	L22760	Rattus norvegicus DNA binding protein	176	26.984
8771	AB032904	Hylobates syndactylus dopamine receptor D4	163	37.008
8772	U97553	murine herpesvirus 68 unknown	346	30.680
8773	X67863	Mus musculus T2	236	40.690
8774	J00123	Homo sapiens preproenkephalin (44	30.000
8775	U49974	Homo sapiens mariner transposase	307	67.742
8776	AB029014	Homo sapiens KIAA1091 protein	1362	61.096

8777	X61046	Hydra sp. mini-collagen	167	47.541
8778	D88587	Homo sapiens Hakata antigen	337	40.816
8779	M12140	Homo sapiens envelope protein	554	32.624
8780	X55777	Homo sapiens put. ORF	245	67.742
8781	M80341	Homo sapiens ORF2 contains a reverse transcriptase domain.; ORF2	320	52.809
8782	Z96047	Caenorhabditis elegans DY3.6	251	28.846
8783	AF132552	Drosophila melanogaster BcDNA.GM01838	1292	79.498
8784	X65120	Homo sapiens alpha1(X) collagen	312	29.081
8785	AL033545	Arabidopsis thaliana extensin-like protein	198	32.812
8786	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	421	54.839
8787	AC002542	Homo sapiens similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619)	1547	62.439
8788	M64793	Rattus norvegicus salivary proline-rich protein	242	30.493
8789	U04267	Gossypium barbadense proline-rich cell wall protein	210	36.601
8790	X86019	Homo sapiens SH3-domain interacting protein	246	29.936
8791	Z14016	Nicotiana tabacum pistil extensin like protein, partial CDS	179	31.579
8792	U57368	Mus musculus EGF repeat transmembrane protein	437	56.522
8793	M11902	Mus musculus proline-rich salivary protein	221	35.789
8794	AF153685	Homo sapiens truncated calcium binding protein	89	28.421
8795	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	184	37.838
8796	X15332	Homo sapiens alpha-1 (III) collagen	294	28.367
8797	AF124663	Mus musculus UbcM4 interacting protein 28; UIP28	515	43.777
8798	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	428	61.146
8799	U97553	murine herpesvirus 68 unknown	390	29.197
8800	S62941	Homo sapiens Ps 2=basic proline-rich protein(PRB1L precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor) {C-terminal}	353	32.915
8801	X61395	Lycopersicon esculentum proline rich protein	185	26.016
8802	AJ243460	Leishmania major proteophosphoglycan	245	30.189
8803	X61045	Hydra sp. mini-collagen	193	35.043
8804	X57010	Homo sapiens collagen II alpha 1 chain	158	37.419
8805	U05342	Mus musculus zinc finger protein	644	50.505
8806	U04267	Gossypium barbadense proline-rich cell wall protein	223	35.115
8807	X55777	Homo sapiens put. ORF	348	72.368
8808	AF055904	Myxococcus xanthus unknown	163	30.682
8809	X60432	Zea mays prolin rich protein	195	32.680
8810	AF055904	Myxococcus xanthus unknown	238	30.712
8811	U25281	Rattus norvegicus SH3 domain binding protein	207	32.035
8812	U35730	Mus musculus jerky	260	33.846
8813	U88895	Homo sapiens ORF2	302	71.212
8814	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	256	44.000
8815	AF019969	Mus musculus Su(var)3-9 homolog	420	49.315
8816	U21310	Caenorhabditis elegans No definition line found	164	32.824
8817	L29169	Chironomus tentans giant secretory protein (sp-Ic)	189	40.800

8818	AL008583	Homo sapiens dJ327J16.3 (novel CHROMobox family protein)	532	59.236
8819	U07973	Gallus gallus alpha-1 collagen type III	346	28.075
8820	D29833	Homo sapiens proline rich peptide P-B	393	73.750
8821	AL034421	Homo sapiens dJ1137F22.2 (core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (MTGR1a, MTG8/ETO/CDR family protein) (isoform 2))	147	32.075
8822	Y10529	Homo sapiens olfactory receptor	1145	75.200
8823	AF055904	Myxococcus xanthus unknown	200	30.545
8824	U03714	Mus musculus alpha 1(XVIII) collagen	165	39.815
8825	AF017777	Drosophila melanogaster waclaw	1208	52.099
8826	X07882	Homo sapiens Po protein	182	34.746
8827	X15311	Woolly monkey sarcoma virus reverse transcriptase (476 AA)	491	47.236
8828	AJ222580	Mus musculus B99 protein	184	27.987
8829	M69297	Homo sapiens ORF 2	109	33.735
8830	Y18620	Arabidopsis thaliana DsPTP1 protein	251	43.925
8831	AF010170	synthetic construct Pol	659	26.002
8832	U68412	Arenicola marina fibrillar collagen	198	34.711
8833	X61047	Hydra sp. mini-collagen	123	33.684
8834	AB032907	Hylobates lar dopamine receptor D4	175	35.811
8835	D64052	Nicotiana tabacum cytochrome P450 like TBP	183	36.691
8836	AF020261	Santalum album proline rich protein	242	26.027
8837	AL078606	Arabidopsis thaliana putative protein	359	45.113
8838	M15103	Plasmodium cynomolgi circumsporozoite antigen	194	26.210
8839	AJ004832	Homo sapiens neuropathy target esterase	1218	58.583
8840	AC006283	Arabidopsis thaliana hypothetical protein	170	29.605
8841	U32305	Caenorhabditis elegans No definition line found	378	40.271
8842	AL031603	Schizosaccharomyces pombe conserved hypothetical protein.	1253	51.969
8843	Z97184	Homo sapiens BING1	484	41.494
8844	AF055904	Myxococcus xanthus unknown	264	31.985
8845	Z81074	Caenorhabditis elegans predicted using Genefinder; Similarity to Yeast ORF YOR070C (TR:Q08484); cDNA EST EMBL:T01610 comes from this gene; cDNA EST EMBL:D36648 comes from this gene; cDNA EST yk303b2.5 comes from this gene	419	35.821
8846	U25281	Rattus norvegicus SH3 domain binding protein	233	31.837
8847	X55686	Lycopersicon esculentum extensin (class II)	56	31.818
8848	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	206	76.744
8849	X64173	Zea diploperennis hydroxyproline-rich glycoprotein	181	33.117
8850	AC006233	Arabidopsis thaliana hypothetical protein	188	42.342
8851	U62528	Equus caballus type II collagen	326	29.173
8852	Z14015	Nicotiana tabacum pistil extensin like protein	253	29.469
8853	AF121861	Homo sapiens sorting nexin 11	68	30.000
8854	U93569	Homo sapiens putative p150	296	42.373
8855	L24521	Homo sapiens transformation-related protein	249	56.667
8856	AF086608	Rattus norvegicus neurestin beta	297	30.802
8857	AF000381	Homo sapiens non-functional folate binding protein	806	89.506
8858	S70011	Rattus sp. tricarboxylate carrier	298	53.846

8859	AF016671	Caenorhabditis elegans Similar to collagen	274	45.361
8860	U49974	Homo sapiens mariner transposase	368	68.041
8861	M22333	Homo sapiens unknown protein	585	49.393
8862	M92913	Nephila clavipes dragline silk fibroin	326	28.439
8863	AL031282	Homo sapiens dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae) bacterial, worm and yeast hypothetical proteins)	1589	55.644
8864	AF017777	Drosophila melanogaster tweety	475	25.971
8865	AB011126	Homo sapiens KIAA0554 protein	426	58.678
8866	Y14690	Homo sapiens procollagen alpha 2(V)	238	30.038
8867	AB028997	Homo sapiens KIAA1074 protein	504	50.575
8868	AC005498	Homo sapiens R31665 2	366	27.083
8869	AF159131	Mus musculus nucleolar RNA helicase II/Gu	174	32.335
8870	D80009	Homo sapiens KIAA0187	827	87.333
8871	AC006085	Arabidopsis thaliana Hypothetical protein	294	28.516
8872	U53155	Unknown Similar to cuticular collagen; coded for by C. elegans cDNA yk58e6.3; coded for by C. elegans	109	34.127
8873	X15081	Crithidia fasciculata MURF2 protein (AA 1-348)	196	32.639
8874	Z70780	Caenorhabditis elegans cDNA EST yk465d10.3 comes from this gene; cDNA EST yk465d10.5 comes from this gene; cDNA EST yk481d9.5 comes from this gene	323	27.626
8875	AC003979	Arabidopsis thaliana ESTs gb Z34075, gb Z34835 and gb AA040488 come from this gene.	424	40.299
8876	AL022537	Arabidopsis thaliana putative protein	172	33.121
8877	AL078637	Arabidopsis thaliana serine/threonine kinase-like protein	220	30.270
8878	AB029022	Homo sapiens KIAA1099 protein	1687	79.878
8879	AL022393	Homo sapiens p373c6.2	538	50.521
8880	U76557	Rattus norvegicus O-GlcNAc transferase, p110 subunit	1063	64.537
8881	X75919	Pseudomonas fluorescens TRANSFERRED ENTRY: 3.4.19.3	53	28.916
8882	X99699	Homo sapiens XIAP associated factor-1 (ZAP-1)	689	64.324
8883	AF026802	Homo sapiens alpha-3 type IX collagen	120	36.735
8884	AF041330	Bodo saltans NADH dehydrogenase subunit 5	144	32.824
8885	AF003535	Homo sapiens ORF2-like protein	231	44.882
8886	Y12713	Mus musculus Gag polyprotein	228	37.324
8887	X55777	Homo sapiens put. ORF	309	54.444
8888	U44091	Rattus norvegicus atrophin-1 related protein	224	36.683
8889	AJ012582	Homo sapiens hyperpolarization-activated cation channel HCN2	113	32.653
8890	AF091234	Mus musculus putative transcription factor	1363	67.341
8891	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	1439	77.891
8892	AL009266	Homo sapiens hypothetical protein	803	67.568
8893	U97553	murine herpesvirus 68 unknown	287	30.478
8894	AJ004801	Bovine herpesvirus type 1.1 glycoprotein C	169	34.746
8895	AJ132828	Spermatozopsis similis p210 protein	177	27.039
8896	AF167320	Mus musculus zinc finger protein ZFP113	567	34.409
8897	Z72495	Carassius auratus ZP2	413	30.882
8898	D29642	Homo sapiens KIAA0053	398	49.612
8899	U45958	Nicotiana glauca pistil extensin-like protein	210	31.780
8900	M64793	Rattus norvegicus salivary proline-rich protein	273	34.701

8901	S71333	Platyrrhini alpha 1,3 galactosyltransferase, alpha 1,3GT	622	65.584
8902	M13101	Rattus norvegicus unknown protein	348	50.794
8903	M16976	Glycine max N-75	274	36.364
8904	X52235	Homo sapiens ORFII	308	43.275
8905	X52851	Homo sapiens peptidylprolyl isomerase	766	74.332
8906	L24521	Homo sapiens transformation-related protein	347	60.638
8907	AF007269	Arabidopsis thaliana No definition line found	525	28.500
8908	M24732	Homo sapiens lamin-like protein	174	40.708
8909	AF055904	Myxococcus xanthus unknown	256	32.090
8910	AB028070	Homo sapiens activator of S phase Kinase	181	36.522
8911	L28802	Mus musculus zinc finger protein	206	31.343
8912	AJ243460	Leishmania major proteophosphoglycan	197	28.854
8913	AF009829	Mycobacterium bovis unknown	183	37.234
8914	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	475	38.871
8915	X68684	Homo sapiens ZNF11B	258	39.370
8916	M64791	Rattus norvegicus salivary proline-rich protein	150	34.127
8917	M17463	Human papillomavirus type 5 ORF E4 from bp 3285 to 4022; putative	112	30.058
8918	AL021086	Unknown /prediction=(method:"genefinder", version:"084"); /prediction=(method:"genscan", ve	1994	52.736
8919	AL035289	Homo sapiens hypothetical protein	2986	69.146
8920	AC006232	Arabidopsis thaliana putative proline-rich protein PRP2 precursor	393	28.254
8921	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	481	40.529
8922	X02585	Xenopus laevis unidentified open reading frame 2	249	48.315
8923	U75308	Homo sapiens TBP-associated factor	232	33.209
8924	AF073770	Homo sapiens carnitine octanoyltransferase	488	98.750
8925	M15182	Homo sapiens beta-glucuronidase precursor (EC 3.2.1.31)	743	55.000
8926	AB023206	Homo sapiens KIAA0989 protein	327	50.000
8927	L10910	Homo sapiens splicing factor	947	59.170
8928	U88895	Homo sapiens ORF derived from D1 leader region and integrase coding region	189	42.222
8929	M13100	Rattus norvegicus unknown protein	214	47.312
8930	AL031581	Unknown /prediction=(method:"genscan", version:"1.0", score:"198.31"); /prediction=(method:	236	25.786
8931	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	319	43.802
8932	M19419	Mus musculus proline-rich salivary protein	217	43.411
8933	A31038	Nicotiana glauca PRP3	157	44.304
8934	AF020261	Santalum album proline rich protein	201	42.718
8935	U58755	Caenorhabditis elegans C34D4.11 gene product	175	43.564
8936	Z47357	Caenorhabditis elegans cDNA EST EMBL:T00822 comes from this gene; cDNA EST EMBL:T00823 comes from this gene	327	43.382
8937	X83543	Homo sapiens APXL	547	39.852
8938	U54638	Mus musculus rhotekin	1149	89.401
8939	AF047690	Homo sapiens ATP-binding cassette protein M-	225	54.054

		ABC1		
8940	AF075575	Homo sapiens dysferlin	341	37.563
8941	A31038	Nicotiana glauca PRP3	155	33.708
8942	AL033534	Schizosaccharomyces pombe serine-rich protein	226	27.891
8943	U07974	Gallus gallus unknown	210	33.816
8944	L22030	Glycine max hydroxyproline-rich glycoprotein	167	31.613
8945	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038)	721	60.476
8946	AF080070	Mus musculus zinc finger protein 54	236	43.220
8947	M92913	Nephila clavipes dragline silk fibroin	276	30.651
8948	D90899	Synechocystis sp. hypothetical protein	392	31.818
8949	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	314	26.752
8950	U09413	Homo sapiens zinc finger protein ZNF135	1055	49.547
8951	AF019236	Dictyostelium discoideum TipD	211	26.250
8952	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	296	35.122
8953	X76203	Drosophila virilis major larval glue protein	180	31.098
8954	U41543	Caenorhabditis elegans No definition line found	262	33.742
8955	Z68747	Homo sapiens imogen 38	697	59.055
8956	AF045646	Caenorhabditis elegans contains similarity to collagens	126	33.775
8957	AF018432	Homo sapiens dUTPase	464	64.615
8958	U97553	murine herpesvirus 68 unknown	214	28.668
8959	L27428	Homo sapiens reverse transcriptase	173	26.437
8960	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	286	75.000
8961	M12099	Mus musculus proline-rich protein	263	33.333
8962	L24521	Homo sapiens transformation-related protein	327	64.045
8963	X13885	Nicotiana tabacum extensin (AA 1-620)	371	25.828
8964	AL050331	Homo sapiens dJ486I3.4 (TSPY-like (testis specific protein, Y-linked like))	1548	94.981
8965	AJ388557	Canis familiaris zinc finger protein	358	45.098
8966	U83303	Homo sapiens line-1 reverse transcriptase	269	43.750
8967	X03145	Homo sapiens pot. ORF II	238	48.421
8968	AB012223	Canis familiaris ORF2	268	53.846
8969	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	731	91.270
8970	AF164612	Homo sapiens Gag protein	272	44.706
8971	AB012223	Canis familiaris ORF2	295	40.426
8972	AL024499	Caenorhabditis elegans cDNA EST EMBL:C10123 comes from this gene	244	34.746
8973	X83413	Human herpesvirus 6 U88	685	36.986
8974	L22343	Homo sapiens nuclear phosphoprotein	2191	86.410
8975	AB012223	Canis familiaris ORF2	361	52.212
8976	M64791	Rattus norvegicus salivary proline-rich protein	253	35.638
8977	Z98204	Hordeum vulgare extensin	209	28.652
8978	AL035423	Homo sapiens dJ20I3.1 (brain mitochondrial carrier protein-1 (BMCP1))	381	51.007
8979	AJ132828	Spermatozopsis similis p210 protein	206	30.047
8980	AF132856	Homo sapiens suppressor of G2 allele of skp1 homolog	209	64.815
8981	U93872	Kaposi's sarcoma-associated herpesvirus ORF	109	31.915

		73, contains large complex repeat CR 73		
8982	X61294	Rattus norvegicus L1 retroposon, a portion of its ORF2 sequence	276	44.521
8983	AL035461	Homo sapiens dJ967N21.3 (novel protein similar to predicted worm, yeast and plant proteins)	2526	95.455
8984	D29956	Homo sapiens This gene is similar to tre oncogene(X63547) .	526	63.690
8985	AJ005282	Homo sapiens NPR-Bi	6054	96.677
8986	Z54141	Saccharomyces cerevisiae unknown	128	31.250
8987	D67066	Bos taurus N-WASP	247	41.221
8988	U01849	Trypanosoma brucei ORF1	178	31.034
8989	AL022537	Arabidopsis thaliana putative protein	193	29.327
8990	AF062389	Rattus norvegicus kidney-specific protein	1344	60.857
8991	AF104411	Mus musculus neuronal-specific septin 3	2395	82.452
8992	Z70208	Caenorhabditis elegans predicted using Genefinder; similar to collagen	246	30.612
8993	M86699	Homo sapiens kinase	644	65.934
8994	Z72807	Saccharomyces cerevisiae ORF YGR023w	171	32.895
8995	AF055904	Myxococcus xanthus unknown	202	29.694
8996	AB012223	Canis familiaris ORF2	199	45.977
8997	AF071172	Homo sapiens HERC2	260	79.245
8998	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	216	43.333
8999	AF087573	Homo sapiens DNA fragmentation factor DFF35	427	68.613
9000	AL031174	Schizosaccharomyces pombe hypothetical protein	215	40.404
9001	AF017777	Drosophila melanogaster tweety	472	30.380
9002	U49973	Homo sapiens ORF1; MER37; putative transposase similar to pogo element	476	41.573
9003	U97553	murine herpesvirus 68 unknown	242	32.783
9004	AF073344	Homo sapiens ubiquitin-specific protease 3	2084	90.909
9005	AB028965	Homo sapiens KIAA1042 protein	979	57.621
9006	M69297	Homo sapiens ORF 3	136	41.096
9007	AL117589	Homo sapiens hypothetical protein	902	59.480
9008	L29435	Gallus gallus beta-5 tubulin	2300	95.845
9009	X78928	Homo sapiens zinc finger protein	551	64.463
9010	L41827	Homo sapiens sensory and motor neuron-derived factor	1404	98.643
9011	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	298	79.688
9012	AL035632	Unknown /prediction=(method:""genefinder"", version:""084"", score:""113.36""); /prediction=(meth	673	55.435
9013	X94910	Homo sapiens ERp28	468	74.074
9014	X53476	Mus musculus HMG-14 (AA 1-96)	211	79.167
9015	M15386	Homo sapiens gamma-globin	556	71.094
9016	S39127	human, testis, Peptide, 331 aa cathepsin S=cysteine proteinase	157	67.442
9017	AF115384	Homo sapiens LRB	279	82.456
9018	K02212	Homo sapiens alpha-1-antitrypsin	2458	98.223
9019	A12029	Homo sapiens MRP-14	322	51.923
9020	AB028997	Homo sapiens KIAA1074 protein	189	69.811
9021	L13440	Nicotiana tabacum cysteine-rich extensin-like protein-2	202	52.459
9022	M15386	Homo sapiens gamma-globin	898	98.621
9023	U10362	Homo sapiens GP36b glycoprotein	506	53.741

9024	AB011157	Homo sapiens KIAA0585 protein	332	88.525
9025	Z32683	Unknown cDNA EST EMBL:Z14902 comes from this gene; cDNA EST EMBL:M89155 comes from this gene; cDNA	711	28.841
9026	AF000560	Homo sapiens TTF-I interacting peptide 20; TIP20; Transcription Termination Factor I Interacting Peptide 20	224	52.381
9027	AF171099	Xenopus laevis Mi-2 histone deacetylase complex protein 66	648	61.137
9028	AB018341	Homo sapiens KIAA0798 protein	1398	62.281
9029	AF026954	Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDP α	1070	71.374
9030	U93569	Homo sapiens putative p150	256	57.143
9031	AB017614	Mus musculus OASIS protein	276	34.091
9032	L10110	Octopus dofleini alpha tubulin	369	74.667
9033	AL023706	Schizosaccharomyces pombe hypothetical protein	358	34.300
9034	Z70683	Unknown cDNA EST EMBL:T01585 comes from this gene; cDNA EST EMBL:D72333 comes from this gene; cDNA	750	33.613
9035	AB007198	Agkistrodon blomhoffii siniticus phospholipase A2 inhibitor	248	37.143
9036	X80433	Mus musculus tex292	278	80.597
9037	Y09945	Rattus norvegicus putative integral membrane transport protein	173	56.863
9038	X52574	Mus musculus GTP binding protein	2154	84.635
9039	U63840	Rattus norvegicus nucleoporin p54	1202	69.381
9040	AB011169	Homo sapiens KIAA0597 protein	260	43.011
9041	D14336	Mus musculus RNA polymerase I associated factor (PAF53)	697	71.233
9042	AB029008	Homo sapiens KIAA1085 protein	2554	99.482
9043	M37190	Homo sapiens ras inhibitor	708	40.431
9044	AL050262	Homo sapiens hypothetical protein	543	39.922
9045	AF071059	Mus musculus zinc finger RNA binding protein	3718	96.721
9046	X58636	Mus musculus lymphoid enhancer factor 1	1428	94.009
9047	U05681	Homo sapiens homologous to members of the I-kappa B family; protein binds NF-kappa B proteins	329	32.534
9048	AL117557	Homo sapiens hypothetical protein	1432	83.600
9049	AF125455	Caenorhabditis elegans No definition line found	231	29.167
9050	X52063	Escherichia coli orfB	397	42.553
9051	AL031770	Homo sapiens dJ20B11.1 (ortholog of rat RSEC5 (mammalian exocyst complex subunit))	2189	99.432
9052	AF132953	Homo sapiens CGI-19 protein	2422	100.000
9053	U47024	Mus musculus MEM3	1159	92.708
9054	AF007109	Arabidopsis thaliana similar to yeast dcpl	347	34.416
9055	U41534	Caenorhabditis elegans No definition line found	380	31.724
9056	AF120499	Homo sapiens DEM1 protein	764	88.406
9057	X89401	Homo sapiens ribosomal protein L21	350	57.759
9058	Z82271	Unknown Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from	756	42.804
9059	M26312	Oryctolagus cuniculus unknown protein	204	33.571
9060	AF077188	Homo sapiens cullin 4A	425	98.571

9061	AC005546	Homo sapiens R29425 1	2564	93.271
9062	A52744	unidentified unnamed protein product	237	37.624
9063	L27428	Homo sapiens reverse transcriptase	399	72.043
9064	Z70783	Caenorhabditis elegans cDNA EST yk575f9.3 comes from this gene	372	38.150
9065	AL031579	Schizosaccharomyces pombe hypothetical protein	270	25.993
9066	AF027219	Homo sapiens ZNF202 beta	431	52.857
9067	Z85986	Homo sapiens dJ108K11.3 (similar to yeast suppressor protein SRP40)	1223	96.296
9068	U88587	Nicotiana glauca 120 kDa style glycoprotein	303	35.622
9069	D90868	Escherichia coli GLUCOKINASE (EC 2.7.1.2).	923	98.639
9070	AL035461	Homo sapiens dJ967N21.3 (novel protein similar to predicted worm, yeast and plant proteins)	3064	99.786
9071	AL096749	Homo sapiens truncated by frame shift; corresponding STS: EMBL:G37487	274	26.433
9072	U73379	Homo sapiens cyclin-selective ubiquitin carrier protein	787	79.762
9073	AL078630	Mus musculus 573K1.15 (mm17M1-6 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein))	669	86.667
9074	Z81505	Unknown similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene	486	34.672
9075	AF132956	Homo sapiens CGI-22 protein	2064	98.433
9076	AB025793	Bos taurus casein kinase I-alpha	149	71.429
9077	L29457	Mus musculus dynamin	423	60.484
9078	S60885	Mus sp. LYAR=cell growth regulating nucleolar protein	1188	74.532
9079	L05147	Homo sapiens phosphatase tyrosine/serine	212	45.783
9080	AF126736	Homo sapiens ubiquitin processing protease	2997	98.468
9081	AL080125	Homo sapiens hypothetical protein	442	75.510
9082	U64856	Caenorhabditis elegans weak similarity to TPR domains	583	44.845
9083	AL022117	Schizosaccharomyces pombe hypothetical protein	289	38.621
9084	AL110241	Homo sapiens hypothetical protein	1458	97.510
9085	AJ005698	Homo sapiens poly(A)-specific ribonuclease	712	82.639
9086	AF117897	Bos taurus rab11 binding protein	1302	82.609
9087	AB033168	Mus musculus nuclear protein ZAP	1451	93.627
9088	M58378	Homo sapiens synapsin I	1816	97.872
9089	AF051098	Mus musculus seven transmembrane domain orphan receptor	1745	92.000
9090	AJ131693	Homo sapiens AKAP450 protein	1238	97.500
9091	AF183910	Rattus norvegicus frizzled receptor 4	915	96.947
9092	AF067608	Caenorhabditis elegans No definition line found	57	42.857
9093	X76717	Homo sapiens MT-11 protein	200	75.610
9094	M64488	Rattus norvegicus synaptotagmin II	306	73.973
9095	AF000422	Homo sapiens TTF-I interacting peptide 5	439	41.714
9096	AF125569	Homo sapiens tumor suppressing STF cDNA 6	187	47.674
9097	A18812	Brassica napus extensin	324	32.143
9098	U73682	Homo sapiens meningioma-expressed antigen 11	196	29.703
9099	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	199	36.000
9100	AF180920	Homo sapiens cyclin ania-6a	1370	90.361
9101	AP000063	Aeropyrum pernix 175aa long hypothetical	158	35.780

		protein		
9102	D88315	Mus musculus tetracycline transporter-like protein	553	71.901
9103	AF051400	Gallus gallus fibulin-1, isoform C precursor	241	47.500
9104	X92521	Homo sapiens MMP-19 (matrix metalloproteinase)	600	41.356
9105	AF106702	Mus musculus testis-enriched protein tyrosine phosphatase	457	32.646
9106	Y17113	Xenopus laevis ribosomal protein L24	1009	68.037
9107	AL031447	Homo sapiens dJ126A5.1.2 (novel DnaJ domain protein) (isoform 2)	427	92.754
9108	M34024	Homo sapiens immunoglobulin heavy chain	734	82.270
9109	X59727	Homo sapiens 63kDa protein kinase	2621	98.765
9110	D90741	Escherichia coli ORF2	378	52.055
9111	AF091624	Drosophila melanogaster Pelle associated protein Pellino	840	55.285
9112	AF125158	Homo sapiens zinc finger DNA binding protein 99	4417	100.000
9113	X07311	Drosophila melanogaster heat shock protein	197	40.000
9114	Z83826	Homo sapiens dJ473B4.1 (novel protein similar to predicted human and worm genes)	494	72.131
9115	X03145	Homo sapiens pot. ORF III	274	59.000
9116	AL050008	Homo sapiens hypothetical protein	1449	88.281
9117	Z49909	Caenorhabditis elegans weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene; cDNA EST yk549e12.3 comes from this gene; cDNA EST yk618d6.3 comes from this gene	584	38.839
9118	X63546	Homo sapiens oncogene	2573	80.467
9119	AJ223782	Mus musculus CDC10	1675	91.958
9120	X85991	Mus musculus semaphorin B	1074	78.641
9121	M55264	Saimiriine herpesvirus 2 gene products	125	42.857
9122	AB028997	Homo sapiens KIAA1074 protein	602	56.970
9123	X76104	Homo sapiens DAP-kinase	5061	100.000
9124	X58826	Drosophila melanogaster RNA polymerase III second-largest subunit	517	69.912
9125	D89821	Mus musculus RhoM	766	53.202
9126	AF092091	Rattus norvegicus cp431	1700	82.647
9127	D87908	Mus musculus nuclear protein np95	401	47.134
9128	U38979	Homo sapiens hPMSR3	1141	94.444
9129	X51760	Homo sapiens zinc finger protein (583 AA)	373	59.292
9130	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	338	69.620
9131	AF098796	Mus musculus SLM-1	1278	96.618
9132	Z81030	Caenorhabditis elegans similar to citrate lyase beta chain; cDNA EST yk302b4.5 comes from this gene	255	45.000
9133	AF098863	Mus musculus Ets-protein Spi-C	459	46.199
9134	U95097	Xenopus laevis mitotic phosphoprotein 43	611	71.523
9135	AF000413	Plasmodium berghei merozoite surface protein-1	153	33.621
9136	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	801	38.074
9137	U62940	Rattus norvegicus mt-GrpE#1 precursor	258	60.204
9138	M13100	Rattus norvegicus unknown protein	255	50.685
9139	X67155	Homo sapiens mitotic kinase-like protein-1	4436	98.844

9140	U83303	Homo sapiens line-1 reverse transcriptase	356	58.416
9141	U79260	Homo sapiens unknown	335	69.048
9142	AF022821	Mus musculus putative potassium channel DP4	336	52.885
9143	AF055077	Homo sapiens zinc finger protein 42	932	86.061
9144	U16790	Mus musculus putative collagen alpha-2 (XI) chain	212	32.716
9145	AF071172	Homo sapiens HERC2	324	57.009
9146	Y17793	Mus musculus Dutt1 protein	644	87.156
9147	X98259	Homo sapiens M-phase phosphoprotein 8	380	55.285
9148	X85124	Mus musculus PACSIN	435	87.342
9149	U64833	Caenorhabditis elegans B0507.2 gene product	888	40.000
9150	M93017	Rattus norvegicus , gene product	1094	92.228
9151	AB026190	Homo sapiens Kelch motif containing protein	675	32.159
9152	AJ388555	Canis familiaris hypothetical protein	1163	88.559
9153	AB002312	Homo sapiens KIAA0314	597	39.384
9154	AF055636	Homo sapiens leucine-rich glioma-inactivated protein precursor	723	53.000
9155	D50930	Homo sapiens The KIAA0140 gene product is novel.	198	31.217
9156	AF006492	Mus musculus FOG	1384	68.652
9157	AF043179	Homo sapiens T cell receptor beta chain	758	58.768
9158	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	1436	63.772
9159	X55777	Homo sapiens put. ORF	351	70.513
9160	AF076167	Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T6	1118	91.892
9161	U67549	Methanococcus jannaschii spore coat polysaccharide biosynthesis protein E	675	35.770
9162	AL022325	Homo sapiens ff27C3.1.1 (protein similar to C. elegans protein B0035.16) (isoform 1)	922	75.115
9163	AL031266	Caenorhabditis elegans VM106R.1	275	42.105
9164	U00051	Caenorhabditis elegans coded for by C. elegans cDNA yk50b2.5; coded for by C. elegans cDNA CEESV26F; similar to lipases over a short region	827	31.369
9165	AB007898	Homo sapiens KIAA0438	198	80.556
9166	AF072509	Rattus norvegicus glutamate receptor interacting protein 2	826	84.472
9167	U40942	Caenorhabditis elegans No definition line found	759	45.956
9168	AB020649	Homo sapiens KIAA0842 protein	352	84.932
9169	D80009	Homo sapiens KIAA0187	864	93.750
9170	AF155110	Homo sapiens NY-REN-45 antigen	1914	51.565
9171	U88165	Caenorhabditis elegans No definition line found	616	48.374
9172	L04159	Plasmodium falciparum 3' end., gene product	204	27.723
9173	AF022985	Caenorhabditis elegans No definition line found	465	43.478
9174	AF098505	Caenorhabditis elegans similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891)	525	37.379
9175	AL021997	Homo sapiens dJ874C20.1 (Zinc Finger Protein ZFP47 LIKE)	266	59.770
9176	D80006	Homo sapiens KIAA0184	738	99.138
9177	M23613	Homo sapiens nucleophosmin	737	93.600
9178	L15309	Homo sapiens zinc finger protein	250	77.778

9179	U47619	<i>Drosophila melanogaster</i> ovary2	1262	42.715
9180	AB014536	<i>Homo sapiens</i> KIAA0636 protein	803	47.482
9181	U80741	<i>Homo sapiens</i> CAGH44	704	68.478
9182	U71363	<i>Homo sapiens</i> zinc finger protein zfp6	887	78.409
9183	X85786	<i>Homo sapiens</i> binding regulatory factor	358	49.600
9184	L11275	<i>Saccharomyces cerevisiae</i> selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	180	27.317
9185	AF177203	<i>Homo sapiens</i> cerebral cell adhesion molecule	492	72.414
9186	D79994	<i>Homo sapiens</i> similar to ankyrin of <i>Chromatium vinosum</i> .	305	37.453
9187	AF041083	<i>Rattus norvegicus</i> RoBo-1	189	29.710
9188	AF099742	<i>Rattus norvegicus</i> putative short-chain dehydrogenase/reductase	921	73.575
9189	AF035209	<i>Mus musculus</i> putative v-SNARE Vtila	843	95.238
9190	AF181655	<i>Drosophila melanogaster</i> BcDNA.LD27873	298	42.754
9191	M29852	<i>Oryctolagus cuniculus</i> cytochrome P-450 isozyme 5	479	50.340
9192	AF151820	<i>Homo sapiens</i> CGI-62 protein	994	97.297
9193	AB007876	<i>Homo sapiens</i> KIAA0416	1001	56.554
9194	U38980	<i>Homo sapiens</i> hPMSR6	340	64.634
9195	U26397	<i>Rattus norvegicus</i> inositol polyphosphate 4-phosphatase	384	28.378
9196	AE001058	<i>Archaeoglobus fulgidus</i> adenylate kinase (adk)	178	31.034
9197	L05147	<i>Homo sapiens</i> phosphatase tyrosine/serine	242	45.833
9198	AF126746	<i>Mus musculus</i> zinc finger protein splice variant FIZ1-A	474	42.021
9199	M27685	<i>Mus musculus</i> ultra-high sulphur keratin	432	47.934
9200	AF064604	<i>Homo sapiens</i> KE03 protein	2308	99.717
9201	AF036145	<i>Homo sapiens</i> meningioma-expressed antigen 5	1458	99.099
9202	AF184919	<i>Rattus norvegicus</i> artemin	142	40.000
9203	AF010144	<i>Homo sapiens</i> neuronal thread protein AD7c-NTP	357	76.471
9204	AB002803	<i>Homo sapiens</i> BACH1	324	38.571
9205	X90849	<i>Gallus gallus</i> polybromo 1 protein	2847	88.200
9206	AL080125	<i>Homo sapiens</i> hypothetical protein	982	64.082
9207	AB007898	<i>Homo sapiens</i> KIAA0438	198	80.556
9208	AF155352	<i>Mus musculus</i> ankyrin repeat-containing protein Asb-1	374	41.667
9209	AL050110	<i>Homo sapiens</i> hypothetical protein	4147	100.000
9210	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	179	80.000
9211	AF177942	<i>Xenopus laevis</i> katanin p60	655	48.918
9212	AL080125	<i>Homo sapiens</i> hypothetical protein	540	61.074
9213	AF016508	<i>Mus musculus</i> C-terminal binding protein 2	1107	79.916
9214	AB018308	<i>Homo sapiens</i> KIAA0765 protein	400	32.530
9215	U37263	<i>Homo sapiens</i> KRAB zinc finger protein; Method: conceptual translation supplied by author	548	39.464
9216	M14268	<i>Homo sapiens</i> T-cell receptor V-region (V-D-J)	736	92.742
9217	AB014594	<i>Homo sapiens</i> KIAA0694 protein	523	60.140
9218	AF180920	<i>Homo sapiens</i> cyclin ania-6a	1016	70.044
9219	X01655	<i>Homo sapiens</i> type III procollagen (aa 892-1023)	143	39.231
9220	U33007	<i>Saccharomyces cerevisiae</i> Ydr449cp; CAI: 0.18	337	31.959
9221	AJ005073	<i>Mus musculus</i> Alix	1066	95.455

9222	AL110151	Homo sapiens hypothetical protein	240	38.760
9223	D66904	Homo sapiens suppressor for yeast mutant	436	77.778
9224	U58332	Mus musculus receptor tyrosine kinase	362	81.159
9225	AF092091	Rattus norvegicus cp431	215	71.154
9226	AF106682	Homo sapiens spindlin	688	100.000
9227	AJ131730	Homo sapiens DREAM protein	205	41.111
9228	AB025259	Mus musculus granuphilin-b	405	40.123
9229	AB002336	Homo sapiens KIAA0338	1185	84.163
9230	X57206	Homo sapiens 1D-myo-inositol-trisphosphate 3-kinase	1194	87.081
9231	AF002197	Caenorhabditis elegans short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1	453	34.061
9232	M63963	Rattus norvegicus H,K-ATPase catalytic subunit	285	91.667
9233	AJ388557	Canis familiaris zinc finger protein	327	62.366
9234	AC006264	Arabidopsis thaliana unknown protein	802	43.408
9235	X98507	Homo sapiens myosin I beta	2935	97.650
9236	AF152963	Rattus norvegicus NADH/NADPH mitogenic oxidase subunit p65-mox	319	36.216
9237	U89280	Rattus norvegicus oxidative 17 beta hydroxysteroid dehydrogenase type 6	418	69.697
9238	Z21507	Homo sapiens human elongation factor-1-delta	511	72.308
9239	Z73619	Saccharomyces cerevisiae ORF YPL263c	438	34.014
9240	AC004484	Arabidopsis thaliana hypothetical protein	611	42.029
9241	Z83760	Ciona intestinalis COS41.5	181	33.333
9242	AF061025	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1	1628	99.184
9243	J02638	Escherichia coli polynucleotide phosphorilase	601	44.091
9244	AB013607	Mus musculus c29	671	62.983
9245	AJ243310	Homo sapiens Cl4orf3 protein	357	36.910
9246	X14046	Homo sapiens CD37 (AA 1-244)	217	57.831
9247	M69181	Homo sapiens non-muscle myosin B	9236	99.384
9248	X00947	Homo sapiens alpha 1 antichymotrypsin	275	58.889
9249	AF104246	Gallus gallus enhancer of filamentation 1 homolog	319	39.490
9250	L24521	Homo sapiens transformation-related protein	227	51.220
9251	AF021231	Mus musculus acetylcholinesterase-associated collagen	177	30.833
9252	A31036	Nicotiana glauca PRP2	197	36.275
9253	X80433	Mus musculus tex292	278	80.597
9254	X61047	Hydra sp. mini-collagen	183	43.038
9255	AF118838	Homo sapiens citrin; adult-onset type II citrullinemia protein	1574	99.605
9256	D90869	Escherichia coli similar to	1633	97.048
9257	AF114817	Homo sapiens KRAB-zinc finger protein SZF1-2	271	82.143
9258	M15530	Homo sapiens B-cell growth factor	156	55.102
9259	M15386	Homo sapiens gamma-globin	476	67.241
9260	X55777	Homo sapiens put. ORF	157	50.877
9261	V00488	Homo sapiens alpha globin	364	74.684
9262	U36771	Rattus norvegicus sn-glycerol 3-phosphate acyltransferase	226	60.714
9263	L10910	Homo sapiens splicing factor	161	52.941
9264	AB019438	Homo sapiens immunoglobulin heavy chain variable region	506	82.105

9265	X53777	Homo sapiens putative ribosomal protein (AA 1-184)	513	69.369
9266	X03725	Mus musculus ORF 2 (466 aa)	183	42.466
9267	AF115435	Rattus norvegicus syntaxin 17	236	90.244
9268	L38717	Rattus norvegicus titin	345	65.000
9269	U23452	Caenorhabditis elegans No definition line found	224	29.921
9270	AF134983	Mus musculus energy-dependent regulator of proteolysis	286	62.857
9271	D10653	Homo sapiens cell surface glycoprotein	393	66.990
9272	L07955	Bos taurus factor activating exoenzyme S	582	72.656
9273	J05459	Homo sapiens glutathione transferase M3	597	75.424
9274	AB000910	Sus scrofa ribosomal protein	356	89.286
9275	L07599	Homo sapiens ribosomal protein S6 kinase 3	550	81.188
9276	A12029	Homo sapiens MRP-14	534	71.296
9277	U01317	Homo sapiens G-gamma globin	287	58.140
9278	AC002550	Homo sapiens Unknown gene product	181	51.724
9279	AF028808	Mus musculus hemin-sensitive initiation factor 2 alpha kinase	2818	81.714
9280	X56411	Homo sapiens alcohol dehydrogenase	230	87.179
9281	M15386	Homo sapiens gamma-globin	295	61.039
9282	V00488	Homo sapiens alpha globin	228	94.595
9283	AB025026	Homo sapiens brain carboxylesterase hBr1	242	87.805
9284	M15386	Homo sapiens gamma-globin	455	70.588
9285	M15386	Homo sapiens gamma-globin	199	91.176
9286	M15386	Homo sapiens gamma-globin	382	67.010
9287	U14966	Homo sapiens ribosomal protein L5	1157	96.667
9288	V01514	Homo sapiens reading frame AFP	460	69.725
9289	AF115435	Rattus norvegicus syntaxin 17	236	90.244
9290	X02515	Homo sapiens T-cell receptor beta 1 chain	209	53.425
9291	X00497	Homo sapiens putative p33	294	54.167
9292	AL035593	Homo sapiens dJ310J6.1 (novel protein)	164	61.905
9293	M15386	Homo sapiens gamma-globin	491	73.786
9294	AF079873	Rattus norvegicus splicing factor 1 homolog	252	49.451
9295	AF150089	Homo sapiens small zinc finger-like protein	163	56.818
9296	M15386	Homo sapiens gamma-globin	333	55.670
9297	M15386	Homo sapiens gamma-globin	415	65.000
9298	V00488	Homo sapiens alpha globin	370	90.323
9299	M15386	Homo sapiens gamma-globin	205	53.030
9300	D13891	Homo sapiens Id-2H	38	32.000
9301	AF016370	Homo sapiens U4/U6 small nuclear ribonucleoprotein hPrp3	1798	91.613
9302	X55777	Homo sapiens put. ORF	248	62.963
9303	X17617	Mus musculus zinc finger protein (AA 1-580)	661	54.023
9304	U80955	Caenorhabditis elegans contains a domain found in band 4.1, ezrin, moesin, radixin and talin	822	48.561
9305	X55777	Homo sapiens put. ORF	319	58.537
9306	M13100	Rattus norvegicus unknown protein	158	39.241
9307	M36899	Cricetulus griseus uridine diphosphate N-acetyl D-glucosamine dolichol phosphate N-acetyl glucosamine-1 phosphate transferase	1050	91.765
9308	A67508	Mus musculus MUS MUSCULUS GENOMIC DNA CONTAINING THE FV1 GENE.	405	44.253
9309	AF143241	Mus musculus ADP-ribosylation factor-like protein 3	241	37.838

9310	D37885	Rattus norvegicus choline kinase R2	304	41.401
9311	AF126062	Homo sapiens Arf-like 2 binding protein BART1	292	55.952
9312	U38979	Homo sapiens hPMSR3	177	35.354
9313	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	450	77.907
9314	AF045641	Caenorhabditis elegans No definition line found	1008	44.789
9315	U54644	Homo sapiens tub homolog	600	65.922
9316	S36219	Homo sapiens prostaglandin G/H synthase, PGG/HS	204	73.469
9317	X55777	Homo sapiens put. ORF	248	62.963
9318	AF055985	Onchocerca volvulus pyrrolidone-rich antigen	117	28.395
9319	AF043724	Homo sapiens hepatitis A virus cellular receptor 1	1578	77.640
9320	U78294	Homo sapiens 15S-lipoxygenase	193	54.237
9321	AF037402	Bos taurus butyrophilin	253	42.308
9322	D90903	Synechocystis sp. hypothetical protein	211	51.667
9323	AF017368	Mus musculus facio-genital dysplasia protein 2	299	78.182
9324	U66220	Nannocystis exedens unknown	166	32.584
9325	Z30425	Homo sapiens orphan nuclear hormone receptor	332	92.308
9326	U87965	Mus musculus putative G-protein	972	41.667
9327	Y08685	Homo sapiens serine palmitoyltransferase, subunit I	958	94.737
9328	Z47072	Caenorhabditis elegans similar to acid phosphatase	722	36.607
9329	L27428	Homo sapiens reverse transcriptase	220	43.836
9330	A22096	Homo sapiens plasminogen	854	90.845
9331	D63477	Homo sapiens The KIAA0143 gene product is related to a putative C.elegans gene encoded on cosmid C32D5.	1332	98.030
9332	AF115435	Rattus norvegicus syntaxin 17	236	90.244
9333	AF008203	Homo sapiens homeobox protein	442	42.424
9334	AF067972	Homo sapiens DNA cytosine methyltransferase 3 alpha	1036	82.902
9335	AJ243460	Leishmania major proteophosphoglycan	212	34.653
9336	Z80220	Unknown similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST	433	50.806
9337	AC009322	Arabidopsis thaliana Hypothetical protein	232	50.704
9338	AL023284	Homo sapiens dJ406A7.2.1 (Microtubule Associated Protein E-MAP-115)	401	59.804
9339	AF055077	Homo sapiens zinc finger protein 42	469	63.025
9340	Y11354	Homo sapiens subunit of RNA polymerase II transcription factor TFIID	215	29.646
9341	AP000001	Pyrococcus horikoshii 305aa long hypothetical L-asparaginase	173	44.928
9342	AB020690	Homo sapiens KIAA0883 protein	179	50.000
9343	AF045640	Caenorhabditis elegans No definition line found	665	45.378
9344	AF173378	Homo sapiens 60S acidic ribosomal protein PO	442	89.333
9345	AC005328	Homo sapiens R26660 1, partial CDS	694	73.600
9346	AF022465	Mus musculus high mobility group protein homolog HMG4	492	83.333
9347	X66357	Homo sapiens serine/threonine protein kinase	257	91.111

9348	AL024499	Caenorhabditis elegans cDNA EST EMBL:C10123 comes from this gene	452	35.961
9349	AF076167	Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T6	48	23.404
9350	AB014555	Homo sapiens KIAA0655 protein	965	87.952
9351	AB014074	Rattus norvegicus semaphorin Y short isoform	668	86.441
9352	D89103	Schizosaccharomyces pombe unnamed protein product	211	46.602
9353	Y10392	Human endogenous retrovirus K gag protein	335	41.026
9354	AF176514	Mus musculus E2F1-inducible protein	169	38.636
9355	AB024075	Homo sapiens B120	394	50.000
9356	Z14310	Human endogenous retrovirus tripartite fusion transcript PLA2L	170	59.574
9357	U55366	Caenorhabditis elegans Similar to cuticle collagen	186	29.775
9358	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 ..	147	30.345
9359	AF022985	Unknown Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA	187	29.730
9360	U56964	Caenorhabditis elegans weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386)	371	31.939
9361	M26312	Oryctolagus cuniculus unknown protein	161	40.000
9362	AL050156	Homo sapiens hypothetical protein	547	49.756
9363	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	204	58.462
9364	AL021481	Caenorhabditis elegans cDNA EST EMBL:T01200 comes from this gene; cDNA EST EMBL:D72618 comes from this gene; cDNA EST yk343c3.3 comes from this gene; cDNA EST EMBL:Z14821 comes from this gene	395	31.050
9365	AC005498	Homo sapiens R31665_2	305	56.098
9366	AJ011523	Caenorhabditis elegans CHE-2 protein	405	41.135
9367	U49974	Homo sapiens mariner transposase	227	55.422
9368	S61069	Homo sapiens reverse transcriptase homolog=pol {retroviral element}	291	86.275
9369	X55777	Homo sapiens put. ORF	332	64.557
9370	AF010314	Homo sapiens Pig10	223	35.593
9371	X07858	Saccharomyces cerevisiae ORF (1 is 3rd base in codon) (266 is 1st base in codon)	109	41.667
9372	U41020	Caenorhabditis elegans coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor	407	50.450
9373	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	222	73.333
9374	U50193	Unknown coded for by C. elegans cDNA CEMSG95FB; coded for by C. elegans cDNA CEMSG95RB; coded for b	255	33.113
9375	AB020709	Homo sapiens KIAA0902 protein	624	70.896
9376	AL021571	Caenorhabditis elegans predicted using	312	36.943

		Genefinder		
9377	AF050640	Homo sapiens NADH-ubiquinone oxidoreductase NDUFS2 subunit	211	91.429
9378	AL031432	Homo sapiens dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	226	37.838
9379	AC002291	Arabidopsis thaliana Similar ATP-dependent RNA Helicase	1818	42.125
9380	U53585	Mycobacterium avium fibronectin attachment protein	136	37.179
9381	AJ243460	Leishmania major proteophosphoglycan	265	36.404
9382	AF116268	Mus musculus G-protein XLAS	157	29.570
9383	AF090867	Rattus norvegicus guanosine monophosphate reductase	976	67.727
9384	U49974	Homo sapiens mariner transposase	348	70.000
9385	L20319	Rattus norvegicus developmentally regulated protein	1188	63.869
9386	X66285	Mus musculus HC1 ORF	182	44.828
9387	Y00638	Homo sapiens LCA (AA -23 to 1281)	322	76.389
9388	M31013	Homo sapiens nonmuscle myosin heavy chain (NMHC)	173	73.529
9389	Z70208	Caenorhabditis elegans predicted using Genefinder; similar to collagen	180	30.000
9390	AF055995	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100	646	80.645
9391	AF045646	Caenorhabditis elegans contains similarity to collagens	245	32.143
9392	U41021	Caenorhabditis elegans contains two LIM domains	240	61.111
9393	AF022465	Mus musculus high mobility group protein homolog HMG4	492	83.333
9394	X53581	Rattus norvegicus ORF2	181	55.814
9395	D90710	Escherichia coli Hypothetical protein HI1731	1041	91.515
9396	U00039	Escherichia coli overlaps end of previous orf	566	93.258
9397	D64006	Synechocystis sp. asparaginyl-tRNA synthetase	997	42.359
9398	Z74036	Caenorhabditis elegans predicted using Genefinder; similar to collagen	176	32.847
9399	X89715	Saccharomyces cerevisiae AOF1001	221	32.616
9400	X99302	Homo sapiens Pop1	762	96.610
9401	AC003682	Homo sapiens ZNF134	827	51.429
9402	Y17918	Drosophila melanogaster CRAG protein	1790	48.253
9403	X94976	Brassica napus cell wall-plasma membrane linker protein	250	27.551
9404	AF146396	Homo sapiens soluble liver antigen/liver pancreas antigen	234	100.000
9405	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	753	71.338
9406	AJ388555	Canis familiaris hypothetical protein	735	67.832
9407	AF024636	Homo sapiens STE20-like kinase 3	681	87.500
9408	D49835	Homo sapiens DNA-binding protein	253	97.368
9409	AC006284	Arabidopsis thaliana putative ankyrin	205	40.659
9410	U09366	Homo sapiens zinc finger protein ZNF133	428	60.360
9411	A58792	unidentified unnamed protein product	201	90.625
9412	U42208	Oryza sativa OSBZ8	82	64.706
9413	AF118838	Homo sapiens citrin; adult-onset type II citrullinemia protein	401	90.141

9414	U27121	Danio rerio G12	212	73.810
9415	X99145	Canis familiaris overexpressed in thyroid tissue after TSH stimulation	608	92.000
9416	J03535	Mus musculus embigin precursor	167	60.000
9417	U35022	Rattus norvegicus cis-Golgi matrix protein GM130	681	68.639
9418	X75090	Homo sapiens PHAPI (Putative HLA DR Associated Protein I)	838	65.517
9419	AB011137	Homo sapiens KIAA0565 protein	219	47.222
9420	D63881	Homo sapiens KIAA0160 gene product is novel.	3129	98.323
9421	AB020716	Homo sapiens KIAA0909 protein	348	100.000
9422	Z75330	Homo sapiens nuclear protein SA-1	651	100.000
9423	AJ005890	Homo sapiens JM1	169	100.000
9424	AC004697	Arabidopsis thaliana unknown protein	226	29.143
9425	AF140691	Mus musculus melusin	733	51.376
9426	AJ006591	Homo sapiens cysteine-rich protein	256	97.500
9427	X90875	Mus musculus FXR1	183	96.000
9428	Z27170	Homo sapiens IG light chain variable region (VJ)	518	76.238
9429	AF061034	Homo sapiens FIP2	377	65.060
9430	D64062	Rattus norvegicus annexin V-binding protein (ABP-10)	1326	73.448
9431	L22557	Rattus norvegicus calmodulin-binding protein	420	80.723
9432	AF111168	Homo sapiens unknown	759	100.000
9433	U16800	Xenopus laevis ribonucleoprotein	1367	79.688
9434	AF105378	Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-4	1257	99.474
9435	AB014536	Homo sapiens KIAA0636 protein	1756	61.358
9436	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	226	53.448
9437	U85055	Mus musculus rap1/rap2 interacting protein	703	93.694
9438	AB007903	Homo sapiens KIAA0443	416	49.682
9439	Z66568	Schizosaccharomyces pombe hypothetical trp-asp repeats containing protein	522	42.941
9440	AF157706	Human herpesvirus 6B B4	157	36.923
9441	AC004908	Homo sapiens zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333)	855	99.180
9442	AF153191	Homo sapiens nm23-H7	890	79.558
9443	AF059569	Homo sapiens actin binding protein MAYVEN	519	100.000
9444	AF065414	Homo sapiens COBW-like placental protein	188	90.625
9445	AB019440	Homo sapiens immunoglobulin heavy chain variable region	486	79.310
9446	AB019439	Homo sapiens immunoglobulin heavy chain variable region	577	89.320
9447	V00488	Homo sapiens alpha globin	331	81.356
9448	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	251	35.577
9449	AF062146	Homo sapiens immunoglobulin heavy chain variable region	866	93.525
9450	AJ131730	Homo sapiens DREAM protein	142	70.370
9451	AJ224819	Homo sapiens tumor suppressor	572	42.132
9452	AF084521	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2	186	100.000
9453	M93017	Rattus norvegicus , gene product	491	92.500

9454	M33328	Homo sapiens calpastatin	152	95.833
9455	X00452	Homo sapiens DC classII histocompatibility antigen alpha-chain	255	95.238
9456	AF117888	Homo sapiens myosin-IXa	5696	99.649
9457	X60221	Homo sapiens H ⁺ -ATP synthase subunit b	284	53.750
9458	X75785	Rattus norvegicus SCP3 protein	191	58.824
9459	V00488	Homo sapiens alpha globin	374	98.246
9460	AB020716	Homo sapiens KIAA0909 protein	195	79.412
9461	AC005825	Arabidopsis thaliana putative glucokinase	265	48.193
9462	AE000854	Methanobacterium thermoautotrophicum Na ⁺ /H ⁺ -exchanging protein:Na ⁺ /H ⁺ antiporter	191	37.391
9463	A31039	Nicotiana glauca PRP3	176	38.272
9464	AC002988	Homo sapiens OLF4	303	78.689
9465	AF151826	Homo sapiens CGI-68 protein	201	68.889
9466	X52128	Mus musculus domesticus pBS13 precursor polypeptide, testis-specific	543	40.609
9467	AF070663	Homo sapiens HSPO07	297	71.875
9468	U31449	Homo sapiens tetraspan membrane protein	252	74.510
9469	D14340	Mus musculus ZO-1	174	100.000
9470	V00488	Homo sapiens alpha globin	118	100.000
9471	AC003007	Homo sapiens Unknown gene product (partial)	468	89.024
9472	AC007842	Homo sapiens BC331191_1	290	54.545
9473	M74090	Homo sapiens TB2	356	63.043
9474	A06100	synthetic construct synthetic antithrombin III	459	92.105
9475	AL050062	Homo sapiens hypothetical protein	259	94.872
9476	L06498	Homo sapiens ribosomal protein S20	387	84.211
9477	X56932	Homo sapiens 23 kD highly basic protein	963	100.000
9478	AF151830	Homo sapiens CGI-72 protein	935	85.556
9479	AL033503	Candida albicans conserved hypothetical protein	334	40.299
9480	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	234	55.556
9481	X57821	Homo sapiens immunoglobulin lambda light chain	484	79.787
9482	J02828	Gallus gallus beta-tubulin	1224	82.692
9483	AJ006710	Rattus norvegicus phosphatidylinositol 3-kinase	1147	93.855
9484	AF041207	Homo sapiens midline 1 cerebellar isoform 2	285	33.113
9485	X63797	Gallus gallus decorin	519	55.245
9486	AL023799	Homo sapiens dJ322P7.1 (zinc finger)	276	89.130
9487	U09368	Homo sapiens zinc finger protein ZNF140	296	62.500
9488	X93207	Homo sapiens NRD2 convertase	285	100.000
9489	AF017369	Mus musculus faciogenital dysplasia protein 3	2523	80.328
9490	D83268	Athalia rosae vitellogenin	141	43.662
9491	U23514	Caenorhabditis elegans similar to S. cerevisiae SSD1 protein (SP:SSD1_YEAST, P24276) and to E. coli VACB and Ribonuclease II genes	231	39.560
9492	AC005594	Homo sapiens R26984_1	786	47.566
9493	AB023231	Homo sapiens KIAA1014 protein	1009	51.908
9494	L42324	Homo sapiens G protein-linked receptor	654	96.970
9495	AC004262	Homo sapiens R29368_2	906	83.140
9496	U29488	Caenorhabditis elegans No definition line found	578	44.915
9497	AF116826	Homo sapiens putative protein-tyrosine kinase	818	96.923
9498	U95044	Homo sapiens zinc finger protein	402	69.565

9499	U05343	Mus musculus zinc finger protein PZF	2307	93.151
9500	Z74031	Unknown Similarity to Yeast D-lactate dehydrogenase (SW:DLD1_YEAST); cDNA EST EMBL:C12235 comes fro	662	44.017
9501	AJ011118	Mus musculus skeletal muscle and cardiac protein	988	87.709
9502	X78927	Homo sapiens zinc finger protein	439	98.529
9503	AF030131	Mus musculus Plenty of SH3s; POSH	382	58.163
9504	Y18208	Rattus norvegicus serine-threonine specific protein phosphatase, glycogen-binding (GL) subunit	228	80.952
9505	AC002130	Arabidopsis thaliana F1N21.13	346	48.148
9506	Z73428	Caenorhabditis elegans similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene	391	34.197
9507	AF061258	Homo sapiens LIM protein	227	100.000
9508	AB002584	Rattus norvegicus beta-alanine-pyruvate aminotransferase	448	78.049
9509	D42054	Homo sapiens KIAA0092 gene product is distantly related to smooth muscle myosin.	191	46.970
9510	D87455	Homo sapiens Similar to S.cerevisiae hypothetical protein 5 (S49634)	1099	82.775
9511	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	263	45.556
9512	X68670	Mus musculus deoxynucleotidyltransferase	442	39.906
9513	AF149414	Arabidopsis thaliana contains similarity to Pfam family PF00145 (C-5 cytosine-specific DNA methylase); score=10.4. E=0.051, N=1	390	36.946
9514	AF155739	Mus musculus axotrophin	302	88.235
9515	U49385	Mus musculus CTP synthetase homolog	2213	93.820
9516	X72467	Homo sapiens Ig kappa light chain (VJC)	717	90.517
9517	AF109907	Homo sapiens S164	380	26.140
9518	X17617	Mus musculus zinc finger protein (AA 1-580)	198	69.767
9519	U28831	Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies	712	59.556
9520	AJ222636	Homo sapiens hypothetical protein	288	41.618
9521	L11672	Homo sapiens zinc finger protein	270	43.548
9522	U25691	Mus musculus lymphocyte specific helicase	427	96.774
9523	AB011097	Homo sapiens KIAA0525 protein	660	57.297
9524	U35376	Homo sapiens repressor transcriptional factor	729	39.655
9525	Z81030	Unknown similar to O-sialoglycoprotein endopeptidase; cDNA EST EMBL:D73065 comes from this gene; cD	472	42.593
9526	AL049608	Arabidopsis thaliana extensin-like protein	241	27.372
9527	AF019085	Homo sapiens BRDT	231	24.869
9528	AF039720	Caenorhabditis elegans No definition line found	974	56.452
9529	D25215	Homo sapiens KIAA0032	277	48.148
9530	U29096	Caenorhabditis elegans coded for by C. elegans cDNA yk44f2.5; similar to P59 protein (HSP binding immunophilin) and to TPR domain	272	40.351
9531	D82080	Gallus gallus leucine-zipper protein	283	40.816
9532	S45663	Rattus sp. SC2=synaptic glycoprotein	220	42.667
9533	Z54327	Caenorhabditis elegans similar to oxidoreductase	449	31.707

9534	AL050159	Homo sapiens hypothetical protein	832	60.215
9535	U83176	Mus musculus ROSA26AS	622	67.808
9536	L31840	Rattus norvegicus nuclear pore complex protein NUP107	1227	84.071
9537	AF155595	Homo sapiens CoREST protein	225	47.619
9538	L01042	Homo sapiens TATA element modulatory factor	1129	100.000
9539	Z93386	Unknown Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes fr	180	38.889
9540	AL022393	Homo sapiens p373c6.2	605	52.151
9541	Z48475	Homo sapiens glucokinase regulator	1390	99.074
9542	Z30425	Homo sapiens orphan nuclear hormone receptor	573	98.734
9543	AB023191	Homo sapiens KIAA0974 protein	241	34.146
9544	AC002337	Arabidopsis thaliana G-beta-repeat containing protein isolog	156	37.349
9545	AF109134	Homo sapiens 7-60	195	80.000
9546	K02401	Homo sapiens chorionic somatomammotropin	789	96.000
9547	X15187	Homo sapiens precursor polypeptide (AA -21 to 782)	1315	99.057
9548	AF129756	Homo sapiens NG32	839	100.000
9549	AF085279	Arabidopsis thaliana hypothetical protein	538	49.032
9550	U42208	Oryza sativa OSBZ8	82	64.706
9551	D78132	Homo sapiens ras-related GTP-binding protein	435	57.798
9552	AC004886	Homo sapiens C-terminus matches KIAA0559, N-terminus similar to Bassoon protein; match to PID:g3043642; similar to PID:g3413810	422	100.000
9553	A52806	unidentified unnamed protein product	677	83.186
9554	D50310	Homo sapiens cyclin I	245	55.556
9555	M63180	Homo sapiens threonyl-tRNA synthetase	729	44.492
9556	AC004382	Homo sapiens Unknown gene product	968	100.000
9557	AF099973	Mus musculus schlafen2	680	50.000
9558	D16200	Sus scrofa sp32 precursor	2428	82.118
9559	X74504	Mus musculus T10	1514	73.089
9560	AJ007970	Mus musculus interferon-g induced GTPase	168	87.500
9561	Z18946	Mycobacteriophage l5 predicted 21.3kd protein	120	31.624
9562	AB002819	Perilla frutescens actin	178	96.667
9563	AB011089	Homo sapiens KIAA0517 protein	986	94.118
9564	Z66521	Caenorhabditis elegans similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene	698	54.688
9565	AF005497	Bos taurus butyrophilin	655	43.421
9566	D14168	Bombyx mori 50kDa lectin	221	29.268
9567	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	1418	96.413
9568	AB018340	Homo sapiens KIAA0797 protein	855	100.000
9569	X51760	Homo sapiens zinc finger protein (583 AA)	669	66.258
9570	AJ132889	Mus musculus kinesin like protein 9	537	86.667
9571	L38933	Homo sapiens the longest open reading frame predicts a protein of 202 amino acids, with fair Kozak consensus at the initial ATG codon; an in-frame TGA codon is seen at nucleotide 8; ORF; putative	243	92.683
9572	U19617	Mus musculus Elf-1	1020	91.525
9573	AF022962	Mus musculus Sec8	748	98.333
9574	X96586	Homo sapiens FAN protein	1216	100.000

9575	Z74043	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene	369	65.476
9576	AF067855	Homo sapiens geminin	567	98.901
9577	Z83107	Unknown cDNA EST EMBL:D69907 comes from this gene; cDNA EST EMBL:C13424 comes from this gene; cDNA	202	26.994
9578	AB023187	Homo sapiens KIAA0970 protein	436	60.185
9579	X68249	Xenopus laevis Proline rich protein	983	66.376
9580	AF166261	Xenopus laevis nuclear protein Sojo	303	61.644
9581	AF056034	Rattus norvegicus F-actin binding protein b-Nexilin	625	93.269
9582	D13626	Homo sapiens KIAA0001	735	47.393
9583	AB020684	Homo sapiens KIAA0877 protein	427	69.880
9584	K02113	Unknown Gallus gallus vitellogenin	186	22.280
9585	L36315	Mus musculus zinc finger protein	925	97.727
9586	AJ001810	Homo sapiens mRNA cleavage factor I 25 kDa subunit	265	100.000
9587	Z78542	Unknown cDNA EST EMBL:D72182 comes from this gene; cDNA EST EMBL:D72353 comes from this gene; cDNA	158	28.409
9588	AF067430	Mus musculus Smarcel-related protein	895	52.140
9589	AL031266	Caenorhabditis elegans VM106R.1	242	46.237
9590	U23486	Caenorhabditis elegans similar to S. cerevisiae zinc finger protein GCS1 (SP:GCS1 YEAST)	323	64.407
9591	U00483	Macaca mulatta mucin	164	24.000
9592	X77953	Rattus norvegicus ribosomal protein S15a	257	78.431
9593	U80753	Homo sapiens CAGL79	1936	98.962
9594	D50919	Homo sapiens The KIAA0129 gene product is novel.	218	97.222
9595	M68864	Homo sapiens ORF	197	50.820
9596	AB023432	Rattus norvegicus aspartoacylase	261	50.769
9597	AC004997	Unknown match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and	1762	71.131
9598	U29659	Human endogenous retrovirus pol gene product	626	100.000
9599	AF134726	Homo sapiens NG22	741	41.053
9600	X66405	Mus musculus collagen alpha1 type VI-precursor	2251	92.837
9601	AF153366	Mus musculus tubulo-interstitial nephritis antigen	1246	50.578
9602	Z99118	Bacillus subtilis similar to hypothetical proteins	345	50.526
9603	AC004780	Homo sapiens F17127 1	186	82.759
9604	AC004849	Homo sapiens similar to KIAA0662; similar to AB014562 (PID:g3327138)	1459	94.286
9605	X72012	Homo sapiens endoglin	479	82.609
9606	X05562	Homo sapiens alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon)	2224	100.000
9607	AL050272	Homo sapiens hypothetical protein	667	99.000
9608	X84692	Mus musculus spermatid perinuclear RNA binding protein	1617	98.387

9609	A31038	Nicotiana alata PRP3	161	40.323
9610	Z74042	Caenorhabditis elegans predicted using Genefinder; Similarity to Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene	266	43.000
9611	AJ010317	Fugu rubripes Sand	481	46.860
9612	Z47808	Unknown similar to beta-transducin; cDNA EST yk489h7.5 comes from this gene; cDNA EST yk399d9.5 com	1099	40.643
9613	V00639	Bacteriophage 434 reading frame (rex1 protein)	1128	100.000
9614	AB016816	Homo sapiens MASL1	336	36.032
9615	AF071317	Mus musculus COP9 complex subunit 7b	537	98.864
9616	AF182426	Rattus norvegicus arylacetamide deacetylase	755	42.748
9617	AB014557	Homo sapiens KIAA0657 protein	2375	100.000
9618	S69232	Homo sapiens electron transfer flavoprotein-ubiquinone oxidoreductase, ETF-QO {EC 1.5.5.1}	219	97.297
9619	AF123880	multiple sclerosis associated retrovirus element gag polyprotein	170	37.838
9620	AB020625	Homo sapiens butyrophilin like receptor	225	27.612
9621	U09367	Homo sapiens zinc finger protein ZNF136	1402	52.308
9622	AB014888	Homo sapiens MRJ	441	87.838
9623	AF132726	Mus musculus FLASH	665	88.793
9624	X90849	Gallus gallus polybromo 1 protein	196	30.392
9625	S83545	Homo sapiens Na+/H+ exchanger isoform NHE-3	260	97.500
9626	AF151904	Homo sapiens CGI-146 protein	208	96.552
9627	AF181645	Drosophila melanogaster BcDNA.GH12144	292	45.263
9628	AJ243895	Mus musculus basic-helix-loop-helix protein (bHLH)	417	66.364
9629	Z80223	Caenorhabditis elegans predicted using Genefinder	258	27.152
9630	U72661	Homo sapiens ninjurin1	356	56.190
9631	Y18265	Homo sapiens zinc finger protein SALL1	149	26.901
9632	AF111943	Dictyostelium discoideum development protein DG1124	196	45.614
9633	X56958	Homo sapiens ankyrin (brank-2)	580	98.936
9634	AL050231	Drosophila melanogaster BACR37P7.g	272	46.988
9635	AF080171	Homo sapiens zinc finger protein ZNF232	595	100.000
9636	AF005392	Homo sapiens alpha tubulin	519	90.588
9637	AF011566	Homo sapiens immunoglobulin-like transcript 4	136	35.000
9638	Z46935	Caenorhabditis elegans weak similarity with quinone oxidoreductase; cDNA EST EMBL:C13104 comes from this gene; cDNA EST yk264f3.5 comes from this gene	247	40.385
9639	U09367	Homo sapiens zinc finger protein ZNF136	207	33.835
9640	AC002339	Arabidopsis thaliana hypothetical protein	185	29.851
9641	Z22866	Mus musculus skelemin	573	74.603
9642	Z50028	Caenorhabditis elegans cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene; cDNA EST yk360f12.5 comes from this gene	616	33.793
9643	AF067211	Caenorhabditis elegans contains similarity to 26S protease subunit	194	27.219

9644	L12018	Caenorhabditis elegans putative	375	47.656
9645	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	573	70.492
9646	U19614	Rattus norvegicus lamina-associated polypeptide 1C	874	66.667
9647	U79260	Homo sapiens unknown	229	56.757
9648	U30883	Homo sapiens SRp55-1	1635	99.213
9649	U97667	Rattus norvegicus RSP29	248	42.045
9650	U64598	Caenorhabditis elegans weakly similar to S. cervisiae PTM1 precursor (SP:P32857)	285	26.531
9651	X74764	Homo sapiens protein-tyrosine kinase	3799	94.842
9652	AL032643	Caenorhabditis elegans similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene	283	50.000
9653	AB018353	Homo sapiens KIAA0810 protein	668	100.000
9654	AF056618	Homo sapiens BWSR2 associated zinc-finger protein BAZ2	273	53.571
9655	AB014593	Homo sapiens KIAA0693 protein	298	60.274
9656	AF073883	Danio rerio myotubularin related protein 2	134	33.871
9657	AF090133	Rattus norvegicus lin-7-A	474	98.684
9658	AF119668	Rattus norvegicus lipolysis-stimulated remnant receptor alpha' subunit	1383	85.897
9659	U37263	Homo sapiens KRAB zinc finger protein; Method: conceptual translation supplied by author	461	49.664
9660	U00017	Mycobacterium leprae pimT; B2126 C1 165	397	34.862
9661	U65092	Homo sapiens melanocyte-specific gene 1 nuclear protein	301	91.667
9662	AF041378	Homo sapiens cell death activator CIDE-A	302	54.023
9663	AB017508	Bacillus halodurans truA homologue (identity of 62% to B. subtilis)	206	38.636
9664	L29162	Homo sapiens immunoglobulin light chain variable region	733	93.162
9665	AL096844	Streptomyces coelicolor A3(2) probable 3-oxacyl-(acyl-carrier-protein) reductase	165	36.111
9666	AJ010469	Arabidopsis thaliana RNA helicase	806	42.901
9667	Z14020	Nicotiana tabacum Pistil extensin like protein, partial CDS only	223	44.444
9668	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	195	100.000
9669	AL009193	Unknown /prediction=(method:""genefinder"", version:""084""); /prediction=(method:""genscan"", ve	178	39.286
9670	AC007228	Homo sapiens BC37295_1	407	96.970
9671	Z81109	Unknown predicted using Genefinder; cDNA EST EMBL:D71433 comes from this gene; cDNA EST EMBL:D74134	188	33.981
9672	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	268	83.333
9673	D10631	Mus musculus zinc finger protein	230	44.776
9674	AL049943	Homo sapiens hypothetical protein	180	70.270
9675	AC009465	Arabidopsis thaliana unknown protein	192	50.000
9676	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	371	41.436

9677	AL023781	Schizosaccharomyces pombe N-terminal acetyltransferase 1	237	49.351
9678	AF008554	Rattus norvegicus implantation-associated protein	478	82.955
9679	Z48334	Unknown similar to ribosomal protein L10 (QM protein); cDNA EST EMBL:T00732 comes from this gene; c	719	80.469
9680	X62639	Drosophila melanogaster hrp48.1	675	52.174
9681	AF053356	Homo sapiens nucleoporin	1484	96.087
9682	L00923	Mus musculus myosin I	1299	97.073
9683	M57547	Rattus norvegicus ER alpha-mannosidase	849	85.507
9684	D83776	Homo sapiens The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.	443	41.143
9685	Z68006	Caenorhabditis elegans K09C8.4	231	21.429
9686	U58728	Caenorhabditis elegans C54H2.1 gene product	239	31.884
9687	AF031903	Mus musculus ADP-ribosylation-like factor homolog ARL6	373	95.238
9688	AL117204	Caenorhabditis elegans Y116A8C.9	249	43.617
9689	AJ005821	Homo sapiens X-like 1 protein	410	79.452
9690	Z66524	Caenorhabditis elegans T13H5.6	150	30.928
9691	Z36715	Homo sapiens Net	420	92.537
9692	Y09501	Homo sapiens NADH-cytochrome-b5 reductase	347	79.730
9693	AL096768	Homo sapiens dJ858B16.2 (novel protein similar to hamster PSSC (Phosphatidylserine Decarboxylase Proenzyme, EC 4.1.1.65)	535	96.386
9694	AF160893	Drosophila melanogaster BcDNA.GM10765	272	45.745
9695	AL110477	Caenorhabditis elegans Y113G7B.24	184	34.211
9696	U94363	Homo sapiens glycogenin-2 beta	297	97.959
9697	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	335	47.872
9698	AC003682	Homo sapiens F18547 1	199	65.217
9699	AB006628	Homo sapiens KIAA0290	1144	57.746
9700	AB011110	Homo sapiens KIAA0538 protein	801	83.448
9701	AB018288	Homo sapiens KIAA0745 protein	1007	65.086
9702	AL031856	Schizosaccharomyces pombe putative DNA repair and recombination protein	241	38.542
9703	Y00978	Homo sapiens PDC-E2 precursor (AA -54 to 561)	129	100.000
9704	AF017433	Homo sapiens putative transcription factor CR53	522	69.159
9705	M64488	Rattus norvegicus synaptotagmin II	967	85.882
9706	AF053368	Mus musculus lysyl oxidase-related protein 2	1035	90.244
9707	X85750	Homo sapiens expression associated with monocyte to macrophage differentiation	450	68.966
9708	AB014566	Homo sapiens KIAA0666 protein	472	63.025
9709	AF126736	Homo sapiens ubiquitin processing protease	353	38.211
9710	U29244	Caenorhabditis elegans No definition line found	379	39.860
9711	X67469	Mus musculus AM2 receptor	409	49.020
9712	AB018293	Homo sapiens KIAA0750 protein	1014	56.877
9713	AF006829	Coturnix coturnix slow myosin heavy chain 2	702	69.231
9714	U23484	Caenorhabditis elegans No definition line found	582	52.201
9715	Y00204	Xenopus laevis nucleoplasmin	468	53.147
9716	AF059569	Homo sapiens actin binding protein MAYVEN	329	67.089

9717	AJ002204	Zea mays polyamine oxidase	228	45.946
9718	U28831	Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies	613	63.855
9719	AJ242723	Drosophila melanogaster hypothetical protein	209	49.254
9720	AF132480	Mus musculus Ese2 protein	990	94.839
9721	D63877	Homo sapiens KIAA0157 gene product is novel.	708	37.500
9722	U18771	Rattus norvegicus Rab26	215	57.143
9723	X58483	Pseudomonas putida urocanate hydratase	280	34.513
9724	AF067165	Homo sapiens zinc finger protein 3	547	98.765
9725	AL009195	Drosophila melanogaster EG:30B8.1	757	79.412
9726	A26182	Mus musculus beta3-adrenergic receptor	249	30.488
9727	AB018315	Homo sapiens KIAA0772 protein	222	94.444
9728	AL050306	Homo sapiens dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein)	272	75.000
9729	AC007055	Homo sapiens unknown	570	35.593
9730	D86969	Homo sapiens similar to Human zinc-finger protein, BR140 (P1:JC2069)	321	49.020
9731	U97006	Caenorhabditis elegans No definition line found	172	67.568
9732	AB025258	Mus musculus granuphilin-a	1425	87.967
9733	AB029016	Homo sapiens KIAA1093 protein	295	40.559
9734	U96174	Onchocerca volvulus OvB8	509	39.908
9735	AF151824	Homo sapiens CGI-66 protein	379	74.157
9736	X80754	Homo sapiens GTP-binding protein	968	100.000
9737	AL009066	Caenorhabditis elegans Similarity with Human adenylate kinase KAD protein (PIR Acc. No. A33508); cDNA EST yk265c3.5 comes from this gene; cDNA EST yk265c3.3 comes from this gene	172	36.709
9738	AB011167	Homo sapiens KIAA0595 protein	270	100.000
9739	AF090326	Mus musculus AE-1 binding protein AEBP2	1535	97.788
9740	AB014558	Homo sapiens KIAA0658 protein	830	100.000
9741	Z84476	Homo sapiens dJ25J6.2 (zinc finger protein)	280	28.877
9742	AB020629	Homo sapiens KIAA0822 protein	355	58.511
9743	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST E	208	29.333
9744	AC003682	Homo sapiens F18547_1	212	74.419
9745	D10923	Homo sapiens HM74	1065	94.410
9746	U40419	Caenorhabditis elegans No definition line found	962	47.416
9747	U42436	Caenorhabditis elegans C49H3.6 gene product	290	35.616
9748	X78898	Saccharomyces cerevisiae N1342	892	48.252
9749	AF069291	Homo sapiens ht41	505	65.179
9750	L15309	Homo sapiens zinc finger protein	242	87.805
9751	U53421	Sus scrofa betaine-homocysteine methyltransferase	297	82.000
9752	AF173867	Homo sapiens DNA binding protein p79PIF	763	92.481
9753	AF070530	Homo sapiens unknown	160	46.053
9754	Z12017	Caenorhabditis elegans predicted using Genefinder; basic-rich; cDNA EST yk328f6.3 comes from this gene; cDNA EST yk328f6.5 comes from this gene; cDNA EST yk393c3.5 comes from this gene; cDNA EST yk641d11.3 comes from this gene	377	33.453
9755	D87438	Homo sapiens Similar to a C.elegans protein in	3322	100.000

		cosmid C14H10		
9756	AL034364	Caenorhabditis elegans cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene	719	30.582
9757	AF170301	Mus musculus nuclear body associated kinase 1a	702	94.595
9758	AF026565	Mus musculus ring finger protein	170	47.368
9759	Y08134	Homo sapiens acid sphingomyelinase-like phosphodiesterase	1362	100.000
9760	AF056116	Fugu rubripes unknown	252	79.545
9761	M96629	Canis familiaris homologue to sec61	691	96.262
9762	AF125385	Drosophila melanogaster L82B	188	42.667
9763	AL022603	Arabidopsis thaliana hypothetical protein	214	28.426
9764	U19729	Saccharomyces cerevisiae Ylr409cp	183	36.082
9765	AB003930	Homo sapiens rap1GAPII	370	45.985
9766	Z95397	Schizosaccharomyces pombe Ths1p	308	26.780
9767	AJ007012	Mus musculus Fish protein	740	78.295
9768	U23037	Oryctolagus cuniculus eIF-2Bepsilon	631	88.679
9769	J05499	Rattus norvegicus L-glutamine amidohydrolase	1770	95.307
9770	L14684	Rattus norvegicus elongation factor G	709	85.606
9771	U00051	Caenorhabditis elegans coded for by C. elegans cDNA yk50b2.5; coded for by C. elegans cDNA CEESV26F; similar to lipases over a short region	192	35.922
9772	D89340	Rattus norvegicus dipeptidyl peptidase III	806	99.187
9773	AB023189	Homo sapiens KIAA0972 protein	332	58.333
9774	AF022789	Homo sapiens ubiquitin hydrolyzing enzyme I	839	91.729
9775	AF139185	Rattus norvegicus myomegalin	269	65.152
9776	AC003682	Homo sapiens F18547.1	206	45.833
9777	D10884	Bos taurus neurocalcin	595	100.000
9778	D63876	Homo sapiens KIAA0154 gene product is related to mouse gamma adaptin.	657	76.923
9779	M15888	Bos taurus endozepine-related protein precursor	489	39.698
9780	AJ011033	Mus musculus KCC2 protein	900	97.761
9781	AF160973	Homo sapiens p53 inducible protein	1474	100.000
9782	Z81547	Caenorhabditis elegans predicted using Genefinder	194	36.036
9783	AJ011855	Homo sapiens PAK4 protein	265	63.333
9784	X87143	Helianthus annuus cytochrome b5 containing fusion protein	173	42.105
9785	AC005328	Homo sapiens R26660.1, partial CDS	623	98.925
9786	U85494	Zea mays LON1 protease	325	27.019
9787	M96625	Gallus gallus cardiac muscle tensin	687	60.326
9788	AF020351	Homo sapiens NADH:ubiquinone oxidoreductase 18 kDa IP subunit	177	90.909
9789	AB002354	Homo sapiens KIAA0356	445	87.500
9790	Z73423	Caenorhabditis elegans cDNA EST EMBL:Z14908 comes from this gene; cDNA EST EMBL:M89403 comes from this gene; cDNA EST EMBL:T00022 comes from this gene	435	46.512
9791	AL032657	Unknown predicted using Genefinder; similar to DnaJ domain; Thioredoxin; cDNA EST yk433f3.5 come	960	37.945
9792	AB003503	Mus musculus Guanine Nucleotide Regulatory	622	71.053

		Protein		
9793	U51000	Mus musculus DLX-1	1344	99.515
9794	U09367	Homo sapiens zinc finger protein ZNF136	429	69.149
9795	AB004664	Mus musculus Rab33B	859	94.815
9796	Z98601	Schizosaccharomyces pombe zinc finger protein	236	27.778
9797	AB017016	Homo sapiens p25 alpha	213	91.667
9798	X82018	Homo sapiens ZID, zinc finger protein with interaction domain	768	96.032
9799	Z97055	Homo sapiens dJ388M5.3 (Sulfotransferase (sulfokinase, EC 2.8.2.1) like protein)	1395	100.000
9800	AF030131	Mus musculus Plenty of SH3s; POSH	1571	94.017
9801	U35113	Homo sapiens metastasis-associated gene	785	73.446
9802	U25842	Saccharomyces cerevisiae Similar to several members of the Cdc48/Pas1/Sec18 family of proteins (Swiss Prot. accession numbers P25694, P24004, P18759)	165	31.507
9803	AF033566	Mus musculus cdc2/CDC28-like protein kinase 4	686	93.684
9804	AC007193	Homo sapiens Putative homolog of hypoxia inducible factor three alpha	1917	99.653
9805	U60644	Homo sapiens HU-K4	285	39.695
9806	S73488	Rattus sp. zinc finger transcription factor, Kid-1 {KRAB A and B regions}	267	62.500
9807	Z81135	Unknown cDNA EST yk345g1.5 comes from this gene; cDNA EST yk496a3.3 comes from this gene; cDNA EST	156	38.272
9808	U63818	Xenopus laevis RING finger protein	493	31.641
9809	AB002377	Homo sapiens KIAA0379	506	81.633
9810	S71659	Mus sp. LIM-type homeodomain=Gsh-4 {C-terminal}	398	93.651
9811	L15313	Caenorhabditis elegans putative	1088	58.885
9812	AB032904	Hylobates syndactylus dopamine receptor D4	216	31.206
9813	Z82215	Homo sapiens dJ6802.2	2663	100.000
9814	AF180919	Homo sapiens RNA lariat debranching enzyme	2176	100.000
9815	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	348	38.235
9816	X79510	Homo sapiens protein-tyrosine-phosphatase	485	100.000
9817	AF077000	Rattus norvegicus protein tyrosine phosphatase TD14	879	99.265
9818	AF050182	Mus musculus PERIOD 3	518	63.830
9819	X79828	Mus musculus NK10	368	65.000
9820	AF002714	Homo sapiens centromere protein B; CENP-B	182	31.532
9821	AB011146	Homo sapiens KIAA0574 protein	278	100.000
9822	AF161181	Mus musculus P55T protein	252	97.619
9823	Z83760	Ciona intestinalis COS41.4	324	66.667
9824	X96973	Mus musculus Lasp-1	800	84.127
9825	AC002457	Homo sapiens Rap2 interacting protein; similar to U73941 (PID:g1916018)	819	98.387
9826	AF008915	Homo sapiens EVI-5 homolog	839	77.711
9827	Y18881	Mus musculus midline 2 protein	311	29.064
9828	Z38062	Saccharomyces cerevisiae orf, len: 432, CAI: 0.15 similar to dnaJ proteins	218	47.059
9829	AF053970	Homo sapiens outer dense fiber protein 2/2	260	100.000
9830	Z83123	Caenorhabditis elegans T04A11.2	405	49.275
9831	AF030558	Rattus norvegicus phosphatidylinositol 5-phosphate 4-kinase gamma	1106	95.322

9832	AF084530	Homo sapiens cyclin-D binding Myb-like protein	883	100.000
9833	X99145	Canis familiaris overexpressed in thyroid tissue after TSH stimulation	736	53.646
9834	AB029025	Homo sapiens KIAA1102 protein	464	46.023
9835	M20823	Mus musculus mdm-1	1013	75.000
9836	U41534	Caenorhabditis elegans similar to yeast MAK16 protein (SP:MK16 YEAST,P10962)	644	59.864
9837	AB007869	Homo sapiens KIAA0409	300	68.571
9838	D14076	Rattus norvegicus testicular dynamin	701	99.091
9839	AF109907	Homo sapiens S164	1178	100.000
9840	AB014536	Homo sapiens KIAA0636 protein	400	50.794
9841	AL031667	Homo sapiens dJ620E11.1e (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein, similar to KIAA0308)	913	100.000
9842	U33821	Homo sapiens tax1-binding protein TXBP151	869	33.190
9843	AL080080	Homo sapiens hypothetical protein	1065	100.000
9844	AF168362	Rattus norvegicus protein associating with small stress protein PASS1	1052	79.888
9845	U58280	Mus musculus second largest subunit of RNA polymerase I	832	85.211
9846	AF119569	Homo sapiens patched 2	176	89.286
9847	M35297	Rattus norvegicus G-protein coupled receptor	477	89.333
9848	X83226	Saccharomyces cerevisiae global transcriptional regulator	734	49.057
9849	AB007872	Homo sapiens KIAA0412	175	90.000
9850	D29640	Homo sapiens KIAA0051	548	75.000
9851	AL080125	Homo sapiens hypothetical protein	473	64.103
9852	AF041207	Homo sapiens midline 1 cerebellar isoform 2	190	28.276
9853	AB029334	Halocynthia roretzi HrPET-1	350	42.857
9854	AB011370	Mus musculus Ankhzn	1122	91.237
9855	AL117407	Homo sapiens hypothetical protein	442	47.468
9856	AF125053	Homo sapiens pyruvate dehydrogenase E1 alpha subunit	169	100.000
9857	U97191	Caenorhabditis elegans No definition line found	276	46.316
9858	X71997	Rattus norvegicus myosin I	1848	63.699
9859	AJ012409	Homo sapiens hypothetical protein	211	93.750
9860	AB000776	Rattus norvegicus semaphorin Z	424	87.671
9861	Z27080	Unknown cDNA EST EMBL:D33198 comes from this gene; cDNA EST EMBL:D32867 comes from this gene; cDNA	345	55.422
9862	AF027514	Homo sapiens zinc finger protein	791	99.174
9863	Z78019	Unknown Similarity to Yeast LPG22P protein (TR:G1151240); cDNA EST EMBL:T00686 comes from this gene	1006	75.258
9864	AF051155	Rattus norvegicus G beta-like protein GBL	1358	80.934
9865	L28174	Acanthamoeba castellanii disulfide-like protein	349	45.794
9866	AL096857	Homo sapiens hypothetical protein	1028	98.101
9867	Z98531	Schizosaccharomyces pombe hypothetical protein	184	38.158
9868	Z92669	Mycobacterium tuberculosis hypothetical protein Rv0235c	166	31.858
9869	U96781	Homo sapiens Ca2+ ATPase of fast-twitch skeletal muscle sarcoplasmic reticulum, neonatal isoform	1370	99.539

9870	L13687	Homo sapiens ADP-ribosylation factor-like protein 2	390	37.838
9871	U26358	Rattus norvegicus S100A1 gene product	167	36.585
9872	AB026190	Homo sapiens Kelch motif containing protein	1392	43.254
9873	AB000199	Rattus norvegicus CCA2 protein	306	82.143
9874	AC003682	Homo sapiens F18547 1	223	74.419
9875	Z69902	Unknown predicted using Genefinder; cDNA EST EMBL:D27579 comes from this gene; cDNA EST EMBL:D64778	595	32.419
9876	AB011527	Rattus norvegicus MEGF1	353	69.620
9877	U69262	Mus musculus matrillin-2 precursor	276	73.016
9878	AF168418	Homo sapiens activating signal cointegrator 1	221	97.059
9879	U40342	Mus musculus ninein	2234	89.390
9880	AF016430	Caenorhabditis elegans contains similarity to a BR-C/TTK domain	184	37.647
9881	AL031685	Homo sapiens dJ963K23.2 (novel protein)	276	41.304
9882	AF073879	Mus musculus myotubularin homologous protein 1	382	87.302
9883	L14745	Caenorhabditis elegans homology with glucose induced repressor, GRR1; putative	328	29.944
9884	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	664	50.971
9885	AC004890	Homo sapiens similar to zinc finger proteins; similar to BAA24380	514	84.375
9886	AJ243591	Xenopus laevis hnRNP-E2 protein	694	83.594
9887	Z19153	Unknown similar to Sodium/phosphate transporter; cDNA EST EMBL:D67894 comes from this gene; cDNA ES	710	43.882
9888	AL022157	Homo sapiens SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	274	72.000
9889	U29096	Caenorhabditis elegans coded for by C. elegans cDNA yk44f2.5; similar to P59 protein (HSP binding immunophilin) and to TPR domain	354	39.548
9890	AF016452	Caenorhabditis elegans similar to 1-acyl-glycerol-3-phosphate acyltransferases	327	44.792
9891	AC004557	Arabidopsis thaliana F17L21.21	523	39.768
9892	AF003136	Caenorhabditis elegans F28B3.4	184	42.353
9893	X52022	Homo sapiens collagen type VI, alpha 3 chain	244	74.510
9894	L20303	Gallus gallus actin filament-associated protein	666	45.387
9895	D80009	Homo sapiens KIAA0187	338	88.333
9896	Z46242	Unknown similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532	869	50.871
9897	AB012725	Mus musculus zinc finger protein	483	91.429
9898	AJ001693	Drosophila melanogaster PRUNE protein	502	36.071
9899	AJ235271	Rickettsia prowazekii PUTATIVE ENOYL-REDUCTASE (fabI)	419	46.825
9900	D79983	Homo sapiens There is a C3HC4 zinc-finger in the C-terminal region.	381	54.348
9901	U95044	Homo sapiens zinc finger protein	396	86.301
9902	D90899	Synechocystis sp. hypothetical protein	251	34.884
9903	AB016496	Mus musculus intelectin	791	76.510
9904	X03342	Homo sapiens rpl32 (aa 1-135)	172	84.375
9905	AF022891	Drosophila melanogaster Fuzzy	165	36.000

9906	AL096751	Homo sapiens hypothetical protein	1004	100.000
9907	AF156271	Homo sapiens RING finger protein terf	196	77.419
9908	AB014561	Homo sapiens KIAA0661 protein	462	65.766
9909	AF059569	Homo sapiens actin binding protein MAYVEN	253	46.667
9910	AF019082	Borrelia burgdorferi virulent strain associated lipoprotein	249	26.506
9911	AF058693	Mus musculus M-RdgB2 retinal degeneration protein B subtype 2	435	94.118
9912	U95044	Homo sapiens zinc finger protein	675	69.677
9913	U60666	Homo sapiens testis specific leucine rich repeat protein	225	33.155
9914	AB018374	Mus musculus GARP45	647	51.915
9915	Z68014	Caenorhabditis elegans Similarity to Human DRA protein (SW:DRA HUMAN)	291	43.333
9916	Z82095	Caenorhabditis elegans similar to PDZ domain (Also known as DHR or GLGF).; cDNA EST EMBL:M75803 comes from this gene	413	53.390
9917	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	221	41.414
9918	AC005328	Homo sapiens R26660_1, partial CDS	169	72.222
9919	AC007369	Arabidopsis thaliana Putative RNA helicase	315	41.667
9920	X14549	Chlamydomonas reinhardtii spoke protein	428	46.207
9921	AF117610	Mus musculus inner centromere protein INCENP	570	79.798
9922	AF151835	Homo sapiens CGI-78 protein	248	100.000
9923	L14745	Caenorhabditis elegans coded for by C. elegans cDNA GenBank:CEL16D4 (M89109); putative	278	30.808
9924	AB007865	Homo sapiens KIAA0405	266	53.731
9925	X90840	Homo sapiens axonal transporter of synaptic vesicles	2660	100.000
9926	AF175969	Rattus norvegicus Leman coiled-coil protein	371	39.181
9927	U80747	Homo sapiens CAGH3	188	34.375
9928	S62597	Drosophila melanogaster, Peptide, 753 aa neu=neuralized	186	23.757
9929	U63131	Homo sapiens CDC37 homolog	181	37.079
9930	Y09723	Homo sapiens Miz-1 protein	838	31.299
9931	D86728	Mus musculus TIS	219	86.842
9932	X67683	Homo sapiens keratin K4a	824	100.000
9933	AC007136	Homo sapiens Putative map kinase interacting kinase	2718	100.000
9934	Z79755	Caenorhabditis elegans predicted using Genefinder	186	54.902
9935	AC002131	Arabidopsis thaliana Contains similarity to hypothetical protein C18b11.05 gb Z50728 from S. pombe. EST gb H76601 comes from this gene.	367	31.696
9936	U00050	Caenorhabditis elegans No definition line found	377	35.979
9937	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	377	38.806
9938	AB005541	Rattus rattus PCTAIRE3	341	67.416
9939	U63648	Mus musculus p160 myb-binding protein	651	73.913
9940	Z78201	Unknown Similarity to E.coli 2-oxoglutarate dehydrogenase (SW:ODO1_ECOLI); cDNA EST EMBL:D32590 com	226	29.878
9941	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	67	75.000
9942	AC007067	Arabidopsis thaliana T10024.10	364	61.905
9943	U41663	Rattus norvegicus neuroligin 3	968	96.479

9944	X91617	Mus musculus 5'-3' exonuclease	745	100.000
9945	AF167411	Mus musculus pendrin	347	56.627
9946	U80953	Caenorhabditis elegans weakly similar in serine repeat region to rat thyroxine-binding globulin (PIR:A39567) and to D. melanogaster ecdysone-inducible protein E75-C (SP:E75C DROME,P13055)	163	37.805
9947	AC007633	Unknown similarity to several hypothetical proteins- Arabidopsis thaliana	226	61.818
9948	U35245	Rattus norvegicus vacuolar protein sorting homolog r-vps33b	431	98.507
9949	M94315	Oryctolagus cuniculus neurofilament-H	226	24.528
9950	AF096896	Drosophila melanogaster pushover	197	24.291
9951	Z68117	Caenorhabditis elegans similar to Probable rabGAP domains; cDNA EST yk325d7.3 comes from this gene; cDNA EST yk325d7.5 comes from this gene	280	37.705
9952	AC007018	Arabidopsis thaliana unknown protein	308	33.163
9953	U29156	Mus musculus involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	1222	92.857
9954	M95762	Rattus norvegicus GABA transporter	1153	89.730
9955	U09284	Homo sapiens PINCH protein	1648	85.020
9956	AB007872	Homo sapiens KIAA0412	320	73.913
9957	U95825	Homo sapiens androgen-induced prostate proliferative shutoff associated protein	704	83.607
9958	U68535	Mus musculus aldo-keto reductase	1175	68.110
9959	AF003151	Caenorhabditis elegans No definition line found	241	25.987
9960	AF060173	Rattus norvegicus SV2 related protein	745	96.522
9961	AF004841	Homo sapiens CDO	243	41.489
9962	U66561	Homo sapiens kruppel-related zinc finger protein	273	56.338
9963	U09367	Homo sapiens zinc finger protein ZNF136	199	72.093
9964	U34925	Drosophila melanogaster TH1	665	62.025
9965	U32626	Drosophila melanogaster unknown	317	57.333
9966	L08239	Homo sapiens located at OATL1	179	100.000
9967	M61866	Homo sapiens Krueppel-related DNA-binding protein	226	60.377
9968	AB007144	Homo sapiens ZIP-kinase	222	33.884
9969	U75321	Mus musculus chromaffin granule ATPase II homolog	487	65.574
9970	AF036706	Caenorhabditis elegans strong similarity to class-I aminoacyl-tRNA synthetases; most similar to glutaminyl-tRNA synthetases	558	50.000
9971	X82018	Homo sapiens ZID, zinc finger protein with interaction domain	540	63.415
9972	X97324	Homo sapiens adipophilin	312	44.340
9973	AF080070	Mus musculus zinc finger protein 54	240	48.052
9974	AF169548	Homo sapiens gamma-synergin	1069	100.000
9975	AF056302	Drosophila melanogaster eIF-2alpha kinase	454	39.891
9976	AC003114	Arabidopsis thaliana T12M4.6	143	39.759
9977	Z78198	Caenorhabditis elegans Similarity to E.coli glycerophosphoryldiester phosphodiesterase (SW:UGPO ECOLI)	203	46.154

9978	AF098505	Caenorhabditis elegans similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891)	498	44.578
9979	D31763	Homo sapiens ha0946 protein is Kruppel-related.	383	55.660
9980	AC007591	Unknown Strong similarity to	221	41.667
9981	Z48758	Saccharomyces cerevisiae unknown	404	46.043
9982	U29187	Mus musculus prion-like protein	716	76.471
9983	AB013607	Mus musculus c29	528	70.833
9984	X63337	Homo sapiens high sulfur keratin	839	77.397
9985	U09824	Rattus norvegicus 30 kDa S-type lectin	328	42.857
9986	AJ006692	Homo sapiens ultra high sulfur keratin	732	76.068
9987	U43292	Homo sapiens MDS1B	384	65.000
9988	AL117204	Caenorhabditis elegans Y116A8C.9	593	40.773
9989	X55126	Mus musculus Zfp-29	354	84.375
9990	AF153208	Homo sapiens GC-rich sequence DNA-binding factor candidate	719	100.000
9991	AL023781	Schizosaccharomyces pombe N-terminal acetyltransferase 1	522	52.564
9992	U59240	Rattus norvegicus N-tropomodulin	267	50.000
9993	AF070651	Homo sapiens zinc finger protein 4	835	74.847
9994	AP000399	Oryza sativa EST AU056133(S20320) corresponds to a region of the predicted gene; similar to Caenorhabditis elegans cosmid D1054; hypothetical protein (Z74030)	486	43.478
9995	U21549	Mus musculus Ac39/physophilin	379	69.620
9996	AL022318	Homo sapiens bK150C2.7 (PUTATIVE novel protein similar to APOBEC1 (Apolipoprotein B mRNA editing protein) and Phorbolin)	1280	100.000
9997	AJ242977	Homo sapiens p243	371	100.000
9998	Y10495	Mus musculus CDV-1R protein	1736	92.384
9999	Z93394	Caenorhabditis elegans similar to Probable rabGAP domains	829	50.211
10000	U97571	Mus musculus signaling molecule	892	90.714
10001	AL021068	Homo sapiens dJ206D15.1 (Reduced Folate Carrier protein RFC LIKE)	764	64.458
10002	AF056116	Fugu rubripes All-1 related protein	427	35.156
10003	AP000059	Aeropyrum pernix 115aa long hypothetical protein	54	29.787
10004	X51760	Homo sapiens zinc finger protein (583 AA)	345	80.952
10005	AB020710	Homo sapiens KIAA0903 protein	602	67.717
10006	AB025259	Mus musculus granuphilin-b	256	30.769
10007	AJ011855	Homo sapiens PAK4 protein	391	72.000
10008	U06944	Mus musculus PRAJA1	262	66.102
10009	AF186469	Rattus norvegicus TM6P1	288	29.605
10010	D45913	Mus musculus leucine-rich-repeat protein	299	83.019
10011	AL117203	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	171	33.036
10012	AB020678	Homo sapiens KIAA0871 protein	759	77.397
10013	AF017368	Mus musculus faciogenital dysplasia protein 2	315	57.732
10014	U13878	Mus musculus neural-restrictive silencer factor	361	34.615
10015	S73488	Rattus sp. zinc finger transcription factor, Kid-1 {KRAB A and B regions}	173	57.447
10016	AF099011	Homo sapiens EH-domain containing protein testilin	396	62.921

10017	D61689	Mus musculus SOX-LZ	1050	96.933
10018	AF070651	Homo sapiens zinc finger protein 4	423	82.432
10019	D63478	Homo sapiens The KIAA0144 gene product is novel.	600	58.282
10020	U40802	Caenorhabditis elegans similar to other protein phosphatases 1, 2A and 2B	420	35.407
10021	AC004472	Homo sapiens P1.11659 5	223	35.593
10022	AF051944	Gallus gallus Xin	298	33.645
10023	AF007170	Homo sapiens unknown	177	44.262
10024	AC004997	Unknown match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and	532	55.833
10025	Z25535	Homo sapiens nuclear pore complex protein hnup153	273	100.000
10026	U43503	Saccharomyces cerevisiae Lph2p	198	45.455
10027	D86043	Homo sapiens SHPS-1	337	43.704
10028	AB011093	Homo sapiens KIAA0521 protein	1394	97.309
10029	D17577	Mus musculus Kif1b	1152	97.159
10030	U89264	Drosophila melanogaster kinesin like protein 67a	642	47.926
10031	D14663	Homo sapiens KIAA0107	305	94.118
10032	AF132856	Homo sapiens suppressor of G2 allele of skp1 homolog	183	90.625
10033	AB023189	Homo sapiens KIAA0972 protein	331	62.025
10034	AF031939	Mus musculus RalBP1-associated EH domain protein Reps1	1647	92.636
10035	AL117600	Homo sapiens hypothetical protein	326	67.123
10036	AL031788	Schizosaccharomyces pombe conserved hypothetical protein.	429	51.079
10037	AL031276	Homo sapiens dJ1118D24.1d (part of novel protein similar to worm proteins T08G11.1 and C25H3.9)	586	98.901
10038	D42063	Homo sapiens RanBP2 (Ran-binding protein 2)	825	86.014
10039	AJ011306	Homo sapiens guanine nucleotide exchange factor (long isoform)	317	100.000
10040	AF047010	Drosophila melanogaster asteroid protein	196	40.244
10041	Z54096	Schizosaccharomyces pombe hypothetical protein	328	52.294
10042	X89571	Mus musculus human homolog is GPI-anchored protein	436	52.713
10043	AC010077	Homo sapiens MTDM_HUMAN ; DNA METHYLTRANSFERASE; DNA METASE; MCMT; M.HSAI	249	77.358
10044	D86971	Homo sapiens no similarities to reported gene products	967	49.684
10045	AF099973	Mus musculus schlafen2	258	36.111
10046	X78077	Equus caballus link protein	214	36.250
10047	U80448	Unknown coded for by C. elegans cDNA CEES55F; coded for by C. elegans cDNA yk84a1.3; coded for by	185	54.000
10048	U39703	Mycoplasma genitalium DNA helicase II, putative	183	25.087
10049	AF100657	Caenorhabditis elegans Contains similarity to Pfam domain: PF00614 (PLDc), Score=13.8, E-value=0.2, N=1	481	33.660
10050	AC007259	Arabidopsis thaliana Hypothetical protein	189	31.915
10051	AF099973	Mus musculus schlafen2	338	37.267

10052	U41559	Caenorhabditis elegans No definition line found	300	38.095
10053	AB018341	Homo sapiens KIAA0798 protein	423	70.787
10054	S44213	Saccharomyces cerevisiae, Peptide, 323 aa YKL522=mitochondrial ADP/ATP carrier protein homolog	211	35.294
10055	AF111423	Xenopus laevis chromosome condensation protein XCAP-G	719	64.162
10056	AJ242978	Homo sapiens p621	1835	100.000
10057	AL023777	Schizosaccharomyces pombe hypothetical protein	428	32.464
10058	AB018285	Homo sapiens KIAA0742 protein	166	40.000
10059	AC006528	Arabidopsis thaliana putative DNA replication licensing factor with an MCM family domain (prosite:PDOC00662)	228	29.612
10060	AF077818	Mus musculus syntrophin-associated serine-threonine protein kinase	205	62.000
10061	U15173	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2	449	40.722
10062	AC002328	Arabidopsis thaliana F20N2.6	53	50.000
10063	Z98974	Schizosaccharomyces pombe hypothetical PSU1-like protein	323	45.918
10064	AB018413	Homo sapiens Gab2	551	58.462
10065	AF151816	Homo sapiens CGI-58 protein	289	100.000
10066	AF099973	Mus musculus schlafen2	204	40.187
10067	Y12090	Lycopersicon esculentum putative 3,4-dihydroxy-2-butanone kinase	1197	41.199
10068	U49046	Mus musculus Zfp64	1594	89.494
10069	L39211	Homo sapiens carnitine palmitoyltransferase I	252	58.730
10070	AB000199	Rattus norvegicus CCA2 protein	554	84.848
10071	AC007228	Homo sapiens BC37295 1	252	65.000
10072	AF060246	Mus musculus zinc finger protein 106	264	97.436
10073	X81058	Mus musculus tex261	1140	99.422
10074	AB020675	Homo sapiens KIAA0868 protein	439	46.715
10075	AJ011928	Drosophila melanogaster Fidipidine	586	52.174
10076	X98834	Homo sapiens zinc finger protein Hsal2	706	100.000
10077	AF151363	Mus musculus Cdc42 GTPase-activating protein	499	69.608
10078	AF149413	Arabidopsis thaliana contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1	641	53.093
10079	AC007842	Homo sapiens BC331191 1	834	51.711
10080	AB002334	Homo sapiens KIAA0336	213	97.143
10081	S76838	Mus sp. Dbs=Dbl guanine nucleotide exchange factor homolog	287	59.420
10082	AB015306	Homo sapiens Leukotriene B4 omega-hydroxylase	750	81.818
10083	AB029000	Homo sapiens KIAA1077 protein	329	88.679
10084	AC002528	Homo sapiens Genscan gene prediction; 90% similarity to AA023673 (NID:g1487590)	765	99.099
10085	X54618	Listeria monocytogenes phosphatidylinositol specific phospholipase C	197	28.571
10086	X57303	Homo sapiens REC1L	398	63.043
10087	AB023178	Homo sapiens KIAA0961 protein	331	68.421
10088	AF061243	Homo sapiens metalloprotease 1	1936	98.913
10089	AF038563	Homo sapiens membrane associated guanylate kinase 2	665	100.000
10090	AJ010017	Homo sapiens zinc finger protein	200	44.615

10091	AF067806	Mus musculus cAMP-specific cyclic nucleotide phosphodiesterase PDE8; MMPDE8	300	54.167
10092	U44731	Mus musculus purine nucleotide binding protein	2293	74.730
10093	Z70269	Unknown predicted using Genefinder; Similarity to Yeast hypothetical protein YHG1 (SW:YHG1 YEAST);	167	54.348
10094	AB014516	Homo sapiens KIAA0616 protein	235	45.669
10095	AB018293	Homo sapiens KIAA0750 protein	487	66.038
10096	D90400	Human papillomavirus type 58 open reading frame E5	71	44.444
10097	AB011128	Homo sapiens KIAA0556 protein	325	100.000
10098	X89426	Homo sapiens ESM-1 secretory protein	197	33.588
10099	Z48334	Caenorhabditis elegans F10B5.8	787	76.471
10100	X14971	Mus musculus alpha-adaptin (A) (AA 1-977)	688	100.000
10101	U81788	Drosophila melanogaster kinesin-73	402	50.400
10102	L12579	Homo sapiens alternatively spliced	380	88.406
10103	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform	408	60.177
10104	M22743	Oryctolagus cuniculus lambda-crystallin precursor	202	81.081
10105	U44129	Rattus norvegicus p58	479	46.154
10106	Z92813	Unknown similar to WD domain, G-beta repeat (3 domains); cDNA EST EMBL:D69452 comes from this gene;	213	34.579
10107	AF031370	Rattus norvegicus PLC-b4b	1014	95.425
10108	Z35639	Caenorhabditis elegans similar to TNF-alpha induced Protein B12; cDNA EST yk579c8.3 comes from this gene	224	45.055
10109	AF175292	Mus musculus neuronal IL-16	393	84.286
10110	AB012099	Pyrococcus kodakaraensis Glycerol Kinase	223	36.047
10111	AB023658	Rattus norvegicus Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha	1070	89.205
10112	L06940	Escherichia coli tetracycline resistance protein	296	32.515
10113	U75329	Homo sapiens serine protease	173	41.026
10114	L22557	Rattus norvegicus calmodulin-binding protein	673	99.010
10115	AL035528	Arabidopsis thaliana hypothetical protein	207	55.738
10116	M15888	Bos taurus endozepine-related protein precursor	1198	86.829
10117	AF079974	Mus musculus Rac GTPase-activating protein	588	77.778
10118	Z72511	Unknown possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D715	1343	57.576
10119	M83679	Rattus norvegicus RAB15	552	82.524
10120	AF023450	Homo sapiens Down syndrome cell adhesion molecule	518	60.000
10121	U80955	Caenorhabditis elegans contains a domain found in band 4.1, ezrin, moesin, radixin and talin	335	45.192
10122	U15002	Rattus norvegicus COUP-TFI	271	74.000
10123	L40378	Homo sapiens cytoplasmic antiproteinase 3	354	100.000
10124	AL121764	Schizosaccharomyces pombe putative ATP-dependent RNA helicase	491	60.000
10125	AC003682	Homo sapiens F18547_1	210	67.391
10126	M58583	Homo sapiens precerebellin	234	48.485

10127	AF055017	Homo sapiens unknown	398	32.917
10128	AL050284	Homo sapiens hypothetical protein	216	70.213
10129	AF078828	Homo sapiens talin	652	72.180
10130	U58746	Caenorhabditis elegans weak similarity to regions of guanine-nucleotide releasing factors	168	48.980
10131	Z81521	Unknown predicted using Genefinder; cDNA EST EMBL:C09934 comes from this gene; cDNA EST EMBL:C08308	259	32.877
10132	AJ010585	Rattus rattus PTB-like protein	753	97.581
10133	Z68297	Unknown cDNA EST EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA	335	37.415
10134	D89928	Homo sapiens HKL1	647	86.555
10135	L16559	Caenorhabditis elegans putative	224	33.793
10136	AB009372	Rattus norvegicus Lysophospholipase	1408	86.585
10137	AL035496	Homo sapiens dJ437022.1 (novel VHS domain containing protein similar to predicted worm and human proteins)	200	96.552
10138	AF187318	Homo sapiens F-box protein Fbx2	229	43.243
10139	Z83760	Ciona intestinalis COS41.5	248	32.283
10140	U81788	Drosophila melanogaster kinesin-73	927	66.351
10141	AB024400	Rattus norvegicus LAT4	1006	64.103
10142	U23522	Caenorhabditis elegans No definition line found	180	32.061
10143	AJ243460	Leishmania major proteophosphoglycan	173	21.577
10144	Y08774	Silene latifolia Men-2	115	37.097
10145	Z71262	Unknown similar to serine/threonine kinase; cDNA EST EMBL:D27596 comes from this gene; cDNA EST EMB	161	29.032
10146	AB010363	Mus musculus mszf51	164	37.500
10147	AF000196	Caenorhabditis elegans No definition line found	160	30.556
10148	AC005306	Homo sapiens R27216 1	423	98.507
10149	X98709	Homo sapiens COL1A1 and PDGFB fusion transcript	146	31.068
10150	AF099053	Mus musculus phosphatidylserine synthase-2	2504	89.776
10151	U02928	Dictyostelium discoideum Rab7	362	36.207
10152	X98475	Mus musculus vasodilator-stimulated phosphoprotein	164	29.412
10153	AL080200	Homo sapiens hypothetical protein	138	37.113
10154	AB002374	Homo sapiens KIAA0376	712	36.215
10155	L04733	Homo sapiens kinesin light chain	504	53.521
10156	AL023592	Schizosaccharomyces pombe zinc finger protein	295	45.055
10157	L07063	Mus musculus FKBP65 binding protein	819	87.234
10158	X82200	Homo sapiens gpStaf50	907	62.679
10159	AF106682	Homo sapiens spindlin	256	68.421
10160	AF125385	Drosophila melanogaster L82B	173	44.444
10161	Y17282	Homo sapiens cytokeratin type II	818	59.244
10162	AB029023	Homo sapiens KIAA1100 protein	784	50.000
10163	Y17282	Homo sapiens cytokeratin type II	294	43.972
10164	AF173681	Mus musculus thioredoxin interacting factor	348	38.372
10165	AF125963	Caenorhabditis elegans No definition line found	159	25.743
10166	X78925	Homo sapiens zinc finger protein	162	60.870

10167	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	773	66.667
10168	AB017437	Gallus gallus avena	1096	93.143
10169	X75760	Drosophila melanogaster LRR47	485	29.443
10170	AJ007014	Homo sapiens AMMECR1 protein	1134	55.000
10171	J04802	Homo sapiens open reading frame A	161	96.154
10172	AF057170	Homo sapiens bestrophin	401	70.370
10173	U70855	Caenorhabditis elegans similar to the RAS gene family	382	48.305
10174	AB025410	Mus musculus Ten-m1	835	93.893
10175	AF091434	Homo sapiens secretory growth factor-like protein fallotein	184	49.180
10176	U95044	Homo sapiens zinc finger protein	525	76.786
10177	M20681	Homo sapiens glucose transporter-like protein	201	83.784
10178	AF067165	Homo sapiens zinc finger protein 3	240	55.072
10179	D88026	Mus musculus Dhml2 protein	385	82.090
10180	AL035419	Homo sapiens dJ1100H13.1 (putative novel protein)	252	100.000
10181	X97064	Homo sapiens Sec23 protein	2794	100.000
10182	X79828	Mus musculus NK10	531	90.588
10183	AC002332	Arabidopsis thaliana putative NAD(P)-dependent cholesterol dehydrogenase	245	40.336
10184	Z48166	Schizosaccharomyces pombe gar2	176	28.175
10185	Z81525	Unknown cDNA EST yk282b7.5 comes from this gene; cDNA EST EMBL:D28011 comes from this gene; cDNA ES	512	39.640
10186	AL110487	Caenorhabditis elegans Y39E4B.7	491	47.794
10187	AB018341	Homo sapiens KIAA0798 protein	396	74.074
10188	L42178	Ovis aries carbonic anhydrase I	620	64.615
10189	L11275	Saccharomyces cerevisiae selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	191	24.876
10190	AB018260	Homo sapiens KIAA0717 protein	260	94.595
10191	AF118767	Homo sapiens endothelial lipase	2456	99.446
10192	AF096771	Homo sapiens kinase related protein	200	26.596
10193	U47920	Pseudomonas aeruginosa dihydrolipoamide acetyltransferase	444	72.917
10194	U18009	Homo sapiens similar to Pacific ray VAT1 protein, Swiss-Prot Accession Number P19333	422	49.618
10195	AL035086	Homo sapiens dJ44A20.3 (novel protein similar to worm F32F2.1)	369	55.455
10196	L01089	Homo sapiens profilaggrin	447	38.095
10197	AL035702	Homo sapiens dJ593C16.1 (ras GTPase activating protein)	2171	73.131
10198	X92969	Mus musculus odorant receptor	360	52.525
10199	AF062249	Homo sapiens immunoglobulin heavy chain variable region	699	85.593
10200	AF125569	Homo sapiens tumor suppressing STF cDNA 6	718	83.333
10201	Z99118	Bacillus subtilis similar to hypothetical proteins	159	32.143
10202	AB020654	Homo sapiens KIAA0847 protein	2158	98.795
10203	Y18102	Oryctolagus cuniculus titin	436	95.652
10204	D90706	Escherichia coli PhoH protein homolog.	1451	100.000
10205	D90708	Escherichia coli Putrescine transport protein.	704	100.000
10206	D90717	Escherichia coli Hypothetical 38.9 kd protein	515	100.000

		in ding/rarB 3'region (o361).		
10207	X56958	Homo sapiens ankyrin (brank-2)	179	96.429
10208	D90730	Escherichia coli Hypothetical protein 63 (MukB 3' region)	655	98.058
10209	X55683	Lycopersicon esculentum extensin (class I)	122	59.259
10210	Z70683	Unknown Weak similarity to Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 c	291	41.284
10211	AE001373	Plasmodium falciparum predicted secreted protein	383	25.198
10212	U28377	Escherichia coli ORF f141	792	96.825
10213	D90754	Escherichia coli Hypothetical protein HI0761	995	98.000
10214	AF109134	Homo sapiens 7-60	681	40.152
10215	M13934	Homo sapiens ribosomal protein S14	885	99.265
10216	AF055666	Mus musculus kinesin light chain 2	524	88.542
10217	X70032	Mus musculus nebulin	423	42.143
10218	D42167	Ciona intestinalis myoplasmin-C1	246	28.477
10219	AF034580	Mus musculus TSG118.1	811	54.426
10220	AF128535	Mus musculus cytoplasmic phosphoprotein PACSIN2	1389	56.891
10221	AF084928	Homo sapiens erythroblast macrophage protein EMP	811	98.450
10222	AL050321	Homo sapiens dJ717M23.1 (novel gene)	576	98.864
10223	AF113615	Homo sapiens FH1/FH2 domain-containing protein FHOS	833	62.189
10224	Z49967	Unknown cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA	173	34.694
10225	AB025412	Mus musculus Ten-m3	1096	96.471
10226	X99145	Canis familiaris overexpressed in thyroid tissue after TSH stimulation	184	48.980
10227	AF037454	Mus musculus ubiquitin protein ligase	447	98.551
10228	Z21878	Physarum polycephalum myosin-related protein	453	43.085
10229	X70208	Homo sapiens immunoglobulin M chain	631	90.291
10230	AB018285	Homo sapiens KIAA0742 protein	258	31.667
10231	X82157	Homo sapiens hevin	466	98.684
10232	D90832	Escherichia coli ORF ID:o341#12; similar to	234	100.000
10233	AE000186	Escherichia coli orf, hypothetical protein	1155	100.000
10234	X73413	Escherichia coli ORF2	247	95.000
10235	D90743	Escherichia coli Rod protein FlgC	550	96.667
10236	D90703	Escherichia coli Lipic acid synthetase (lip-syn).	480	100.000
10237	X01563	Escherichia coli L5 (rplE) (aa 1-179)	779	100.000
10238	U28377	Escherichia coli ORF o492	762	95.935
10239	U00039	Escherichia coli treF	1305	99.468
10240	D90872	Escherichia coli similar to	545	100.000
10241	AJ001614	Escherichia coli catabolite gene activator protein	228	96.970
10242	U14003	Escherichia coli ORF o243	436	100.000
10243	X05173	Escherichia coli NR(II) (glnL gene product) (AA 1-349)	570	89.423
10244	AE000336	Escherichia coli orf, hypothetical protein	852	100.000
10245	AE000396	Escherichia coli orf, hypothetical protein	858	98.571
10246	U28377	Escherichia coli ORF o179	611	97.872
10247	D90769	Escherichia coli Sn-glycerol-3-phosphate	416	100.000

		transport system permease protein UgpA.		
10248	D90699	Escherichia coli Hypothetical 16.8 kd protein in nfrA 3'region precursor.	520	100.000
10249	AE000406	Escherichia coli orf, hypothetical protein	469	95.588
10250	U00006	Escherichia coli No definition line found	502	85.542
10251	AE000458	Escherichia coli putative enzyme	378	90.323
10252	D90809	Escherichia coli Superoxide dismutase (EC 1.15.1.1) (Fe)	566	100.000
10253	AE000396	Escherichia coli orf, hypothetical protein	426	100.000
10254	X15996	Escherichia coli narX	165	100.000
10255	X12614	Escherichia coli uroporphyrinogen III cosynthetase (AA 1 - 246)	1188	100.000
10256	AE000402	Escherichia coli orf, hypothetical protein	576	100.000
10257	X04711	Escherichia coli put. 16S rRNA methyltransferase (ksgA) (AA 1-273)	451	100.000
10258	U00007	Escherichia coli yehW	434	100.000
10259	D90740	Escherichia coli ORF ID:o231#4	321	98.000
10260	U29579	Escherichia coli alternate name ygbC; ORF1 of L07942, has different start due to frameshift in L07942; ORF f255	1112	98.837
10261	X14436	Escherichia coli ORF4 (AA 1-197)	1119	99.465
10262	AE000334	Escherichia coli orf, hypothetical protein	748	99.091
10263	D90756	Escherichia coli Protoporphyrinogen oxidase (EC 1.3.3.4) hemK	638	98.958
10264	AE000242	Escherichia coli orf, hypothetical protein	563	92.784
10265	U29579	Escherichia coli ORF o433	591	95.699
10266	U82664	Escherichia coli hypothetical protein	927	100.000
10267	AE000142	Escherichia coli putative esterase (EC 3.1.1.1)	634	100.000
10268	AF009205	Homo sapiens unknown	163	96.429
10269	D90872	Escherichia coli similar to	1280	98.020
10270	AL032654	Caenorhabditis elegans similar to Heme-binding domain in cytochrome b5 and oxidoreductases	386	52.830
10271	AB019280	Mus musculus sprouty-4	453	83.750
10272	U40953	Caenorhabditis elegans No definition line found	437	32.365
10273	AB002349	Homo sapiens KIAA0351	347	63.529
10274	AF043695	Caenorhabditis elegans similar to zinc metalloprotease family of peptidases	168	37.363
10275	L47274	Encephalitozoon intestinalis beta-tubulin	351	39.333
10276	S66427	Homo sapiens retinoblastoma binding protein 1, RBP1	812	82.759
10277	AB011166	Homo sapiens KIAA0594 protein	847	99.242
10278	U49973	Homo sapiens ORF1; MER37; putative transposase similar to pogo element	302	35.461
10279	Z93785	Unknown predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain)	490	65.347
10280	AF132177	Drosophila melanogaster unknown	222	66.038
10281	AF033664	Mus musculus cbp146	1932	88.785
10282	U93305	Homo sapiens synaptophysin	601	66.667
10283	X58636	Mus musculus lymphoid enhancer factor 1	932	100.000
10284	AF009329	Rattus norvegicus enhancer-of-split and hairy-related protein 1	529	98.718
10285	AL049558	Schizosaccharomyces pombe hypothetical protein	267	37.725

10286	L15309	Homo sapiens zinc finger protein	237	85.714
10287	Z98596	Schizosaccharomyces pombe putative SMC family protein	302	55.000
10288	U13152	Mesocricetus auratus guanine nucleotide-binding protein beta 5	362	53.636
10289	X93302	Saccharomyces cerevisiae Msn5 protein	173	35.200

TABLE 7: Neural Network SignalP Program Data

SEQ ID NO.	BEGINNING AND END NUCLEOTIDE LOCATION CORRESPONDING TO AMINO ACID SEGMENT	MAXIMUM S SCORE	MEAN S SCORE	AMINO ACID SEGMENT CONTAINING SIGNAL PEPTIDE (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown)
1	188:323	0.946	0.85	MLKSSVDLLFLFSMCVLSINNLRSSLLAVHALS GDTLVTEIQTGN
2	916:1051	0.94	0.875	MLSAILLLLQLWDSGAQETDNERSAQGTSAPL LPLLQRFQSIICR
3	13559:13424	0.99	0.968	MLTLALLVLRICVCEAASTFVCPCLPWLSLLFL HLLPRLFQVQIW
4	11219:11354	0.984	0.936	MLRSLLVYMLFLLVTLLASYGDASCHGHAYRL QSAIKQELHSRAF
5	34:169	0.983	0.936	MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGR CGEGYSRDATCN
6	7698:7563	0.99	0.928	MESELTWQIAWRLLLLPVVAATVVAVAVRAG TQDRVLADRKLGS
7	13595:13730	0.966	0.884	MFRFLGVLLGIAIRTGSPLSLNLAEPVWKQLA GMSLTIADLSEVD
8	1527:1392	0.997	0.92	MWYGVFLWALVSSLFFHVPAGLLALFTLRHHK YGAAIAGVYRAAG
9	1683:1548	0.997	0.92	MWYGVFLWALVSSLFFHVPAGLLALFTLRHHK YGAAIAGVYRAAG
10	466:331	0.95	0.651	MGKSLASQFPITLIFSAFSSTFCLLDGLFISCP TSTELPKVNSL
11	768:633	0.956	0.821	MVLSGIHWYSVLLLAVEFCRYCPLRYRCSTFS SWARVSSTPQASS
12	604:739	0.991	0.957	MMCLVMASFGFILCGLCADSSVCLGLCHLLNL GSFQPLVLWIFFS
13	189:54	0.969	0.795	MYLVKGLLIGLHSILLCLREQGGLRRVERDEG TASWYSSQNTYNI
14	1012:877	0.993	0.897	MIQLFFVLYGILALAFLSGYYVTLAAQILAVLLP PVMLLIDGNVA
15	191:326	0.958	0.769	MTNFFWCCLSLVVGQLQSRFREYLTSTFLVLGE SPCHTHLLKGCSV
16	206:71	0.941	0.726	MPWGSLFGVESLWCSLTFLPFDDL SLLRLWE GNCVYCFVLMYYS
17	284:149	0.972	0.902	MLHSQLLAVSFRLIVTLPLSIQDWDDAENMKG LQYIFNTLWSVSS
18	311:176	0.974	0.852	MHLPTLFFFRLRIILPTQGPLQFPYEFEDGLFHF CRKGGHWNFDRD
19	154:289	0.962	0.784	MVLHRKLVSFFSIWIFSFSVIHLKRLSFPQRM FLACSSKISWLE

20	112:247	0.951	0.839	MSKVKPLHGAPAPLLVSLCLLSWCGLPGVIVH VTYVSPRHLSNTR
21	252:117	0.927	0.649	MFPCPAVRFCCLAWSAHISCQKFHVKYALAEK QVQAKCFISKGGR
22	845:710	0.906	0.558	MAPARPWWLTPVIPALWEAEEDGSRGQEFKT SLASMVKPRLYYKY
23	300:165	0.944	0.695	MVTLPPPLASTWKPSTSPAPICLSWLCLFMNFVI HMLPGGLLFRRW
24	165:300	0.885	0.695	MSFSCPALNLYSLWLGEFPFAPCTMTALWTR KCLVHPHLSDKFSE
25	306:171	0.954	0.656	MVALNGLLGFWLVKLDEWWGPELQWGILGG DGIQEGDREFRLQAW
26	261:396	0.951	0.692	MWKQISPIGNLVTAFIFCVLCQQRQWLARDA FNTQSILSPPIWV
27	410:275	0.932	0.623	MLHETLRVCWSRIRVWPLMPALLGPPRALSS LAAQMGEHRTMWNP
28	54:189	0.947	0.775	MRQINKKGFWSYGPVILVVLVAVVASSVNSY YSSPAQQVPKNPA
29	222:87	0.994	0.93	MFQFLSQGFYCGVGLFTRFLKLLGALLLLALAL FLGFLQLGWRFL
30	176:311	0.974	0.942	MFTCLFLFSAVLRALFRKSDPKRFQNIFFTITL FTLLTDDWSL
31	127:262	0.984	0.794	MLGLCFYLFQIFFYFSLNFFVYPCHSETNCVILI YFCGFEFILVF
32	185:320	0.966	0.835	MFIKFLRILISLQCSSFKFTVTAKVLFMTYKKRA QSDFFLVFVDR
33	209:74	0.992	0.926	MIITSIFLGVITVIIIGLCLAAVTYVDEDENEILELS SNKTFIM
34	294:159	0.972	0.842	MWAFRAINFLITALAVSHRFWDVLFVLIGYKE LLSSALISLFIQ
35	255:390	0.912	0.742	MVTQLTLEVLHLSLVVGQVSNLLHIGPLASE QMFYAVATKIRD
36	131:266	0.906	0.746	METQRGLGWGLGALAAFSGLGGTLALGLSED LATLSPSSHAGMMQ
37	550:415	0.989	0.944	MTIATFMTVILFFSLLSITLWRNSRRAFSVSLFA SGRRMTRRFKA
38	145:10	0.965	0.869	MASASFSLICGFLASLSLQRIEELGLGLGLGF GLRECCGWFGLL
39	301:166	0.919	0.733	MFKSKLLNFYIFVNCMNFLMLSASFNPFWSEII VCNIQFFYYTL
40	220:355	0.894	0.695	MPSSHLVWRLLTCSSLGPGLPSPHSYDPAPP RPRLGRGWEVGEGT
41	91:226	0.941	0.715	MHLTLIAVRTPTVLFSPWTLSSMSVLRRIRPEA AYCIATAVFMNL
42	360:225	0.94	0.797	MNCFSLRLETRQACPLLLAFSIVLEVQACAIK EEKVKDIPTGK
43	330:465	0.993	0.921	MYREVCSIRFLFTAVSLLSLFLSAFWLGLLYLV SPLENPKEMLT
44	91:226	0.986	0.819	MFWRGWGAPLWAWPTLLTPIKCSSLYDSFFS PTDALGLESLLGTA
45	443:578	0.964	0.897	MGTWPVLCCTLVAGETAILISVKTLPWRLYL ARVAIIARIKVYT
46	47:182	0.931	0.827	MPQIYLPVLLLFVSRNYAALNIHIYISWSSHLKV

				SLGIYIVVKLQ
47	840:705	0.93	0.759	MLQNSVYVNFLLTGLVAQLACHPQPLLRSFLL NTNMVFQPSVKSL
48	205:340	0.99	0.952	MSFNSLYCLIWVLSFTVLLQISVTVHIWDWQTT TTTKPEWRRRAP
49	293:428	0.966	0.664	MSLEWLVAWSWSDGLRDCIATGIQSVRDCD TTAVITVACLLVLF
50	397:262	0.904	0.719	MEQEFKLLTGFIATILRLLQLTGFLGNHQPLDR SSHLDQKALDLP
51	15:150	0.962	0.677	MVPVFFDGHWTCLCVKWTQKTGPLPWPKT WRWLLLLARQHGSWV
52	299:434	0.994	0.949	MGYNLLFFLIILYCGWLFMSLSVHLQYYFEWL NNVSMCTYILVYL
53	298:433	0.897	0.718	MVLIYSGLSSLPWAPPMILLYCVLGTSLNTQKV PVGKIGAYNLGV
54	77:212	0.992	0.903	MFFLIYLSRFFLPALLNCFKYFFCSQCALPFR MLDFSSPSVLIA
55	184:319	0.942	0.832	MPWWALICANTSPLCAPPLCSPLPQPRPGLQ APFSPGPPRRWGHK
56	189:324	0.951	0.874	MRMQCCSTGLCSSRVVLIILLPLXXXXXXXXXX XXXXXXXXXXXXXXXX
57	6:141	0.896	0.69	MCGSPERLCVRCARVCAVFMRALCVVCVYLR RRIKYERFLGWELR
58	217:352	0.965	0.752	MNICTNTMPCSIIFYTAIWLIXKYLEILLMFHP WLSWICPITSL
59	250:385	0.984	0.797	MLVLSFWFAFVCLQGNVMFKEKRKSYQSMLS EHFNQCKVKSQMTP
60	196:331	0.979	0.869	MIMNMCFLLSYVSFCYTCFMAILSDAYKFRIVL SSCRTDLVIIMN
61	65:200	0.947	0.86	MSVRRALTPSALGLVFILQIFAHGLPGPGPCHL GPGICLRICQCA
62	970:835	0.952	0.832	MLCHPHVHHHLVCLLATLTFSLNASCAEQTFH SQQSNGEFMATLP
63	98:233	0.969	0.895	MLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGL NSIKVTRTKLDCF
64	537:402	0.947	0.677	MTWAGLFLFLRVGSPNRKWAASGGSGGDGV DGEDWSLARSHQPSP
65	293:428	0.976	0.843	MTLATILFLLGILIVISKVKCRKADSRSESPTC KSCKSELPSSA
66	267:402	0.984	0.926	MAVAVLLCGCIVATVSFFWEESLTQHVAGLLF LMTGIFCTISLCT
67	107:242	0.92	0.794	MCTPVRVSIVCMGAVGAVWTAPLPLPWAPT PSIHLREEGAAPF
68	78:213	0.97	0.762	MTSLMFLWRALLETISTNMTFSLPLAAVVRW MKPTGSGMFLYQY
69	263:398	0.973	0.719	MSPMSYMVFPFKGVLLCMPKCMALWIRHSGN NGQLRSQDNLGAHI
70	118:253	0.929	0.864	MFSTRNTILAFMLSCIIYCKLNFCMVLYKGCSS FSPCECPLFQFY
71	236:371	0.992	0.973	MLLLFLIVLLGLFAWHRRRQKEKGRDLAPRV SYTPAMRMTSTDY
72	60:195	0.99	0.918	MMNILMLITIIVMTIMANILVYSCLIIYVISLILENNL LLGPVIV

73262:397	0.951	0.834	MADEKTRIGFIVLGLFLLALGTFLMSHDRPQV YGTIFYAMGSVMV
74424:289	0.962	0.688	MCFILLLLQCVNLPKPQGERALERGAGGWTG CHLPLCPHLHKAQT
751349:1484	0.958	0.667	MSTSCVCRRLQVVLVQEMGLGPVPLDSSAQ LTFMASLRLVSALF
76656:521	0.996	0.969	MSLLLPPLALLLLAALVAPATAATAYRPDWN RLSGLTRARVETC
77221:356	0.985	0.927	MVPIFLLKCLLLHVPLCMSSNLSFHSSHHLHIF LPSFSSHLPRPL
78264:129	0.994	0.964	MQPLALWTGLVMAALSGLCYALLYPCLSGAF TYLVGGYAALIGFM
79118:253	0.928	0.786	MGRLWLWPWTPGATTWGASAVRTTVSYCVQ DCTGCSGAALAAEL
80176:311	0.892	0.659	MKLCRLCVGRRPSICATSLSRLYGWGRLEQ EGPPSPEWRVCICT
81195:330	0.962	0.911	MKFQGPLACLLALCLSGEAGPLQSGEEST GTNIGEALGHGLGD
82633:498	0.932	0.643	MHLLCFLDFPLMQQTFLHHVKRMRPFSSQN FYLAITFHHRLTMT
83339:204	0.945	0.667	MHMMVHFYFQINVMLIAAIQKSDQFLHIKLVSC KLAIIIIIIMM
84175:310	0.964	0.835	MCSSPAVLLCALVVGCPVGFPEADPGSMQR ASSLGLHQASVSA
85190:325	0.93	0.758	MMWAAGAVAAMSSITFAVSALVSRTADADQ QGELIGTSDNYLKV
86370:235	0.992	0.747	MSFLAGLGLAVGLALLLYCYPDPKGLPGTRR VLGFSPVIDRHV
87186:51	0.988	0.806	MYTLLFCCCFPMFLLVLPQVTHYGKKVGGGRI RRGFYILLGKRN
8839:174	0.962	0.821	MISFVLVKGLFLKCTHFHPLFNHRHIMSCSFLRS DFMHGDSMCFSS
89166:31	0.956	0.797	MHALQWISFCRGWLSVRLSHPCLLVDVGRTP PAGPTCRPAVLVAP
9018:153	0.948	0.798	MSIPYQIYGLQFFCLSMGCLFTVLIVPFDARKF LILMKSCLFFFY
9119:154	0.931	0.672	MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSP PQILVHPQDQLFQG
92387:252	0.949	0.816	MERRRLGGMALLLLQALPNPLSARAEPQV RGRGRLGHVGSWGS
93288:423	0.943	0.847	MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCL AAGITYVPPLLE
94147:12	0.994	0.903	MLMYMFYVLPFCGLAAYALTFPGCSWLDPWA LVFAGGIGQAQFSH
95127:262	0.937	0.701	MQLEALNLLHTLVWARSRCRAGAVQTQERLS GSASPEQVPAGECC
96187:322	0.956	0.864	MGVVLYVLVCGALPFDGPTLPILRQRLVGRKI PDSVFHVRRLRAP
97167:32	0.965	0.884	MVRLQVLVLVFRVVGSSQMLRQGAAGARSH RVLASLHFQHGFGTF
98536:401	0.975	0.94	MSLRFCFCLPVCPSLPISVFHVFLSVSDHPVSL CLTVSGHEMSVI
99285:150	0.977	0.94	MLAYLFFFSGTLLNQLLDRGPSLSCFWPRG

				VQACARLQQLLEW
100	299:434	0.96	0.852	MPVWLGGTFAPLCLACRISDDFGECCCAPYL PGGLHSIRTGMRRER
101	335:200	0.959	0.932	MLYVYFFLLWGVEACGHFRGPGPCGGRVGS CSWPGRSQVSRGPD
102	269:404	0.968	0.924	MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPH WNTRCPLASHTD
103	401:266	0.891	0.656	MRASCPIGRLSLTALSVMSSSNSTWMSLLPVA VSTRKPRILRTML
104	154:289	0.951	0.626	MANIECFHTKIRNKIRILGLILLFTIVMKVLHGV NTHTHKRNR
105	145:10	0.987	0.723	MFLILLGVCLTRVLDVDCTLGFITQLASNNRKEI VLFFKSRPFS
106	177:42	0.949	0.697	MPCLLRALAVLTCPSSPSPVLFPLLLCPHLHL QEYRTNLSLKA
107	333:198	0.902	0.786	MSFLLVILVSHLRNHCIIQTHEYLCLFYEFNSVS SYAYYLCPLMS
108	46:181	0.918	0.747	MIVYVWLMSNLFNTGKFIFNFIHHINDTDILS TNNSNPVICPS
109	35:170	0.894	0.617	MITHLGRRWWSGQCWLALSSRRIMELPAPG TVPGTGWEAGQGW
110	192:327	0.956	0.554	MAPFALAVPRCTGPEGSGGGPWVACFCVLR MFWAVSRLGLVSLRR
111	125:260	0.96	0.64	MGADRWNALALLSGSYVTLVYTRTFSTNTIEG LLFTWLLVLVSSH
112	482:617	0.956	0.688	MRCRCCLCSCFWGLWDPCKSVWSPWSS SSLGAFSVGSELASAA
113	355:220	0.951	0.795	MSSDVILAFIWIQKWLLHLLIEVGIDYLVVIPPQI PVLNYFWLRW
114	156:291	0.948	0.807	MFLSSSFIVSGLIFKSNLFWFLYVIYTGVSFFC NRHLVFLAAFI
115	179:314	0.986	0.907	MKGLFCLWPLVRSVSSLMTSSTSCPSPTLP PWRPCLPRLMRVL
116	223:88	0.968	0.715	MKRSNILAVMLFLISWMSTSISPLYPSLLXWIS RYTTASSCPSL
117	236:101	0.938	0.676	MGQVPCCWAWWSLLQGRGSWCEHKELRG WRRPGPGACRTPARGQ
118	1248:1383	0.99	0.906	MPSIRLGLSHLFLTAGIYCLLLCARCCALGRGT AWAACPGGACGL
119	380:515	0.982	0.9	MFSRLYAVCMLYMWGFVDKMCVWSVMQVC YCLVFVYVFLCMVCRV
120	316:181	0.942	0.768	MLTSKSCIICLLYLHNPAGIELYECCEFGRG VFPFFPTWISNQ
121	129:264	0.907	0.805	MRTRVMTIFFSTVYIPSCLAQCNLHIVKCMNLK VHGLVLINVYIH
122	150:285	0.969	0.953	MTFLILSIAPVLAVTGMETAAMTGFANKDKQE LKHAGKQLKLWR
123	242:377	0.977	0.856	MPLICLPVRVLLQCLSGPPLREVSLLVFGCS FIGGIHLAHIGI
124	35:170	0.901	0.564	MLQAHQGAFHFWMNQVFPQLFCTFLSIDLEC LWNTQSVPCVNHP
125	542:407	0.928	0.622	MVLWNLMLHSLSAVTYPPDLVSWNLHFKQNP DHSPLPQLTWEVLP

126	630:495	0.896	0.652	MITTSKSSSRCCFRRSIFFTATCFPVCFSVA MHTMPVEPSIL
127	212:347	0.905	0.64	MLIIFNAVWVRCLKPKIPARPTTNDTMISKTKQ HTQYTSYAPSWP
128	29:164	0.978	0.876	MHTCMYVWGCVCCTCVCTLHVYMQVWVYVCV QYMHTCKCVGVCVHY
129	25:160	0.901	0.694	MFFTSGCSFFFLGGGVKPLFLPNPFGPPCWG GGYQTKKKRPPPL
130	126:261	0.924	0.736	MTVLSFQYEYLIFLLTSLTTIYNTLSRSGDGR RTCLVFNLRKV
131	171:306	0.952	0.641	MWYSPASPSSSVLQKLTKLSRIYFCLLQLVFS ACVSKHICIPWE
132	29:164	0.996	0.941	MYLNLQLCLWTCLFFFYQCQLCFINFEVIKDTN LKFLYCCTELIL
133	246:111	0.993	0.92	MRSALLIMLFMSFTSAGIFATFIFLDSERFVKIS NTVFCLFILTS
134	87:222	0.891	0.57	MRKRPTELSCACGLFLFRTVSVVSPKGRDHR DGRARPLSSGQAXT
135	72:207	0.955	0.81	MCVRRSLVGLTFCTCYLASYLTKVGRGARE AAIARGRFESENLP
136	412:277	0.949	0.781	MELRKFLSIPIPCVCVCLIMNRGELYHMLFC LLKQYDTLFVLS
137	227:92	0.97	0.796	MLTWQPVHLWLLSADTCPASRSLSSVFLIL TLLLSLHPPPELPC
138	99:234	0.922	0.64	MAYTMIPVLHFFCCTSSLVRTKVWWEAINMV FAKSMNGGPDRCI
139	94:229	0.987	0.789	MPSYFKTCSLFTLLSSVFLVCIWIFKTNIKSSVS ESPPDSGLGQV
140	147:282	0.962	0.798	MWRLPRVPWGRHPALWLCCSGLLSHSFWRL WVSINILSLKCGKI
141	384:519	0.992	0.84	METAVIGVVVLFVVTVAITCVLCCFSCDSRAQ DPQGGGGRSFTV
142	157:22	0.989	0.971	MLIFVFLFSYIALAGTFSPRLNRSGESVHPFA LHPVLRRKHPVI
143	353:488	0.993	0.908	MCMFRRIVLYMCFCLCVWYVHVCGCCGDVW DVHVCGAHCIXLLC
144	55:190	0.994	0.966	MICKYFFLILWVVSFFFMFLDAQKFIILMKSNS SFLLLLHMLLE
145	167:302	0.934	0.788	MRMLLTGGLPQMCLKFHGTPLTCPQGVPCP HDSQRIQGIPKAPT
146	25:160	0.985	0.818	MYPGFNLSTSSSTLAIICLFAFSILMSMKCYLVV LICIPLMATDA
147	260:395	0.994	0.966	MFCCVICPVSFILIIICIFLFLSLAEGMPILLFSN THVVHRFLP
148	271:406	0.992	0.807	MLRLGLCAAALLCVRPGAVRADCWLEIGDK GYVWLAICNQNPQA
149	160:295	0.989	0.927	MRGWLWTWLPQPILLRLGQKPFLYFVLKETIIP SPTGRARLSMQG
150	244:379	0.951	0.74	MGVSFCTALLVYVSILPRPYCLDDYTYAANLSI RVIPPTLLVWLF
151	239:374	0.941	0.566	MLCLPMLDYFKCCLLLKFLKNDFCQHIPPLOII KEKILKLPIVT
152	92:227	0.951	0.701	MNMEYLSIFVCPLQLFTSVFYAFYYRDLSSLW

				LSLFQGFYFVCSY
153	247:382	0.903	0.731	MQKLQQVIQKMKVALLTLLGTSAGDFKLQSV LIYHSVNHRTLRI
154	97:232	0.989	0.781	MSSVSLIEFPLYMICPFALAAFKTFSALILDILL TIFLDDIHFV
155	406:271	0.943	0.901	MLLLWGRLTWRKMCRKLLDMTFSSKTNTLVV RQRCGRPGGGVLLR
156	18:153	0.977	0.826	MFSCPLQTVPLAVFFLLAGIAVHLSHLVLKLLK SLIFYVDFDHPP
157	150:15	0.921	0.745	MAPGGAKGQGASALALLFILASPATGGGPRL WRAGGLGFTHCQAN
158	115:250	0.955	0.862	MHRLPAATRATLILSLAFASLHSACSAEASSSN SSTLTAHHPDPG
159	816:681	0.939	0.87	MILLSTFFCCFREDSCFYKKYVGLVQWLMPV IPALWEAKVGGS
160	243:378	0.937	0.751	MFLYASLITVYGFVKIQPVAFTCLLHDLYNPLG SQPATHRTFPCA
161	70:205	0.884	0.588	MVVGAFPMAKLLYLGRQVSKPLANRIKEAAR RSEFFKTYICLPP
162	213:348	0.987	0.932	MLHFYILIIFILNCLFLPQALRTFILFLDDSVICLIS FALAFLLW
163	508:373	0.989	0.875	MKALCLLLLPVLGLLVSSKTLCSMEEAINERIQ EVAGSLIFRAIS
164	18:153	0.941	0.818	MVPWHFLFSLIRKITPALLGWRPQVSTGGRGL DEQGVVRGPGAQGP
165	20:155	0.957	0.763	MLMCFICTASTVWNTLRAGHCVYLMSCQSWK SPAEFSAHLSNFTV
166	292:427	0.984	0.861	MLPLLLWPIPLLSLPSPCWAPGFSSDSKYAVIL EPLSLLSHLPGT
167	244:379	0.964	0.826	MQKFFLITYVLRFALDVANYIFICIFINMFIMISM PLSFKFWGII
168	241:376	0.981	0.822	MFFWRLLILYSSPEITVCLHLFTSSGLKMQHLR SHCHLFRQALFL
169	8:143	0.932	0.681	MVQSLWKTVLAVFYKTKCTLTIQFNSAIVLLGI YPNELKTDAYKD
170	131:266	0.971	0.585	MLFAWKVSFFPFQFKLCFLREDLLISLFIKQAP GARKPLHQHSIC
171	107:242	0.937	0.766	MKSFILPSSRYLSLVCSFWPTLVGWGFSNNLI FSKVILVYFIHGL
172	33:168	0.953	0.862	MDHCGALFLCLCLLTQNATTETWEELLSYME NMQVSRGRSSVFS
173	198:333	0.983	0.903	MLSFKSFIVLYFIFRSMICFELLVKGIRSLSRFV FYMWVSICSS
174	138:273	0.888	0.626	MPCSGSSVQTFRPLLIFHNVTFILPVKCFNALI NVLERPFWQLL
175	362:227	0.924	0.818	MMRVIIWFRISKGTQFHSTTKCDVCFRVFLL SNCSFLSLNYKL
176	146:281	0.944	0.622	MGGFKVNLVVKVKAEGSPLCWLKLACLGAWL LSLLISQKSDEQLC
177	59:194	0.972	0.68	MSSSGQLGHPPRAPHSWRRWCWWLFMLAT SLSRRRRPSTPLIHYR
178	58:193	0.975	0.788	MATPSSPWWAHSGLPPLFSSGLSWRLVPLF WCLQSLTGFLGPCLP

179	48:183	0.956	0.623	MKIFLSRVLPGGELAVLCLPWWPLNPEGQCC VFTPWHMGRENPGR
180	222:87	0.986	0.917	MPALLVLKVVKVLLPMVLTGLGVEELKEMVLL LPVPCAAIIGSFK
181	174:309	0.926	0.71	MTEHLAQQSEFAATLLLLWAPLKTGRLTNSFV NGPGQHGMCCIL
182	102:237	0.931	0.584	MQYWNGHKTGRSLYTKMATMGLIGAGLPAAF LLVVTYEAQATTCA
183	91:226	0.959	0.811	MRSNLGLWLYENVLLTVALLTTGVVHHIFNT APKLFHLNVEWP
184	99:234	0.969	0.927	MKMLSQTYLLLQLLSLSQTEFLKELCIITFFPF LHFPLTLFQPP
185	92:227	0.981	0.858	MVGFGTNRGRRLPSLVVLLVIVVLAFFNY WSISSRHVLLLEE
186	699:834	0.907	0.56	MCTRNALLFAPSVFQTDGRGEHEVRVLQELI DGYISVFDIDSDQ
187	148:283	0.911	0.687	MTIILQIETVIFLLYLAPDVRPLTIITGMAGIVKQ QIDSHITDP
188	181:316	0.959	0.818	MLHPETSPGRGHLLAVLLALLGTAWAEVWPP QLQEAPMAGALNR
189	28:163	0.95	0.685	MRIISLTLMLLELFDSEDPQRQREYLKNILHRLY GRMLGLRPYIHK
190	239:104	0.954	0.645	MFAYTSGGSSTCAGKARLCLLVTLAIMSTILA PLNCRDRALGRF
191	77:212	0.977	0.902	MRLAVSCITSFLMLSLLLMAHRLRQRRRERIE SLIGANLHHFNL
192	8:143	0.958	0.838	MKVLWAGVLGTFLAGCQAKVEQAVETEPEPE LCQQTEWKSGQRWE
193	11:146	0.973	0.925	MVPCSQVFSIAFGFLVFGIFMVVITVGSFKGIIL WYIFYFLLIPW
194	134:269	0.965	0.692	MKAFCIFYLFFSPLNSWLFLCSHPKPEGLAA AKKLCENLLQTVS
195	129:264	0.914	0.74	MVHLLLVFWSGPHNLGRFQPMKLFACLNQS GYIIAFFVLYTNRM
196	122:257	0.97	0.898	MPSPSGLWRILLVLGSLVSGSARAAAPLRLV RQTALCCATEALV
197	110:245	0.978	0.797	MLLALPLAAPSCPMLCTCYSSPPTVSCQANNF SSVPLSLPPSTQR
198	93:228	0.985	0.928	MAFLYHVAYVLVCMGLGFCHEFFYSFLLFESV YRHQTLLNDIPCV
199	173:38	0.984	0.859	MWDVLYFCSMVVCELGLGGCLGWRISSEFCIG YLGLVLGVLSWGLL
200	130:265	0.942	0.817	MXISALCLHPSLYISSCLFLYITFSILSLDLLS SYYSLSLLLL
201	52:187	0.94	0.686	MRKAGCLLELCCPLYTVLITSQGCFLPHLRPL PPHHFHHPSYLP
202	302:167	0.89	0.589	MAWKPLGRQAVLRETPLATLCIDRRQVSSSLV QEGFHKSCHCLG
203	271:136	0.923	0.811	MXXXXXXXXFLSTTGFLPAAAFSSDLACSAAX TXPLCYCRSLRFL
204	93:228	0.995	0.941	MVPFSYFWFYVAFLLISPWAASVITRKMLSPS YGFQASTLLLTGV
205	4:139	0.978	0.74	MLYFQLVIMAGTVLLAYFECTDTFQVHIQGGF

				CQDGDLMKPYPG
206	122:257	0.919	0.798	MLWELVLLGEPLVVMAPSPSESSETVLALVNC ISPLKYFSDFRPY
207	315:180	0.924	0.674	MERTTARLATCMLLAWQGCRRSRTDCMLSL MLHGSDIFSIVFYE
208	395:260	0.924	0.831	MWLFSLVSVCMSAHEIQHFVDVLPHTLHRC PTSRYRGYHLLAQD
209	19:154	0.958	0.789	MLVLFVATWSDLGLCKKRPKPGGWNTGGCR YPGLACPLGRPPGQW
210	27:162	0.968	0.919	MKWVTFISLLFLFSSAYSRGPKAEFAEVSKLV TDLTKVHTECCHG
211	84:219	0.96	0.876	MRRRALKHWVALCLTWTAGESTGPWPSPEP SVRAKEADPSGRRSL
212	677:542	0.978	0.886	MAASPARPAVLALTGLALLLLCWGPGGISGN KLKMLQKREAPV
213	426:561	0.968	0.935	MHPSLHPWALSLLVSVALAAASCHPKLQHEG CISCAILNRLGNYL
214	101:236	0.921	0.771	MIIQICTISRIEFICLCVCVFFRVIWLPVEFYLET KILKVVFVIV
215	39:174	0.903	0.61	MTLCSAAQLALICHSSSGTLVHSQPKHLNHLQ LLEPGSGAQEPQA
216	345:210	0.916	0.677	MFLTIGRILLACYSQAVQTDPAKGISLESNLKR RAWEEEGWEEEG
217	336:201	0.991	0.872	MLSWVFPGSVFGCLSVVFWHQASLGRAS GCAPALRVGLIPGCR
218	80:215	0.985	0.962	MKPVVWATLLWMLLLVPRLLGAARKGSPEEAS FYYGTFPLGGHSA
219	711:576	0.897	0.772	MGAVLLVCLQTSIAARDDLKDAVDSGLLLANS LSHFVPLVVRNYL
220	182:317	0.934	0.749	MVFLLPILVMAPKIEADMSWSARSPTLPSGS LWRKVRDPRRTINM
221	257:392	0.929	0.775	MGLIAVTVIAATAGVALRQSIQTVHFVDKWQK NSTRMWNSQVLIK
222	43:178	0.996	0.874	MIIWFLFTLLLFNKYDVMSFFLFEYVKTSLHP WDKSQLIIVNYL
223	193:58	0.982	0.864	MFIGIWSLYQVLWLKELLWGHYIFWVSRKMF VYGGVGGKTANIC
224	191:56	0.96	0.749	MLLKFLCECMPSLLLSEFLDSPRSGIDGSNGN SMFNFVKNCHFPT
225	223:358	0.988	0.904	MFGLLFRGQGFWSWMPMLFLCIFQPSLADLR TQYLGVACRSRQGV
226	334:199	0.997	0.949	MFLLLFCLMFDFTKVFFILLHIFCLSTCLFLGL HICASFHARAL
227	103:238	0.939	0.728	MHMMKLSIKVLLQSALSLSGRSLDADHAPLQQF FVVMCHCLKHGLK
228	48:183	0.978	0.793	MLWPWGPRLLVGAPSALLQLRQVEELSGVG RGLGGIRMGWGGLP
229	143:278	0.992	0.925	MTIAMIFYLLEIFFCAWCTAFKFVPGGVYARER SDVLLGTMMMLII
230	196:331	0.996	0.971	MCISKVCWGLCVFLCWCLHTVFRCLWVSI VQVKSASYCRGCWA
231	86:221	0.979	0.947	MACYLLVANILLVNLLIAVFNNTFFEVKSISNQV WKFQRYQLIMT

232	361:496	0.995	0.973	MDILLLLFFMIIFAILGFYLFSPNPSDPYFSTLE NSIVSLFVLL
233	150:285	0.918	0.863	MSPQHLLLTLPPLRSPILFSHTAQLLVLTRIAF RACELFFFVMV
234	207:342	0.914	0.656	MPVFHLTPCLLPPTAVPIFFPTEKREINKNRGQ RKFRREMGVTRP
235	338:473	0.971	0.86	MESWWGLPCLAFCLFLMHARGQRDFDLADA LDDPEPTKKPNSDIY
236	234:99	0.977	0.93	MWIVLLGGFVGPLYLTPAPSPCTHTLGVRAPV LVTGLTSQLWLNA
237	125:260	0.968	0.864	MVTGVLWTMEVLLWIPLPSQIIYQAVTVLSFHR GGRKAVLEVTEV
238	53:188	0.988	0.939	MGVMAPRTL LLLLGALALTETWAGECGVGR ERASAGRSEWPARP
239	457:592	0.962	0.871	MPVPLAYFQSSIVLFPLIFSLVTCVSLDGEPKS VVGVISISAYYR
240	382:247	0.951	0.655	MLAEQVELWWSQQPRRSALCFVAVGLVAG CGAGGVALLSTSSR
241	358:223	0.95	0.705	MVFGWVSGGLQAGWMVLDWVSGALQAGW MVFGWVSGGARLGSFW
242	1814:1679	0.994	0.957	MPALRPALLWALLALWLCCATPAHALQCRDG YEPVCNEGMCVTYH
243	157:292	0.947	0.754	MLLGLFTLQFPHLLKGDGILVARPPAWCGFPL LSFFTEIEELDSS
244	223:358	0.915	0.795	MAGSPLMAICWMFRLGMAGDGLDSIPEQAGP ASQPAGQSGTHRSF
245	208:343	0.979	0.863	MKFALFTSGVALTLSFVFMYAKCENEPFAGVS ESYNGTGELGNLI
246	566:701	0.987	0.792	MENCVGERNHPLFVVYLALQLVLLWGLYLA CPGVCGCGPAGSCS
247	251:386	0.936	0.72	MILQVLYEWIFLHVAAPSSSHVCGSSPLHCIAD VYEGKRKIHPVC
248	334:199	0.957	0.882	MLEILLKLVRLTTQPYLTLFQAVRNALNLSTS SGSLGPAPGEP
249	88:223	0.958	0.882	MMHFLTGGWKVLFACVPPTTEYCHGWACFGV SILVIGLLTALIGDL
250	291:156	0.99	0.952	MSFTTFVALLSLCLWVTSTNYPTRSLRISSFN KEESDVASYSPQ
251	35:170	0.987	0.761	MNIIFCWXLTKLSLIRLPGFPLLSYLSASLPLF SLPTSSDSWIS
252	79:214	0.995	0.954	MPWVLGCTPFIALAYFFLWFLPPFTSLRGLWY TTFYCLFQALATV
253	341:206	0.973	0.907	MRSSCWLTRVTVFATIWTASAPGPVTLTDV WRLTGVFCTSVLST
254	298:163	0.924	0.567	MGSSVLSIWILSPSIYPILSPLAMPCLSRDILR VRRIQGAWPSE
255	496:631	0.992	0.949	MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLG LVHLGQLLIFH
256	9:144	0.894	0.666	MTTTFPPRKMVAQFLLVAGNVANITTVSLWEE FSSSDLADLRFLD
257	203:338	0.989	0.82	MENCVGERTHPLFVVYLALQLVLLWGLYLA WSGLRFFQPWGLWL
258	435:300	0.989	0.968	MPIWKPFMAWMAAWALAVLSKLTKEPIHLLWM

				VARSINTEEMILP
259	55:190	0.914	0.729	MYGCLGAWCHVTTVTRLTFSAYQGNLSM YHDSPCSNQYVYIP
260	247:382	0.966	0.687	MINLGFYCLGLIPMTFLVVRKPGMAFNSAGIIN KTS DHSEILDN
261	29:164	0.989	0.884	MWLLGPLCLLLSSAAESQLLPGNNFTNECNIP GNFVCSNGRCIPG
262	204:339	0.991	0.578	MTGSRCEEHVFSQQQPGHIASILIPLLLLLLVL AAGVVFYWKRR
263	247:382	0.979	0.849	MVGFGANRRAGRLPSLVLGVLVIVLAFNY WSISSRHVLLQEE
264	184:319	0.92	0.844	MVARVWSLMRFLIKGSAVAGAVYLVYDQELL GPSDKSQAALQKAG
265	53:188	0.962	0.61	MRNRRTERCTPPLASPYNLVPHLQNLAVLL MILVLTMPVLNPH
266	349:214	0.971	0.879	MVVVLPFAVLKLLFGQSKLQPMQPSQSGLD PVGAGMSASIA DGS
267	193:58	0.904	0.774	MTMLPCDIFPAVFTLGLNSVFWQYNKNSP ENLLDESAFTKSPN
268	324:189	0.961	0.867	MTPIQSLLYWWTFRIFIHFCYCMECTHVPIRVG QGGQFHVPIFA
269	341:476	0.923	0.708	MLPQVFLGFTKVRLLRLRNPWGCVEWTGAW SDRWGSGVGVGLDP
270	159:294	0.888	0.694	MTLLADLLLQTKSAMSLSGCGYFSVKPDL SWL PSRAVSFTWQPSW
271	59:194	0.887	0.64	MDLGRVFITLILNLLRETIFKRDQSPEPKVPEQ SVKEDRKL CERP
272	6:141	0.949	0.835	MRS LWKANRADLLIWLVTFTATILLNLDLGLED AVIFSLLLEVR
273	126:261	0.989	0.858	MLKKIFLIKLSILSITLKLCLILESMLLSLAGTKL PELKKNFKI
274	354:219	0.964	0.794	MFIIFLAFIALKRKSVIGAFLYLASIFLAHGVAA HIVFMSAFYQ
275	149:284	0.924	0.683	MYFSGPFLIQKMISLKLQATYFFSFFWCLTFG HFSHYYYEREIK
276	287:152	0.975	0.909	MLTEALTLLLHSALEALILSELIHRGLYYFGWW FVLHCSVFGQI
277	6:141	0.968	0.925	MRNPGFPLFVCTLFSLPLCLALDFIFSLPFLSI SLLFFAFHPNF
278	22:157	0.963	0.661	MQRGRNEWIGKIRPWVVRNCLLSLTCLLPLV NFGCIFVSKCHIR
279	33:168	0.971	0.781	MCIELCIIFPVMSSPSFFILVSENNNNDFLIL MVL LLSLGLT
280	148:283	0.909	0.564	MFIINMHILEGCTKFCFDCFFWLVCWGMWSN KFGELSLISHNLA
281	79:214	0.914	0.597	MLLSRVFLSTFQSPHSHLPGLLEPLPLGLHNS DRVSLTLSYSGIF
282	172:37	0.926	0.684	MEVEGGGLVLIGCVTFVFCIARLEGLVIFHV GCCSLFGVFRWE
283	360:225	0.982	0.822	MWFAAPWALVRGPGFCLLDYPRGGSGGGI TVLLAFGLLGEDAEG
284	21:156	0.949	0.774	MMGVSGCMVLLAPLLARRSQSSLWKQFEKC SAGPKMLLSKFLPWG

285	146:281	0.948	0.714	MLFSAVKLYCCQFWHLILNRVPSPSLLYSCGL STNVLNTTVCYVR
286	30:165	0.91	0.654	MLMMDTLWPILLQTLKVISQVGHAGPLANMIH DNPCIAYRITLR
287	72:207	0.945	0.801	MICSTTFLILKCFSVLKEILKPILTNVHCRSGVE AQAFFLQQFTS
288	190:325	0.955	0.831	MIDIVRFAGLPSTLLHALCLISLTYPSSFRHSSY LISPCASFWIL
289	46:181	0.908	0.638	MPIVVACARISSILFARLFADPPNSHLLLPNPNV TGCSSVPVYER
290	61:196	0.926	0.615	MGATDSLRRRCRQGPWRPSPWMFLLGRLFEL GSGAWLVEGPWPTGP
291	261:126	0.98	0.81	MGWHRLWALLSPFACFRICGSFESQNNGSAS LPSTPPVGGWPRGC
292	615:750	0.972	0.926	MIALTQLLTFILSCNSSLHIFPFCEQVLVNGT KAGHSLLMDAR
293	175:310	0.948	0.782	MIFSPSPRLCLFLVPCAHSCSLQSQPGLGIVN SFSFFSYCFLYSP
294	231:96	0.97	0.853	MTHTNISLLLFMFAYFDCTCTLDLVGSLAKQVY FLKYTREVGVHS
295	49:184	0.928	0.636	MVLSWLTLEALADVMTTDGNMLQLFCVERTN LLVNQIRMTLYAQ
296	178:313	0.96	0.835	MLSCFSSCRRLFLALWGASQTAWMDSLVMFP SSTLAPANSYLSLG
297	274:139	0.955	0.65	MCVWLAVLRGILLKGPQIGGHSSWPLTPGCE PSPAVLVARAPGAW
298	153:18	0.939	0.649	MVIGSLHTFTLLAASSLVDTPKQIQLLMQNLMMN DPRKEVKILAIQ
299	415:280	0.969	0.734	MWVSLVGKCLCGLFTVQKAAQQCNGLTALDR ESEAWVLVVALAPP
300	441:576	0.937	0.722	MSTPHFFCPFLILPCWSDWKWGCSSLDTGK EGPWGCHFLCPFGW
301	297:162	0.986	0.878	MKCFHCASALAFFLCLTFSVSPTCHLSQVAL NRNLSFYVCFNSP
302	111:246	0.94	0.712	MIWDVHWSKKAIELTLALLWPVVATVFISEPE IYDTCILTEKKT
303	207:72	0.976	0.959	MKIALLLLILARCFTMESEVSVQVSEFSNHIGT SIFKLLVFWFNT
304	50:185	0.954	0.602	MWTVLWHRFSMVLRLPEEASAEQEGELSLSSP PSPEPDWTLISPQG
305	226:361	0.98	0.947	MILMLLLLIVDLVQLAGNAVISSGSWDSACTGT PSPSTPSTWPGP
306	35:170	0.901	0.784	MLLIFTFDPSTSLCVLSFPIINSTGICFSGQELN VSPMPSNKVSD
307	9:144	0.891	0.71	MDHKSLWAGVEVLLLLQGGSAYKLVCYFTNW SQDRQEPGKFTPEN
308	116:251	0.928	0.697	MQCAICILLYLLNKKTWRCRIHHNNTVVLTR ESSPFLTCTLS
309	173:308	0.904	0.611	MKRAQGIFLEPLFTFLYIMDVHMPATFSLHTE LPQYRDGTPASS
310	142:277	0.948	0.676	MIFYVILSSPSSRTFFKITLIMSLGLISKLLITSCT FDTVTFMML
311	293:428	0.986	0.881	MLITELFITWFIYLLFDFKHLLLVDLHMLGLGNF

				NIQVGIPVAIV
312	146:11	0.942	0.695	MSPFSKLFFWLYPGSLIPEALRVVMLVDTLRD PYPATSAGDIMGL
313	40:175	0.945	0.759	MLLCTCHVPNFSLVVLIPYTAIEMNFHFFSCGR LSFTIVFMLPKV
314	100:235	0.977	0.867	MPAKAWPIWILKAASFLIKLYIFARFSTIPSFLKK NLYASFTPSL
315	297:162	0.891	0.703	MIELAWKFIMHINALLSFGTTSCLKIKFAHVFSFL QLCIMNKITLI
316	317:182	0.995	0.938	MYALLGVFCLAILVFLINCATFALKYRHKQVPL EGQASMTSHDW
317	97:232	0.943	0.839	MGMGTLIIMNVWVLFIPTRLRIDQQPVHIKPSM RVLDKWWSAFVH
318	70:205	0.946	0.733	MIIFYGFGVCVFMRVQPALYALWNIRITIFIVDFI LFSHLCTYYW
319	175:40	0.931	0.551	MELETFVRFLVLLLPKNKGKQWQHIEMKKPQ VCNTLKGKRGPKFV
320	187:322	0.981	0.933	MWHYAFSLAFYFFGACLAFSHSGIIKDLIAHLH PFVLSQISSHD
321	55:190	0.974	0.879	MNLIWGRIPWFSVPAWLSVIPYDVLVSPRVH SPRVVLKLGTPN
322	401:266	0.909	0.59	MSNFFLQRAILWSILPDTQCIPRFFHSDLWSH VPFLALGDLQELF
323	65:200	0.959	0.738	MPHIQTLRLTLFASHLLVSLWQSEPMKPRMR KYNTSSEYLSELD
324	387:252	0.885	0.73	MGRNPVFTLLFMISQGFGLGYNIQLQVMVESTI REYFYKEKMAKL
325	414:279	0.974	0.944	MVCTLPVLLKVVCLNKTPTTLDMPRAGITQY TWLRPDENLPRSG
326	58:193	0.99	0.849	MKWKTGVAIFVVVVVYLVTTGGLVFRALQPFEE SSQNTIALEKAE
327	66:201	0.933	0.811	MSYVVAGFHFFLTAFICYRYSTGIFYLVINIT NQISIWKILL
328	266:401	0.991	0.9	MEFSYFCLIFFQALCCIRGFFAFCINSVC SHGD LTFLNPPLQFLW
329	35:170	0.969	0.724	MALALAAVYCGWVVDRETWPVPMPCNKGGRR ACNLEMGMWLNLC
330	31:166	0.986	0.595	MRILSLSSFTDYNVKNRLHVCILTSFCCGLLA LFLVLAVQGYLA
331	424:289	0.932	0.581	MVFLLATSGFCASGCRYLSDAVDTEAVATSD REGCFPTQSQTQW
332	472:337	0.982	0.809	MIIAIGGVIVASGLVFIVLLMIRYKVYGDGDSRR VKGSRALPRVR
333	16:151	0.955	0.704	MILCPPCSFKQFIVFIICLIERIHIYYRKLNVVK KKKKPAEIP
334	182:317	0.986	0.889	MCVIAVLTFASASTVFIALKVCVAWAAAAASR CLGGSLLNLSAV
335	33:168	0.942	0.568	MSLPPSLACVGRACCLLPLGRQRPGGCGALA RVTRSGCGRQGGCD
336	280:415	0.959	0.742	MHLIGSATLARSTINLPSTLIIVTMLILLTILEIAG DLIQAYVFT
337	275:140	0.944	0.709	MLSSVFLDLPVLLGGFQDVITVAPLAGLVPGP HQSTLCCDPTSG

338	321:186	0.957	0.807	MSSTAAFYLLSTLGGYLGTSLLLKYPTLLHQR KKQRFLSKHISH
339	477:612	0.984	0.921	MFLHSVNLWNLAIFYVFMVFLATLGLWDVFFG FEENKCSMSYMFY
340	316:181	0.937	0.757	MWRRFLSFFQCLVKYNVCKCSVMLRFSWL DSTCQTKLPLGCNEF
341	125:260	0.904	0.724	MRQWGOHWWTFGWREFGALWRTQQGVV CLGHRAGGEGQTHHPTL
342	30:165	0.965	0.775	MNKPFINASISYCLYILSAITLWALVLVSSV ASLGPFGFSW
343	313:448	0.992	0.961	MKLYKWSFSLILLSLLLINFSYDLLIIHQFQSD SMGLFGLPQG
344	34:169	0.975	0.903	MYFFLFFLFAEMGLYCNHPSFFYLHTIPSYGY TVIYLVSSLCFR
345	269:134	0.978	0.896	MFSFSMFMMFFKTFNSLVQVEFILIVVGIEPF PQIVKQSQSLIL
346	42:177	0.972	0.646	MGCDGRVSGLLRRNLQPTLTYSVFFSFGLC IAFLGPTLLDLRCQ
347	384:519	0.996	0.96	MVSKFLLSHLVAVPLRVLLVLWALCVGLSRV MIGRHHVTDVLSG
348	37:172	0.969	0.681	MMALFTGKLLQVSVKVLWLYQTNFSLHTHYSF NRGQIFKRKTQVN
349	274:409	0.958	0.867	MMLVLPRLPEWWLVSVACMRTGTMIPGVTQ LTEKDLKYRLQASR
350	87:222	0.964	0.752	MLTFKSDNGKTXIXILLCLLLLFISFLDDPRAS IFSSPIPNCVS
351	295:160	0.962	0.603	MLGFRKPCQCLRLRWVCLHLLRRDFSILGLSF PICETKGPEERKL
352	209:344	0.951	0.857	MNHCLSFHLLFYGWAYTLQASLPSLLTIHNISK TQFFLPSECHI
353	262:397	0.973	0.905	MSFVKILIWELFIACFPQGPLVHSGKMLKHGLD WHRTLLQKHPCI
354	206:71	0.963	0.916	MCTVTAWWPLVTTAGCWPSRPAGMSPGSW CPSCGSTASQALCSAL
355	368:233	0.943	0.775	MPTFFAWLLPAGPGATTACSLHSQAAQRRRA PLSCAAEPVAAGSG
356	370:235	0.976	0.927	MLDLIFNFWLLPFAVLIPKWLLLRPAVLIPKP WLLLRPAVLIP
357	119:254	0.968	0.784	MDLPFFHLSLSTTALGFSWAVCLFKIFLSALNP ARNLGHVFLEST
358	581:716	0.971	0.875	MPVQAGSGTPLLFSISLISALNIISVLLFSVLFC CPFSNFLKRD
359	86:221	0.954	0.782	MSVRFIHVAVRSIVCACSLKTSIVWLYRSSQI HFTVSQACPMHA
360	128:263	0.973	0.806	MNQKNPEKLFPAFLFLLMPFLSLCVPPHLCH QFKMTLKVLLHPS
361	620:485	0.985	0.881	MCCWQFASILLRICTSMFIKDTGLKFSFSVVS PGFGIKMMLAS
362	319:184	0.992	0.902	MFLLEPCLLVCTCTGXAALILCQHRLRLEHKCV AVPSGIQQUREL
363	255:120	0.899	0.62	MIKSLYLFFDIIFISMTTLPSSKHRNILLYKWKR HRAVRELHNNV
364	174:309	0.979	0.778	MIVCLLFMMILLAKEVQLVDQTDSPLLSLLGQT

				SSLSWHLVDIVS
365	14:149	0.923	0.717	MKMLPSCKAALSLHLIWLQSGGHRPVCLA PAQTVKCAWCMPMV
366	402:537	0.984	0.872	MPTYWLANLRPGLQPFLHFLLEWLAVFCKI MVLAAAGLLPTLH
367	141:276	0.962	0.646	MSLLSDFILAIVFSTSRISIQFFHIAIPTDTLCL GKYISYFIS
368	423:558	0.96	0.791	MLIVSHLHYFLFIPFAGFGGSRKLIKFLSKMEK SLFAYFLLTSLV
369	186:51	0.901	0.76	MAIWSYPSRWVALIYAEVNLANLICLIAPKAF RGRPKKILIYNP
370	59:194	0.956	0.624	MSWLANGVCLYEYLFRCGFLILQPCSFASL TDEESRKNWEEFG
371	318:453	0.939	0.764	MCVALLVLGLTVQSDRCFPELPGGRSLLFCAL RRSERPLPQASRG
372	222:357	0.903	0.669	MQVLHHCWGALKAQWRLVGFCEKRLHLCHH VRKDLLARFLLTT
373	110:245	0.915	0.72	MRSVLVWLIQQLTPLYKGETWTQTCTEDHVT MKAEIRVMLEARE
374	167:302	0.9	0.696	MNSNPLLVIKLSSLFLCHSSQNLFVLMHKNV FKIVCLFSLKKHA
375	18:153	0.931	0.657	MYVPGRIKCKMTLLFSPWGLTLDKLNKSILY SVFSIYCDIFDQ
376	162:297	0.967	0.719	MLLFYTLXVFFYKXEYFHAQINFFHMLQKV QEFILVRKTRESN
377	96:231	0.956	0.802	MADSVLTLVFTSCLLSELSLVCSDFRPTPISYQ SRYGSGDGWIRC
378	165:30	0.888	0.572	MLSSQRLGHLPRLPWGLLSWTPRVSAVIFID KKESCFLDKNLHS
379	248:383	0.994	0.871	MLLFGLCWGPYVATLLLSVLAYEQRPPLPGPT LLSLLSLGSAKAA
380	177:312	0.911	0.74	MANYSLCQCIMVISFLCHGTFISYFLKVIIVSFRI EKPKLYYLV
381	204:69	0.969	0.786	MVRASHRSLLAFFACWTSILRLIRTSTRGSRL PTFCSECTISIK
382	24:159	0.989	0.923	MKVLLAVALIARTVFFLLLAGPSAADDKKKGPK VTVKVYFDLRIG
383	167:32	0.921	0.562	MLPYYATSLFFFVIGKSEIRFSNAYSVMPSAYA NLVKSKNLSEGA
384	234:369	0.96	0.911	MLLSFLFPQTMALPSRMLVCGTDPFIHSFVHS FICKHSSNSHHMP
385	144:9	0.974	0.774	MAAADDTILGFRAALLILVAAAAALSPKVACRV GTVRRRETPQPS
386	158:293	0.938	0.73	MKFFVLAILCIKLRHFTTGKKIWPQELFTRITT QLRVLNHFQK
387	245:380	0.897	0.56	MKMINTMGLFLLNLEMRIOTRIHFIALQLGREK CYWGKNKTDLTC
388	271:136	0.931	0.743	MIIYLTFPVAMFWVSNQAEWFEDDVIQRKREL WPPEKLQEIEEFK
389	72:207	0.94	0.752	MEIPVFSHICFLFSSLLCVRNPLSTMLHFPAWS LPDTSPLPHHTQ
390	153:288	0.931	0.614	MVHRALHLMAPHLTKLTFTCSCSRALRSECI CSCHLEYSPTSP

391	24:159	0.949	0.761	MFCFLVSVLYSKAKLASACGGIIFLSYVPYMY VAIREEVAHDKI
392	702:837	0.966	0.735	MLSQWAMLSLTSAFTYTVLYPKCFSFPLSVQQ TCLLSTVMXPFQA
393	40:175	0.918	0.614	MGRWLRELVVNLSCFHVHCVLELDHHEETSKI SSFIVIGRRQGGP
394	159:294	0.907	0.685	MSLLKSYCKLRANCNLLFLFVARGLHRSNLCF PCHPAFRGWPAI
395	51:186	0.959	0.814	MVLGLLVQIWALQEASSLSVQQGPNLLQVRQ GSQATLVCQVDQAT
396	176:41	0.972	0.935	MALRHLALLAGLLVGASKMENTD TDVPAPPE VLTRSTAGVRGAC
397	422:557	0.907	0.703	MQADRGGVFLVALPGLWETVLRHPGASPEP VSLHTGLAAEPLL
398	325:190	0.95	0.791	MWVFTLTLAASWGMNGYRKGWRQHGVVIG CIRWLEMQGFSSLAH
399	102:237	0.92	0.576	MPWLLSAPKLPVAVANVRGLSGCMLCSQRRY SLQPVPERIPNRY
400	149:284	0.967	0.909	MVDLVLRLSFSALAPLFGSSLFTWSSQMAQI RSLRANPCQVGH
401	184:319	0.989	0.705	MTPSFVSWLGVGKSQTWGPFSFLFLPTLFL CMLLFTQYLPQKSK
402	43:178	0.937	0.61	MSWFRYTFSPMPTYLLHLLQCCSLRNEVHN ENSGTPQYHKLLRK
403	387:252	0.955	0.876	MMYLGQDLFVLMFRVCWDSWMSFSSSMFL PIISSNSFSILPQPW
404	169:304	0.904	0.659	MRKLPLRGSWSCSCHYVRAELVLEWLLVQCF FSLCSSSYVSPRRR
405	255:120	0.971	0.803	MGSTWGSPPGWVRLALCLTGLMLSlyTLHVKA ARARNRDYRALCDV
406	342:477	0.942	0.626	MALDFVNVLLCQLAEVTLGVLREEGASLLVAL GSALFPSAAVVGK
407	118:253	0.947	0.796	MPLALSLPAKILFCALGYNHLGLVDEFGRIFMQ GNNRYGQLGTGD
408	298:163	0.964	0.869	MPRVALVCLPTSWVLSLAHAIPNGCEGVWLF CPCPHLATLLVLPQ
409	305:170	0.96	0.797	MCISVPLTPLLLFLNAGTMVSKDTGKCILTSE SEVEPAACLALE
410	85:220	0.954	0.724	MILINFREICLKVLTPLCVSGGCVLLYILALTC CYTNSLLISHL
411	321:456	0.957	0.649	MGVVLYVMLCASLPFDDTDIPKMLWQQQKGV SFPTHLSISADCQD
412	59:194	0.932	0.558	MHCITGWPNVWLMAGQFLCNTPSCHRWATT QQEYWAGICPKPRLH
413	172:37	0.933	0.742	MASPPPKVCLLAALWGQIFGLSLPCGLSEDL QLTRNSHCKIWET
414	231:366	0.965	0.788	MSCIIPPEAWWGALALLFCALRQRTTSLPLGN EWKPNFFPLPKV
415	45:180	0.914	0.78	MGERAPCFIPLLLHFTITYALEINYVCCVCMVE GTCLRNSTTEIS
416	736:871	0.947	0.686	MSLSCTGFALEKRCAGWVWWLTPVIPALLGG QGRQIMIMVRSRPP
417	265:130	0.958	0.832	MGVIHLKFHCRVLWVNNLLTTCQVFNKVTLPPVS

				YLEEKGLRTSILG
418	101:236	0.977	0.823	MINTLVVSFLLLKIMLQPTAFYVCAGIPIRLIGYC
				WYKDKLFICT
419	78:213	0.937	0.617	MLGTPLEIILFFLCYLTEETHGRLHVLACPVG
				QGSLEAKPLVRS
420	262:127	0.922	0.588	MFCALSLSGHALLNSTLLSTHLGGIGTAQKPK
				LYLAHQVFIGPR
421	183:48	0.965	0.812	MRRRWWGLWASVGILLPAELDSRLWREGTTL
				GACESGGSPARSWA
422	1542:1407	0.982	0.832	MACKGLLQQVQGPRLPWTRLLLLLVFAVGFL
				CHDLRSHSSFQAS
423	82:217	0.976	0.87	MGAFMVVAIAMGVFLGGVNGKLFGGLVAT
				AVGTFTMLVWLSPW
424	165:30	0.964	0.617	MKFWLPGGRGCVLLISVPIVPTPVSHSMYSTN
				ADECARGARGWHAL
425	132:267	0.958	0.864	MCVHICLILVKWIFPITYNGYLTFCLCKLFMFA
				HFSIDVSVFHI
426	195:330	0.99	0.965	MLLLFSLCVYACLCNVIIYCDVSRLLSGIGHHM
				HVENLFQNKIYW
427	304:169	0.973	0.845	MRPLFSWSCFCSCGILLLSLKYQALTRVKCWV
				NIYEVFHLFELKD
428	98:233	0.961	0.799	MSTGRFFLVYTFSVLNLVPLACRRHPHDGSQ
				RKFLNNGRWNFLTY
429	221:356	0.967	0.792	MTIIILLAKKALCPLAEVQTLPLPARLGNXKEL
				QKEGQQSISFC
430	166:301	0.924	0.595	MWSENVNLWRNTATSLQVLFFQSCFVPPFY
				LVHFMPPKPNRFYK
431	349:214	0.974	0.892	MSTCLPPPLLYHLWSLFWLPLLRGVQAGTRR
				PSGGCCTKEAQSPN
432	240:375	0.99	0.77	MMVMTLKCLFPVLNSMSMFLAGFLTFSPGSP
				ENTSSACSNSDGL
433	242:107	0.989	0.791	MAGLWFVVAACAEEKCLSLPWSLRQLEVAPRS
				RQGRGRAGAASFL
434	208:73	0.936	0.785	MKLMRPLMLLYISQLYMLMKRNSPHIGDCLSL
				LFLQEKQKEVYT
435	140:275	0.985	0.814	MQPSGLEPGTFRGWPLLSLLLLLLLQPVTC
				AYTTPGPPRALTT
436	402:267	0.885	0.73	MGRNPVFTLLFMISQGFLGYNYIQLQVMVESTI
				REYFYKEKMAKL
437	160:295	0.942	0.725	MRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRA
				AVPHTGRKNQ
438	388:253	0.891	0.726	MSRRWGACLAWPCPACMGAPPSRKLRG
				ASLLPREDPPWWVEV
439	347:482	0.933	0.731	MKWRRKSAYWKALKVFKLPVEFLLLLLTVPVD
				PDKDDQNWKRLN
440	1220:1355	0.923	0.565	MLQAPPLTSLQLSLKYLFAVRWSPVRPLVFAA
				ASGKGDVQLFDLQ
441	135:270	0.907	0.855	MFVFMLLVGSGIYAPEAVKVYHYDMETESGQ
				LLSELKSRPREP
442	91:226	0.968	0.582	MTTRGEDFLYKSSGAIVAAVVVVIIIFTVVLILL
				KMYNRKMRTR
443	32:167	0.934	0.678	MWELFTFRVFLSPSFLKNLNEPGEQYLKEACV
				SLKTHLLKIQRLY

444	215:350	0.969	0.777	MLLCTASVMTLLHCFKVPFVAHCALSHICS HVQFLTCKRMHT
445	57:192	0.882	0.769	MAMKILTVVIVIRHLGSPDTRGLEFLPLPDLEA KLFPVFCPLGF
446	196:331	0.995	0.962	MSHLLAQLILAMLASWFLNQLVVLPISGPLPG CSFLEILAILSK
447	9:144	0.948	0.686	MFTHLSHLVLTAAALCQGEERWLHPQFPHKEN MDSPSGPVTSKGRV
448	317:182	0.968	0.792	MPNTSVLSLSFLVILWFWEKMKLPPLCGFYPL KKPGFGVFGDQIN
449	1181:1316	0.98	0.897	MLALSSSFLVLSYLLTRWCGSVGFILANCFNM GIRITQSLCFIHR
450	136:271	0.98	0.936	MGIKHFSGLFVLLCIGFGLSILTIGEHIYRLLL PRIKNKSKLQ
451	76:211	0.949	0.808	MLASRVSWGRGWGKPFCCGALGLLLVLLPETL LEWQPCHSPLQWKI
452	244:379	0.989	0.914	MRTGFLAPTSMFTFVVLVITIVICLCHVCFGHF KYLSAHNYKIEH
453	129:264	0.93	0.791	MHRGVLVTLLKITVLKSMHRGILVTLLKITILKS MHRGVLDTLK
454	17:152	0.957	0.812	MCAHYVYGVVTSTYVIFSLFAFIIIFISISYFFILI NILIHGEA
455	371:506	0.987	0.553	MVGSEGEFSSNSRVDSVMRRCLLWLSSAV FLAMTLSSALSAAG
456	50:185	0.954	0.716	MGRGLISRLWAGAGFSSFLKLSQFSLFMVVL IYKVATNPKLANT
457	93:228	0.938	0.808	MCYGQLGLWVFWHLAEGLDCHVHLHQPR GPRRITWFCWVKIP
458	169:304	0.991	0.858	MFLVSIICVTLFFPIVALFDLYATLAHCVYAFST DSLLPAVMLTA
459	99:234	0.978	0.911	MVPAAGALLWLLNLGPRAAGAQLTQTPT EMQRMVLRFGCSVI
460	238:373	0.922	0.862	MKVWTWPSWFSGLTPTFCQAHLVALSCLKS CSSRGLPNCGGKTM
461	165:30	0.998	0.977	MWRLLSALCLCAWLLCLVLLSVLLVCVDVSP VVRVSCSWRPRL
462	70:205	0.93	0.56	MLLKILKGCVVFHHLPCSTQVYKPSLGMWGFL SPLWEVVFCHTPC
463	318:183	0.976	0.887	MVNACWCGLLAALSLLLDASTDEAATENILKA ELTMAALCGRGL
464	234:99	0.984	0.798	MAKVTAFLYFFTRCTTWAFWSGVTLQQITVLH MQASSRRSFLTSL
465	462:597	0.994	0.903	MLMYMFYVLPFCGLAAYALTFPGCSWLPDWA LVFAGGIGQAQFSH
466	152:287	0.98	0.739	MWSRCLLRHCYGLWFICLPAYVKVCHSKVRA LKTAYDVLKMQSK
467	76:211	0.998	0.958	MLLLLTWPYILLGFLFCFVVVNGGIVIGDRSS HEACLHFPQLFY
468	198:63	0.962	0.755	MMTQLIAVTLLMLLDNRCSLGSPLRTRGPR HAFRGDEPGLRL
469	266:131	0.992	0.728	MTVFRFESLDSVVCXGXFGVGLLVLCGLVVCF WFFLCVSCPSCL
470	35:170	0.983	0.94	MPIGLRGLMIAVMLAALMSSLTSIFNSSSTLFT

497	105:240	0.983	0.955	MKKLVSFLLILLVFLKFGSKDVFSSLQYNIEK LGNKPLTKFMN
498	277:142	0.959	0.881	MYILVVHAMWWSRLSGISTATWALVVSSHGP EMSKLWKARSWVGL
499	136:271	0.925	0.788	MWKPLTSVLMHFPAVCPHSLWAGGVRVCHH ADRSPEAGQADCFGF
500	334:199	0.919	0.645	MGWGAAREQALCLGCMLAPVPTKLLPLASKG VGTRVPGQGAGPAR
501	60:195	0.936	0.758	MNPAVRQRCLLFCFQQKLILSHFFLLQVPQWC AEYCLSIHYQHGG
502	707:842	0.965	0.764	MSRFLLPREGCLLIVFMLCEKTLFPFLFTLKEYT FIPEHRTTDINC
503	353:218	0.946	0.78	MRSDWFLYDCRLLRHVALGLFCCGISVYLAAL SIYALLFEIETG
504	208:343	0.984	0.564	MRLHSGKSQDPSTKVHIKALQTVTSFLMLFAIY FLCIITSTWNL
505	165:300	0.923	0.63	MAACKLLKHLNGFSLLLPRLECNGVISVHCNP LPPGFKRFSCPSL
506	54:189	0.966	0.913	MIIRVLLFLLPRTLQEDYGFFRAISLWPPLVLI GIYATALSASM
507	136:271	0.967	0.799	MGCWGLVIYAATGAICSALLQKYLDNYDLSVR VIYVLGTGFSVG
508	292:427	0.965	0.577	MLEQQSPLSTCRGHISGLSKWSYLLSCVLC CVLCYPVLGSPSLS
509	62:197	0.97	0.762	MKTKCKPNITFFNTIICFFLTFLFCIYIDSLCTV PKNPAQAVQL
510	350:215	0.913	0.788	MSSPWLTCLYILSILHADSNTSYTSTHLGREN GLYSDCFDFFLC
511	46:181	0.976	0.946	MAVVRVMVVVRVTAVVRVMVVVRVVVRVM VVVRITAVLRVMVVV
512	401:536	0.922	0.801	MPRAYLSTLLQVNWILSVSAELAEAVCLVNANI WQPLSSGMRGKA
513	940:1075	0.975	0.709	MLTWLEFFGIYSTIWIPTIPIAPDMRGQATMVL SAHFWLGLFLGP
514	182:317	0.988	0.728	MIHPTTDQALFPVAKGFIFFALFFMHALICITGSI PLVLLISLAP
515	13:148	0.918	0.668	MSCFGLLLGGLTPRVLSTEEQLPPGFPSIDMG PQLKVVEKARTAT
516	92:227	0.992	0.873	MVVS AWIGLEATVVAACLALLG SVVRETSTSA SPTPAALRAAWTV
517	92:227	0.944	0.812	MSHNLPISLR IEVALIFLCFCWHPALSTTICIRTI RTIMCSTLFI
518	83:218	0.935	0.804	MTNWMLLLASRIFQSLAIPKQLGLRREMPSGS PTTNSSSGCIRNL
519	365:500	0.993	0.985	MLLMFLLATCLLAIIFVPQEMQTLRVVLATLGV GAASLGITCSTA
520	364:229	0.938	0.758	MCFS AALLGTGFVAATVGGKSQMQTRSASPR FCSHDPCCDFSFV
521	12:147	0.992	0.962	MIPPAIFWVLIIFGWTLVYGFVYFTTGETIMDKL LRVLYWILVKT
522	151:286	0.889	0.765	MPKYNCISLLIALLSDFAIRFC SKMHG TKMWKE KNAKRSCFQGV
523	174:309	0.961	0.767	MLGKVILL SLLWNIFEKFYEAKLKNAYYKHMY

				MDIWRRLRPRSG
471	227:92	0.905	0.593	MYSLARMLRPLRYSWSFWAAPRRAPSVSPGL SPSLCPSNAPTGPA
472	272:407	0.889	0.562	MISWSFRFRPVIARALRRSRCFPFVFNMMNNINI KINVCVFLCIHK
473	88:223	0.954	0.862	MFSTLLLVIRVQVIQSQLPVFTRFDNPAAVSP TPTRQLTFNYLL
474	17:152	0.884	0.594	MLRGGCLFWETPGLGMAVLGEATQPGEGETA MEGDLSLLGEPVGER
475	37:172	0.994	0.956	MLFFLQSLFMLATVVLYFSLHKEYVASMVFSL ALGWTNMLYYTRG
476	1466:1331	0.979	0.918	MSPKPFISIPFLAFILSFSLSLFFFFSFPVLSFFL SVLSPFSWFPF
477	242:377	0.949	0.881	MNRVMRGLAITTTCLLSMLQAITISPSILWNHA AVQYVHGHSLVQ
478	66:201	0.94	0.831	MTARLMRSLAAQLTFVYRVAHLMNVAQRIRG NRPIKNERLLALL
479	75:210	0.997	0.628	MYFGEGENDHKKQILGRKLAFWLSTVFLAWVI VVAWWRILGVCGM
480	157:22	0.907	0.746	MSTLRMLHVIRVFYSLQRTFTPIISLDLDHSL GKWTRERTGRFC
481	180:315	0.928	0.68	MFTNYKLFYLFYLTLSFQSEPDNTSLIALESIH SYSTLQNYLAF
482	38:173	0.962	0.866	MCRALLLLCSPNSSFQWLPLPVHPHTTIRYR SYNMVPVKLTNVQ
483	137:272	0.956	0.819	MLTLFAAMLSCGIHLQRLIQEKGFVSTIIRLLDS PSTCIRAKAFL
484	16:151	0.969	0.86	MHTIIHLRFLSIVLCFSSVSYGYLHFPQFISHQA SPRSRSLAFSSI
485	196:331	0.979	0.942	MVANMFYIVVIMALVLLSFGVPRKAILYPHEAP SWTLAKDIVFHP
486	23:158	0.993	0.674	MDWTWRILFLVAAXXXXXXXXXXLVQSGAAEK KSGASVTVSCRASG
487	168:303	0.944	0.78	MCLITSLSWTIFELILGMPSWCRPKESCLELHS RGRNSICGFHFP
488	117:252	0.93	0.698	MMHNIIVKELIVTFFLGITVVQMLISVTGLKGVE AQNGSESEVFV
489	73:208	0.966	0.777	MNVEGNIVLLWNAGTLTGVTFSFLSLFSFWST LFVCSVSSILWDS
490	231:366	0.921	0.587	MTIHLCSNLMCHFLQRMGTILLCPNMQPHQNL TTVICSKGNLLRA
491	102:237	0.987	0.959	MLVFFFRIFAASCPFYFSIFHPFRPRPPAFRS SSPCTAIFPPTP
492	47:182	0.89	0.605	MSGRWVLAWYRARRAVTLHSAPAVLTADCS RPAVAPDLFWGTYRP
493	281:416	0.992	0.909	MYALYITVHGYFLITFLFGMVVLAIVVWKIFTLS RATAVKERGKN
494	201:66	0.964	0.876	MNHWGAKRNLCLLIFSLPLKHFLFGSCFGLL STYFIYTCIHIEC
495	438:573	0.969	0.916	MVKSVIFLSFWQGMLLAILEKCGAIPKIHSARV SVGEGTVAAGYQ
496	90:225	0.951	0.632	MTEPPGASSHLRQALRCCQWLAGIPSQWVLF WEVLWKWVLQTDAA

				GNSRSWKNCVLS
524	61:196	0.922	0.69	MGAAWSSATQAI SVFCFTIPLQDFCLQSYLLV QEEFQQFQIVGRP
525	6:141	0.988	0.875	MFYVKA EFLVSFSCPWLTACALLMSCSWFLTL TILSVKGGTPAGM
526	862:727	0.937	0.653	MPLSPLLFHLGPFPFKAESWLNFLPPFFPPLL PLLFLAKAEIQWA
527	168:303	0.893	0.576	MIRCSCLEQLHLQMLLLPPSCEAVAPRGWRR SCSCPECCRVCSSP
528	907:1042	0.984	0.924	MQCWQLLALCAPLFLPQHHLWYVKQQLQR HADPRSETGQYATYC
529	273:408	0.947	0.671	MFTTLGYLICGFRVVL MYRFEEELFLRSLQDY KIQSALLVPTLFS
530	2134:2269	0.951	0.849	MWLWPPTHCVWRSTGLCWRMRVSISVRPPT PWARPRPQLTSTLKL
531	174:309	0.983	0.856	MLNLAF TVGSFLLSAITLPLGIVMDKYGPRKLR LLGSACFAVSCL
532	207:342	0.996	0.97	MTIFFSLLVLAICIILVHLLIRYRLHFLPESVAVVS LGILMGAVI
533	113:248	0.898	0.687	MASSSSLSWPTSAWPLSWTLVFSPERMRRMR TRRTTSGLRCTRTWM
534	164:299	0.905	0.619	MFFFCTFSRTGVQTFRRDHRFWVLAHPN LNLFAAGKGHFLSF
535	236:371	0.923	0.755	MRFLTDLWLLPLGPPAMPLGNPPTLDPIFFSF TSDTLPTSRLLCF
536	227:92	0.984	0.829	MWDMLPWGITWVLLTTQLHSPLLYVIGFTYW VCKGDRDSYLEENS
537	49:184	0.951	0.758	MTQDLVLTVPFMGCLLILVDGLKPNRPAYIQT GSQATQAGVQWHN
538	213:78	0.925	0.659	MGFFGVGSLFVFLNGSTPTNYP SIRD FCFFWV KAKGVECSQKLTH
539	39:174	0.948	0.722	MRLQWGDAQEWASLHVLLIALLRAAQTFHPH SSQPASKAAETQSS
540	271:136	0.953	0.807	MVASAAQLLSHVCLGGLQLLHSLSSLQLPAL LLKLAPEALALFT
541	38:173	0.981	0.819	MRLGLLLARHWCIAGVFPQKFDGDSAYVGM SDGNPELLSTSQTY
542	118:253	0.917	0.752	MGSTGISKFLFILAADTLAYTFLSNQNI FPSLLY QGKFKPERETS
543	180:45	0.918	0.636	MDLFSLKCASFVLIGYVRICLEQFVLEVYNLE VMSWYKSESLQ
544	199:334	0.917	0.69	MPGSLCGRRTVCWLLG SVTSKQVLTDFLRKF SRSSRLQEDQERSL
545	11:146	0.944	0.668	MCTLYLISTPHLLGRLLISKESAAPALKRKQA PGPTNPYSISEG
546	388:253	0.989	0.789	MCFLNKL LLLAALDWLFQIPTVPEDLFFLEEGP SYAFEVDVAPE
547	183:318	0.954	0.716	MPCLLCHQICLILAHLRHSVLVFSFAYNIFGIAD SSFTFSLSSPQ
548	253:388	0.894	0.552	MQLLQILEPKMFRYAHLPSPQLATLLTPHLFQ VLLQVAGPTGTS
549	201:66	0.964	0.723	MATLPQASNLATRILLTLLFEEMKLPCA WVE SSGILNVLIKLL

550	88:223	0.892	0.743	MWADASILASLLWPHQSLQLWHPHLANKNM GVPPPTTCKPWSTV
551	58:193	0.915	0.583	MISVCPLWAARARGVNPYVLCGSGCAPETSIS FTMSSLPSLAASW
552	139:4	0.952	0.581	MFRPLPTLFFTGLMILKTMKKKYDSRSRVWNE HSALPAGELREDP
553	305:440	0.985	0.902	MYILTFMKVGLKLSGCFVLLALISINWYINLPH CRVSFIRTGSW
554	124:259	0.924	0.622	MSSSSAKVFYLLQYPVLKPLLRTLCIPAGVILP YHYLFTLHSLLL
555	199:334	0.965	0.821	MMRLEKFVTWSVMALGWVFRQQNCWALW SKSVLISWSRPLTRSM
556	144:279	0.957	0.882	MLVWLYGTIRWPALGAPRWWPWVWPPGVW SGIETPSSTPRARSLR
557	281:146	0.961	0.882	MRPEAAGSSAVFLASLLALRTTSLCLATREY FWAKTWGLGEDGA
558	284:149	0.897	0.553	MLPGSPSPQAAGLSQFQWAPGCHWLQPLLW VKVYVLLVPDGTGR
559	380:245	0.991	0.957	MFLVWKRLFAASLLASDSSTILCSRDLILESIA LIIAFCSLRIL
560	53:188	0.966	0.914	MCTFLIPILSLFAIQLAQNLSHFYLVSLSPVQLT QLVFLICYFIF
561	267:132	0.916	0.658	MYFKWKSSQKITGFAILPVLLPALEYLHSCFPC LPGWRKGTGLGP
562	3:138	0.981	0.91	MRALVLLGCLLASLLFSGQAEETEDANEEAPL RDRSHIEKTLMLN
563	27:162	0.941	0.861	MRTLTLTVGSLAAHAPEDPSDLLQHVKFQS SNFENILTWDSP
564	178:313	0.892	0.66	METGRLAIWAIVAACVGTEAGRWLLREMRGP GPASKGQLPGRGLL
565	199:334	0.953	0.691	MWPSVHLCRCVEWFLPFAFHFGHRSRATNW LCTFEHFLSSLGLCF
566	158:293	0.969	0.778	MEYRLQKGAGFHLDLFCVAVLMLLTSALGLP WYVSATVISLAHMD
567	301:436	0.968	0.864	MAWGLATLLCVEGAAMLYPSVSRCEGLDH AIPHYVTMYLPLLL
568	69:204	0.9	0.589	MPFSTCTALPSWATLSTWSWTPKVSLAGEER GETCQDPDFPPHPS
569	101:236	0.899	0.681	MCAMALVHARILRVFYGAPSPDGALGTRFRIH ARPDNLNHRFQVFR
570	134:269	0.951	0.882	MINFIYFLAFLIASDAMSVQYYECGPNHKTGFS YRLQLCLLKIRD
571	8:143	0.964	0.931	MSLVLLSLAALCRSAVPREPTVQCGSETGPSP EWMLQHDLPDGL
572	32:167	0.945	0.75	MXPPTRPRTRGVGIFYFYIIISFLVVVNMYIAV ILENFSVATE
573	139:274	0.896	0.684	MGNRAVIIARQLSSVHTLICNFFWLLLRRTGGD LDSLKCSYESIG
574	49:184	0.992	0.794	MLWALWPRWLADKMLPLLGAVLLQKREKRG PLWRHWRRETPYYD
575	252:387	0.995	0.965	MMNLFFILLNQIVLSLIYFLCCLQVDKLGVMMSM FFPLYSHKYNLQ
576	525:390	0.984	0.911	MLLMLLFRCCSSKDLWPVLIHLVPQGGQEG

				NVGEQTKGKSNRVL
577	69:204	0.932	0.753	MAAARALGDVTVLGSLLLQHLLHFSTPGLVLR SLGALTGPQLLSL
578	171:36	0.92	0.794	MCSAFSSFWVWPPLAGSGVKLQFTASVTAH KRSTDPKSEQQLDL
579	220:355	0.98	0.875	MLIGEIFELMQFLFVVAFTTFLVSCVDYDILFAN KMVNHS LHPT E
580	159:294	0.976	0.944	MPSASLLVNLLSALLILFVFGETEIRFTGQTEFV VNETSTTVIRL
581	108:243	0.988	0.863	MGIYQMYLCFLLAVLLQLYVATEAILIALVGATP SYHWDLAELL P
582	80:215	0.905	0.64	MLWFSGVGALAEYRCRRSPGITCCVLLLLNCS GVPM SLASSFLT G
583	88:223	0.983	0.932	MKLLLILTAFQANLCITMPASACQRSTFPSFCT TIGILPLSVGKT
584	73:208	0.951	0.764	MAFIEMIISFCFLLLGKGEHGKPYPLTEEDHDD SAYRENGFNIFV
585	333:468	0.969	0.909	MAIWSRPLLFI LYV FVGELGMQTYRDPWVARC PWESWKPLLTLKD
586	363:498	0.985	0.905	MGGSGVYGCFYLFGLSAGYLCCVLWGWF S ACGLDIVLWSFLLAV
587	172:307	0.994	0.97	MLFYLVSVCLCVAVIVAFQLTAFTFRKNLAATA LLLSLFGYATLP
588	56:191	0.977	0.82	MCKFLCYFFYKNFAFTMVHFWFGFFCGFSAQ VINVPSPLLCKSVN
589	27:162	0.917	0.605	MCWARCWTRWNTCTIWTSSSTD PFRKCWMA PEALNFSFSHKSDIWS
590	84:219	0.993	0.853	MSERVERNWSTGGWLLALCLAWLWTHLTLA ALQPPTATVLVQQGT
591	174:39	0.983	0.878	MAIQLVPCWVAWALYPAGSIVVTYTSLLQQEN SRRKLWEPFQPQQ
592	138:273	0.93	0.672	MSSQARFLGQAGLCLWVRSLSGASGQQRAL RSQGVSSGSPRWVPI
593	338:473	0.891	0.753	MNFASVFAVL FNGCTGIMAGANMSGELKDPS RAIPLGTIVAVAYT
594	139:274	0.965	0.9	MMFICSHLIFLRVCTYSLPVSPSSIPSQSFLVT TEHCMRWKVHH
595	68:203	0.982	0.872	MILSLLFSLGGPLGWGLLGAWAQASSTSLSDL QSSRTPGVWKAEA
596	392:257	0.929	0.73	MPARLVLASLQVALHDDL SGLRVKGLWRRG LGLLDLLRGWGQHT
597	94:229	0.93	0.732	MTKLYALFFFRQYLQTLHLQSWDLLDIFGGIRS FPLDIMTYLKNQ
598	1026:891	0.983	0.824	MLCSRLGTTASWRRLGIRAWAPLLLLFPWDW HFILSFSSRPWAGT
599	215:350	0.962	0.672	MSVIPALWEATVGGALVWMIKLLDNIDTYVSF FAGSQKT VREIR
600	343:208	0.979	0.6	MLIGKSQREGEVALPQLFDVSGLLFIWCGFVL VSVLSNCLVLACD
601	145:280	0.955	0.808	MPSLLIVLFFRLFPDGVKLWLRQWYRRQPGPL FPGALCLPEAFAG
602	496:361	0.93	0.697	MPPRCTSLYVCTQVCLWCFFGPPRPLPSFA SNPFKGFSEPNLTE

603	92:227	0.947	0.791	MNEQVPKGQLHFPLLCLFTWVTLWHCIDPSP SPNQSMPLVLRPS
604	67:202	0.967	0.724	MALKSFLSTFLSKILVKILILKYERRSLYCTPGN LWLEMYSISSE
605	63:198	0.915	0.767	MRSSPWSTFSKGFCLQWLFNALAQQLQAHF KNVRSCMKTLRYDS
606	127:262	0.967	0.744	MQWWLELVYRHMQWWLELVYRHMQWWLEL AHVVSLLCTSLPSLEF
607	177:42	0.964	0.768	MLEQASLWLGRSFLLAGFLVSSSCPSLEQAA KGECSPIPCFAHC
608	235:370	0.952	0.749	MVDVASLCIQFYIWIRCLWMISLGGSSIQRMLP RIEAAWALWVAG
609	319:454	0.95	0.88	MVASFRESRVLLLGLVVRVLTDFLTQVVRVG SECGDELVRLYSF
610	140:275	0.971	0.925	MHMLNGALLALLFPVWNTRLLPFLEIYYIQHV MLYVVPYILLWK
611	330:465	0.925	0.666	MVRETVFKYAWFFFELLVKMAQHVHNMDKR DSFRTRFSDRFMD
612	310:445	0.973	0.865	MSVWMLSYLLSAFFSQANTAALCTSLVYMISFL PYIVLLVLHNQL
613	60:195	0.942	0.762	MFRGLAGAITLPMVGATSLAVATGALAYAWY QGNSTLSDFNKTIV
614	166:301	0.936	0.682	MNVIYFPLHLFVVSRYATSLVLVGCTNLCAVL FARCLDDHLVSL
615	346:211	0.895	0.714	MLHYICTPARQFRLSPVLFGLLMRFGLTIRNCV RKSRDELVSQVA
616	239:374	0.958	0.672	MGLGKTLQCITLMWTLRQSPCKPEIDKAVV VSPSSLVKNWYNE
617	252:387	0.994	0.972	MLIDVFFFLFLFAXWMVAFGVARQGILRQNEQ RWRWIFRSVIYEP
618	733:868	0.984	0.846	MKEIKYLFPLIFLSLASPLPLSFLNACRFTRPE HLGSSAKIKCS
619	317:452	0.903	0.556	MCKSSATRLLYCTTGVLRRLEGDTALQGVSH IIVDEVHERTEER
620	188:323	0.973	0.748	MLAAGVTSAAGLALAFSGDYLKAFIDVPTVPA ALVFLLLVGLLNA
621	62:197	0.971	0.837	MLQLIFMHMAGVIQLLILKRELISFVYMLAVKN RMTVRLKNEGLF
622	877:1012	0.993	0.893	MWAASWCLSLWCCWVWSGTSESITANSSQH LPLSPWWESPSSAS
623	170:305	0.975	0.857	MSVFAVFYSWLAVFYINNLLIVFNFTLLKFPFIL FINVAESYLY
624	254:389	0.938	0.762	MSFLQAVLALAASWTSRQVGERTLTGIVIDSG DGVTHVIPVVSRI
625	10:145	0.974	0.778	MLQQTEKKIQFVWFSIIAIVILVSSLSTWFLA RRIAKPLREV
626	193:328	0.965	0.852	MLPQGFAGQFLCLLLAHSRSYVQLERQLGW TVQDGHIHMSNRWH
627	389:524	0.982	0.899	MFPLGYWLSSALCGFLLCQGCTEFKCRVSQS LYSSSPRSTHSLFT
628	144:9	0.988	0.682	MGLGVIIWHAFSLDPEETRFRTQYFLPAMMW RRFLFIFYFTYSI
629	202:337	0.99	0.918	MTAWRRFQSLLLLGLLVLCARLLTAAKGQNC

				GGLVQGPNGTIES
630	160:295	0.978	0.932	MLWTTLTGVSLALFPVAQAPTALVALAVAYGF TSGALAPLAFSVL
631	415:280	0.99	0.949	MTVMVTVTVTVMVMVMVMVMVTVMVTVTVM VTVMVTAEMTMVGV
632	221:356	0.92	0.848	MLIVQFIFELVSSILVSNVKDMLDFESGFCSKIL SYFFSSPRYRL
633	370:235	0.973	0.89	MKSWRLPACMLAFWASSTAGAGLLKASSRL PRAQPGAPGAPSES
634	42:177	0.907	0.631	MISVLHGRFCVFGVGLSHSSPALSFTCCHNLC QPPWPAFPSC LCS
635	309:174	0.968	0.719	MCKWKALGLKLSRGLLWRVVPACCR LIPA GFNWADTGQGNIFL
636	290:155	0.894	0.597	MSFLMVVHRLWTQGVFLSRGLLSSYCLPKH TPAISLGCLTPPKP
637	221:86	0.946	0.857	MPPGLLTTGILLSLWLHNRMLLDIAVQFLGVVY EELNDMHIVSLE
638	4:139	0.944	0.69	MATQRM LPCVIHQWLLITTTVRYHYIAARTAKS GKR SRNQCGYRE
639	161:296	0.914	0.554	MLCWKTTSGRLKDILAILLTDVLLLLQEKDQKY VFASVDSKPPVI
640	342:207	0.977	0.915	MAIPSVVISGLAVLLVAMALPSLSGSEAIKSMTI PGLVPTVVR
641	12:147	0.971	0.927	MRVYGTCTLVLMALVVFVGKYNKLALVFLA CVVLSILAIYAGV
642	194:329	0.899	0.813	MELLKLLTCFSEAMYLPPAPESGSTNPWWQF FCSTENRHALPLF
643	141:276	0.986	0.932	MCNPWWSLLGAVGSLIMFVIQWVYTLVNMG VAAIVFYIGRASP
644	15:150	0.989	0.834	MYFSSLFPYVVLACFLVRGLLLRGAVDGILHM FTP KLDKMLDPQV
645	375:510	0.988	0.93	MYASSWFLTLFTTFPLPVATRVDIFMYEGLE IVFRVGLALLQV
646	132:267	0.983	0.916	MWK FVSPLCMAVLT TASIIQLGVTPPGYSAWI KEEAAERYLYFPN
647	3:138	0.922	0.66	MKMFVAHG FYAAKFVVAIGSVAGLTVSLLGSL FPMPRVIYAMAGD
648	271:406	0.99	0.858	MVGKIKRLKKS AFVVLILLITAKLLVLP L LCRKM VELLDKGCIAA
649	60:195	0.967	0.83	MKIVHVLQVTRAVAPLLLSVTVAYISTTIPAIQT HYHARRGRRLQ
650	135:270	0.916	0.637	MGLLMMILGQIFLNGNQAKEAEIWEMLWRMG VQRERRLSIFGNPK
651	231:366	0.95	0.664	MTIGFLFPMLSIAYLISPRSNLGLFIKPPFIKFI HTASYLTFLS
652	159:294	0.967	0.644	MQQPEVKTWGGVTAAMVIALAVYMGTGICG FLTFGAAVDPDVLL
653	128:263	0.986	0.762	MLQLGPFLYWTFLAAFEGTVFFFGTYFLFQTA SLEENGKVYGNWT
654	215:80	0.945	0.663	MGFLVLKQPM L VAKVFPTLAGVEIILFTLKGFP LGIPVQLPPTV
655	34:169	0.991	0.954	MCVVVRFLGRRG L LFMILTALASLLQLGLLN LIGKYSQHPDSG

656	49:184	0.933	0.775	MIQALGGFFTYFVILAENGFLPIHLLGLREDWD DRWINDVEDSYG
657	86:221	0.993	0.665	MEGWFAVLSTANDVLGAPWNWLYFIPLLIIGA FFVPTLVLGVLSG
658	119:254	0.977	0.622	MAPPGLRRGWFTSRLELYSLQHSLSTEPAVV LGLALALAFATLLL
659	66:201	0.985	0.844	MLMTVIYLLFAGTMTVSTTVGYTLLLLMKYPHV QKWWREELNREL
660	461:596	0.912	0.697	MVVAVLAFWHIQGFPEVGEEELVSPDAKFTK GEFQVVMKVQQL
661	277:142	0.997	0.907	MAATEPKWWSVWSRFLWVTLLSMVLGSLAL LLPLGAVEEHSSSV
662	387:522	0.898	0.565	MQLKTPSGQVLSFCILQLFPFTSESKRMGVIV RDESTAEITFYMK
663	277:412	0.947	0.659	MKISTLMFFQLTLLKIDKDSQELQILRNKLD SKL DKVIGTFLEGS
664	190:325	0.994	0.977	MYPIVLFGLLAVIFAVFVQFLLPEFTNMGMALP TFVGLPVVLSIV
665	22:157	0.916	0.79	MIHGRSVLHIVASLIHLHLSGATKKGTEKQTSE TQKSVQCGTWT
666	76:211	0.967	0.798	MLVYVWSRRSPRVRVNFFGLLTFQAPFLPWA LMGFSLLLGN SILV
667	517:652	0.966	0.936	MKKVLLLLWKTVLCTLGGFEELQSMKAEKRSI LGLPLPEDSIKV
668	1426:1291	0.998	0.958	MFLVAVWWRFGLSICMLCVGLVLGFLISSVTF FTPLGNLKIFHD
669	1079:944	0.936	0.578	MVTGLGNVFPCLLELGVWDDGLRGDGFSAF RLAAMANNQFLFSG
670	1761:1626	0.986	0.898	MGLLLLKASLLQLAAIYILSYMAVFKEKNKRTS QQRKTIHLQSH
671	176:41	0.982	0.885	MDLGYFLVILWPSVFLARSLQCVAACCLVSME NTALPQGNEHGHT
672	839:974	0.947	0.849	MKSENSLQLQPLVLLLWWLHLIHLHPRVRTP QEERLKNAKIAMM
673	74:209	0.909	0.758	MIITLFVPSCLLKNKMYIWTFFFQNCFCFKMKIL YLIDYLLKSIL
674	759:624	0.983	0.878	MFLSYNFPISILFFAFPYFCLPVFHFKLSSPN CFILPLPINLS
675	183:318	0.966	0.855	MQGVFWVARLAGIWGTANVLMVVPQLVEECF GKAVGAVEGALGLK
676	84:219	0.903	0.696	MSFSKISLVIFTLKLMYFSVKNEEVVKCNGGW EPGSSLLEWEVTD
677	14:149	0.986	0.975	MRQGLLVLALVVLVLVLAAGSQVQEWYPRE SHALNWNKFSGFWY
678	172:307	0.992	0.675	MLRWGFLEILFLRSWFHSWICLLPTPQLPPNG ASAGSQDEGSRRR
679	134:269	0.972	0.836	MFWSCSLFLTLLHFPTYPEPPLFTCSSCPLI FLEPDPCFLHLG
680	849:714	0.992	0.96	MLGPFSSFLLLWSFTRFCIHFYLAPSHHCLTA ALLPFSLHPLYS
681	135:270	0.932	0.6	MPITCFLLRSNFGYFIFIRKNTVENLTLAMKML NMVKFLFTDLF
682	122:257	0.98	0.778	MALVLTPLSLLELSLNCLLFIILQPLFNLQRLC

				TEPSQFELISQ
683	505:370	0.935	0.817	MHPPLTPPTPLCLWLRLKQAQILSYVPRFET
				HSLISRCSQVPPT
684	218:353	0.939	0.607	MFGLKPKVIKLYCYICYIFLCNVYYLSFYENVLL
				IVKNFYSSGYL
685	167:302	0.98	0.825	MRSFRVLVPSTLLCHFLGCFIHLHVEAGSPS
				HPLTFHWKTLSTM
686	34:169	0.906	0.593	MSRILSRSLSFVLCNTGTALRKGLMMLGSSW
				GGGPEGFRPPGDYL
687	105:240	0.973	0.828	MVYLYIYDLFQFLITVLQGFLVFEMEFHSCR
				PGQSAMMQSQLA
688	149:284	0.973	0.762	MLILRSSLPFLFCHFTKICLEIYKFCLDSIVLPEL
				EDQCLSLIME
689	443:578	0.989	0.941	MAILLWTPCQLALELLASAARLLASFVLVNLTG
				LVLLACVLAVTV
690	139:274	0.99	0.947	MWLSFPKLFIPLSIFLVFLLMANSFRIFKSKNIFI
				SLLFWNDTFA
691	244:379	0.982	0.866	MVSHCIFCNLLFSLLTVFLRLLHVDTCFLFIRFN
				CCKIFFCQDIL
692	3804:3669	0.981	0.951	MTVLRPFRRLCIFSLLSFLSQSLEQANLTANIT
				TILHLSSHCGN
693	567:432	0.965	0.728	MMSATSSPLILTVXPAXRRIMLLGTVRLLVAPA
				NLLHIAFLPNHS
694	99:234	0.985	0.909	MWLLCLMTKFVFRGVAAHRENDWLGGGLGQ
				AINFLAVHWDQPLLP
695	171:306	0.98	0.953	MVYFARILFLIQVLFIVNGFFKIVIIIPFYNNLEN
				YKNFLFNII
696	68:203	0.9	0.684	MQPCVQRLSRVFGILASLYASISIFCSMITSSQ
				MLARRSVWRETL
697	301:436	0.99	0.965	MLILVYLLCVSFTSTVVLHPGSGNWFETLYFTV
				LGPNTLSSQKY
698	1654:1789	0.983	0.865	MWGWEALFLFCSCSSFSLAGRPLLLHSGPVG
				AAVAGALLLSAQQ
699	194:329	0.986	0.866	MLFIQYLLPCLLLSAELSGTFFLYNTCHLHVPC
				CHSLVPTGPPSL
700	252:117	0.954	0.796	MADHRLQLLAVLQLLVLERSPAHGGPHVLPP
				RSHLPGQESSLST
701	371:506	0.987	0.912	MLSFLVVFQVLVLLRFSGRSHSHQLITITFPLFQ
				WLYFFFFMFFCT
702	1888:2023	0.995	0.971	MGRYRCASLLFCFLLLFFFFWLWVRDIFKLAQ
				KGRGWSLDPHVS
703	130:265	0.951	0.616	MLTCCVNAVVCVCGVCMWGHWYTRPLCMSQL
				CRSVATCRLSVYSPG
704	1256:1121	0.971	0.941	MATGLLAFLGLAAGGQTLCPAGELPGHARAQ
				ASGAPGSVLIAPVG
705	126:261	0.991	0.962	MSLWNQLVVPVLFMVFWLVLFALQIYSYFSTR
				DQPASRERLLFLF
706	31:166	0.967	0.768	MVLPLPWLSRYHFLRLLPSWSLAPQGSHG
				CSQNPKASMEEQTN
707	367:232	0.995	0.936	MTWLVLLGTLLCMLRVGLGTPDSEGFPPRAL
				HNCOPYKCICAADLL
708	531:396	0.964	0.83	MQHTWPRVSCRLVLLKALLKLICDVARDPNL
				TPESVKSALLQEA

709	1161:1026	0.967	0.913	MARAPSVLAQLWLICLPESLASFVQAVPW KVLQPSSNRSTDCS
710	300:435	0.963	0.724	MPCTWGPGLLAADFWSLLTPSLSSDPQLCN DLELCDEAMAPLDE
711	540:405	0.984	0.853	MLLVAVTILIVAVFTANTYGMWGGAMLGVAG LLSRLEEDRLLLL
712	132:267	0.959	0.808	MIIFKKMLLNGFFCLFFRKVTVDIFQVLKILPYN SPMKFSMGEYR
713	57:192	0.991	0.888	MWPALLSHLLPLWPLLLLPLPPPAQDSSSSP RTPPAPARPPCAR
714	172:307	0.98	0.797	MVFSIISSFFSFMPPELLWFFSFFLNQAHEKFM FYLYFIIRKLSL
715	746:611	0.908	0.656	MKTVFTKKLTAALLITVPNCKQPRCPMGEWL NKLQYIHTMKYYS
716	1368:1233	0.895	0.655	MQQRKMRLVWRSYWSMVQTPMLWMATEIP HFTGQPLRTMLSVCGI
717	234:369	0.915	0.638	MICSTELLNFSCPPLFLTVDIFFPMTAFICK NLPKIWYQFYF
718	85:220	0.881	0.629	MLLVVSSVRTGISLSCSLLYHWFLEPCLAYK FSINIYLLLSNFW
719	475:610	0.965	0.754	MMRLWNYLNKCLSLALVGSIVRCWELPLDRS TNGGPTALGWAIGP
720	213:348	0.925	0.795	MWQTSLLSLEIATVTAVFSTHYDPQSAIHIKT LHKQKDNLLKVQ
721	267:402	0.982	0.925	MLPTLTAPTALLLLKPISCLLTSTHPRTQGSR AHFPRAWRLDPG
722	173:308	0.911	0.774	MCWSPLTGWALSSSRCRLSWPLTSFGSTAS CRPTTGWRGLMWLQA
723	713:578	0.994	0.89	MPILFYCPLCLLSFFLFPWRLFHGLWITITHG RAAVPKWVLVQA
724	839:974	0.947	0.849	MKSENSLQLQPLVLLLWWLHLIHLHPRVRTP QEERLKNAKIAMM
725	506:371	0.984	0.863	MGEVPKAHLRLRWLFPVSLCRAPLLSTAHLA LLLPCCLLCSCSY
726	1144:1009	0.94	0.74	MKPQRFSPILSSRSFIVLGFTFRSVTLFRLIFIIG CEAWIKVYLF
727	18:153	0.928	0.69	MLLQTFVTTCSIFYWHFNFVWIIQFNVCVLS FQPERLTLAFLIG
728	137:272	0.971	0.831	MSGLLSMGSTLTFVSLIFCLDDLSIENEALTF STSIVLQXIKL
729	236:101	0.977	0.894	MKGRFLFPLRLLWMCLHLQRQASELHQPSM PGCPLTSSSRIFDN
730	635:770	0.998	0.868	MLAMLVVLVLLVHLFMSFLHFLHLLVYYH CWSNHARSQGIH
731	491:356	0.953	0.719	MVRSIRLLFFFGWGFSTTQQPSLCQNSLMFP DGSSFTPLSEAPKG
732	177:312	0.971	0.849	MASAETLTVFLKLLAAGFYGVSSFLIVVWNKSV LTNYRFPSSLCV
733	1373:1508	0.977	0.945	MQAVRKVFLFLWLIKFLRKMFSFHNLFSLWK KLNMLLPLKNIAF
734	89:224	0.947	0.593	MASSWGGYLNFTLTQGCVVWSLALREGKLS VFPWSFLSWASSST
735	111:246	0.928	0.657	MIKAVLLGWFGCELSTRFEMDNQLQLIPGVSG

				FQISNPPILLVCF
736	91:226	0.993	0.892	MMMPSTVLAYTQLGTFMMLIMCISWAFATFFF QCMCRCLGPQGTC
737	136:271	0.924	0.731	MLRCLLFYFSSLGKGSFSSTIYLPEVCVGEAA RTTPSAMCSCRAA
738	219:354	0.989	0.971	MFTFMFMFMFRALCGLGRLRTRSLTQPQATV LAHSATSSSRILN
739	208:343	0.992	0.938	MLAAKLTILELLHLLCSLFILILHTVLD SHFQAA SLDIVQQSML
740	20:155	0.994	0.926	MHVCLHIWGLGVCVFMHMMCACVGVVCPF MRYGMQICACIHAHS
741	1432:1297	0.99	0.938	MKASVLSPSFLLVLWSCFLSCSCMEPQSGFP RPSCFTVGFLRRR
742	24:159	0.963	0.751	MFAXQYWFMLFPIYIFLRDISPNRKIPTSIKWF HFIRRVKYFFMS
743	112:247	0.956	0.746	MMCKVCFSTKSLATFVTCVTLSSMNSYGMK GMNYPKPKCHKPYV
744	172:307	0.992	0.675	MLRWGFLEILFLRSWFHSHWICLLPTPQLPPNG ASAGSQDEGSRRR
745	157:292	0.968	0.703	MHMMYVYMPVSVYLYLCLCRSMYVYVCLCLE CEGYTPSLWRVFTY
746	159:294	0.954	0.616	MLAINTLVRMSRLVQKVGSGRWQGGRLWIW TLPVSLGLNEILNL
747	663:528	0.888	0.696	MRSMGFRAQGLPFGIRQTWLRILDLLLTCTLP FGSRDVKWRCCHL
748	95:230	0.915	0.659	MPARSCHLPSLSTGLLLWEMSGSGSLSGSE EDPRQGYLSLLPAW
749	263:398	0.983	0.915	MFTLLVLLSQLPTVTLGPHCARGPKASKHAG EEVFTSKEEANFF
750	209:344	0.887	0.594	MCQHVLIFVFFVETGFHHVAQAGLKLGGSSD LPTSASQSAGIKG
751	755:620	0.969	0.804	MQLILWLPWYVDQTFCHSVLQCCCPGQLCQS FHSNRNDARLLGAK
752	1387:1522	0.889	0.558	MLGLLQFDSGFICLCARVYPSCLEPGQSFITEE DDARSESSTEWD
753	1401:1266	0.954	0.673	MQMWWLGAQSAGRCWLRARTATSWWTCS WKRLVRGCCGRKTSSLV
754	1524:1659	0.979	0.685	MRNLSQRVTFRMVFAACSRYSRNMQPCCVLI FLKILLCLFYQSVG
755	172:307	0.992	0.675	MLRWGFLEILFLRSWFHSHWICLLPTPQLPPNG ASAGSQDEGSRRR
756	209:344	0.964	0.658	MWNVAFLFQWFLSLKKEGRSSVETKDRRSVR DLWGMPKKMVSFGG
757	1947:1812	0.953	0.88	MPGLVLMWGLGGAWGRVGISRLGNLRCPS RVPAARFGPRPSWRG
758	203:338	0.973	0.747	MSSGELRLPSSAALVSLFAPAAPCSISFLTIYV VSLLA VIMATTL
759	209:74	0.998	0.975	MGSQVGWLAWLTWLRWLIWCFGSDCCLGPS LPVYVTSAGAAFER
760	131:266	0.984	0.967	MLLATLLLLLLGGALAHDPRIIFPNHACEDPPA VLLEVQGT LQRP
761	121:256	0.962	0.624	MILHFGLGSGAGWFCPPWGSPMWCSWELSC TCIVRGS LGQDCWQQ

762	50:185	0.974	0.619	MPSQGSTLLGVLLQQSCSHLLLCVCSPGPE ACPAGEAWGGRRAR
763	893:1028	0.958	0.836	MWYFWTLNSVPVIYMSTLMSIPHYFDYCCFIV SDIMLPEITFST
764	274:139	0.915	0.619	MPLHTCLVHVGVSAAARGSPVCPSVLWWWF CVHFQVIHMWAHECV
765	26:161	0.896	0.771	MWAAAGGLWRSRAGLRALFRSRDAALFPGC ERGLHCSAVSCKNWL
766	1271:1406	0.989	0.979	MVCGALMWIMLILVGLGFPFIMEALSHFLYVPF LGVCVCGAIYTG
767	328:463	0.998	0.913	MVSCIIFFFVLLIVFLTIFSFWWLSYWLEQSG TNSSRESNGTMA
768	888:753	0.98	0.88	MFLSSNFPIFSILFFAFPYFCLPVFHFLLSSPN CFILPLPINLS
769	234:369	0.98	0.725	MPFASEFFPRTWKQNFVLACISFFTGACAFLA LVLHALEIKALRM
770	257:392	0.946	0.751	MKIIIFIQTRTIFGLKGVLLIICQDSKLELNCPVK PGHRPPTHG
771	464:329	0.997	0.977	MTTALSFMVITVLWVLLHLLANICIPRKCSFVC FYINGILLHAV
772	209:344	0.975	0.852	MCLLGRPFVFLFMLRLAVTNVTKGRCIFKTTA PPTQMAFTMCQAV
773	140:275	0.987	0.933	MPLTLFLLYFLHVILPEVILFGNCLFFTIGLCPVY HCNPITHIES
774	34:169	0.952	0.855	MKMVLGSSLVWLFPCLEAYALTSQEFKQAGG RRVLTALKKFTFQ
775	391:526	0.929	0.591	MKNLRLGEVVTLSWVLVVELEVKAHSVLLAIL TTEFSLNQSLKM
776	291:426	0.976	0.856	MFGKWFPALGGFKTLIIGIIIVIGTCLLLPCLLPV RLQMIKKLHH
777	34:169	0.91	0.626	MWNSSEAFLLFFIYFKYHKILLIYISVNWIPYT SLLFHCSSFIP
778	96:231	0.954	0.651	MFRLYSFSTVKLGANLAACLLHKNLRGHVYM DFIAACCWKFFCLL
779	792:927	0.918	0.69	MPFWLIFVETGFCHVTQAGLKLLGSSDPPGSA SQSAGITGVNHCA
780	97:232	0.959	0.633	MPELPTWVLALLPHPVLLIDSGELEAFEQICR STLKAVWHSVHG
781	410:545	0.992	0.86	MTLRPGTMRLACMFSSILLFGAAGLLLFISLQD PTELAPQQVPGI
782	320:455	0.989	0.959	MSALACLYACLFMCVYACLRHLHSLIALTFLSAI TSPLLPLSPIP
783	105:240	0.942	0.736	MFNLYFYRFLTILLWSDTRFYMKPIIQHLLRV KLSSTWSVFANV
784	62:197	0.986	0.742	MVLVILVDVSSSPDVCFFFSFFKFFVCLCWISI SLYFFLLMDFS
785	910:1045	0.991	0.952	MHCCTLGFLSCSLFLHMSFELKLLLLLWLA SCSLFLHSHAWLS
786	754:889	0.937	0.586	MGHLLLQAKAMQLLYCLKTEHSEDQVQSKQW LTHFLDQFTNIKNS
787	145:280	0.923	0.675	MLSGAPGEVGSVLFSLFWSVQGSLLSWCYLQ LKSTDSGAKDLAVD
788	536:671	0.967	0.675	MASSPSSGSHSSLLSPXDMSLLLSLIAWWLL

				GSELSQACFGNRQ
789	149:284	0.898	0.746	MIQAVFMLLFQHTHIKLCPSEEALPAEVVALS YSVVAAPLRAL
790	447:582	0.992	0.959	MVFINVVGWVTFVLVLLIFSNNVFLVGTASL GLFLSSTFPSML
791	967:1102	0.994	0.913	MVCFLFITPLAAISGWLCIRGAQDHLRLHSQL EAVGLIALTIALF
792	397:532	0.987	0.795	MMNVSKISFFAMFLMYLLAALFGYLTFYEHVE SELLHTYSSILGT
793	554:689	0.882	0.6	MVLPFICNLLRRHPACRVLVHRPHGPELDADP YDPGEEDPAQSRA
794	684:549	0.973	0.907	MQLMGLWLLRVVNRVVGIGLGGNPLLLTKL CKDGEKHCPIPR
795	8:143	0.972	0.906	MAAPWRRWPTGLLAVLRPLLTRPLQGTTLQ RDGLLFEHGRGRFF
796	345:210	0.992	0.934	MTYFSGLLVILAFAAWVALAEGLGVAEYAPAA LPCAACATILLSS
797	161:296	0.988	0.869	MLCLYRLALKFLKSHFFLLLVPNFSSRHSCV VPYFYNWVLLRI
798	211:346	0.977	0.884	MWSLIQTLQILPGSLSILLCSSAGWKDCQSAL WLNHVFRRAWWLL
799	628:493	0.901	0.712	MSYVRHVLSCLGGLALWRAGQWLWAQRLG HCHTYWAVSEELLPN
800	148:283	0.989	0.938	MIGTIFLWIFWPSFNAALTALGAGQHRTALNTY YSLAASTLGTF
801	484:619	0.897	0.802	MFSAVFPAVSCQISLLSTCNSLQHFPYAGVLC FRPVLCLCPGQDF
802	331:466	0.932	0.758	MTCPLHTTFFPFLPCLPTFFLDFPSCSLSSCL PICFPFLSLXQI
803	1569:1434	0.991	0.923	MGFSFRFPVLYMLAGLFTAFCLTWPLPGDLTR LFTPSVVGDTSD
804	433:568	0.949	0.551	MSMAFLTCLLKCVKSKRRRSNRSAQLWSQ LKDEDLETVQAAYL
805	3865:4000	0.947	0.607	MVFSPGSVSVIDSLLTLPAIVSIAAGGSLLLIIV IIVLIAYKRK
806	3865:4000	0.947	0.607	MVFSPGSVSVIDSLLTLPAIVSIAAGGSLLLIIV IIVLIAYKRK
807	5915:6050	0.987	0.941	MKGCGFPFYFFTFPFLWVFLSFLYAVDAFFLL QFWMWSYMEKLH
808	210:345	0.986	0.803	MPSVHRLGPOQVPSRRLRLALALLSLQVVV FFLVVLGQGRLLQ
809	109:244	0.986	0.92	MVKFAWVQYVSILLIFLWVFERIKIFVFQNGV TTIPVTVTPRGD
810	167:302	0.925	0.734	MLFIFPLSLPWRPSCWKESCSTGQRQAGRSR EDSVTPPPSSPWPT
811	591:456	0.961	0.744	MKTVSFFILPWLGTCCSLGYSQSSNDCFLTQ LRCHFLDEDLSSY
812	162:297	0.993	0.97	MGCAIAGFLHYLFLACFFWMLVEAVILFLMVR NLKVVNYFSSRN
813	212:347	0.966	0.804	MGAFNRRKRNSIYVTVLLIVSVLILTVGLAATT RTQNVTVGGYY
814	1120:1255	0.978	0.806	MLHILHTFIQILPFLKPFCLYILCFDTLARKKM SVFWCTFLK

815	606:741	0.88	0.771	MLFYWGLWGMGGKGLFEYFLKGKQYQGDQP YLDLGIVLGQRKLRS
816	205:340	0.968	0.899	MDCVFFSTLFLSLKLWLALVVAGISLQAANLY GYILCKMGGNSDI
817	763:898	0.964	0.661	MLRVLPAGLFAHTPCLVGLSLTHNQLETVAEG TFAHLSNLRSLML
818	223:358	0.92	0.728	MLYTTLWCPLPHSLPALSPHSVPTRPVCATHL PFSSQSSSWGALP
819	723:858	0.987	0.96	MVTCFIIGLLFPVFSVCYLIAPKSPLGLFIRKPM KFICHTASYL
820	965:830	0.934	0.856	MTGTHQYAWVIFVFLSTYRISPCWPGWFQTP GLRWSACGLPGCW
821	324:459	0.925	0.558	MARDPSFLMGAARCLPLAAVRDTSASLQQ ARARSLVFSILLAR
822	1112:1247	0.957	0.891	MFCRVRNLAGLVSYTALIFVMLPLMSALMGVN TGDPQSKKGGRW
823	1121:1256	0.9	0.758	MFSCFFSTSLATSVSLEAQSCFAWPLIVSFPQ GSLLSPFLMSYN
824	2326:2191	0.993	0.933	MMALRWSTAFWSSLSFLIWSSMWMSVLSS RRWSCSNSSSVSPSQ
825	182:317	0.977	0.831	MTYILVYKLGSIILSFFLICFEFSSSENSGPGIFF VERVLILNLI
826	785:920	0.97	0.756	MCVAACFSLVAWSILQWGKRKYPEGNSSWQI KEKVWRFSTAFCSV
827	1336:1201	0.969	0.94	MEAPAQLLFLLLLWLPDITGEIVLTQSPATLSL SPGERATLSCRA
828	916:781	0.991	0.956	MQLLSMVWVTWTCFLPWMCKDLFPPIILMG LRTSVEKQKLRQF
829	1843:1978	0.963	0.759	MHVHFWLVTASFSSSVAVTTAEITGGVSGVA AGVGSWEGGSEKGD
830	58:193	0.965	0.886	MFGSRGLLCMCVFFFNILASQCKVISSGMLC CRTPTLLDYLRQH
831	1006:871	0.992	0.943	MWPLSLCTPWALFQLFARTLHWALVALSHCS LTLLVPWWAYFRR
832	150:285	0.991	0.751	MLIFTVLELLLAAYSSVFWWKQLYSNNPGVSM LTCRLIPAVSQVQ
833	3871:4006	0.947	0.607	MVFSPGSVSVIDSLLTLPAIVSIAAGGSLLIIV IIVLIAYKRK
834	37:172	0.986	0.916	MPAGCWKTLLRWLPVFLQTMLTAISMSAIATN GVVPGKGCPAAA
835	130:265	0.943	0.843	MTRMLNMLIVFRFLRIIPSMKPMVAVSTVLGL VQNMRAFGGILV
836	449:314	0.992	0.946	MIQYAVFVLCGFLYLCFMLFFFSSVTQAGVSE PRSSHCTPAWATE
837	1669:1804	0.99	0.968	MLGIYASIFLLLLITVLICAVYSCGSLFPKALQRL SRSIVRSRAH
838	175:310	0.906	0.707	MGVTTATLIAPALRTLRTSAVCSTTAETSFSAC TFVSTSCSKKGT
839	76:211	0.989	0.715	MVGDTVGAQAYATAKCLNIWALILGIFMTILLII IPVLVCQAQR
840	4411:4546	0.956	0.917	MHYCSLLLIFYAFILANMKFCEKKPFDLKKKKP PPPSVAGNKLLVL
841	4274:4409	0.985	0.905	MSMLWRWLLIFLNIQISNPVTKFRLLWVLLKLV

				LITWAQVSSWAS
842	73:208	0.991	0.624	MALYELFHPVERSYRAGLCSKAALFLLAAA LTYIPPLVAFRS
843	278:413	0.977	0.924	MCLLICVLTIVDLGFSYLRGRPTGSAPGHEG KETACTNDEIVDP
844	423:558	0.987	0.938	MVTVAMACSGALTALCCLFVAMGVLVPWHC PLLLVTEGLDMLI
845	225:90	0.987	0.797	MTLRMLVPRLLLTRQLVWFFSAATERDPEMM NGIPRKLMSPFPSS
846	120:255	0.982	0.867	MLTALPKSFVKVVGWWWLFICLVLAADGK RHKYSYDANVFLQ
847	212:347	0.939	0.669	MDTPRSTVFSWFGIHKAAAGIFQVLVQLLLLT PYPRYPSPSPPLP
848	4:139	0.94	0.697	MFFNTLSFCFHSILSIISGWPSTWVKPASYLFL YKLAKNSFNIFK
849	500:365	0.923	0.855	MKTRAALLFLHSYVLSAQNSAWHSVNIKRMEE VLTKCLAFCGHLS
850	215:350	0.989	0.832	MHVLVLFARGLLLKGWLDHGLFEQSVNLS LNPSSAIYLSVIWA
851	1981:2116	0.939	0.605	MSSGGILRQCLRLVCAVAVRNCLECCQHSQ KTRGDKALKPMHSL
852	74:209	0.983	0.896	MHNNYTALLGVWIYGFVLMLLVLDLLYSAM NYDICKVYLARWG
853	421:556	0.955	0.751	MYVLTVPKFYIIFLLAISCCFEIDSISSLNNVITS GWIFTPAQK
854	263:398	0.96	0.635	MEAETPCTIFTFSPSLKYRFWLLLLFSMASSEP MPQYFLSCTLSE
855	1665:1530	0.948	0.674	MRLIRIWFSGKFFPAGLHSQSLPSISAAIGLLM LFTNLFTCSKCF
856	185:320	0.984	0.941	MPSVCLLLLLFLAVGGALGNRPFRFVVTDTT LTHLAVHVRTGEV
857	1964:2099	0.941	0.809	MFHRCGIMALVAAYLNFVSQMIAPAFQCQHS KVIEIRTMEAPYF
858	598:733	0.988	0.96	MNLSLPFLCLFLLSFSFKLALQLRKVSLLSLRL WGQSICCCEKEG
859	91:226	0.99	0.665	MVGDTVGAQAYASTAKCLNIWALILGIFMTILLII IPVLVAQAQR
860	319:454	0.98	0.925	MSYISGSFMTGLLLLFYFPFQIFSVQCTLGSHA DGLSGKGSMDGRD
861	58:193	0.941	0.799	MISVSAMAI AFLTLGYFFKIKEIKSPEMAEDWN TFLLRFNDLDC
862	159:24	0.964	0.629	MVAASSRSEKYLEMVVWKAYTLVLTAFTLSST LSWIATGSSFPSS
863	139:4	0.982	0.792	MLILTFLWPFSNLCLVGSSEEKEHVAPSLEAG ALLXKVNSYSYFK
864	158:293	0.934	0.709	MKIVCILNVHVGMMFLNLVIGGIFSFIGPLAY DLCISIRSSSR
865	208:343	0.966	0.902	MLCAPVQTNLIFHCFFLLTLISGLTGMPSFQSY FLAWECAFLCSQ
866	121:256	0.921	0.574	MAWDHLA LRCFSVLQWLWNEQGSSGSYCY RKHNTGPYGCRSVQR
867	14:149	0.96	0.624	MQNANRGKDSESVGFWLALALILHLFQPSSF LSWGKPKHNCHQA

868	88:223	0.931	0.764	MQMVVPRLLSVPQLLNTAPLFLPWEKTVKTQ YSGIIFKFKSRIET
869	2:137	0.917	0.782	MHAKRIFVFFFMQVVTSPQHSASCFIGHTIYL RDLAMSVHNKHP
870	100:235	0.951	0.806	MFLRFINVVCINPSLLMLSSIPVYEQITVYLSIFL LVDSWTLSNL
871	82:217	0.994	0.936	MAFLIQWLLLIIMTTCILEVYVEEGECCFSSDTI SEKVCDCLLHT
872	95:230	0.95	0.858	MFYLGLLKRLVILIPPYFQASTLLPVTKKAHFKY ILSLKITVGA
873	38:173	0.981	0.896	MAGFCVAHLFLPLSFPFASLLGSHHPTQIAFS LSTEGRVGLRCS
874	61:196	0.988	0.845	MFFCLTRQSLCTLLMLKRCIFFSYCVICRAK SFELFTSEITFP
875	159:294	0.976	0.902	MCPLLKYKILVFAAMFFFSQGSQVEIRSHEGE HCVGTVHLLSHF
876	222:357	0.992	0.871	MAGPRPRWRDQLLFMSIIVLVIVVICMLYALL WEAGNLTDLPNL
877	280:415	0.902	0.73	MKTLLILHGVPHAGLASVFLRYSRLLYRLAVVA RTCKLSTLGGLG
878	2021:2156	0.961	0.875	MFNLKEIPLILYVLLSVVCFVSFSYGVPEPKSWS QGKKGVTGDSL
879	189:324	0.954	0.733	MTLPCAQMFAAVQVLSVTYLDLQPHLNESLL TVSLIFRFIFNL
880	243:378	0.987	0.555	MEEPTPEPVYVDVDKGLTLACFVFLCLFLVVM IIRCAKVIMDPYS
881	331:466	0.937	0.823	MRRQMSISTFMAFSWILVSSSDRLLMSPLKT TSSAFNCSTFSAS
882	185:320	0.902	0.607	MCNTRRFATQILLVKTSTSPSCGSMNRKSSP SRLAWTSDSDLQ
883	204:339	0.97	0.908	MIALYFTSIWFTCILIYNDCSDEAFSNRQNSFT HTLQPLCTPTS
884	55:190	0.883	0.712	MCVFFPSFFPLPFSSSSSYITTLTSSSSSTPL PKINKPVTPKVP
885	67:202	0.996	0.923	MIWVLLAVPLVNCWFQTLTVVDLWHDCKFN SSSGQEYSTGPIL
886	1167:1032	0.907	0.617	MVRWKREIHELLWPLWFCSWPRVFEKQRSM TDFTCSAFSAFLFC
887	216:351	0.974	0.793	MFTGLGCSVFLLSAADSFFPLLFCRWFLNL TPFSCAQCGNKSS
888	1436:1571	0.969	0.808	MLFMVAVAIFTEGLYNVTLALWNYIVIPNQVIL NIFMLSCLNVL
889	37:172	0.935	0.731	MSMRTQIVSSFYILKLNLTVCCLWKCYCTIDH SLVGPFVRVDRSV
890	29:164	0.936	0.659	MFLSRVGMTCPILGELLVCAGGLPPLDDDLLRI AERFINLSALGL
891	158:293	0.966	0.829	MLFSLQTAIVYCTITVLCRHTLIFSSMHKCIMLF PIIHICSYVFF
892	759:894	0.974	0.795	MWCAEMLHILFMGLRVNLNHFETFLICCEIYQA WMISVFLVCCF
893	163:298	0.901	0.672	MLSSRFGKTYKQAVYGLFISLLCIFLDIYRLFDI STHYQILGYGI
894	113:248	0.918	0.669	MPLQFLISIGVGVLAHAVSQGKNTCMLEKSTR

				YLFIFPQPD TIP
895	224:359	0.927	0.562	MTSLQKRLSHCMQCTMLLGICGQCKDD DILA SWVIQEFTAMQSR
896	165:300	0.89	0.708	MPKSECQTILVEALLLPLGTGITADNINIGHMT PQLIPLQRLKA
897	131:266	0.984	0.967	MLLATLLLLLLGGALAHDPRIIFPNHACEDPPA VLLEVQGT LQRP
898	57:192	0.928	0.649	MFC SNFYFVDQSSIALVLPVLLTLYNILKRAV SRTALLQLQSA
899	215:350	0.993	0.914	MFFVLVLT PVECCLCFWLNIYRALFEKLNSDP SRDEGNKAETLIT
900	189:324	0.998	0.986	MIWLIHFSRLRLSVLVCFAICLWLGC FQFQTCC NKHL CNILLFTL
901	55:190	0.955	0.812	MGLPGLFCLAVLAASSFSKAREEEITPVVSIAY KVLEVPKGRWW
902	43:178	0.889	0.638	MCVCEGLLPIPLAPGAWCLKRWCVPCQATLK NIYVQQQYNSTRER
903	161:296	0.995	0.918	MKSHWRFCFALLFAFWGFRSGVLGIYIQT VQ YTGQLYTIYCIY
904	412:547	0.968	0.932	MFSRLFVFLILYKLLGKYYGIRFKIVITCVWRY VLGGRYILCSF
905	179:314	0.928	0.644	MIQGPLACEFFLQGALLSFCMMRLEAWHGSL KTTIPLGWGPSPSG
906	450:585	0.965	0.932	MPAIVVFLCFVISDGLTSPRLDCTGLNLLSS SDRPTSASPVAG
907	159:294	0.971	0.887	MRSWYLASFLLSFLLTTEGRFSLYFPQRPLCL AQHWTTANVSTWG
908	169:304	0.975	0.766	MSWLPFIVYSLKAATVCESFLTICTVKSCWIDS GMRQIKQPAYKI
909	248:383	0.965	0.744	MLGASNLLQVLWRAIWHCLVKLTKLPHGSG GLSLHVCVCSRKPS
910	163:298	0.93	0.56	MTGLTRLMHRRGV LWIT IARPRHPMRSVMDT LSVTRKAMRRFHSG
911	29:164	0.921	0.658	MFYLTFLCAYMGVGERHTFHVSAFFFLQSPH SLYLPLLEEEGRKW
912	84:219	0.994	0.962	MALALSCLRAFLCSLLCLGAPFRLVQMVRI PM TQTHFNGTPPKYA
913	40:175	0.986	0.944	MWLLVTLSPRLLSPSHFTLEG PQIDQA HSEL QVLPLVRPSAVPL
914	66:201	0.95	0.871	MLLLSMIFLTTIVERQSSPFTCIFT CNVIFDAYY VLLFNQPILFY
915	120:255	0.959	0.788	MITPLRILSIFSLPCLACKEYNHDPFYKQNTSIE RTEILGFKYFK
916	17:152	0.884	0.646	MSLLPPWCLLKARVAFSEWKSNRVPPAQTPQ HSLSSPLSSVTSS
917	110:245	0.946	0.794	MLSTLSIGTLSMLIIVSDSWSYSSNSPAMFGS DAGFIPSN CIFA
918	17:152	0.944	0.67	MGRCLSLGILRQGLCCPCWSVVAESGLTASL GGSGHPATSCSKEA
919	102:237	0.922	0.777	MKMFQMLLTSSFCSLSHLQSCQHISFLSISNH SKIFLYLQPTCYL
920	88:223	0.963	0.733	MLPLGVFLPLFFSWTRKPGDLFLRSQKRKNR DSSTQTQPLALMTS

921	533:398	0.982	0.735	MWTILLPTHLSSLSFLSFTVEPLFSVMPSLVR VNCYSIHFPFQ
922	245:380	0.964	0.615	MLLGCSLLTTWVSTEMGRTVKGWRHLLTVLF PCADLSFACGHPRS
923	232:367	0.885	0.587	MGGRTQRLGPGALLTVGTPSYVWGSPYQTK VPDLSLAREADTAQ
924	56:191	0.946	0.753	MSHAAAFSTWLSMKLPSLPLHTTLFLHERPL GLFSSHPESCGTD
925	466:601	0.907	0.589	MGGTPWAQAPTQTSLTTLAMSSLSWLVRSGA IFTRTAGLCTLRKP
926	774:639	0.953	0.871	MRKLIAGLIFLKIWTCTVRTSTDLPQTEDCSQC IHQVTEIGQKVA
927	276:411	0.987	0.877	MISRLFPWNVTLMCFCLFTALLEPCSQASSFIH FSPFSYQGGECV
928	153:288	0.924	0.789	MHAAFVPGRIRWRTLMSLSRQRTGIINSSTKE SRRDLILMCSAWC
929	146:281	0.972	0.756	MAFASVLLARASPAVVRACL SRCAYGVGSDC PHLVTLAALILFWV
930	151:286	0.987	0.674	MSLLLHFYCAFMCTHTLLSIFDLYNPLHILCLV MCLTNDSVFSAL
931	51:186	0.965	0.865	MLFIVAFEMFFIGPCFSNILCTLQSLIEIWLTKS YLLQSFYNIA
932	23:158	0.988	0.789	MWLFIAASKCIFLLIVPNFIFVFWRKVFSHDLNI AYSFELSSKYI
933	44:179	0.998	0.974	MIVLFPLLLLFQALPVSILCFFCLVISSLKSSRYF LKIFFKEIMF
934	38:173	0.895	0.712	MVEVVSLHLHYAVACARKGPFNPNTKDLSGWT PSSGREELWK GKRA
935	286:421	0.981	0.887	MLVPTFFLLSLDQSCLSICVSQDYFSSIVVQIR QIGSLCLNKS
936	24:159	0.944	0.717	MPTLAKWILSLSMTSTTWSPCSSMIPLMASST APSRLRTGSLPSM
937	78:213	0.938	0.789	MPRYSHFYCSRLLQSRLIFFLILCCHLQKIIRKI GLTLCPIYIWS
938	190:325	0.932	0.711	MRFIVLTSLLKLNFEVLVIGNHKLMIKLCYLSRISI NPVTHDIHKQ
939	450:585	0.965	0.932	MPAIVVFLFCFVISDGLTSPRLDCTGLNLLSS SDRPTSASPVAG
940	145:280	0.962	0.797	MKNTWGLLMYLFHFCVSCRM SLMYKCSIFSVK TQMILLEDGGRKHIL
941	151:286	0.972	0.736	MTVLCWAFIFIFPHICPYGGDAFEYFHFSFQLF GLKLC SHGVPPN
942	939:804	0.961	0.885	MQDAVFSIICLKVLLIGMLL FCTVDGPVLQEVV WYIFRTWGFRI
943	178:313	0.958	0.829	MALKCNGQLGRLLSHVGPLYFLV FVVVLP TPNVWAPLLLD SG
944	156:291	0.972	0.913	MELGCWTQLGLTFLQLLISSLPREYTVINEAC PGA EWNIMCREC
945	127:262	0.962	0.632	MRIFFAFQSGLLASASFLPTKNSVDSQINIFKL VHSLRRSSRRSS
946	147:282	0.97	0.722	MVTFVLWKIILQLETHWHYLLITASFYILLNAKL CKKVMVGEKSR
947	174:309	0.912	0.577	MVFAWGLAVNKTSLVPIFMDLSLAGKIYIKQR

				MRMEENLLGDNEV
948	99:234	0.997	0.974	MLALFFFHWLLTVMSLCFASTVSYQVFRTHLI
				FFLDTVLLLLLS
949	168:303	0.929	0.586	MLTSLHLSLHILCKGKLRFFREQKLTTWASQLV
				SKPACCRRKGLE
950	333:198	0.953	0.784	MVSVVPIISFFKLLLFVKSNYLNRMEVKLRLLKR
				ANGGGGGGVMTA
951	139:274	0.985	0.932	MSSLHCALNCLLSCTMFLFFWFGWNLRLLK
				AMTDGDSRFLLSQ
952	19:154	0.98	0.751	MSTVYLFGLRAWALAFDCLGWSPSSATVAHA
				VGLHPGVHGTYHSR
953	163:298	0.985	0.932	MELHRTFFVCSLSIVRLVIAACICRLLALVATW
				DSFVWIYHAFL
954	92:227	0.92	0.66	MLRSFITAIIEWMIILKLQKGIWHIFSKPQNNVL
				QDNTHLDIKQ
955	25:160	0.934	0.661	MATLGRCSLCFPACLGHEAWMGSSLPGLIL
				GSLHSGRLHGPLVW
956	29:164	0.982	0.951	MLLKSVSIQHFCLLVFLMAHFPLLFAMMNYS
				PSLPQKQLMNDWS
957	80:215	0.978	0.907	MIRCGLACERCWFLTLTLLLSAIAFDIIALAGRG
				WLQSSDRVQTS
958	177:312	0.931	0.725	MGNEIGVVLGLSLLPARLLLKAVQVIHFSFHLV
				TGKEGRWYFLH
959	69:204	0.98	0.807	MLFPSLVMGHIFCCFSCLYIVNFTLSFARLLLY
				SFKQCWAFSQDA
960	106:241	0.967	0.661	MNVSGLLCFTSLSLICLLYKMEQIAPRTSGYCK
				NEMKLDRAVQAD
961	156:291	0.943	0.694	MKSKRTIFFSKFLGSLQESVGVLLFLLVPVSA
				AGVGRREAILCL
962	433:298	0.935	0.575	MFALVSCIILYRGALEFWKPVPSTGEQLPCLQ
				QETSVHGDNAGVQ
963	263:398	0.988	0.653	MISKLLACAGGWLWGCLLIRENKGRAKVQVR
				VKLEVKAFDSFWMK
964	1352:1487	0.932	0.765	MFLRFPLRFGILADKLILYKASHFTMLSVPGLY
				LSTLLEGIFILK
965	73:208	0.927	0.666	MWGILQNGLRRGVFGFLQLFQSHWKQRPNLG
				RLTVINQVLAIFSQ
966	90:225	0.935	0.669	MAKLNFIWLPYLKFTCLTIRVNMNGTKDYQN
				KIGDELFTREDFN
967	80:215	0.946	0.707	MSTNLIFGSYFPDHFLFVFWLLHAIGVTTTTLISG
				KFSRVSTLSPH
968	1311:1176	0.977	0.843	MCVYTYVCMCACMYVCIMCIFSSSLPLLLLALE
				RDTKYWLGAIFFF
969	223:358	0.944	0.621	MLSTLTMVGLADLLFDLFLAPKRSYTTKSCCSI
				AHIRKSPSKGII
970	59:194	0.963	0.806	MGVILIACVLGSLHCQVLKQILFLQMVKALLP
				SSCLKFGFFPSH
971	137:272	0.915	0.69	MGWKPVQHGQGGGLGFISSATAFLCSFGIVL
				WMFSQYPPVSYEL
972	210:345	0.937	0.764	MVMPTLQVEPLCVCFWKLLFKNWGRGVVPLV
				LHVSLEFQACWRA
973	53:188	0.963	0.822	MDCWTMGLALMWLWRSWLPQRGSYHVQV
				PTVKHEGKYSFKGFCV

974	98:233	0.909	0.753	MLMYVTNISFCNLLFLHARETCISFNVCAKHN KDHPQLLSRAL
975	42:177	0.92	0.763	MLANISMLVSLVIIIQYITQEIPDPSRLPLVASWK TYPLFFGTAI
976	311:446	0.978	0.853	MVPTFLCLLALSTYPLSTTHITPPIQPIIGFQV CQSSYGFLNM
977	94:229	0.893	0.559	MGRERGLLPLALRQLSIFWAPPGRWDALLGH WSLSDLRRFQSGFT
978	259:394	0.967	0.888	MTLWPFISYPSKLYFLLIFLYSYFTSAILAPKLF YLGSSYLSLHA
979	12:147	0.987	0.961	MSELMGLSVLLGLLALMATAAVARGWLRAGE ERSGRPAWSCSVTQ
980	43:178	0.965	0.875	MYFQRILWARKLFCLLKSVLHYFEIATINNQLIR SLQLCGNKRQT
981	298:433	0.982	0.878	MIMIIVIIFLKFSMPITVSCVGTDKNELQKPLYI SDSGAALNCF
982	224:359	0.953	0.76	MIISHICLLFYNLVGFVSITPLSAVRKHFGPVGA WGRLLSSQGDTC
983	135:270	0.952	0.902	MLFVFMLCQWLVLQQQSSVVRDNHVFAAEP TLFTFWAFADERGQP
984	60:195	0.905	0.555	MIFSDHAVAVSQSLFCALYLLCMYDENGNFSS VFFSSSQSTSKAL
985	55:190	0.883	0.645	MLKITSHIFNLLHLATIPPSFLIYIGHMQGPFNVL YSFPPKRNLS
986	111:246	0.971	0.734	MFSGLLPFLPLFFSAIPHTGHCFPLSLFDHGC FNSLHIFVKHIL
987	185:320	0.999	0.965	MAFHLLLSFSLFVFSLKFFLLIFLFSPIVHFVKHLV YTIGVNMFFS
988	122:257	0.993	0.766	MTTIYKILFALKSVFPSINAATSTFFCIFAWHVF FFILSLSTFL
989	55:190	0.967	0.875	MTHTTCCIFSLFLMKITITCPIYSVLNALKGNRQ GIQSFNLSEIA
990	152:287	0.986	0.794	MPVHSEPGSFLFSTGFGVLILFLLSLHLLES TLQNLSPSTSCQD
991	168:303	0.926	0.622	MQRQGSVLCRLCLIRRGVSWWNLRHCSGQ GGRGQGALVPEIHLG
992	121:256	0.932	0.675	MESTALSIHSAIFSVTWVLPFLSSRRQAACAL FTMGYGSDIHIV
993	444:579	0.918	0.651	MFILCPVLTIIENGLLQFAISIIDLRIFSFNSVSF CYAYFEALV
994	175:310	0.948	0.555	MYLFKYWLLTGKCILPHSLLEHTVTSKAVTHF GKKKIFFGKNCIT
995	564:429	0.939	0.87	MILLSTFFCCFREDSCFYKKYVGLVQWLMPV IPALWEAKVGGSL
996	232:367	0.911	0.688	MHGSLGLVHFLKLLKKYLGINQLQFSSFSLSF SNWCCVTCFWVR
997	34:169	0.964	0.841	MLHISSAFHCYAFPLPFALTNFIFLYLLSLSP KLECKFQEGRD
998	377:242	0.983	0.897	MIKIAVSLVMFLKVLLKVIFIIILRTRERFLVWL PVPLLLISLK
999	34:169	0.975	0.917	MKRRRQLRARVFALALAWSLGPCWALRVAVP KASXTIRGPQRLL
1000	125:260	0.965	0.703	MVALVTKPGQTFAPLLGTWLLCFYTGHDLFQ

				QSLTPVGS AHPWP
1001	218:353	0.914	0.647	MRCRAPAWLRRRCGQLSERLMRPNQVQAV VRGILEGAGAGAAGG
1002	19:154	0.969	0.872	MSLPWTFVTVLILAPSLSGSLSGKSSTCAPAPS APGSRSSGPRRNH
1003	31:166	0.978	0.941	MASEVVCGLIFRLLLPICLAVACAFRYNGLSFV YLIYLLLIPLFS
1004	269:404	0.917	0.668	MPIIGLLQIFFCLEDIFPCWKNSAFLPHTDTNSS PSRASVWGIFV
1005	128:263	0.924	0.78	MLFLLLAIGKATDLQNVRLGWQAEHTLRSFI PKCCHFRQTFDIL
1006	90:225	0.996	0.977	MSFSIWGLSLSFCCFLSIYPICFLILSSFPGF FLITFLLFHLL
1007	148:283	0.989	0.938	MIGTIFLWIFWPSFNAALTALGAGQHRALTNTY YSLAASLTGTFA
1008	183:318	0.917	0.658	MAIRQATGWSLPRAPWTFVMMDFVLDPILDI WAPLWYPYVLDLL
1009	139:274	0.988	0.959	MCEIADLWIGLLWLFVYICFSFNSLTTCRAA VFWRSAPDPGA
1010	413:548	0.954	0.64	MMTVYPLLGYLARVQLLGHIFGDIYPSIFHVLIL NLIIVGAGVIM
1011	126:261	0.914	0.636	MKISLIFLKVNNFFLILFPDYVHNSIVNFIRVPYF HVSHPPNYTF
1012	359:224	0.958	0.821	MAKYASMTFKLFSLCVCMYIHACTHTHISHTDI DIKQFYAQEYQG
1013	128:263	0.969	0.764	MLQRRGALCLVLPWSLVRISSFIQIVPSAPGKP IYFRSPIHMLSS
1014	133:268	0.893	0.776	MRLLFSCRGRGMFLFRRMLPSRDRYYKDVE LIFNYLGLIVSGL
1015	80:215	0.971	0.817	MLTSLFTSLCRHLIFQILPTNFMKAIGQSVLIQ NLKLFICNWAG
1016	61:196	0.941	0.777	MLRFYLIAGGIPLIICGITA AVNIHNYRDHSPYC WLVWRPSLGAF
1017	94:229	0.919	0.605	MVFFTASFTSWMLHISHYFKNNSLPEDHGCTV SLVLLSQRVHVFS
1018	59:194	0.966	0.89	MSRPLGILRSFCFLWVLYSVQQNMGVESKT VIWLLCVPPAKHLD
1019	193:328	0.974	0.921	MVHHVLVVMWFSAWVARWDHLSGFENSQCL DPSLGISLQFVWGLL
1020	320:455	0.945	0.798	MAQSQRGWFPVHLKCSLLALLQMLSTQQTQFQ SLLRVQHGAHGSGR
1021	148:283	0.957	0.636	MILLCPGLTDLVSFLFSLTIGHFSRVRGQTITAC PSSRIPAGFQD
1022	45:180	0.924	0.812	MPGFKFCSSLRFLYLINFPIGKFVCLAILLPHFP LLSCCPLODHL
1023	223:358	0.92	0.604	MSVFSNCKFHESRHLVFFVPWWICLFLIKEP CTPMGRSVVYNPG
1024	141:276	0.952	0.849	MNTYFFSIGICFLCITARSNHCIVYFCRKIEEF YFNTIFPIPA
1025	342:207	0.916	0.578	MSTGLGAWLTVVWVGHGRGPQQGLQENSNSN GNCSAQSTCQSPNNLR
1026	340:475	0.937	0.821	MFLFTSWVKGLTSLRDWFSVWESNLGSGCE SMESSPLEYRLDCPF

1027	209:344	0.934	0.771	MNTFLAPRFLKGVTVGFMIIYFDSTSRLPAFVI ECFCAWVVCFG
1028	135:270	0.938	0.76	MSLHSHVITQSLLFILEFTLSFVRSVGLDKFIIA CFHHDSSIKS
1029	106:241	0.956	0.761	MSFALLRSFLILWKQLEVLKEHWGRLKLQGG DINSVSLHKRFSEL
1030	34:169	0.901	0.752	MPLESIPSILTFTLILALIHPPQTSTLIPLPLALN LLIYPAYYL
1031	127:262	0.951	0.725	MKCFPLLFLRLNFKLVKKCKELMYQTLEMC KRKTFKIVFSKIL
1032	160:295	0.899	0.67	MNPYLLHFPLYPLLPLSSSLSQPFVPSLLTFE TLHGASFPWALG
1033	95:230	0.966	0.928	MITFFFTFIIRYLSLYLKTRCQLLLPKLSVLHLT LLFPFRKVYS
1034	105:240	0.943	0.765	MPISGPSAFFFYLGTCFTFFLSFKFNISLYTSV GVPVAVSFYSII
1035	222:357	0.992	0.871	MAGPRPRWRDQLLFMSIIVLVIVICLMLYALL WEAGNLTDLPNL
1036	46:181	0.968	0.924	MEWPALLTSALLGWGMPCGSPCVRRESEL NDGECHCRSMHRQQ
1037	146:281	0.941	0.791	MPYLILCLSPILSHLKDIVWFFCLSQMSSSGIWI LRQFREVACAL
1038	222:357	0.992	0.871	MAGPRPRWRDQLLFMSIIVLVIVICLMLYALL WEAGNLTDLPNL
1039	232:367	0.937	0.731	MCLGERRSRIEFCVLLHIYKILKALLCVCHLFF TSKVGLQIFRF
1040	108:243	0.943	0.642	MQKLPLIKPFPLLLVEDWLPEDQLWLLKFYS SYKGLLKHNLLW
1041	185:320	0.965	0.895	MGHNQRQVFLILAMTKLITCLWWLGKTVCCQ NLVKKQSQQGGVGL
1042	737:602	0.95	0.684	MVCLVGFELEILYVYRFRQSLALSHRMECNGTI LAHCNLRPGSS
1043	324:189	0.922	0.567	MPLRKRKVGEVAHLVVTIVLRSSSPFSGGWR SVWLIQHVFHTCFL
1044	236:371	0.967	0.875	MARAHLPPTSAGFLLTLFMSLSKEQGPPVREQ NTYVQRNEDAGRR
1045	16:151	0.934	0.795	MELVVIYSLLLYKIFPLKSLCPICTLFIGDWTRL DTLEQWFSKNS
1046	213:78	0.889	0.675	MPGLKLHLITAAVATPLHGASQECEPNATQMS DFQEKLGICIFNG
1047	514:649	0.98	0.953	MNSLSWGAANAVLLLLLAWASPTFISINRGV RVMKGPSAFLSGD
1048	115:250	0.957	0.65	MFLFGFPTSYMILNMSLVLPARFPQQQMNFNE YKLVKVTTWTAVT
1049	120:255	0.999	0.987	MFYKLVLWFWWWCLTTRGNLLCLACIFATLSLE SKNFPTLQATLLI
1050	206:341	0.927	0.635	MLQALKSTVSALATAFWDLDAATILAVSIFH HSPCFAALVPES
1051	273:408	0.946	0.626	MGPVSGCWHMSLCLRVYLALDPAHQELMPP GSSLQPITLGIGIEI
1052	245:380	0.978	0.762	MTLPLFISVLKCRCTCIALFLSPTSCSHFPPQDF MTLQKKTNTFLH
1053	91:226	0.984	0.937	MTITALAFTYVLLAHSFMLAHYFPLNSWFLASII

				FFLVWIKLLSL
1054	375:240	0.968	0.902	MATLLIILLMVCDEWGIHRILYGIFLKSFKFLQ ELMGETEPQE
1055	195:330	0.946	0.612	MQAGSALWHLWAEGRWLVAGFGNFGERP HLKTHTDYPGPTEASC
1056	283:418	0.9	0.673	MGMLHGSAFSCSLGLLSSSRTLWATCITLQK SNHCKEAGGGTHE
1057	88:223	0.91	0.731	MLRPCSWFYLQSLAQGLLHSCFIDHCRMSE QINVWNRLCLPGTT
1058	172:307	0.962	0.707	MVMMGVRMMLKVMKIPLLLTEALPAFTVACW KDASGAYTIAVSGS
1059	200:65	0.929	0.733	MRRARTKFVLLAFIASRNTDDFCCPRWSSYLF TSWNWTGPSDLTG
1060	121:256	0.926	0.762	MLLSCFSVLTPTSFIPSSPSILLRHEYRACLFS QNFQHLHLTQRI
1061	13:148	0.991	0.951	MLCVWIKVLFLLIAESNTWLLSPRTKDVLSKSEP TQIYPHTSRKQF
1062	133:268	0.933	0.808	MKSLCFYLSFTFTLDALSLRERGTAGHPHVQT TSSLSVLLSKPLP
1063	72:207	0.934	0.83	MIKSLSTLAFYVFWVNMYSRLPCLIPVMLQVP REKDGTRSSPVWG
1064	152:287	0.936	0.573	MTRHWVLSVLVALKKQKEFTHWVLSILVALKK QKEFRHWVLSVLV
1065	61:196	0.934	0.83	MIKSLSTLAFYVFWVNMYSRLPCLIPVMLQVP REKDGTRSSPVWG
1066	201:336	0.951	0.704	MIVCVCTSAFKWILSGIWIFSKTHSHASARASS FGWVKRKPLWLE
1067	69:204	0.91	0.639	MTVTVMYVPCHLLVYRLRLPGVKACVSLSSF QRMEGWWGWENCLR
1068	199:64	0.894	0.558	MFFQTHGLLIAKFLSTVQIKESNKEKMIEHEITL LPVMLSGTTKE
1069	50:185	0.964	0.901	MNRHKYAAALCFLLQALLSRALYMGGHDRHVY XXXXXXXXGGPFGK
1070	972:1107	0.922	0.717	MFQVGGRVFKRCIFSFCCHFIGLGLGVCFS LNGTRMFADSSV
1071	1504:1639	0.961	0.849	MAFRTCFLSCLTVVKVCSKASPSFSTQQPCVT TKVELSLICCCFS
1072	58:193	0.939	0.685	MFSFHTFSLIYFTLFSHYMEKNFHSPGDKFPH SVSLLSFFTKIVS
1073	156:291	0.908	0.655	MLMHRWGVTAKIMQLTFVMMRVSSEVWEEG DTPDRRDPIAAFND
1074	268:133	0.966	0.856	MVLWFFYLWGEGLATLNNHQSILHRTAWA MSSSFNNPLATHSG
1075	89:224	0.949	0.841	MPLSVVFMAFAWWKSCGGYVEIKTRINFCSR SKYIFLKSRIKFPI
1076	38:173	0.963	0.875	MLNSKLHFTVMVTAFFLWGLQGKQPLVSICEH TCSLCLGRVPGAS
1077	425:560	0.988	0.962	MWLRKCLLGLSLISFRVCGPLIALWVSDSSIR RLNPLVFLCVC
1078	181:316	0.97	0.832	MCLLLSLCSFRFALKIGRNEEFPSFSPSAVNI SVLVILFGRLR
1079	187:322	0.907	0.778	MFQFTFYIRLHFKVYNLVFCRFIMFRIFLKCFYT HLIYCTLPLLK

1080	25:160	0.931	0.741	MSVRSYPIGVLICTFRVFKLLFPYQSTLWEVG YFTFSYHALYYF
1081	14:149	0.887	0.56	MKFHLSFFSLKRAIFYICAKADKISGGYLYKCR TVSYSGKNVRSG
1082	25:160	0.968	0.856	MRLHCKTLHIVLFTLLYKILMDHQNLSEHVL MVLYLIELGLEN
1083	130:265	0.972	0.904	MWSVTSTIFICRLLIVRLLGNTAVRTSVVFLPH KAGRHWEKSTSL
1084	77:212	0.933	0.796	MFSALSFFIHLPERGACLLCQNLFWILLIWP RIMNLTNGRLY
1085	107:242	0.974	0.916	MMFKTGPWLLQRCWAELCRCFIVNSNCEHG LEPAICIFSLHGVK
1086	240:375	0.892	0.751	MTPLLVWSGLSGHYHWYGRFKHITPIVLGS GFSTSLPLFWISG
1087	111:246	0.936	0.731	MVLHCLAPTSLFHFLPHSLASALEAHWLIAGL RTDHVCFQCRPLH
1088	1949:2084	0.908	0.617	MPSRLKALGTLVSHVTLRLLKPECVLDKSWC QEELSVAVKRAVML
1089	152:287	0.953	0.815	MGSEFVFISAPCFFHWVGSALVTSPTHPPVS HPWWEVEGHLPGK
1090	73:208	0.984	0.928	MKMMVVLLMLSSLSRLLGLMRPSSLRQYLD VPLPPCQEQQPKAS
1091	11:146	0.99	0.832	MLFVYLFVWGRVYFLLQPCPLHMCHMSLLC AHLSTAVLGHWT
1092	119:254	0.987	0.963	MNRRASQMLLMFLLAICLLAIFVPQEMQMLRE VLATLGLGASAL
1093	173:308	0.964	0.844	MACSSLVLPALSSWSLSLSLCHRLPGRNAYR PSFVFSLTLLGAAL
1094	199:334	0.955	0.91	MSLSPISLFFLPHALLYTPRFLSAPPSHPLL CLLYFQLYSLLF
1095	118:253	0.916	0.868	MALLPRWFREAPVLFSTGWSPLDVLLHSLLT QPIFLAGLSGFL
1096	110:245	0.93	0.886	MGIALLOIFGICLAQNLVSDIKAVKANWSKWND DFENHWLTPTIS
1097	564:699	0.965	0.83	MSPLPLHAPLAFFPFIFIYLLTFMKFPLPSDPYC PCCPDHPSQPS
1098	66:201	0.891	0.731	MVVLPVSWVANAIIRDFYNSIVNVAQKRELGE ALYLGWTTALVL
1099	1:136	0.983	0.815	MALSWMTIVVPLLTFEILLVHKLDGHNAFSCIPI FVPLWLSLITL
1100	157:292	0.98	0.724	MMLGPVTLHLVGHLLAFLDLLCPRGPIHSILPM TFEAVKQDHGFM
1101	184:49	0.933	0.792	MVMVIFYICVCCSNFSENMLCICTYQNLNFTET IFLVHVNKHKKK
1102	1526:1661	0.963	0.593	MHAHSASLWVAFFYRSPFLFFTGPPTSSS PAGLPLESTVDA
1103	1528:1393	0.991	0.596	MSDISPLLYEIWLGDTAGFFTCVTVLHVLLL LSSVLHFLCPRD
1104	685:820	0.992	0.963	MNETGVIVWYALCLLLAWLIVGAALFKGIKSS GKVYVFTALFPY
1105	891:756	0.942	0.88	MPTLGDALILYLHLVLGVAGVLQPPGPRPSQA LGPTGDRAPGKWN
1106	249:384	0.977	0.889	MSRWVRWVRGVGLVCVVCVKRLLGRAW

				QLFISNSLLSVLPTSL
1107	200:335	0.905	0.717	MYRCNIVLFASLVSCHGCPGILRESRLSFKGR LSHDKYSCDRFLW
1108	322:187	0.911	0.64	MKKITVILKTMAYLNFTIYLTQDTATTYFYFQA MEIFYLMFFS
1109	336:471	0.908	0.643	MQRKRQRYPGHLGLVFIVLGSILNKHSLKELL IPRSKFSLSKVD
1110	891:756	0.979	0.889	MLFSSMTLRLSRCSCSILLFWASAACMFSSR YLWSGRSLVSVEG
1111	698:563	0.961	0.779	MALFCLVYQIIFLIQHTHFSKALLIMALNTLTYC VLVQSNNTQS
1112	105:240	0.974	0.892	MLHWSTRVCACVCVVCFRARTCVLSCTYMG WCVQECVWCGVPGRV
1113	52:187	0.952	0.869	MGPSTPLLILFLLSWGPLQGQHHLVEYME RRLAALERLAQCQ
1114	27:162	0.956	0.769	MGIFKLIHLIAIMAVPVFETICKRVSVENITQQG HLNTQSSKVYA
1115	4:139	0.935	0.703	MRWTERVCFPLLPESLILGGVLCIPPFIVSPPL PLGFTKESELR
1116	25:160	0.949	0.737	MEKKIHLRLHRCLSYFSPLHFVPLLSSLLPFFL ANFSDNCLVVVF
1117	1362:1227	0.976	0.925	MIQKILFKDLFRLLVYLLFMIGYASALVSLNLP CANMKVCNEDQ
1118	1478:1613	0.983	0.904	MWSHFVKVSTQGLFVAMFWPLIPQFVCNCLF YWALYFNPIINIDL
1119	181:316	0.97	0.753	MKMTVRAVAWSLPSLLLLPDQNPMLLSLA WCVVACRLLPGNAS
1120	201:336	0.96	0.857	MTAVNFRMVTWVVICLQQSTCIFEFAAAPSSG SAKTSILGLHFSP
1121	13:138	0.981	0.91	MRALVLLGCLLASLLFSGQAEETEDANEEAPL RDRSHIEKTLMLN
1122	85:220	0.996	0.882	MFAFLTLLHFLWELVLSTFPSLALYSPALHYLES AIMTVSKCGHVR
1123	11:146	0.97	0.829	MVVLIVRAYNHYILCCLSSSLYVLILLVTVYL MLTTSSYNDVS
1124	190:325	0.885	0.613	MRLEELISFLSRLFHLTICTTGRSYLYCFPKALF GHYCIDGKLSG
1125	46:181	0.967	0.925	MGLVLCRCQGCLCTPVMFLLEGGCIEEGVLH AGSSLLLLGLPFLG
1126	148:283	0.991	0.769	MKSDFSLLLKIPPLSYFKILYLLEAFCAFLTFLX FLFLFKXQTL
1127	140:275	0.933	0.757	MPLGVMPTFLLGILSPISPSCSSLNSSHSSQFK CHFLREVFPHP
1128	58:193	0.945	0.789	MGANRRALWTLGFVSGALHTLISQNQVTSQ SIMCCIFQSSLGCM
1129	126:261	0.895	0.62	MSRPWKKEESFTAGCSLLGLCRDLALCLGG LCSAAWPDTSLSMA
1130	131:266	0.991	0.875	MQRPSAWWILFCSNLLARFIQCLQIVNKEVH FFRYIKYYKFWEG
1131	206:341	0.964	0.823	MQLRRCLTLRALILPIQLCRDRQCCLLVRCF WSPRRRCHWSCLF
1132	850:715	0.991	0.965	MAWTPWLTLTLTGIGSVVSELTDQPTVSA LGQTLRIKCQGDT

1133	3:138	0.992	0.962	MISRVIWGFSLSCSLWLSLALTLTLLHSCSPPP SLTLTAEYTVLV
1134	403:268	0.963	0.83	MRLTVCTLYVICFHVFI SRDIWNTLLNNEINCI CPISSHLYHIY
1135	138:273	0.977	0.831	MVCFPIHGNI LGLFWFLAFMHKVAINVLTVAFV FVITEMKTGV ELL
1136	199:334	0.994	0.967	MFIWYISSACFWVLSVLMVPAFEMIFASSHI QCILRGNCNKTG
1137	265:400	0.984	0.899	MGADRGP HVVLTWLTICLPVVFILSFVVSFY YG TITWYNIFLVYNE
1138	13:148	0.944	0.73	MYVTLVFRVKGSRLVKPSLCLALLCPAFLVGV VRVAEYRNHWSDV
1139	238:103	0.982	0.934	MLGKVWWLFFYSLMHSAIRFYIGLYSLTYKPEH AAYGQEP AVNM
1140	51:186	0.886	0.654	MLTCLFSFGQ CWRARGWQRLCEGRRGWPG VGQRTLKVSEPA PLRV
1141	54:189	0.947	0.707	MQGHRWSLCVSLSSCGAFFLQGHQPCWIS SHYYS LGPPNQFGFH
1142	173:308	0.998	0.98	MFFFLLAFLLTLCFFPYMCIYLLITNIYLRVGRG SLQNGGFLSII
1143	59:194	0.923	0.749	MVYTIYLQYCLIFFPLRMHSLIAFKIKKRRENGI EGDGCSLGSLR
1144	210:345	0.963	0.842	MRREATWAGKGLAALLWFLVDFAPNLGMWK ATLSLVGSWPQANC
1145	44:179	0.938	0.834	MMIGPDRKILL LTLIMNVTVSFITNGKLTDSFW SRVVLTLQHHL
1146	2389:2524	0.984	0.893	MPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRK KDPDQPADSVP
1147	12:147	0.97	0.93	MTTTHVVEFVLFFMFPVLGVAGASWICVDSFY EILMFWPVFSYTF
1148	1516:1381	0.969	0.94	MEAPAQLLFL LLLWLPD TTGEIVLTQSPATLSL SPGERATLSCRA
1149	3:138	0.968	0.729	MVMLAALAHHLFYWDVWFIYNVCLAKVKGYR SLSTSQT FYDAYIS
1150	250:385	0.983	0.941	MPSSFLALACFLFSMGLSASPYCLTTPPRKVS TCFIFKHPKREHL
1151	147:182	0.993	0.804	MSRSRLRLYLS ELLAAFSFLERRSCSFLIPLLL FAVLFGWLFCK
1152	109:244	0.992	0.946	MLGLALISVHLLVFSPFIF SCLVYHLNILYLSHL LIDLFSCPIE
1153	58:193	0.89	0.726	MSFPYSFLGATLKVKLTWATFRVPLFSLNSHS FSSSLALPFMSYL
1154	68:203	0.964	0.922	MGRGSELPVCLAFVCLMAALGCCEVLSTVH PEETVLRAPPTNFQ
1155	34:169	0.995	0.962	MNKHFLFLFLLYCLIAAVTSLQCITCHLRTRTD RCRRGFGVCTAQ
1156	75:210	0.946	0.795	MIQPCQPCWSCALWNVLISCLSYECVCICSSY PGLTNLRSPVYKR
1157	242:377	0.986	0.937	MNVVSLVILFWAIYCVTICMDLYLKHFCCKFFK VFFKCVIICAFK
1158	54:189	0.989	0.956	MFLSASFLALLVLHLFGGKVRRTRELGRCFE NIVTKALLNDAQK
1159	76:211	0.902	0.7	MQPRHKSFSFSPWPIWLALCSPWRHCLSTM

				LGPSAVPEGFRPLS
1160	410:545	0.985	0.883	MYLSNTTVTILANLVPFTLTLSFLLICSLCKHL
				KKMQHKGKS
1161	154:289	0.986	0.914	MHQLFGLFVTLMFASVGGGLGGIILVCLLDPC
				ALWHWVAPSSMV
1162	126:261	0.995	0.918	MLWLLRWLIARLLEAWLARADSHVAFWQMPV
				ASLTSAAPIRLPH
1163	202:337	0.909	0.658	MMLMSLGGLLGPPLSGFLRDETGDFTASFLLS
				GSLILSGSFIYIG
1164	309:444	0.987	0.956	MLSFISATCLLLCLNLFVAQVHWHTRDAMESD
				LLWTYYLNWCSDI
1165	208:343	0.886	0.662	MSLITLGHQQLHFFASIYQEVSRCHFNIWISLIA
				GLNMFSYVHRS
1166	40:175	0.993	0.966	MYVYALFPFLMTQFLPTCFFCLFGFILLDDIFFK
				CLVIFGLLLIL
1167	72:207	0.978	0.9	MFLEHAIHCSLLFLSQLPLLPLVFLLLSHLLSE
				VPLIQPPSL
1168	114:249	0.995	0.65	MLSVSDRRQYITEGSRTWLAFMTMPFLLWLF
				YFISCWFSHPGKQM
1169	16:151	0.922	0.799	MPGSATWLCPCPTLACPLPAQPLIMVPGSP
				QTGLAEAPKTHNRH
1170	47:182	0.905	0.704	MYFGAYFTVAPRLAILQVNVISYKDIRHFYL
				RHWRNERNCICH
1171	160:195	0.949	0.556	MLLATSLPLPAHDFRHKDTLLEPTLLALFWVLH
				VTHLPSTSIST
1172	123:258	0.937	0.572	MVSLEFKRLRFPMLFAFGMLSPQSNRCPKIVH
				FPSRKGEKKSVEE
1173	7:142	0.887	0.591	MISIICSQLYLINTWCNVNRTRILNCQIYYILILFP
				CKYVKYLVE
1174	208:343	0.961	0.638	MLLFYSIPFKGMVFLFEHVLLILEHTIKGEFLEIL
				FYNSVYLD
1175	253:388	0.991	0.605	MEQPVREMIPPLVIFPKSSLKWVSSFWLLLP
				WCCHLHCPPLPLF
1176	16:151	0.965	0.848	MHVCMPLCLFLLSFSVSPDRLLRMRERLFRG
				CAQDCPFLALHQGE
1177	135:270	0.915	0.617	MSNLQFIFKDFGILIKFWYLHIKFGFYITSCLLCF
				PPSFMLFFGF
1178	5:140	0.995	0.952	MLPVLLMLVRVSVGQALPLFLFLGGNTSPYM
				SQGNWPFFSTYKPL
1179	159:294	0.932	0.624	MVFSPLYCLLSTDILFNLPSYLFIIYLYLPTLCAPE
				GRALICCGHC
1180	339:204	0.963	0.9	MMVTVIWLSLKLFCRGENTCMPMLWEGFDV
				YLILGEEVHTFSV
1181	255:390	0.926	0.689	MLWKAHFSLVASVWPGSHTWRVSLWGRTG
				HWADGIYIXGTRF
1182	135:270	0.954	0.788	MITIAPWLMERWVTVCTLGALGNLGRSGIFYQ
				LGLRGPPAGPWR
1183	431:566	0.992	0.96	MFWTMIILLQVLIPISLYVSIEIVKLGQIYFIQSDV
				DFYNEKMDS
1184	129:264	0.976	0.833	MLVCLIVHHSPPYTLFTFIHYFFLLLLGLGTFNC
				PIFKFTCSAC
1185	826:691	0.933	0.703	MFLQLLLATLQSGRKKCSCSYCTSNPQGGKY
				AFFSGVRLGLASKM

1186	1197:1062	0.926	0.588	MVLPVAGKAVLFCSVSGEGWMRPLPSSPPRL RPALSLGHSAGRGL
1187	191:326	0.997	0.887	MTAGVLWGLFGVLGFTGVALLLYALFKISGE SSATNEPRGASRP
1188	32:167	0.906	0.658	MLGRGYFIHRRELRSLILICLAAGNFIKIGIFSP WHLETTILLN
1189	1304:1169	0.919	0.688	MTLCCPWATMHPSTVLRMVWSLRSRARRWG SVRTGLSWSSSSDSR
1190	514:649	0.931	0.744	MSSSPGLLFSSLSHLLNNSSTLALLTHRLSQM TCLQSLRLNRNSI
1191	33:168	0.967	0.668	MVLSVPVIALGATLGTATSILALCGVTCLCRHM HPKKGLLPRDQD
1192	1528:1393	0.991	0.596	MSDISPLLYEIWLGDTAGFFTCVTVLHVLL LSSVLHFLCPRD
1193	289:424	0.948	0.76	MPCTTILRIWTFPALLFGPHCQFTPVGIFILEG GNCSNREARDF
1194	250:385	0.929	0.676	MSRGHRSAAAGRAAQLHLLLLSNVFRREGW NLFPSCPGAIPVPS
1195	198:333	0.897	0.726	MPLILAFIKLFNKCLECFVSTRGIECYRSFGSR HQAAYNQGSKNQ
1196	49:184	0.891	0.676	MKFLICLRSHFPFFFNSAIEMCFSKLKIFKIACN MNFTSYISTFF
1197	93:228	0.988	0.954	MMKSLRVLLVILWLQLSWVWSQQKEVEQNSG PLSVPEGAIASLNC
1198	95:230	0.954	0.637	MRKRERNAEWRTGFWHSFLSLLVLPVIKNPS VWTQCPFMAWQESS
1199	227:362	0.972	0.594	MFQGSNILFLLPSPGITSINDRTYFLFVMRSNW LFLTCLIAFQK
1200	95:230	0.98	0.944	MRDYLVSFLCVLLWFRVIFGLLKDSISELLSG GELCGPCLAHSI
1201	49:184	0.928	0.837	MLAPAIINSWLFFIYTLTQSPGSPDFVTAGLR RHIVLSAITSVY
1202	117:252	0.98	0.944	MIPAFGIFRLIIILIVLDMGFALYRRFFVPEDGS PVSFAAHIA
1203	191:326	0.892	0.723	MRVWRCRLAHRGGWMVQELWFRDGYMIWR LAISYVRIGIQMACRT
1204	12:147	0.946	0.641	MLSILLATLTLSLKEKRGERSIHQPEPSEKSV LPVSGADPFRGS
1205	49:184	0.969	0.888	MKILVAFLVLTIFGIQSHGYEVFNIIISPSNNGG NVQETVTIDNE
1206	194:329	0.959	0.612	MCGWCPCGFWPLAFTLHPWTRYVKPVNEHSW VLSIQSNTLNWSLHS
1207	68:203	0.95	0.872	MNKIVFCFLLLGGCREESIVLDGIFKLIRTFFC RGRENETKFFK
1208	6:141	0.96	0.692	MWWCPXSVFIYFVFSHTHKKKPLPPMHQEAP ALPALLTGLTLPQQ
1209	18:153	0.986	0.769	MFLYPFHSSSLVITALFFLTYPHNIIYVRWKIA PNFSKPLWGGK
1210	4:139	0.943	0.803	MVLFYSILFLKTSYIGGMTILFSGSALYESLTILP FVMLELMSTA
1211	57:192	0.979	0.877	MHLNAHRALFVLFCLSLFFMWMRIDRHDLHT PCGQEPSCSFHFCV
1212	125:260	0.988	0.862	MALQWSVLGQASFLLLLGHLLIFFYLDVKKIPSL

				SWRFSNFTRMHL
1213	85:220	0.965	0.856	MWMSVCLSAFICTRILMDYGLLHIVHITRVICM
1214	64:199	0.999	0.98	NTHERYVSKHYG
				MAYFFILLGLFCVALRRIFCFFFLLLCLFLEYSF
1215	130:265	0.903	0.709	PPLLFQTLHL
				MAHTSWLIHCCSPRNASFILRAARCLLWFQLTA
1216	487:622	0.957	0.887	HCCVQSSPPAVV
				MVIALIIFLRSPAMAGGLFAIEREFFFELGLYDP
1217	985:850	0.957	0.772	GLQIWGGENFE
				MFWFLNIFILILSKHSSKSLSLQLPEVLLFLCQ
1218	81:216	0.978	0.897	FCLRLHPVRGL
				MCSILRFIRTCLVILYMFVYSRFPMYFLILLFFHL
1219	127:262	0.98	0.816	DRLFCFMLMR
				MTSILSQLPRYQSLFGLLLPGFFFFPVFFPCIS
1220	71:206	0.956	0.719	MLAKYMC SLGLH
				MGYTLRQKELQRNLKFLIMVVLVYLDWFFE
1221	35:170	0.929	0.808	TIIYIFYMYTLGS
				MSLFLPLKRVFIDHFTCLHEKSPWYKASACC
1222	309:444	0.921	0.575	VGHVGIQLVNIY
				MCLHFLGSEQHMAAHVRVCMCFHNHLSQLL
1223	239:374	0.969	0.855	LCLWSNFNSFSCCT
				MRIHPPLPTPLPVWELLVCRANVLMFLVFLVP
1224	229:364	0.976	0.822	LTLGSRGMPWHI
				MLIYILLERILVKCVLFRVNAVLIYVNMCMNSF
1225	70:205	0.953	0.865	FFSVRTMFLRS
				MLLNLLIPFVLTVGSGSKDSPWLEQPEVQLLL
1226	88:223	0.888	0.612	QTVINVLLPPRII
				MHFCLVLLITEQSLGKEVHPLRLVSFRFDSKNL
1227	69:204	0.969	0.885	PASMLSLPSGFK
				MAKWQRAAWPEGMLTLWCYFMATALSATLV
1228	99:234	0.934	0.588	PDTLYFLLGENNIPA
				MIFGTDCALSKYMWAFVFFLIKARWREKNPC
1229	156:291	0.965	0.684	FDDSLRPEQCLLD
				MFRGLFLLPAPTDFPFYCLLVSQLPNKNNEER
1230	976:841	0.996	0.962	GEEQLTHWAGLNG
				MQIFLLLYALGRFVLLVTFSPVLVLSYPVLVSF
1231	30:165	0.956	0.614	YLRYPVLFVF
				MLWIFAYFRISSMFTETTTLKIVLAIRTGPDRIN
1232	662:527	0.94	0.793	CEQKTWINIR
				MYRSVLFVFPQGFRPLPFMLFEASKTFLDYWE
1233	233:368	0.931	0.558	AVRSSKVQNKKHGF
				MCPFMPPPGLLRLFQIVFWVEHPGSVNPFER
1234	2962:2827	0.913	0.735	STIIGRS AKLKKDL
				MPYVTEATRVQLVPLLVAEAAAAAPAFLEAFA
1235	112:247	0.94	0.69	ANVLEPREHALLT
				MQWKVTLTSRWGLLRHCQVLGALLHLGNIQF
1236	95:230	0.9	0.775	AASEDEAQPCQPMO
				MDTPSSLGLHLVFLSVTHLQGLDFAYNLGEA
1237	28:163	0.973	0.928	LQRAKVLIEGLPI
				MILPLPLFLRCLPQLLHASATFFQALCVWSSLP
1238	295:160	0.986	0.772	APTTPQTVPFQON
				MALLALPQVWCWSHLVFLQGRTQHPNIDTR
				SLQQPASIKDPRVC

1239	3024:2889	0.968	0.925	MAAGVSSVLLLLFTLMESGLKHRVWESWQLF TSWLAFCSPSFSVV
1240	19:154	0.963	0.916	MLSTSVSAILLSICLRAPCFLCPDLKMLGWQD MALGPLRKTKGRT
1241	312:447	0.908	0.573	MRRRSCIVSKQLWCPVTVLEGLTSSXNAGGL VLRNCMGAFLSLHA
1242	1336:1201	0.988	0.974	MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRT ALGDKAYAWDTN
1243	74:209	0.961	0.721	MMRSSQIQVLSVFCSAFVACGFVIPSSGNGG CSPRHNGPLRKKGD
1244	94:229	0.994	0.947	MGLLWLITLLLQKSQFILISLQRTSLATLLKESS AFPSIILVLF
1245	251:386	0.987	0.902	MCWLLLWIKEWKIIKTCTVLVLVELRSLQSRGK REDTSNQHPLTQ
1246	62:197	0.913	0.682	MFFYISIGVLFFPNSLLEQPETFLCHISSAVLCP IELAASLVLQL
1247	3:138	0.938	0.806	MSSLLCLAGLIGGCCPHFSFHTPVAQPAEALM LETLGACREGPGQ
1248	29:164	0.917	0.833	MLGGNFLMFLPPLQRLCSNLLSYVIPNDFSVM SCFIKASLNYTLL
1249	27:162	0.984	0.934	MCVFVCFYFLRCIGLSRYLSVHSLCHCCPD GCVQVAELNKYEL
1250	1381:1516	0.971	0.794	MTVSFCCCWILAVLPSPPLYQDLVGSKEIQA AGDPMMPAASRLFH
1251	284:419	0.952	0.822	MLKIGMHCIYFLKSLNVNLMAVRSARKKPNIT WDCVGIVVLCG
1252	481:346	0.998	0.963	MHFLATFALFFIFGVFFLFAVLTNLLAAEEVNIR GGNFLGSLVH
1253	77:212	0.942	0.835	MSCHCLSPWVPNLCAHFPPFRVLFWLSLAS LSGFIVVLSGEEQG
1254	157:292	0.986	0.914	MLKTHLLAPKWGKVLFFLLLLPLHCRAHLPAL PRAAAQGWQAGEQ
1255	19:154	0.952	0.654	MASHGEEDRHWLRCTWIWALSLSVSSSV GWRRGGCRWLGRN
1256	191:326	0.985	0.937	MCVCLLYLCIHLLSLSHYGWLSSPEPTGRK TGRKDQEQAGTPQ
1257	403:538	0.887	0.553	MAGLKRRVPLHSLRYFISMVGLFSKPGLLPWY ARNPPGWSQLFLG
1258	126:261	0.971	0.865	MSLCLAFLLHWGHFRTCPLSHVEMHLYPKRC PQRNAESRWSPALV
1259	165:300	0.983	0.747	MFVIAFLSPLSLIFLAKFLKKADTRDSRQACLA ASLALALNGVFT
1260	289:424	0.949	0.834	MMSGWLLRAAICRGLLSSESLTFTSAPHISIA VTCRDGNLQTGY
1261	815:680	0.949	0.83	MRIPKVAPPLAVMRCLTSLLVCLGTGSGGTME ASIPACLSLQVRL
1262	138:273	0.897	0.68	MASEPCWWAGMLPCACAGLRRCSHSRFLQR GHGLHSLMGSLPAPI
1263	138:273	0.982	0.911	MASSPWGCVCGLLLLLLPLLTGPALGRGFP RPLENSEIPMIPGA
1264	1159:1294	0.992	0.733	MSFFLILGVGCSLSYSLVPLIILSFCHFYPESVG CPDAPSPVRG
1265	125:260	0.962	0.902	MFKAARKARLRWPFLFWVFSVMECFSLNCDD

				YSDHFQIAFRKNTQ
1266	13:148	0.955	0.786	MRPLKPGAPLPALFLLALALSPHGAHGRPRG RRGARVTDKEPKPL
1267	37:172	0.915	0.646	MSFGPYFYVCFIPILLYSLNTKGYGNPYPCFPS TPPKFPFGQPRE
1268	163:298	0.974	0.838	MLLSLGHLYCFRSSRFLQCILPCSFPLIPFIILV LLYSVFAFSC
1269	296:431	0.935	0.737	MQFVLLRTLAYIPTPIYFGAVIDTTCMLWQQEC GVQGSWEYNVT
1270	126:261	0.962	0.88	MKQLSPLPLPWVLCFLWKPSKLSVLSFASPPS TKPSQQAGLVCSL
1271	523:388	0.945	0.704	MHLFPVLFQPLQNCPLFFIGEPFHSCFLKVFLD ITIIVFLGFLYF
1272	2025:2160	0.993	0.782	MVFTVTLKLALDTHYWTWINHFVIWGSLLFYV VFSLLWGGVIWPF
1273	1366:1231	0.979	0.911	MSFSAYQTAFICLGLLVQQIIFFLGTTALAFLVL MPVLHGRNLLL
1274	1111:976	0.998	0.936	MMLAFTMWNPWIAMCLLGLSYSLLACALWPM VAFVVPEHQLGTAY
1275	919:1054	0.976	0.757	MFKNTSGYTERVAVWLGVEIFCLMMSSVLVP LFYFLMLFGNFLQ
1276	129:264	0.888	0.564	MTMVRVWCMARVRIQSVTRVRAQCVRTRVT QCVTRIKAQCVRIR
1277	172:307	0.943	0.798	MLRHLRLAQCPGPGLLLPALTSLLPLAATQAT VEMTVSMAQVGAD
1278	12:147	0.989	0.586	MAGSSEWNPDSRPASFAGWRAWLPWMVVS LPSLLLQCHTVPGQSR
1279	496:631	0.965	0.846	MHVIVLKLAVAVQILLSIKEYTLERNHMHVISV IKVLVKAQTSL
1280	320:185	0.95	0.787	MHVQWSLTTVLRLPLSFWHKKLHLYLNLEILS SENQALNQINNKL
1281	238:373	0.982	0.879	MAMLRVATFLTRLQMIIVTSVLLAGSLYLPFGL RALRMQTAMFVRP
1282	225:360	0.94	0.625	MRGFFRSEAQPLCCCWCNLLCCGRVVVVVSL SIEGIEGACVAGNG
1283	265:130	0.921	0.725	MTCSSLSLDAVCSSFVQAFCSRDPERWPAIS PHSLSGAFYFLNV
1284	187:322	0.883	0.568	MTTIFTCKMGYWSREFLFFLLPKELANQNRR SRFWSSTSAVLIF
1285	59:194	0.955	0.834	MRGIIHYVLFCDWLCSFSIICLRSTRGMHGAG YCFLIGVFRPAA
1286	138:273	0.967	0.685	MNPFFWSHPSLLGSEGRILWLWGLLEIKLFL HMTRLHVLQSLNL
1287	107:242	0.95	0.698	MSLRAPSVRIFVYLLFRLHTQRGLLAGRRQW GPCPLSFSHFLHS
1288	158:293	0.97	0.77	MSPSLHLCFLPSSFFCKCLFIPVYICKHYFKYW GYNDEKNAQSVL
1289	88:223	0.984	0.874	MTALILLSSPLAWVSGTLASFLGSPKRVSYPAL PSLRIAPVYLSF
1290	11:146	0.995	0.824	MKVWLIFPLFLGAGMKLLSLAWGRKNSCVLSL RRSTWPGAVAQTI
1291	8:143	0.991	0.831	MLWVKIFLLSPVPFLGLLQIVNKIIVSMKFSLCC SFLNDYAPERM

1292	53:188	0.912	0.702	MCSVSAGTLPLLGELLSTVAKTNSAGCHHC QSGEGSLSTHTCIL
1293	315:450	0.939	0.614	MHLRPLASLPQCPLYSTLLFLIDSYLPFKNPLR WPQSNTFHKASK
1294	109:244	0.954	0.91	MLMLILVTGVSSLRNMIMCDYISRAKLKSSHIV LSYCTLKQEYDD
1295	67:202	0.912	0.653	MEYLLHLSFSFHNQLFTYLLPLIHWLLECTQHR ALHLVDPOGMLM
1296	179:44	0.946	0.867	MLNTFISLLWGTARWGDVKKNFLQNKAVAS PGKQGPALTLMT
1297	333:468	0.963	0.898	MMPTNLAHLVFWQALLASGRFSLMEHYPPNV QSNRGITHYMLPRG
1298	192:327	0.898	0.586	MSVIKLLSERLFLVLEPSGSLVAQSQSPAELP MWRWPSSLLTVC
1299	70:205	0.991	0.963	MVASLPFILSRLLLIWCHFGLGQQWWATYL MSVPLTSPCLSVY
1300	94:229	0.983	0.659	MFFLLCRQAHSLSVLPICLHPLCPRVPTAPVT PDLKPKMVGGAG
1301	254:389	0.953	0.641	MQAEHVNSSFVCSPKILIPFSLGSLALLSLLHT LAFGPTFNTLYF
1302	53:188	0.98	0.841	MHFLACKKAFLCLLVHRCLLFPPAQSSFMWS ERIHDSVSSMPLLT
1303	72:207	0.98	0.907	MSLCIYTLTCTVVLITFPWEMRVLLLYWLMFKF VHVCVWRAASQS
1304	18:153	0.963	0.743	MLWKRELSSTTWTWNMIHVLLFKAVAPGLPP SLAHCCCLCLFTIGT
1305	73:208	0.982	0.88	MWMIFPFVLMFISCPSSISARITDEVAIYRLCIF TLGNYKPFPGS
1306	323:188	0.933	0.679	MNVICLTCLVSSKCSVGGTASFVLLCFSLPVS SRRRAFQESQGW
1307	68:203	0.937	0.6	MLKWHCQESICLLSSAMPSSLWASLPGKSRS WWQRWLPAAPTIFL
1308	457:592	0.984	0.901	MVLLVVGNLVNWSFALFGLIYRPRDFASYMLG IFICNLLLYLAFY
1309	625:760	0.89	0.672	MDPPCPWLHPAAWPLQTPLALPLLGTGSSPM PIFRWRPPVHLLSM
1310	125:260	0.984	0.618	MLPPLCWCCVRTMTCCIGTSTGMDGRPPSP WRRIPCWTQTCSCRN
1311	258:393	0.912	0.602	MGDFAGVDFVFLVCFQAQRQGAAEAVGAVLA VLLCDTLGVTRE
1312	74:209	0.921	0.71	MVVLIRLGTCTKVVRGWCTGIVVLHRAVTKG LRIKVAMERARKK
1313	143:278	0.89	0.713	MSASVNITITIVLLPFVRSFHKYVQSGCSEPS VGSRAAQRPER
1314	52:187	0.888	0.593	MGEVPLLLCTFQNWLFTHASPVEQNRGPRT TFCHFHITEFAVNL
1315	242:377	0.964	0.863	MCLLFLPRFPVSWRAGVDGAAPSSQDLWRI RSPCGDCEGFDVHI
1316	49:184	0.981	0.945	MVPGAAGWCCLVLWLPACVAAHGFRIDYLY FQVLSPGDIRYIFT
1317	82:217	0.915	0.634	MLVLLPRSKAMPLLSVNVTLAFFPRNKEIVKYL LNQGADVTLRAK
1318	161:296	0.987	0.896	MALGFGRLLALMVMWLHTGQTDTHMLQSPA

				TPASRVASKIRLSL
1319	781:916	0.928	0.711	MLWGSCKKALTCKFKVFFLRSLRAQGGGLFE TLCDDQLDIPGTIR
1320	179:314	0.957	0.811	MEGSRNTPLWVLPISLWISLTASQAGCVGWL KVRKIELCLARI
1321	129:264	0.952	0.93	METFPLLLLSLGLVLAEESESTMKIIEEFTDEE MQYDMAKSGQE
1322	143:278	0.919	0.7	MCDVLKLPNLLSCFCLPCVFLHTGMAHGN SASNLPFVMWTHG
1323	1402:1537	0.991	0.74	MGLFFFFSGVGSFVGSGLLALVSIKAGWMSS HTDFGNINGCYLN
1324	188:323	0.979	0.861	MLILISCPCLDFFWALRLIGKIRQTDIKIYQRETV QGLAKGQIPP
1325	116:251	0.963	0.727	MLFPQLHLFKGPLPCLLRFLTGLGVPGSSPDI REDGEKNFDLDM
1326	43:178	0.944	0.73	MHVFPVPVSPLLCLPSLSLSPAQSVTPSLPLL QWAVLVSQTLKWH
1327	137:272	0.954	0.86	MFRFYLVVICHFTSVPSFPHMFLGLISLATLW QSFLHHPHQNEL
1328	147:282	0.9	0.764	MPVNPILVLFILPTMLMQKWMVKPLLLSR RISTTEPSLLRLR
1329	279:414	0.982	0.963	MFLFWFILSEGCPLEQLNISWCDQVTKDGI QALVRGCGGLKAL
1330	182:317	0.983	0.94	MTWVISSVWLLFHVXWSKMGQRRNEVKWM NECIFKFISNDALPL
1331	784:919	0.972	0.748	MQTLRGVLATLGVGAALGITCSTAQENELIPS IRYKSLCVLCH
1332	17:152	0.941	0.759	MGALDFLLISSYCPAVLLILYSSHCPILKKILNP RHVVSyenIFT
1333	233:98	0.983	0.874	MNSLLWLKLFAAWCFLKDFSLNNRAKTQTAFI QNKRKSYPELNLH
1334	32:167	0.947	0.787	MAPLYLGNYQTLFLKLISISVLAFLFRNVWSNI GCHFSSWVTMVI
1335	113:248	0.989	0.791	MAGLWFVVAACAEKCLSLPWSLRQLEVAPRS RQGRGRAGAASFLL
1336	37:172	0.988	0.937	MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAE GSGGSGVGIGDRF
1337	177:312	0.968	0.763	MLSYAHITLAVLRIPSATGCWRAFFTCASHLTV VTVFYTALLFMY
1338	891:756	0.942	0.88	MPTLGDALILYLHLVLGVAGVLQPPGPRPSQA LGPTGDRAPGKWN
1339	248:383	0.881	0.688	MFLIVLPLESMAGHLFHELGNCLGGTSVGYAI VIPTNFCSPDGQP
1340	439:304	0.929	0.778	MSAFSHLKHFLQILIEHVLGIVTMISIKTPRKQ KNKNSNSLSC
1341	298:433	0.989	0.89	MTGPRPMILHFILVASASCWEVLFCCWQPCPL GIHATSNSPSQLQ
1342	26:161	0.927	0.712	MGAGLAVVPLMGLLESIAVAKAFASQNNYRID ANQELLAIGLTNM
1343	1444:1579	0.99	0.813	MACCLPCRAFPAYPTGVWPTTWLWCWAVLPI PWPASWPWCCAGP
1344	23:158	0.957	0.677	MAEAFPPFFSPFLGWLGVFLTGSDTSSNALFSS LQATTAHQIGVSD

1345	160:295	0.936	0.837	MNKLLVAATAILFSLGCHEKCKIFFLKSISSPQS LFLADLCASEP
1346	32:167	0.959	0.782	MSQAWVPGLAPTLLFSLLAGPQKIAAKCGLILA CPKGFKCCGDSC
1347	104:239	0.95	0.634	MGGAVAAWAWVQLQCGGEGSSVSPFWAM RLMLGGRVWWALGGGR
1348	89:224	0.949	0.676	MTQLGQGWCFGSLTGPGPLLPAAATHGLFLS LSTSWLWVCAGRSA
1349	69:204	0.97	0.806	MLSSLSLHSSLTFLILLSLNTRPSEPHLQELM SRSFPYNPLSSS
1350	326:461	0.982	0.802	MQTFLGPFLCCGLISLPPWAAVNGSICCLPSS QCSPDAIRNSDGQ
1351	2740:2605	0.997	0.982	MCCWIIWFASILLRIFALMFIRDIGLKFSFFVVS PGFGIRMMLAS
1352	153:288	0.94	0.843	MVRVWSPWPCWVFAKETVLCWGRFHHLIR AVVPKWCSLDHLYKM
1353	655:790	0.954	0.653	MSQEPGRRHSLTLTASRMAPCLWWWTS QAWSMSMGSLSMQTT
1354	94:229	0.883	0.581	MHSHGVSYWTVRTVIWPISSLVSKITTWEFNE VTSMSSEHLKSCPF
1355	375:240	0.991	0.867	MLINGHNFFCSFLIFYHLCHIWQVITCFKICFLIF FLLALLFMS
1356	679:814	0.983	0.712	MEAHQSFKHKSCWAITVWFHFVCFNLTFSC FFNKLSPILESLV
1357	60:195	0.961	0.696	MWRGRAGALLRVWGFWPTGVPRRRPLSCDA ASQAGSNYPRCWNCG
1358	679:814	0.983	0.712	MEAHQSFKHKSCWAITVWFHFVCFNLTFSC FFNKLSPILESLV
1359	32:167	0.966	0.754	MPFAQTGLQLLRCLRVLHVLRLGMLREQM HLLREKLLDLLPPE
1360	53:188	0.923	0.667	MNLEHVIVSLLTFYRVLLYKEIIGLHHCFQHFHV NAFLLSPLPPS
1361	271:406	0.902	0.688	MVGFYLSVLYFYFSQLIYLGDAKSVNIVTSF ILTAAYVNNSKM
1362	637:772	0.891	0.55	MQPIVAKALVLLVHPLQDQAESGRLGHVHL LCAPAALQHALRG
1363	24:159	0.974	0.752	MWQKSLILSFRVSFPLFTYNYKLLSIRTRP LSSFFSKLLQIA
1364	119:254	0.881	0.59	MPAPTAWLLPAVSTCSNLRAGVILGTITTRP YVHTWGSADMAT
1365	203:338	0.915	0.697	MVWSYFISTPVQVPTALVGLVMVHTRPGLGD KGGSSGLEHPTCLL
1366	288:423	0.954	0.907	MALFVVLIAGVDLLQIDISSTYINSRILWILSQLY FIKLYICVK
1367	723:858	0.951	0.765	MLCSSSSLLVILLNTLKKVQSALCIREFCIHGFN QIQIENIWGQK
1368	111:246	0.947	0.848	MYQWGSSIIILWPLSMNIGCYSIYLMVMLLS SKFSWKSFSKLQ
1369	1339:1204	0.993	0.928	MLLTLCIRGCMFVWRCFFLSVGTCIYPSKFLFS FHFYIFMNLFYK
1370	16:151	0.889	0.647	MGRPWCSSGGPGLKSTMVWLMFHYLGFASIN PRPTASARAGTLLKM
1371	133:268	0.938	0.655	MTYLLHMLMITLNETYKQNTTYDAWCQHNK

				KKLFPLKGPFLSFI
1372	737:872	0.987	0.897	MCTFRGLLTGLLTFPLFSPVLYFCNKFPNKTN
				MFLLCFCKNYFLS
1373	279:414	0.985	0.692	MAVEPLLAHFLRWSWLSARDFYSLGNVDPAL
				WVPCFFLLFLLIIT
1374	263:398	0.996	0.684	MENIRIPHPNIWVSVSSAFWIIILVWPFPIFP
				FLLLSFVFYLC
1375	194:329	0.93	0.732	MLMHPVLYIYTYISCTCVYCLFYIFIHTTPRSWR
				LTSIAMSLLT
1376	186:321	0.981	0.948	MKVLWAALLVTFLAGCQAKVEQAVETEPEPE
				LRQQTEWQSGQRWE
1377	1221:1356	0.968	0.936	MNPHLGVLVLVSFFLSLLDSQLHSWIVLHNS
				PSSRMWKSIIFFL
1378	644:509	0.943	0.794	MLWALIRAAALHTEEPKKRKEEKMSPALSP
				PLPSVPISLGQNN
1379	206:71	0.971	0.925	MPCLAVICILFFAGSGSLREGVPCACQVLMIR
				VWGSQHCDYLLS
1380	859:724	0.989	0.929	MAWALLFLTLLTQGTGSWAQSALTQPASVSG
				SPGQSITISCTGTR
1381	22:157	0.953	0.843	MWWNSLMMALKCPLNSVALGVCKTQGDACS
				ERGFQIPLCLQHLPC
1382	995:860	0.985	0.892	MAWIPLFLGVLAYCTGVSASYELTQPPSVSVS
				PGKTASITCSGDK
1383	266:401	0.967	0.814	MGTYLVIYTRSLKLLVYCLYLSSANHTTLPR
				VQIKYIKYKRKY
1384	34:169	0.952	0.792	MPLLHGVYLARRSLICISFCHLCVLSIGLRVIVC
				VVGISEDKRKS
1385	181:316	0.91	0.832	MNQFQPWAPIILYICKTLIRIPALSLISCNTGYL
				TFLSLKILIY
1386	124:259	0.988	0.875	MNPSASLVCLLFAFSSCRIWSVLCQLCVPSPW
				PSPLCLCPQTDVA
1387	22:157	0.947	0.609	MWWNSSGYHMSWVAAPPLCLSSGCCISETC
				RPAITQCSPTRMEDL
1388	451:316	0.972	0.845	MAGCLAWKSPGWLAIEFTLLLLGEMGVRFPFR
				DPCPPIRQPQPNF
1389	1199:1064	0.987	0.938	MWAAVGGGFLFAPRCFLLPWPLRAPLSSSLFVL
				PRLLLWPIYPVLA
1390	1263:1128	0.9	0.82	MLVSKLMLQIVMAVPHYIMPVEMKNQSLIPLLL
				EARADPTIKNKH
1391	136:271	0.928	0.602	MNYRRSTKFPVLIMKVCVFLHPDLDPGLSHS
				GVVRTNVNGASFV
1392	617:752	0.91	0.741	MCLGLVTVAGAGGGGHRLLLLWACVSLKTFL
				SWRPLRRAALDLC
1393	1182:1317	0.984	0.843	MGAGCTPVVLGAALWLWRWFSRWGLGGLC
				WRPCTCTPCHSASPGA
1394	1351:1486	0.986	0.566	MKDHLEFPFLDLLDLSLGLLGFQGLLALLAL
				TFLVMRYVNQA
1395	229:364	0.886	0.699	MTARFLLARPAYSSALLRGLGGPRTPLIQFSR
				CGMMSIRLLGLFP
1396	923:1058	0.894	0.685	MDSTFLATRAVRGQLYLWISMLTIATGKLCAR
				CYPENQDHIIQML
1397	49:184	0.944	0.599	MMAKSVRFCYVLFVEEIRFAVLVQRLAKSDL
				WAKSGLLSIFIFI

1398	684:819	0.993	0.891	MIYFLSTPLLLTLFNILMTFFFVAPPLNLLNKTH FCFFSSYSKLD
1399	2697:2562	0.993	0.934	MLFIVTALLCCGLCNGVLIETEIVMPTPKPEL WAETNFPLAPWK
1400	122:257	0.994	0.907	MLIAVFQQFFFLFIMSFFFPRFILNISMLRDSLW WAGLFSLIYFF
1401	189:324	0.947	0.775	MKVRHNFNTLLGFSLCFLTLKIPIILSFRVRDRP LKSWQYSLSSL
1402	32:167	0.972	0.679	MGPLLCPRLPPTAARTHRHVSCSHLRDWRAL LLLSWWEWLPAGA
1403	398:263	0.989	0.899	MSSGTELLWPGAALLVLLGVAASLCVRCSRP GAKRSEKIYQQRSL
1404	248:383	0.902	0.655	METVVLKLVIVSFRQAPLSLWQVQLVLRCTLA MLGPHAQGEGLPH
1405	89:224	0.95	0.607	MLSIFLLPLSCVCHGPPFNKAFLLVFMAGPPG VASFPDSRSPSPE
1406	735:870	0.935	0.696	MVGLGGMSQLLLASLLPPVPQGSPTRRKLPA SLLVSTALISPCV
1407	968:833	0.988	0.971	MANLLLLIVPILIAMAFMLTERKILGYIQLRKGP NVVGPYGLLQ
1408	75:210	0.988	0.946	MKAWCFSNKFWLAVLPICCASAAYLGQVWLLI YAWRAETSLETEF
1409	101:236	0.991	0.96	MYGLKILSHLWVLLILSLLLFLRKSFKFYAVSFV CFAFVAFWNNL
1410	161:296	0.975	0.877	MLVHFFKVCFFLLFSIPGNHALDKRNCSSAF TNVVVRCGKRGV
1411	132:267	0.942	0.551	MAVFIHPVTLISCLNLLRHRLPPCASGNTSLIS YNATGRHSLST
1412	168:303	0.95	0.835	MSLIKYLFFSFFVSNLFFSPGVLECFVFLGIS QFHHNLLMCY
1413	85:220	0.927	0.739	MIYSLSYTISWLLITSLSFVSQVRNENTTTTHKG RPNEQVQNQHKL
1414	242:377	0.957	0.693	MKMLCGLLRTVQGVRFQQLTRIHGPSTQGHQ LLLLWVGVLQVGXS
1415	50:185	0.934	0.73	MPKELSKCFTSLILMWHIPHFLMPPHSYVCMC SCVCIHTHTNYRG
1416	110:245	0.972	0.71	MLFSLLFVNCSIFNLKFVSKALHFSSVLGRKL NTCEVGVKMSPL
1417	34:169	0.971	0.856	MTLCVLLILAPLQHVLMKTNQQAAREINLIKTKI YFIYIDIPCQL
1418	9:144	0.982	0.771	MRVCVPGLAAPCLLASCVTLTKLCWLAGREIP EAGLYGFLASFLQ
1419	64:199	0.996	0.968	MSLLILSRSWGCFWFFLRLLCSFHLYCWLLLI SLFHEVISFTAF
1420	239:374	0.966	0.821	MLLVVRMEPIKALLRGVLLLLSVTLEEGILSDC SVVSRLIFGSLV
1421	604:739	0.994	0.709	MEAPLSHLESRYLPAHFSPLVFFLLLSIMMAC CLVAFFVLQRQPR
1422	1146:1281	0.971	0.873	MRICNLISMMLLLCHWDGCLQFLVPMLODFPR NCWVSINGMVNHS
1423	2657:2792	0.984	0.944	MAHFTWAHLRVLTFLQVGLLDDVHQLLGPQ ADEDLSIFTVMP
1424	317:182	0.984	0.951	MYSVLVTLFLVSFCALSKTFLDHWFMFIYYILF

				KDSEIGFCHPLL
1425	3917:4052	0.985	0.96	MFRRLTFAQLLFATVLGIAGGVYIFQPVFEQYA KDQKELKEKMQL
1426	39:174	0.982	0.938	MLVPLNLCQSTLALVSLPLPGIGRAFCEWLS GTFKARRQGPKAK
1427	892:757	0.929	0.68	MNPYISIVFIVFLCSENYPWNNMLRITGSSPYL HFLSVLGVLVN
1428	395:530	0.982	0.917	MCSLKFWICFCQAVSMHL CATQLSVSLPAGIS MFVSGLVCDICVW
1429	94:229	0.989	0.946	MPRVRHCMFISLWVPYVWGCFGCGCCFLYTK AKSKTHPVMFVDLV
1430	284:419	0.964	0.906	MLSSFFKSCFCVSWTL SIATSSNLLIFSSAISN LLLILSSVFSI
1431	5035:4900	0.945	0.836	MILLFFTFPKLVSHDMLLNLTNEVYILVQYIMRL TCSDQVQLDYH
1432	179:44	0.881	0.627	MSFAFSLWYPFLRDLRSCFKLSKLSCHSPISF VQYTTMSTRVSCL
1433	1137:1002	0.969	0.912	MHLLCSGHKLCCLIVYISFFLFFKVYGFCFLHA NIVNYTEDTTDS
1434	111:246	0.971	0.902	MLLRTLLFHLSFKHSIVPTIFNSDSFLLSCRHF PICVHSLCLHS
1435	1283:1418	0.991	0.825	MLSMLRAVFCRRLHLVSSILFCCSRNRTL SMKEANLLLRVLI
1436	1669:1804	0.989	0.945	MMPLLSLIFSALFILGTVIVQAFSDSNDERESS PPEKEEAQECT
1437	314:449	0.966	0.877	MGKVGFGHGVFLRLLVRLSEALLHVLVARYGF LLCERHACSCLLY
1438	363:228	0.902	0.646	MVYLMSSMLLIRNLSQFSSFHYRNYWNSNIGY VSLFTNEEYISIL
1439	140:275	0.933	0.771	MHFHCTVFFGSCVNSSCLLVIFYFSLRIFFNLP GYLIVFKNYFF
1440	365:230	0.939	0.683	MAFLSTLLNHYLACKHSELWLQSSLNNLGK KKDKAYIFTVLAL
1441	1991:2126	0.891	0.8	MDEVHVLGLALLTVLIELVSPLDSLRRHSCYIT HTFSCNHTNSHF
1442	58:193	0.906	0.602	MLSCKYFFNVAEHLFLVTTGIMLCSTVPSEFSE LVWSQEGDRSGA
1443	1765:1900	0.902	0.642	MITKTPAQLRSVATILKTLCLASPTVANVKAPP QVAVAAGTPNTS
1444	420:285	0.95	0.791	MVQFIGCQTSKISLVVICLLKVVGGMCVLQQC SHISLISHRTSLK
1445	1026:891	0.94	0.569	MTFILSRPPFFFLFSKRSCSGARWSRWPQFG YSTSPPGSMFFSSP
1446	5692:5827	0.989	0.927	MSMLHWIHFILHVSIVLKFLSVKCSIIYKKSFAS SAFFLVQASFF
1447	2962:2827	0.913	0.735	MPYVTEATRVQLVPLLVAAEAAAAPAFLEAFA ANVLEPREHALLT
1448	775:910	0.993	0.949	MMYILLVFLTLWLLIEMIHLQNGDHRTRPPT ETGWLPLRFHLR
1449	413:278	0.959	0.803	MWIFLLLQRPVPPMLSHSLLSLHSHATRRLCT THARAHAAASSV
1450	193:58	0.897	0.697	MVMLTLAIRLMQFEFRQFFIKVNFMRGLSKM AMLLL CRARPYSY

1451	858:993	0.999	0.866	MDLDNAKYSLLGFALFWVVVGFFVCLFWFLV FLPWCKTVESCLF
1452	331:466	0.95	0.744	MLFTQLWTLLERHFNIFAIYIFLLKNNRNQCLS WFNNSTKLFSK
1453	1371:1236	0.982	0.891	MSPPLLLLPLLLLPLLNVEPAGATLIRIPLRQV HPGRRTLNLRL
1454	30:165	0.963	0.806	MFLYCCLLKLLYMFPKNEKFEFHVRELSPLA SQMFLTLLTDFE
1455	480:615	0.963	0.727	MALRGALQSQSGLLSLLLLGLGDKDPVVRCS ASFAVGNAAYQAGP
1456	76:211	0.964	0.633	MALFFCKIICTMKKVLTLTKFSISHSTNTRLSFL HIRLCCSRCCG
1457	278:413	0.911	0.711	MAGTAQLLGLKQLIGLELLTAQCGQITGYRDR REELLPPRFLATG
1458	252:387	0.944	0.866	MFQPRPLPPALFFMLRFAPPLWWSPGTISPW CTFASLGPSAWNAL
1459	824:689	0.94	0.624	MGICLTWKPPPTGVSILILLSELHMKSPGRLKP KSSPHFSTVLTP
1460	56:191	0.979	0.884	MVCLRLPGGSCMAVLTVTLMVLSSPLALAGD TRPRFLEYSTSECH
1461	184:319	0.908	0.701	MLASRQACCPPVSSLFLPLSPTLSGFFTVCVSV SHLHVPRGPALRC
1462	486:621	0.976	0.794	MFSPSFQGIITKVRVCVSVSLCVCVCVCVCV CVYKEPGMRAGRG
1463	170:305	0.985	0.876	MWLGWVLKPRQFIFKAFALCILLRHIALHICFLK ALCRCVKLFVK
1464	85:220	0.976	0.851	MFLGIIGYTVWAWIWHSTLSGVFKKANQIGLTW PPAKPPDSCGSGN
1465	319:454	0.971	0.834	MQGVRVSFGWAMGLAWGSCALEAFSGTLLL SAAWTLSLSPICGH
1466	399:264	0.975	0.896	MLPNSSSLWLVMRILIFCVIPAGGVLGAPTAAG LRPTGDVALRRP
1467	202:337	0.991	0.97	MGVVWSLLWFGQCSCFSLCSHMMWGGLVF PMIHHSHKVPSSDAGV
1468	262:397	0.981	0.864	MPYLILFFAVYILYKILVKVHLFIAEIALYDFLKFF ELYGICMFK
1469	105:240	0.981	0.868	MRQLVFVILSGPVCCSYHSSAGKLMQKDMW ILRVLCGLWGCCLT
1470	291:426	0.986	0.909	MWKLLFYGAILWLWRSVPGDSMVLKMRQPD GFCMSTTLEFTNSLC
1471	420:285	0.916	0.802	MRKLIAELIFLKIWTFTVRTSTDLPQTEDCSQCI HQVTEIGQKVA
1472	26:161	0.99	0.86	MSLLGFLLSRLGLLLKVLLDWPVEVLYGAAAL NGLFGGFSAFWSG
1473	129:264	0.951	0.787	MISSCLEARFHPALLMSACCQLCLCCSLHITVV TLVPPPRDDAAC
1474	10:145	0.985	0.895	MLWAPCDVTLGFWCLALPIFLLVATNSVSSDC VPKWPHPRVPSSR
1475	74:209	0.937	0.729	MKPHFLLFAPFSSLKLPVLFPRPPLFSVLKAPM CLKGAEEEGNWW
1476	526:661	0.979	0.869	MLGPPEARLSLCILLWISILCPWYRFTLYCSSW PYPIFDSGYRPL
1477	68:203	0.938	0.763	MTPLCPRPALCYHFLTSLLRFSLQAQSAAGLW

				GWHTWVRAAWLEVQ
1478	1541:1406	0.989	0.919	MPSLISIFFLNFLSFFLSFFFLETGSGSVTQAGV QWFDLGS LQPL
1479	283:418	0.969	0.858	MLQTFGIGAVTLFSFTSFSLSWPLLSTRVGC SVFLQFAKHFMQT
1480	706:841	0.934	0.628	MRCGWGPLGCLGTGAPAGWMVLGSPRSQ QRARWSRASLSAFGWE
1481	44:179	0.952	0.659	MVSRHTWLHSTVLCVHLQRCLLLRKDRRSE SRRRHRISPVGCGP
1482	568:703	0.985	0.92	MGWSCLAILSSAIGHLICLWPFAMVVALFPYLG YFSGSLSTQIGS
1483	271:406	0.91	0.6	MSAQWPWGLQSASRPLLLLLGHAAQGEPR GGSPWTPCLSLPIM
1484	203:338	0.966	0.846	MWAGYVIYTLFCRFSFSLISIRIRKLGSIGFEL LGNNSQLGCPL
1485	145:280	0.981	0.957	MAMSVRHLTIFLLSLAWASALPDSAFIKGVWE GICPSASQLASCL
1486	2187:2052	0.978	0.956	MPLPWSLALPLLSWVAGGFNAASARHHGL LASARQPGVCHYGT
1487	63:198	0.97	0.781	MIGRISFWNLFSPLCILSLFLKGTDVKMNCEKD YPEEGAKDRKLR
1488	188:323	0.95	0.792	MKKAFARLVRVLVSFNSVLLHSSLDNLLVS PFGTDLSGLLYRE
1489	20:155	0.953	0.698	MSVLFWRSASFLTCSNSPGFDHWLFPYLLY PFLPDCLNACSLF
1490	4:139	0.986	0.818	MAAWLSLYLLQLSASLPPSLGAFSGQLRTVCS LPCHSPTPRPACS
1491	74:209	0.937	0.819	MSDSLWLGVYIYLLFLEGERCFPGTSLHLLPV HMGLRQSTHLRPP
1492	438:573	0.977	0.922	MARLGNCSLTWAALIILLPGSLEECGHISVSA PIVHLGDPITAS
1493	82:217	0.976	0.909	MLLFSSRFIMFLWPPVSGVCLSFIRDRSFLPM CHFIYVLILCNSI
1494	112:247	0.995	0.906	MLMFVFPLRHLEIILCFLISVVATDVSVFSEIGL LGCLSDFSLY
1495	345:480	0.913	0.68	MASLKLVRNVFIITLSFFNGPGTVLGTLQIQISIT GRPCGRRILG
1496	14:149	0.939	0.678	MFSSQLFKFRQVLVLCVPFDAQIYGHVCAWE AQSSCLHKTDCIF
1497	180:315	0.977	0.925	MPSLTILLSLIELTCLISVLAQQVVQVKPSCRRK YGPFDLKEVC
1498	250:385	0.979	0.876	MLQFIFSTLKPILLFFNSFWLTNIEFKIQWCWL SISIWLSENC
1499	447:312	0.917	0.755	MDWNLOFSLLLWATADISDQLFQPPQKFSWD PLESALCLYSSGSA
1500	185:50	0.962	0.77	MFNKVHLITVLWLHKRMVLWKCTFVSFLLSNR LGETQDRERKRKC
1501	210:345	0.993	0.913	MGSFSFILVLFIDCLCMFPSVLVQLLCTYSSLM KTPLWLQARSSH
1502	134:269	0.95	0.594	MSEFLCFFTQRAIVTTFSLTTEGNSCATWLC VPFPGCSVLWSVL
1503	39:174	0.977	0.916	MFLFLFFLVAILPVNTEGGEIHWGTESKPHSRP YMAFIKFYDSNS

1504	958:823	0.954	0.804	MKPFTVLKGFHFSVFCLLPLITHNINLQTTWQI PSLISRAPSSFS
1505	23:158	0.898	0.641	MPPTSTRWRWVFLYHASSVYEVVGGHPSD WLWAVGHASNIYQEV
1506	19:154	0.993	0.97	MAEFFVLLLVFCLLKHFNLHFLSDWHIFCNK PHFGITFVKVAQ
1507	242:377	0.958	0.741	MSVCYTKILCSCLCSCLMWLRDEQFHNSFN DFYIFTYFCCICCL
1508	1365:1230	0.95	0.586	MQWCNLTATSAFQIEAILLPQLSPVAGITGTCY HAWLIFVFLVET
1509	56:191	0.969	0.784	MILNKALMLGALALTTVMSPCGGEDIVADHVA SYGVNLYQSYGPS
1510	407:272	0.961	0.692	MANFLHPVAFLVHPYILPFCLHLSLLHPDTYVL HLEQRYHRKPCK
1511	31:166	0.901	0.668	MPEFWPHVLLGNSTLLLSTCHLPGLHHIPRIIS DSSPRKDIVTSS
1512	828:963	0.968	0.936	MNPHLGVFLVLSFFLSLLDSQLHSHWVLHNS PSSRMWKSIIFFL
1513	970:1105	0.995	0.983	MLVLLVLRVSLAALVKMELLVRWAPVACLVE VALEPLALLVLVE
1514	34:169	0.917	0.784	MMHAPRGRAPSLVWWATEPALAALVLFERSVE LGSRNVTTPVPGKK
1515	3216:3351	0.992	0.922	MALLVPLALLVIAHLVLSVQLERVVTEEKVAL LALLVLPVLLVP
1516	614:749	0.971	0.879	MLVTRPSGNTWIPFFCWLLFCVVELLSPGNLG PSVLEVVLPDVK
1517	343:478	0.974	0.813	MWSLRARAIWMSFCLWSELGLDGSEDAEPG RNGRKRAQAKQGCE
1518	3062:2927	0.979	0.865	MMLLVSLHILFPFMPFSYGLESNNKQPCLMK LTLQNLQKQVAFE
1519	128:263	0.956	0.555	MGAADCLGVQSQSCGKWSSCLLSLLGGAT GLVGGSGWSQLSEM
1520	136:271	0.969	0.552	MDEASVLKGSSRGYLSVINLTYILTAVIIFVRLI WVFISDYTMV
1521	257:392	0.969	0.843	MNDIPVVLVRELISLLWLLFSTCVFTKDILLGHI LMLFLPWYLSA
1522	1712:1577	0.985	0.907	MASICSWRVMLOWAACWVRAHAALSGHPRS TFSLWLSGISLPXI
1523	1463:1328	0.945	0.9	MLLFVVAEMVAAIQETVATHDPLLLDEALETN SGSAVGVVHQLH
1524	614:749	0.983	0.865	MCVSVRVVCVCVCVCARVCARLCVCVHARLCV HVRVSARVSVYVCT
1525	70:205	0.991	0.915	MGWTMRLVTAALLGLMMVVTGDEEDENSPC AHEALLDEDTLFCQG
1526	3917:4052	0.985	0.96	MFRRLTFAQLLFATVLGIAGGVYIFQPVFEEYA KDQKELKEKMQL
1527	88:223	0.945	0.828	MQVSGPRPQLFLPSVFFVLLFSYFTETTQWT VVILALNSKLSFK
1528	195:330	0.975	0.916	MCCWQSVNILLMILILIPKFMSEISANLKIYDNI YKYILFFFL
1529	221:356	0.994	0.969	MTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSP TDAYLNASETTTL
1530	644:509	0.993	0.95	MLFLTILISFCGFLLLHRLTSMVRLFLGAAIQKIL

				SKRLEFSLLPL
1531	219:354	0.981	0.741	MCPALWICICYTLACFKTPTAYCVGMFQVLHL TDMKSLLRSATFL
1532	16:151	0.966	0.724	MASVVLPSSGSQCAAAAAAAPPGLRLRLLLLL FSAAALIPTGDGQ
1533	79:214	0.91	0.637	MRRSFWTVMRTAWRCS CSSVDRALSHQAGL QGQCLSACLLGNLGY
1534	21:156	0.917	0.725	MGLDIIIFCHFIFNLYFWNILKFGFMLTILDWISL FKYNMTISAF
1535	885:1020	0.966	0.767	MRAWAWPFCTSVTSLSAMASPWRRWPRRP ASRTASRAPSGISGS
1536	245:380	0.963	0.845	MARRSRHRLLLLLRLYLVALGYHKAYGFSAP KDQQVVTAVEYQE
1537	382:517	0.997	0.915	MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFI TGCDSGFGNLA
1538	1617:1752	0.996	0.98	MWFLFLCPNLWAMPVQIIMGVILLYNLLGSSAL VGAIVVLLAPI
1539	192:327	0.991	0.941	MFMHLFMFMFMHFFCNLAPSTMDFLLAGLFY KCFIIVILLRREY
1540	4324:4189	0.978	0.824	MLLLLLLEFGITIKVTCRLRIVLCYRKYKTKRKNK KLKLGNNSKF
1541	2020:2155	0.993	0.97	MGCALAGFLHYLFLACFFWMLVEAVILFLMVR NLKVVNYFSSRN
1542	875:740	0.976	0.896	MSVPTMAWMMLLLGLLAYGSGVESQTVVTQE PSLSVSPGGTVTLT
1543	171:306	0.997	0.985	MLARLFCFWLFFVFWFESPFYFNSMPPPTL LRELSPTFPCGKK
1544	595:730	0.989	0.826	MKMLTRLQVLTALFSKGFLLSLGDHNLRLREI KIEGDLVLGGLF
1545	328:463	0.951	0.851	MSHMVPLALLPLFPTSRRAALPFLPLFFGLM FPATTDLPPPHPS
1546	69:204	0.939	0.661	MCSVRPFPSPLFSQSFGLLFLHSELFYSFLHLL SPTLCKSVVCCP
1547	179:314	0.986	0.942	MMLGSCVLLCSCLSVCTANCTLEACCLVHGV PEPKGAEHWKTWV
1548	47:182	0.953	0.792	MCYHTWLIFILVEMGFYHVQGAGFKLLASSG PPASASQSAGITG
1549	431:566	0.985	0.949	MNCDVLWCVLLLVCM SLFSAVGHGLWIWRYQ EKKSIFYVPKSDGS
1550	49:184	0.934	0.826	MILSLLKFFPLLSSDTPNSSVPLTTTPRDPPYH LSPCSSSYFVKE
1551	172:307	0.94	0.794	MVRFPSCALPCTWHCPIIPLYCRCLFNCLLSL WMLWEQGPYLSSL
1552	418:553	0.994	0.923	MILFCVMVFILFITFHLQLPTVGDVTYCFC SNKL RKTRELKISS
1553	90:225	0.937	0.745	MGPLSALLSQSLLLSCTAPRERLPGGGWPGT PGMGPLRSGTSAPS
1554	103:238	0.914	0.738	MASAPKLGFVSFTSLFSFGGGLPCDFNFLVD LRVVDSAFIQPLY
1555	508:373	0.975	0.763	MFSTAFWPPFLNPSLMFFTLLCSDFMPC EAV CSSIIFYSFIVTKT
1556	564:699	0.928	0.745	MQVKNFSLKIAFCLLNMRLLGNWATWIFISCTK HLAIFKPLHPAE

1557	699:834	0.978	0.714	MCESTELNMTFHLFIVALAGAGAAVIAMVHYL MVLSANWAYVKDA
1558	118:253	0.888	0.735	MCWSLLTHGFGMLGGAHFHKHPGCSLHPLF KVRSLDEQHGSTWL
1559	109:244	0.987	0.798	MLMIWSAGRWTYAVLFHCCQTLLPWKVPLEK VWHHQDQGQVGSGLS
1560	3628:3493	0.996	0.905	MLWWTGPVLAVILILIVIAILLFKRKRTHSPSSK DEQSIGLKDS
1561	847:982	0.985	0.945	MPVIWSALSAVLLLASSYFVGALIVHADCFLMR NHTITEQPMCFQ
1562	159:294	0.905	0.613	MTPPLAAWSLILAQSGFPSVPGSPLGATGGG YRGWDSETPWDLGR
1563	775:910	0.96	0.628	MLRLGVAFHMELLCRGRLLLLIPTAETRCDHR RLQNLKLGSLNTL
1564	25:160	0.933	0.705	MALCFSAGTGLFVGRCCPVQVNLHEIVTLPGA LREGLRTAGPGVW
1565	286:421	0.906	0.632	MLNFISPFGSTILLIPSALPPSPSRCSLLSPP PTTPLPLPLPS
1566	327:462	0.963	0.87	MYLLVLFTLPFWNWGSGHQHSYKSADSLTNS VAVKERWEGMDLAV
1567	807:942	0.931	0.736	MQLHVSLPWLLRFPGLDCTLHPDQPSIQLLQG TIDLLDSVILSCS
1568	1227:1362	0.935	0.689	MLSQLPRCQSSVPALAHPTRLHYLLRLLTFL GPGAGGAEAQGM
1569	113:248	0.994	0.94	MFCFLHVFLVSLPFLTSYSCLQIISYSSFKAWF KYPFLCKIFPTL
1570	222:357	0.971	0.879	MAFLRKVYSILSLQVLLTTVTSTVFLYFESVRT FVHESPALILLF
1571	374:239	0.896	0.635	MSLIPSFPIPALSPPLTLLSCMYSLSSASCQN ALKNNFIWTVCA
1572	167:302	0.988	0.917	MKVVPSSLLSVLLAQVWLVPGLAPSPQSPETP APQNQTSRVVQAP
1573	643:508	0.933	0.776	MSFLPSFFPFSFSSFPFLSLPSSFLPSIFVRA ECVSCLFLRPGL
1574	97:232	0.989	0.925	MAFLGLFSLLVLQSMATGATFPEEAIADLSVN MYNRLRATGEDEN
1575	581:716	0.932	0.778	MLSLRRCTSMRLCLSSSLASPCSTMLSTVVLY KVCNSFVEMGSAN
1576	403:268	0.959	0.768	MFASLLQLSRLRTSWLPEVCHPEDLEIWRQG HHLVILPFLWAGS
1577	1254:1119	0.961	0.882	MAFRTFSWIFSGLLSPTLASPSVSMMTMEVLL SGILCSSRALFSI
1578	1442:1307	0.987	0.828	MVLWESPRQCSSWTLCEGFCWLLLLPVMLLI VARPVKLAAPFTSL
1579	4739:4604	0.993	0.958	MLFVFICSYFHLSLFLLFPFLPVSLPSFLPFFLP SFLEFTEVFPR
1580	1431:1566	0.996	0.852	MVLSAPSLWPCSSFSISCLHVGLTAFLFQVAF LCLCCVELLLDV
1581	2491:2626	0.989	0.953	MAGVIAGLLMFIILLGVMLTIKRRRNAYSYSYY LKLAKKQKETQ
1582	122:257	0.937	0.816	MPVLLWAPWPLGQAALMRERVPSSRLKNQT PGASGIWRDGVAGGP
1583	86:221	0.908	0.795	MTFHRHGFLLRRCLAFRCNPVFSSLPHEALD

				FVRNERKFKNSCA
1584	463:598	0.967	0.909	MAVFRSGLLVLTTPLASLAPRLASILTSAARLV NHTLYVHLQPGM
1585	156:291	0.992	0.899	MFPAGPPWPRVRVQVLWALLAVLLASWRL WAIKDFQECTWQVVL
1586	167:302	0.996	0.897	MGWVWTLCTASACLTLLFWSQTPGKAFQIPC PPPHLSHWCLSPMQ
1587	102:237	0.943	0.737	MFHRCRLKAGLMLWRSLESGLCAGAHRLWL EGPMAFFELGEKDPL
1588	224:359	0.935	0.744	MFPASREAWLALAWALGGAQLAGHSWGSWV RPAPAGGHRHLFTRY
1589	1157:1292	0.982	0.942	MSFCFTFLSLLPACIKLILQPSSKGFKFTLVSCA LSFFLFSFQVH
1590	239:374	0.998	0.965	MVFFSFFFQFFVFFFLPFLILSSFFRCFYWET AIMTVHGELFKE
1591	176:311	0.991	0.936	MLIKIVLLILVTYLLVFSCVWKNKSWLILLKVVIN KIDYADIYTF
1592	270:405	0.969	0.886	MYKNFCLFFIFALYQGLANYGLWANSNPLHVS VYKILLGCVPWLL
1593	92:227	0.972	0.902	MEFGLSWFLVAILKGVQCEVQLVESGGGLV QPGGSLRLSCAASG
1594	817:682	0.982	0.942	MSFCFTFLSLLPACIKLILQPSSKGFKFTLVSCA LSFFLFSFQVH
1595	101:236	0.99	0.903	MGPWGWKLRWTVALLAAAGTAVGDRERN EFQCQDQKCSISKWV
1596	21:156	0.882	0.676	MTDHFTFFSQCPNACLSLFLCHICSLCFGSLG HCLRKVIWLYEVL
1597	119:254	0.973	0.891	MRGNLALVGVLSLAFSLPSGHPQPAGDDA CSVQILVPGLKGD
1598	178:313	0.952	0.848	MSGAPTAGAALMLCAATAVLLSAQGGPVQSK SPRFASWDEMNVLA
1599	62:197	0.988	0.753	MSPIMLRLLTLGGCVHTSVWLSVSVHAMRLSS WVGVPFCLEYKLE
1600	2939:2804	0.954	0.823	MMTPKLMIWLLQAKSSISMLEKSSKCLGRCF SSFKNLVMIQSC
1601	99:234	0.963	0.877	MLLHNLFCITVRFMCIHIKFFLLKIGFNELSRMI ALFVASSVVS
1602	1095:1230	0.961	0.817	MSRFFIFCCLRHFSYFSDFAVLFLGALEHLKYQ LAVGHSVLSEST
1603	91:226	0.953	0.77	MTRVLLKVLVTGWQARSWGWWGGYHSEMPPP LPGWMISLCEYTESH
1604	47:182	0.979	0.885	MVCLRLPGGSCMAVLTVMVLSSPLALAGD TRPRFLEYSTGECY
1605	268:403	0.936	0.798	MMFSPLDFIWCFILEFPSISLGLALSFNLQNKFL YTLYQLISFNA
1606	2217:2082	0.985	0.844	MLTFLMLVRLSTLCPSAVLQRLDRLVEPLRAT CTTKVKANSVKQE
1607	100:235	0.905	0.724	MRRGCFFWTLRSSRALRVGAMGRDGTGEVN RNQLREVSIIRPENS
1608	235:370	0.984	0.946	MIPARFAGVLLALALILPGTLCAEGTRGRSSTA RCSLFGSDFVNT
1609	156:291	0.992	0.899	MFPAGPPWPRVRVQVLWALLAVLLASWRL WAIKDFQECTWQVVL

1610	445:310	0.957	0.819	MGKCYKCFICKLILPVQPLLRLSFLGFHLKPL HHIQPKLSNCSE
1611	1992:2127	0.984	0.843	MGAGCTPVVLGAALWLWRWFSRWGLGGLC WRPCTCTPCHSASPGA
1612	87:222	0.938	0.584	MGLHVLSCVHLMCLSPQPVEQVLPASISGHFV EAMIQPPFIGPCC
1613	274:409	0.916	0.569	MGCVLGTLSLVRMCRWNYKFKDEKICKAVRE AVGWDEDIRDSTRM
1614	972:837	0.937	0.827	MMYILFLQAFILDYYQYFLGLNCVYSYQSKKDF SQIWSQGWFWALL
1615	2578:2713	0.99	0.951	MVGFLCCFYLFQLLGPGLLCLPKAVLSFLGLL EAAHLLLVKGFL
1616	6257:6122	0.991	0.934	MALQLWALTLLGLLGAGASLRPRKLDFFRSEK ELNHLAVDEASGV
1617	29:164	0.995	0.87	MRWLWPLAVSLAVILAVGLSRVSGGAPLHLG RHRAETQEQQSRSK
1618	226:361	0.945	0.691	MRPDDINPRTGLVVALVRVFLVFGFMFTVSGM KGETLGNILLAI
1619	1123:1258	0.993	0.976	MLGNVLLCCFFVFFIFGIVGVQLWAGLLRNRCF LPENFSLPLSVD
1620	120:255	0.925	0.566	MVQPGLWEAGRAGKGAGLGSLLLLAPGHFLL CQPFSPGLDQQHC
1621	581:716	0.932	0.778	MLSLRRCTSMRLCLSSSLASPCSTMLSTVVLY KVCNSFVEMGSAN
1622	155:290	0.954	0.701	MWRVPPLLMHALWSRRTLLIKEHLIKGETVQN ANDGRALSPGHG
1623	157:292	0.987	0.748	MLIETQTYLTQGSSQAFLLLGIFSLLLSGSVMW VMSVLPGAATLC
1624	282:417	0.942	0.858	MKNPSPFLLLILIVLASWSQDDDDDDYSINNY YYYKDNDSSYDL
1625	164:299	0.905	0.561	MLLFLPMSSPFHLPGLPSFLLPCVPGLDTPA SSCLSFRESFLSE
1626	43:178	0.98	0.894	MLQAALWCGIGLYLVTLRLGVEVTPESQHFR PRRADHLRPGGRG
1627	139:274	0.993	0.964	MLIRPLGLCLCWFWGWGACVPSPGSPLRG GAYLQKGHLPTMAFP
1628	423:558	0.888	0.656	MTSYISPHLRISLRMLFPLIKLKFCFSFSTSQLCR LAIFKVTNSH
1629	3628:3493	0.996	0.905	MLWVTGPVLAVILILIVIAILLFKRKRTHSPSSK DEQSIGLKDS
1630	81:216	0.994	0.956	MFFVPILLCLLLLIYNIICFNMEHPTGAGLRCSL LAAPKERQHRH
1631	9:144	0.968	0.946	MDLSLLWVLLPLVTMAWGQYGDYGYPYQQY HDYSDDGWVNLNRQG
1632	540:675	0.887	0.705	MCAPHLLLTVLAQSYGAQEISPLGHRLOGAPK PPLCPTGLPKPAS
1633	2565:2700	0.99	0.917	MVALTIQTHWLMTVAELLSLACYIASLVFLHE FIDVYFIATLSF
1634	2373:2508	0.99	0.94	MLDLVALLYQAVLLPAILLPLCQLEMFLMLQL NRQSLKKKYLL
1635	3216:3351	0.992	0.922	MALLVPLALLVIQAHVLVSVQLERVVTEEKVAL LALLVLPVLLVP
1636	4242:4107	0.985	0.875	MLLYVFKFLGLFQFFHSFCTAYGPPGGCGDS

				GEETSLFFEQLDPA
1637	72:207	0.899	0.569	MVSIQNTQIPSLSLLSLRALPSRGEERGIL GFYIILGGFGLR
1638	229:364	0.918	0.593	MICQRTLFKFIDFCCTFEKALKPQYVLSQKLR EVLTGKMSPQYM
1639	64:199	0.991	0.794	MEWRTRVTRNQRAALRVWWQRIRLWKSUVF LLVFWHLVLLSCGHF
1640	237:372	0.958	0.74	MTSHFFGLISFFLTNTLDLHLPKRWQHLHPSL GSIEIQNEDES
1641	307:442	0.933	0.678	MASSCCFIKFNLLVTHLRAPANLPSLIFCHSFL VLCMSAKLHYSL
1642	4243:4108	0.958	0.914	MLGSICNVMLMLAASIPEICTFGPTKLAANCN WMPSRVARLPSV
1643	152:287	0.963	0.728	MLLLERMALCPVLDVHHLGCIICVFDVALSR ELALLCRKSNWW
1644	47:182	0.974	0.807	MKSGSGGGSPSTSLWGLLFLSAALSLWPTSGE ICGPGIDIRNDYQQ
1645	121:256	0.977	0.708	MGPPSACPHRECIPWQGLLLTASLLTFWNAP TTAWLFIASAPFEV
1646	3819:3684	0.995	0.983	MLVLLVLRVSLAALVKMELLVRWAPVACLRE VALEPLALLVLE
1647	336:201	0.993	0.951	MVILPLLLLITPPMTFLAFLTLILSCKNCSKLA ASMIRLLWGG
1648	4:139	0.904	0.625	MITHIVHHPWPPWAQGVVTASCSFSLPVLTTVC LQPTLFFHVLSTT
1649	6:141	0.987	0.916	MLVMAPRTVLLLLSAALALTETWAGSHSMRYF YTSVSRPGRGEPR
1650	150:285	0.949	0.75	MLFLGALAYPAVKWGC PFGECEFCQVGPDN IAVRWRS LFQTLPV
1651	196:331	0.971	0.73	MCSWVSLFLSSLIISPLIDVFRSGLANYGWQVK SGLPPVYVNKIL
1652	197:332	0.96	0.856	MYKRSSARFFLEIIFFFSLVQASTISCVDSCKT DRVSSFSWPNP
1653	180:315	0.93	0.674	MLLTCCSPAWNVPYLANIILLCD SAGHIPSPE PEQMLPSGLPWT
1654	34:169	0.994	0.856	MLLFLLSALVLLTQPLGYLEAMKTYSHRTMP SACTLVMCSSVES
1655	491:626	0.991	0.946	MGRWALDVAFLWKAVLTGLVLLYYCF SIGITF YNKWLT KSFHFP
1656	78:213	0.901	0.687	MESALPAAGFLYWVGAGTVAYLALRISYSLFT ALRVWGVGNEAGV
1657	1431:1566	0.996	0.852	MVLSAPSLWPCSSFSISCLHVGLT AFLFQVAF LCLLCVELLDV
1658	2375:2240	0.988	0.896	MTSKFILVSFILAALS LTTFSLQPDQKQVLLVS FDGFRWDYLYK
1659	52:187	0.965	0.891	MKITGGLLLLCTVVFCS SSEAASLSPKKVDC SIYKKYPVVAIPC
1660	1362:1227	0.913	0.682	MGR LSSSLAAMLIGILHMRSSFS GWKYSAKD WLMSDV DYFSFLFS
1661	540:675	0.969	0.846	MYRSWSWQQHLIGKVALFLHFCCLAVSCPFT AVSSLPLPDSSFPT
1662	347:482	0.947	0.757	MVMLTSLICISTSL LGDTAGVSFSEECHTTMEL FSIDLEIGNFLY

1663	360:225	0.93	0.851	MRGKVAMMLFGLGAIKMTTDWWQFMDLHK KRELTELALFYPLSL
1664	83:218	0.948	0.642	MYEKLFLRKYKNYPCLPLLIKILLFSPSTLTLY SFNRKRKGLDL
1665	111:246	0.914	0.679	MSACPHWGLLPLAFHISLPNAARSPLIWWETG REMEASQRICKKR
1666	199:334	0.963	0.738	MHVRIILRCVGLLSCVQLRVLPHPWGLRAFLPR HSPAAQSSSSRDF
1667	172:307	0.952	0.581	MVLDHSSFTPLWKSLFIEGLWQPSIRSIVFLL GCLITQCRPQPG
1668	95:230	0.968	0.835	MFFSTTSLVFLHQTAPFLKIILEQSKRPREV GHQGVVFQHPGA
1669	79:214	0.995	0.92	MASHFLLWGFALTLLQHLRLVGSFADFSALS LPQSTCGHFSLFW
1670	237:102	0.916	0.762	MLSVTAFILAETVLASQEVQGGVQVRVYLMNA VPDGLQGGSPVGG
1671	5:140	0.954	0.789	MNFSVPFICVSFSVLLSLFSPGNFLLIFPHLCFT RVPFLYCHLKM
1672	31:166	0.972	0.826	MGSSEFLVLGTVVLLVQSKITLALWSHHSKDP VEIMTECRHKQLY
1673	95:230	0.959	0.908	MVLWILWRPFGFSGRFLKLESHSITESKSLIPV AWTSLTQMLLEA
1674	82:217	0.907	0.611	MHFAQLIHCVQLLKFSHSLVGHLCFEGQRLCC SLLCSSWSVIHFI
1675	475:340	0.987	0.828	MTANITCQFYKLSFSSLSLSPFPFLLSFLPLL CSSMLTHPVL
1676	18:153	0.939	0.65	MTFLKTYLSNIFACTSAWAQFYHLVLLNLLFR YPTLFYTNTHRL
1677	78:213	0.911	0.724	MPLTFLHEGVFLWFSHSLTSYTEFIYVKGSQP FLFIKALKLAEPS
1678	265:400	0.967	0.919	MISLIFNLWLKITIWFDLNTYVCNNILFDLNTYE VGICFFKNVSV
1679	175:310	0.929	0.694	MLLLKHLMMSYHSLHVPRLCLHCNCVSKGK QPCVNCLDSVLSSS
1680	124:259	0.956	0.828	MFYLKSSFHLLICLHCGYVVIKSMRVILSKQ MITWDIDSIKHL
1681	12:147	0.923	0.682	MCLAHLFKLLVYFNRSNSWWQAPFVLETTTGL FSSSVSLICILNL
1682	101:236	0.948	0.693	MPLLYIICLRQLVLFHSKCHSQHSCRAGGIQYS MHVSLFLSSPIN
1683	202:337	0.994	0.948	MATIDIFLLLSLFFKCAFAVYGIFFLHIMTLKFFT YFPNPFLKMV
1684	22:157	0.96	0.912	MTAGSLRRGCGLCLLLPCVFSPPFRCIMIAFIC VRYLNSLVLCSL
1685	2133:1998	0.981	0.919	MVRPLLLNLHFHPLSLVSLSLSLLSVSLSLV NAVRLLRASFC
1686	179:314	0.975	0.897	MICTYFLLFLNCHILLISSHSVHQLFNLIKFWSSI ISLAHLAIEI
1687	217:352	0.933	0.718	MTSWIHSLTCLLSSTPLAFQGGAYGWPTGSGS KNKAVPEGGRAYDP
1688	141:276	0.979	0.698	MADRAGTESFVTFLGSQFWLVSWPLLTLYCT GTCQPFLSLKFSK
1689	299:434	0.917	0.59	MKLYGLAIRILTECIATQCMALVVDEYSMASVI

				CGWSILYMSYSP
1690	245:380	0.988	0.761	MDFLMLAVCAHRLCFLYLFIYESKNKRECEQ FRRLQIYLVRLLS
1691	987:852	0.973	0.814	MFLSLCLLSAALT KISSKILYKPGTKVTSLQFIP TSSSYTHMNCV
1692	477:612	0.981	0.952	MGLFLLFFVLVRVRSNVLKGAIQDRVGLLYQFV GATPYTGMLNAVN
1693	161:296	0.922	0.699	MKAEIVSFMFIIVSPALTQFPNCVTLVTCRCSIE PCLRILLCTIY
1694	299:434	0.98	0.879	MHIGLGSMWSLPLSCPACVCAILANFMCTHV WGNLCVFRKDILQL
1695	83:218	0.949	0.851	MNYVVLLEVSCFLSFSCFLCPYINICTSDVKVT LQPLLILSIGF
1696	104:239	0.986	0.79	MCLSVFMHLLINIWIVYLLLVFTNLCIHRDGR TLMAQQTVLLE
1697	187:322	0.959	0.614	MLCRCLFKVCGLYFDVLHLGYSYTKLRSGQH YKCFLLRVLSLRD
1698	247:382	0.958	0.905	MYFLIVLRHGFGLFHFKAWMVKRKCHLND VYVYVPISYSGHRI
1699	50:185	0.972	0.808	MWSAHLAVLSLKLTLFSLTSDWLSSKDMAIS LAFKISQILCSVL
1700	63:198	0.944	0.713	MTTSSLVLPPLFVLKQRFYPPYLYHPYSICQH VSILVKIVWTWG
1701	204:339	0.991	0.967	MYILNFSFFFLLFFLILVRRRPYDLVELSNID KDCRYKFIFRF
1702	31:166	0.883	0.59	MFFFVGDFFAFLGNILKIVYSYQDPVNKKFYLM GKGYTGAFHICN
1703	169:304	0.893	0.697	MVPSGTVLFGIKVLHCVSCMTHLTLSSASIIN AMSIFPSHLTGG
1704	94:229	0.948	0.689	MLMFVNAVATGKWWIKWFPFATLEISVCIHTG SLATWGSMDCVDS
1705	2557:2692	0.967	0.633	MFPSSLPFLLPSSLSLPTYLIFICHEVFGFANDL LDIMPHVIENK
1706	135:270	0.974	0.926	MCQNYLRLYLVFCALISLPSFLGIRVLFMLFYQ STDPLLFISKFL
1707	101:236	0.936	0.685	MHACYIFQCSRQLASFLITSFLMIYFLRHPTFT KLFLHVTDRYFY
1708	60:195	0.941	0.625	MLLCCPLVAIWETAIKNGTVSVNGTSFQSPVP RRVITPFLPTSES
1709	2971:3106	0.981	0.854	MMQLLFPLPLWGIIPFHLHCCDIVCPLSQVEG GILRLPPALVHSI
1710	944:809	0.986	0.945	MRKTRLWGLLWMLFVSELRAATKLTEEKYEL KEGQTL DVKCDYTL
1711	127:262	0.934	0.787	MRWKVQVNSLMVLPSTVCYSTHLSTGCRHI KVNQVLENIQRIL
1712	192:327	0.992	0.964	MALTYFIFAFLAVILLYFPGGWSLPVLVLQDPN NSLSLFFSPQCN
1713	39:174	0.911	0.601	MNTVSKRLMCLMRMLLTEQIINLQFQVHMEPK DHLFPVNCCHKRL
1714	218:353	0.955	0.793	MVLKLLFAFKKICTLSQYENNHIGKSLANAME IIFYVPFLFLFF
1715	484:619	0.933	0.831	MIWIYFAFIFQRLHLIPGKSSARQVSGFSLLSF NPSNTIFVKLDW

1716	220:355	0.989	0.905	MYPRWVFGVPLCIALSTCLLITLETVLLLRNC LFGFFMTNLKMF
1717	191:326	0.885	0.563	MVTRCLLLCVSHSHTVIPKDRLRAYDLQCLFL KSTNPFSDTLDFP
1718	99:234	0.902	0.671	MASRSNYLTETLTPFPALLSLFMLYLSHTGFD NIITFPTKPAYT
1719	122:257	0.915	0.742	MRFRAEPKSRPLPALCHVLIACIVFRWAFAQP LPSSRSYRSSGEF
1720	189:54	0.936	0.684	MILLMSAAIFCSAEVFTRGSSFFSDMLTLDRVKA KGLQGEAASTC
1721	16:151	0.902	0.594	MFYLKYLKRCVSKSVIFYLLIKAPEKHVEKKLS FSFLIDIFEYF
1722	160:295	0.921	0.681	MKMMFIITNWLNYFFLLFSPSNPQIQSILHEVA PLWFRTLYTLR
1723	25:160	0.992	0.87	MAQLMHLLIKTLGWVWWLMPVIPTLWEAKAG GSLEARNLKPAWAT
1724	684:549	0.982	0.735	MWLWSKQGLQGALLGPVTLWLNSPYLSLNR HKSSLNPSFKKIF
1725	126:261	0.922	0.743	MYSRIGSLGSLIYYATLIVGLAFTSHLKMFD MEYFHIIPSMVN
1726	175:310	0.981	0.87	MNIIFIYLATSLAFLIINLSQLLFTTEYLHFRCCSK CSTCINLLSH
1727	181:316	0.943	0.812	MLPLKKWILYLHLVHNNATYIMALDVSSAFH VNKNCSILRYTV
1728	83:218	0.961	0.594	MTLLGSLHCTLHTNVILLGKYDQLLEVHHSSF AILMSELLQGK
1729	216:351	0.928	0.783	MVAATLSLFFSGYAGATQIDTGLVLIELINQQG EYTKPVNKQKDN
1730	296:431	0.967	0.76	MAWGKAAITVICVLSFTVLKQSNMQSGLRSSV YPIQVLHQDCTP
1731	846:981	0.97	0.866	MLIAVIACICYLSLLHSYDILFGHFSVLSQGLDK HCLTLFLSLGG
1732	1117:1252	0.989	0.907	MPFSLQFLT VSGFVLILVWFSKGIQLKQREERII LFKSNFCPRYL
1733	81:216	0.959	0.642	MLFIFGISELFGCFRLSFSVFPEISIFLFGYLTLS MSHTTLSFSA
1734	214:349	0.943	0.732	MIFTNHLKKILLGVLVSLGYLHILYDEINIFYLINL IEASCLKEE
1735	228:363	0.968	0.825	MLVCVRDAFCFHSSLIIFLLGVQGGLVTNEH FPVTQRGLSREGI
1736	733:868	0.997	0.934	MYLSVAVILSSSPILSIFILLISCSFLCALILLFLL FNVMVSSC
1737	84:219	0.988	0.967	MQNRTGLILCALALLMGFLMVCLGAFFISWGS FDCQGSLIAAYL
1738	188:323	0.947	0.624	MMAIKPTILVTQGLILCWKCHKMICSYFNLQLE RHFLETIQSDSF
1739	17:152	0.909	0.716	MGNPTRLQLLFTHWPSLPGSYFTVLLILAVS HISLIDSVFSRAD
1740	212:347	0.963	0.786	MIVLPGTFGLYYFLYFRVLLGYTHTLTQWKYNI YGELIYNTRLPV
1741	144:279	0.901	0.606	MVLTCLVSLDNSLCVCRPPWHLWQHGMGG QSHAGTDTSKEARAI
1742	156:291	0.927	0.778	MSLYLFFCSISLTISNYNSGNTSSSSNLWNQL

				GTSLYGCRASDYN
1743	560:695	0.985	0.929	MRIWHRWLLVRILFPAPGLQTATFSVCFHVAE SELWHLLCFFFFL
1744	117:252	0.932	0.675	MAKSRRGRVCLHLLQQHVAQLLVFLLKQSSLSF RDATSSWFCSPAL
1745	75:210	0.982	0.799	MCGLHAFWLTALALGVWSARRIDSENCRRHP FSLIYREIGAQRIN
1746	331:466	0.914	0.582	MFYAFTLVFXYFHIFKKSHYLIYYKFILYKKCK QLLDSLPSRE
1747	1824:1959	0.944	0.753	MKLGDFVFKLLVSLAGEILLAPLVASGMGPA GVEALEEVSALSV
1748	97:232	0.963	0.893	MYWVTVITLIYGYAWVGFWPESIPYQNLGPL GPLTQYLMDDHHT
1749	151:286	0.896	0.648	MKGKWCCSLCQSPQVQTALVCPLSLSLGPP GPQCPLWLQGEDL
1750	172:307	0.939	0.804	MAIRQATGWSLPRAPWPFVMMVFLDPI WAPLWYPYVLVLL
1751	1275:1140	0.936	0.601	MGRKEDIFLNILFVPSLKCINILWIFYNFSFIIS QLSFVVALQH
1752	363:498	0.908	0.72	MMTVITVTIINILFCRGGNQNEGLFLSPNPK LARFPDPPSP
1753	202:337	0.958	0.755	MTLLFIYFCILLNNISRTVSYHYCSLEITFYWLH SIPSGYITIY
1754	25:160	0.966	0.605	MPAFTCCCSCRLIWIYLLPGPCTNIHDIEARL MAMARVNYKIIHL
1755	101:236	0.973	0.92	MKVSVLLLLLQILLQGLTTKPGPKGSFSPSLPT ALCLLGSIAFFG
1756	113:248	0.95	0.79	MFSSHKVLYLFLDVFIVCSFLNIRKIRHYFLLQV CREVLVGEALRV
1757	154:289	0.928	0.6	MVIINCSPRFWFLFPFTIQHTCKCPLGVRYHTR HLEQIAANKKHC
1758	172:307	0.979	0.922	MFPWKNLFFLAWCIPLSLASRSRKHYSHERD GVSRPCWLFSGGHV
1759	168:303	0.923	0.65	MNLKLNKLTSLMIRFSCAVFENELQHSVSFS QQIFFNKVQPCIA
1760	359:494	0.981	0.886	MTVCFILLACACVFISETDFFSLLCLHPVWESN FTWLTRELGGSP
1761	174:309	0.996	0.899	MLFVLCFLFHLLPVPLHFQIPAPLLLFLCLSP SPPLPCLVPFE
1762	608:473	0.959	0.854	MVSISHALFCIIFPATLCSMHYYSLFIEEMKVL ESEVIFPTRSH
1763	191:326	0.982	0.824	MKMETVVWLMMGHHCCVCLQALCTLCPTTP HPPVWRRAEKKLSLQ
1764	260:395	0.944	0.672	MSIIPLLAISAHVTLCKAQIIGRQSLDLFFIILPIQ FGFLSQSC
1765	57:192	0.967	0.935	MLQAIFLICLLVHLEGELFFKIYVGIGDSDGHSK LTVTVLGGLLF
1766	81:216	0.978	0.799	MPNRIELSALFRVPFHVWLLFAFVFFPLCYVL GFCLPSTVKTHS
1767	76:211	0.95	0.658	MDFLPGPLALLVGYQVLLTHSRASGKAVRK WLSSEHFCPRGERS
1768	57:192	0.932	0.561	MIFGCFIKMWLKFNGWHIHNKVHSAVADST WLKSHISHECLLH

1769	93:228	0.954	0.809	MPKGHILWGHILISFICFRAAGCSSGFSRGLQV GSRLSPGCWNL
1770	46:181	0.965	0.904	MLSEHSHTHLLCLLWLLQCDGRVEELQQA MTCKAENIFWPLNK
1771	16:151	0.972	0.773	MSVAVFVLLKLLCHLHLKKRGEPPVCAHVAVG TSAPCKGCLRTQS
1772	415:550	0.929	0.684	MVGILYTTYFVKCLICISKLISFNGXRSLTSTYK LCDMQLFYVAG
1773	104:239	0.913	0.844	MFIFFSYLSLPLISSQHLSGGAQYSEANAMYP QCCNVVGCQTLGW
1774	125:260	0.928	0.634	MVHVQSFAYTVLCALSSGEISGSRIINAKSVGI LRLSIPIGKLLH
1775	82:217	0.953	0.789	MREPLALCCCCLCLVFRSPVAGRNVYRSPN GTESGLGCLVQME
1776	68:203	0.975	0.778	MGGRLWIFLQLCQSLGLSTVVSSRPVACLESV PGMCMSVCMPLNY
1777	239:374	0.938	0.561	MSAAPWLGHVARPFINHLLCVLNAVPNPKH ELSACREEGAASVG
1778	26:161	0.888	0.668	MIALRXPPRIKRRHFSWALLPQCLLLNHDS PKKSLDCLLPLNH
1779	43:178	0.884	0.551	MLIPIPVHIFPLSSLLGDGTMRLLPDISSDWLCL NQEFAPVQSAI
1780	674:539	0.91	0.645	MDASTWRGPLKWQLFIFNAVFLNLQAKEAHS HHRDWRTPKCKKLG
1781	1182:1047	0.971	0.79	MMVWNLFPFCFPPLLLQFIDCQQSSEIEQGFT RSLLGHPIFFCPD
1782	159:294	0.897	0.673	MNRASSKTKVTWGCLAGLFSMFTAFESFLL STTLQPQPLPPQT
1783	117:252	0.99	0.894	MFIRFFLYITLERMLIPLLILLAHTFSCRHSTIYP YNFIYVQLRG
1784	103:238	0.914	0.738	MASAPKLGFSVFTSLFSFGGCLPCDFNFLVD LRVVDASAFIQPLY
1785	19:154	0.979	0.956	MMSIWPFFYVFLFLGVSFARIEGWPSDIHPTGL CGHQEQSWSQNPR
1786	581:446	0.96	0.829	MLPLISSIKLKLLYYFSVWGWGFFFFFETEFRS CCPGWSAMVRSQ
1787	80:215	0.9	0.554	MSLLFLGFKQYSLQAALVKPSICSACGEGRGA LKWRKVEFSHVKS
1788	94:229	0.948	0.689	MLMFVNAVATGKWWIKWFPFATLEISVCIHTG SLATWGSMDCVDS
1789	56:191	0.951	0.701	MVTLLIAKQFWIFTVDLHLSDYVLELSRYLINAC FYSPCSQPIEK
1790	376:511	0.949	0.843	MKKGRLTAYLLFLFAFPCSHQPDLSLIRTPHE CHQLEPINMPC
1791	710:575	0.903	0.72	MERHGFFLDVCLILGLIPLSIKYSLQKRGKNSA ADNAGWSDLSLG
1792	30:165	0.991	0.938	MFACLFHLKLYFSWILYFPVVLHMIQMSQKCP FLFFTTLGSMF
1793	78:213	0.886	0.606	MGSRVEAIRLFLHSAHPGLGTAVLLFRVTLQT AVGLAGGDSKQTP
1794	141:6	0.943	0.886	MPEIGPTLILLPILLGLTGFTPPDHKLDLSLE KFLITNAWADA
1795	171:306	0.963	0.845	MWHLVNSWICFHC SVLGWEVLGSPWEENSI

				LATLAKECHFVKIT
1796	6:141	0.987	0.882	MWTVGLFALLSCLHAAGIQAFQAHPVLQ QGGGPVLFPLRTH
1797	167:302	0.953	0.829	MVLHILAYKYSVLFRCIPIYLIFLNPKANFVIVIL YAFSYRGLF
1798	168:303	0.939	0.733	MPCVSAFCYCSTLFLVSESVPIIFCHVTTTTKF HGLKQQCGQAWV
1799	139:274	0.939	0.733	MPCVSAFCYCSTLFLVSESVPIIFCHVTTTTKF HGLKQQCGQAWV
1800	230:365	0.888	0.723	MICFCLPVC PKTHLAHPMLATLAFVSLLEYAKH CLRDFILVSFLL
1801	1779:1644	0.942	0.716	MKIAFGNLWMEILYLKPPWTLLHLLQCFFKKHW LAVFGLVMEKNLL
1802	172:307	0.893	0.766	MFVYLLIYLNICDGRQFTLTSYSITLCKVYFQ EIINRNKFIQT
1803	41:176	0.939	0.691	MLLCPQLMNVCCYLMVGNKLVGSAVSTAIRV QFYIILINIMIKLT
1804	839:704	0.906	0.633	MNRCELRACTLMWLKILSTSYKMVSSGGIFQL ASISTDDTVHRLT
1805	691:556	0.974	0.74	MVVSILNXLVIVFYRCFMLFISNYFSKMGLHTS SDFQRNSLMNLS
1806	279:414	0.957	0.797	MYALCLALLFCRKTLDLIEKRKTLNWAELVA PTRALLHSDTVH
1807	141:6	0.972	0.814	MAFVASISFLLTARTLTLVQGSNIFNRNYSQPP RDGQVTQSEFHR
1808	342:477	0.948	0.866	MKGILFFFFWKGVYFSPSLKPRGEIWWNCPQP WGEGGPIGGKIKN
1809	175:310	0.906	0.725	MYMNTCLYLHVYVLTCSGCNVDMCSRLFLST KLKAHVQIVLYWVF
1810	43:178	0.924	0.641	MLWTTTTPSLITPEVRTSLLCLLWVSPHPPLTS QQVLIPSRLLFS
1811	323:458	0.96	0.879	MLVHMLFPLPGISFLPSLLRNSSLKSKQFSHY CPQRAFFDLCQA
1812	187:52	0.96	0.787	MPCLLYLVILIEVFTLEKLLHIYTRSHIHKDAQG SIVRHCKKAET
1813	27:162	0.944	0.633	MWFWLTTPRHQMTLTTLHPKIRTLPRCHKIKKT PDSIYLSVSWGKT
1814	37:172	0.962	0.78	MLSSWILAIHFLAGTKMPFRAVFPDHAHQG DFTAVLRVMVFRV
1815	225:360	0.956	0.859	MSTSATLFIATLTCDTATQASIPNTCRDLPCH GVFAHVETHRF
1816	509:644	0.952	0.831	MYSLVFLTYYWIFITIHFTDEEIEAWQCAITYLG ARGNSDLLSP
1817	195:330	0.932	0.79	MFLLETLKILLKPPLEAIPPCTVSLGFKTSLP PLPNELLMGIF
1818	109:244	0.891	0.621	MVILDVLELYHMWFLGILYDAIFYCFVHAINAD KFFGLKLTKSAT
1819	1803:1938	0.972	0.64	MYWLEYILLFHILKISTLFRIFYFNLEPRLLCQ MYFHNAIKYK
1820	168:303	0.937	0.838	MEHCRVYLSIFCITVSLGAIVMFLMPPKIIKVNQ DMRRVQNEIQT
1821	297:162	0.982	0.774	MFLFSLMLFRVILQLQGVGGFLLGLFNFMQ VMLRSPSTPPPQI

1822	527:392	0.945	0.765	MVGLGKGVPLPLSCLALGDTGLMLIQNPGR TVVTAWPSRREEA
1823	393:528	0.975	0.901	MKTARVIFQIMLCVTTILSLRLNLMVIFQHLSS MKIKKDFKVAL
1824	24:159	0.968	0.785	MTLGFDCLSVCLLCLVQNASPTDFGVLCRSM GTSLHPSTLHPFI
1825	45:180	0.98	0.954	MPVRLIYNVLSVLLCVFLVALGITEDTCNLSLF AGIHVLPLHVK
1826	955:1090	0.892	0.676	MLGIIPSLRRALLQVHGSLSIGRRPGDTGEA RERGQVAPPDSL
1827	60:195	0.992	0.953	MAWACIYSCALALLWESLLIDTHLSPRINFLP MTLAPTAFTG
1828	322:457	0.992	0.743	MFCFPAVCVVCLSMCELLLADRTTGFRGLIQ RQAACSSCAEFXH
1829	178:43	0.933	0.725	MLHHSQILIFVFLVQTGFHHVALSGFKLLASN LPTLDPKVLGLQV
1830	66:201	0.978	0.931	MTVFLILVIFDTAVISFLLQEIAFLLPPAFFAGVK KQNIFCFMHF
1831	33:168	0.977	0.813	MISCAGLGLVLLQSVFIRTFHFHNEAFCKTYA WKLSHFLLLRFS
1832	31:166	0.946	0.674	MLKCTRVSAPALLCGLTQIEAPLQCCLCPEAS QVALSISGTLLPG
1833	85:220	0.966	0.756	MELLSPCHASCALSRTLFLVLLSNIALRVVCLM CVSLPHQRVGSW
1834	234:369	0.969	0.808	MSTALLRSLWGLFLTGEIPTSLGLQAPSFFGF SRSHVPVMPNCF
1835	151:16	0.947	0.864	MHKAKIYKNLFIFLVCISCILTFLYVEIYSEAPPE TKVFASC SHY
1836	148:283	0.961	0.714	MALNILFFLCGEFLVDYITEGINVPDKFSGKLS FILIGVSTQKN
1837	86:221	0.944	0.639	MLVERGLWLGFWYCWRSHRLDKCSSRRRFA RGGSEMSLGPTEFAV
1838	250:385	0.974	0.849	MPKGFVFTYLRKHFAAYFLFTLLMLLLNWR MSAKRHESACAGV
1839	232:367	0.927	0.869	MQPSRLSVSFIFFGLIYILASYRKVIVMEMVLVH RMAHEFCPVEV
1840	94:229	0.989	0.892	MVSDCLAWVKCLSLCLCLSLTCTHARTHMP CTFSVEDFKVFGGC
1841	396:261	0.905	0.63	MYMPIYSLKILSQILSGLTMTACKEMKVSTSP KKKSGAQRGQEI
1842	68:203	0.983	0.584	MKWQVSGFEISPGLVWSKWQISLKKKWCSLILI LCLLTPPTLHFC
1843	44:179	0.928	0.656	MVWSPSQIGSTWFSSALKGLVAWSCLPRAVT APGWTLYTMPHLL
1844	176:311	0.973	0.753	MASWTSPWWVLIGMVMHSPLPQTAEKSP GAYFLPEFALSPQGS
1845	24:159	0.984	0.838	MVINLFRLYISFGVFFKINYIFYVKVSKSFMYP SASFLWLFAL
1846	525:660	0.985	0.854	MGLSKAFLITRTVFLISSLSFYSLGFPSPCLFTG SCMLSTLFIRA
1847	43:178	0.949	0.665	MPFQFPKKARLVPLLGLCLEYSQTLRAPAW MSVSRGPPHSTWIK
1848	5632:5767	0.989	0.903	MSLFLFLMFQVLSEVSWGGVGSVSNQGLEH

				HEIVTPDLQSLAGG
1849	271:406	0.897	0.567	MTPVLFSPLPVISLRHSMPCNPVAIPSGWGLA GCSGGPPKQSLSI
1850	178:313	0.884	0.588	MRARPACTATFPSFHLALDSSYLPCKKGKATF IPKSRIYLQEAKG
1851	201:336	0.932	0.74	MPGLLNWITGAALPLTASDVTSCVSGYALGLT ASLTYGNLEAQPF
1852	276:141	0.918	0.652	MGAHQRLMKIIMLNRYRLVAHFLVFAQKKANR QRTVRHRSGLWLS
1853	64:199	0.926	0.796	MSFLLFWPGSGTASPERPALDSVAKELIKQ RQKPPKFLTFC
1854	323:188	0.97	0.95	MCVQLPQNISLLLLLFFASFSFHLNRKRLKK KSHLTKSCAIRI
1855	66:201	0.931	0.644	MCVLSVAKMVLLFQGWKDALPEYSHAKCIAV GAWVMVPSVHIWQG
1856	167:302	0.993	0.972	MHFSCFLQYLYLLLLSFLGCSQYLLVAYVMD LLRRLPWVIFCSY
1857	56:191	0.992	0.895	MYDFLLLSFIFIVASYWSFLSTIFLDVVCILHC PVKPQTLLKS
1858	217:352	0.946	0.65	MPSTLLALLHCGTSLLRIFKNCLIENTNVFVEM TVTIAEVFYLS
1859	1040:905	0.947	0.685	MGCGSLRFLVKSALCFYICSLPCNPYHVHLF CGFGLLFNCTQVI
1860	8:143	0.98	0.904	MPVPALCLLWALAMVTRPASAAPMGPELAQ HEELTLLFHGTLQL
1861	288:423	0.926	0.865	MEKRLFLFVCLTNSAATTKYLHGKIIINLNAVS LHIQILNVPY
1862	104:239	0.956	0.857	MLGSFIPLFWTLGSQEALFYQHSFVAVNVSH QPDDFSNCKQLY
1863	75:210	0.945	0.682	MFLHRYSLCSVFFMGVRQLTTKKNYLRHFHT QIAAEIRSLPFNV
1864	177:312	0.979	0.945	MFYVEGQFSFLILLIFGFIALRKCWSYFYFLN LLKFSLCLSFH
1865	249:384	0.993	0.944	MKRFLWPILQWLTIKFAIFVLFASSHILEIMKWV HSFYVNKSSAE
1866	303:438	0.984	0.895	MAFQFLISTLLQCLQIGVLHSAMICSPRYRVF LLKLFWLALASV
1867	54:189	0.956	0.71	MPTTPVAYNSLGAVIGIAVLGSLVALVALFIG YRHWQKGKEHHH
1868	376:511	0.94	0.799	MARPSAFPIGVCLTLPMAWISPGLAVPSCPQY ILQAQGCILDMKT
1869	735:870	0.935	0.696	MVGLGGMSQLLLASLLPPVPQGSPTRRKLPA SLLVSTALISPCV
1870	233:368	0.931	0.62	MLVYILWNMYFNVCIVPGVIKSKTGTQDLSGL WPLGTFPLITFLP
1871	137:272	0.889	0.718	MRRWHGFIFLQVSEAWLDRRAWLLRAASVCC DIYCMSRSLWKTPQ
1872	12:147	0.991	0.963	MILFQLPSNVFVLLMFLFLFEFFLTLPVPMWAF GDKTFVSPASSL
1873	15:150	0.975	0.963	MRLVARLLLLIFLGSGQRLGSWETTGSKGWS RMQRVLVARAPGCA
1874	205:340	0.947	0.674	MPPSHPHSSTFYPLILVIDLLSSSFCLLSSSLSL SFLPSLLYPAL

1875	800:935	0.936	0.829	MGMAVLVEKSVVLVIWLG PVAQAGSNWFAVS SLQEY LKQGDSSSL
1876	5:140	0.932	0.842	MKVWDYMIIFIFLLYIKINTLNIFKNPSC TTKNHL LHQILEHSLH
1877	269:404	0.935	0.71	MCFMFILGCMRASVGCKSVYEGEEAE GREEM NIRLGTPGVSLLEC
1878	129:264	0.909	0.68	MRNIPLAKIFFSFLT FYNLNSWPKALLELKET F FGSLIENDIKT
1879	248:383	0.975	0.917	MYLFLHHYYTLFIIVAVVSMPWLESSPWKVSTL WKYHFKTDFNFG
1880	113:248	0.995	0.938	MAHLFASLFLAILGFVLYFLVFWYHDSSIHCHH NSSASSLLYLSA
1881	273:408	0.914	0.725	MRWSIMRKLADLIATTLIPVAATSRASC FALFT ADSVIILIGALL
1882	105:240	0.949	0.64	MVGQVFLQLCVFDYLC LGGRYCEIYFVGCHV FLKCTNLELC SKMQ
1883	241:376	0.963	0.707	MGMIIIVIMECILIGMIIIVTKTYHNKPLYSFQESF GSLVFFGGA
1884	549:684	0.89	0.559	MTGNLCFFSIKGYLLTSEILMIYLTLEFCILRGK HLNVSFKAGDT
1885	451:586	0.934	0.701	MSRCRGLSVLCLGLGVHFQSEDLYIYLIR TLL LSLHIFMNFHSM
1886	128:263	0.955	0.862	MYVLSSAHLCLFLCLQCSSLLEVYLISSLTSFRSV LNCYPPERSSLT
1887	26:161	0.919	0.691	MSRWGYGAGQLVAWVWILEGIRGGEISESPA YRWRLRP RDQLISF
1888	158:293	0.919	0.79	MNKILFMLFLFIDVFHTQGNRFRNTSLCPRHLP SHSLWLKTKKL G
1889	318:183	0.993	0.92	MLSLIFFEICVFLACVFLPLVETWISKQFTFNFTI KNNNCSNACK
1890	595:730	0.925	0.556	MCFVCVFRNFFIVPITEKFHVIGIEKPEVSSLLP RELQSALGTLF
1891	11266:11131	0.984	0.912	MIKLAIWSIIIGLRLTILFCIETRES DICKILQYTES TIFWRFFP
1892	36:171	0.884	0.665	MWLPGLGPHSTVQLIQCVQPRLLL VFYVCLIC KTYDTLMCSNGSL
1893	125:260	0.923	0.624	MRYYLIFTGLAKFTLITPTLGEMRRNRSF SLLLI VNWYNCFRKNL
1894	110:245	0.945	0.636	MQSLVCFENGLGVFDVLGCPGFLFCLMATMW LVSISLYTEVPFGS
1895	175:310	0.924	0.625	MPLACTGLNTQRFSYLRDLFLPWGLC ILYSILS AIFPDLSSSAKL
1896	193:328	0.932	0.729	MAAAAWIALYWVSPAEG LQQVTAYWLLMFI QGPRALYSAGDECC
1897	221:356	0.891	0.714	MFEIHRAHGVFLLLSIQLTTSLKRKSGEGDRES PASWFSPFSQMF
1898	493:358	0.985	0.899	MLLRALTAMCVIALVANVTSLTLQRPQPLSCLL REYKKGKGRSL
1899	744:879	0.985	0.953	MLSIFIFLRFPLPGFCWKELHPEAEQSEKVDF RKPWYLTGHAASL
1900	87:222	0.933	0.861	MHSNIQIPFLWLTSQAFIILNSTEWGKRVLTY NRSLSLLNPFL
1901	173:308	0.988	0.93	MTCSFLYFSVFIFLKLTS DISLFLVDVYHLPK

				RTDGQFHSPHS
1902	134:269	0.953	0.644	MVKFIGPRVRRGLESPLCHACYLALCTLALVR LCALSRSRSLSLM
1903	230:365	0.937	0.791	MPWNGKSTRLWPLNLCWTFDPYVWAVVGA RWIFTDGGTRGRKCK
1904	318:453	0.989	0.708	MAEKLEAVDAYWPLQFCHFCLVCFSFVLFLL TLLITSQSSPSV
1905	109:244	0.991	0.937	MKPYCMYPFLSGLLSLLFWVESLMLLCVQM VLFLMLCVLDYRIY
1906	191:326	0.98	0.896	MPNLFTLPPSLLTWLLYCPFHYLCVLDCLDT LLEGGCFSLQLCA
1907	271:406	0.979	0.868	MFSCFHVYLLSCFATPLYSSLDCLLLVLQDAG VSFPGKHFLKSGD
1908	50:185	0.994	0.956	MGEFCIILYFLFACFLLSMHCLKILKIDWFCYYF KRMKGRLSNYC
1909	545:680	0.961	0.781	MFSVLMLHLVVLQKIYRQPLYVVFIPNCKYIY FEVCLVRVREC N
1910	165:300	0.983	0.865	MCYFYNTIILTQGSMLFLLFSVVTLYLFSSH PTPISIFSDVFN
1911	211:346	0.992	0.863	MLTQPLLLSLLLYCACRLVLLPVSLKTQPEVG WLCVHNFNFTCGA
1912	324:189	0.991	0.929	MVLPVVLALTYLNNWSLSFLTCKMEMTLCAEC LQYLSQGKCSIKK
1913	117:252	0.93	0.663	MYTVSLLLCLFFKKSDPDGPFQNNLFHNHGT QSQSCMGSKVGDV
1914	403:538	0.998	0.987	MFLSLSLTLCLCFSEFFCLYLSLALYLGSEFFCLP FHVSFVLCFLPS
1915	214:349	0.982	0.846	MPHCGLKECGWLVAALGVALSPLCCCACPS WQRDAVTQEWWLPGY
1916	119:254	0.988	0.931	MLGATALCWGLAGTFFTWGMTAAGAALGSY SLWTEADLKMEVLSL
1917	7:142	0.989	0.918	MAAAPGLLVWLLVLRPWRVPGQLDPSTGRR FSEHKLCADDECSM
1918	240:375	0.948	0.702	MWSVIPPNNTFSKFLLLIHFQFGTMASSAVC TLCYPGFVPFYLL
1919	1485:1620	0.955	0.585	MAIRFYIPTRNVEVISNFCFLRIVGWAQWLTAI LALLEAEAGGS
1920	92:227	0.953	0.869	MPPRACVLNVSLWLLWAEIPGHTGWITTPW AKVKTDNIWTRKAT
1921	77:212	0.994	0.917	MAATLQFLVCLVVTICLLSGVTTTQPHAGQPM DSTSVGGGLQEPE
1922	244:379	0.889	0.701	MTLFILGLASHGCRYFSSGAGKYVQHTNRIE KKIEDFLLVFFSK
1923	323:188	0.998	0.884	MKRAYRFFLFLFIFLFWGLVLRVLITITLPSSTN TFHNVNFDKCP
1924	81:216	0.975	0.874	MPGYVPLLLLLLLLRCSQRGGGVNFGEKDAK VPGTWRDGVVRPGE
1925	225:90	0.977	0.818	MVVGIVRVFVRVFGCVLSLQHPSSQPLKII RLFFSLRIFIKIS
1926	239:374	0.994	0.916	MLWALQHFLFMAVPDLFAVCLYLALCLTIETVS VVNYLAVCESSFE
1927	264:399	0.958	0.879	MKAGFLICRWTGFLIGQAIFPSCRFGRFLNMAI CGYVLITAHLYI

1928	288:423	0.992	0.871	MQSPFLINMKTVMFFILNPFIFACVFLIVLVL LRHFMFLTLK
1929	174:309	0.9	0.591	MGLAESSLGPLSLKVPIICLLYFVFFNKSRLFIV GSKWVHFICGF
1930	226:361	0.959	0.634	MKLVCRCFVGWCLNSWRLSPFPCINRSKDLH CTDYVLLPQCNEFVR
1931	174:309	0.971	0.939	MINLVPLFLLLYLVYPNHLVSRSPCTIYISKRHI ACIWLYVFLFR
1932	193:328	0.988	0.903	MMCFTIWEAYFFIFS FYL FLL RYDFLLTQTLN RKNFHSLRDEG
1933	148:283	0.893	0.572	MFIDLFWVVVTQMYTITKRYPKPIKTEYVKYLC LLYASCTSMGKK
1934	125:260	0.952	0.699	MPLPSAFCWVLVGEAGIGDFVGACGLNQLPH PHLLLLAAMLFMSP
1935	101:236	0.984	0.965	MMVVLVFLVSIYNALITFLNNVLFSTNTLLEFLT KLRGYKINSFL
1936	229:94	0.917	0.63	MMPCSLSPPALCTHCFFLSFCKNSYLSCKSQL RCSFLQKDFLVS
1937	207:342	0.943	0.723	MKFLMLSPYRHLFCITQAILSEIAEGIRNDPFK FYLYSVLALFL
1938	46:181	0.904	0.719	MVCFLLYHFNITSTFIISNTHREKSVDFLQFQTS DHLTFLSTFAF
1939	99:234	0.975	0.901	MICMHFLLFVSIFSFKIISQITNVPTNRKAKYYAL VVL TGNFRIH
1940	58:193	0.934	0.776	MCEVISIVLVIQTILNLTISKDLWPFFAELIGKG TINMQYVTH
1941	172:307	0.949	0.866	MILAITLLPQAALTLP RRPFLHCSTVIPVVVLT KFTMHLFKLKD
1942	81:216	0.963	0.79	MHQHILVPLPMKVAEIVFSFVCTAVCVTGLYLV FIFSEQCQMCIF
1943	116:251	0.945	0.734	MFKIFLHISLPVPCHPFSNLAFFAFVGRVPLGL TNYLLFLFKIS
1944	383:518	0.881	0.644	MNLFFFDLSLMDLLISLTLFGTRDSLFFGGGGLP HTHWDFFSPPPL
1945	48:183	0.964	0.807	MMNNFVILNGQLAILPLRLYFSLFFLLFQAEVI DVSYGMADDLK
1946	185:320	0.924	0.763	MGEAPSKLILYIMLISLVIWFPSHQEIRKDGLLM TAGWSRGKVTT
1947	656:791	0.983	0.932	MLFVPVTLCMIVVATIKSVRFYTEKNGQLIYT PFTEDTPSVGQR
1948	32:167	0.913	0.696	MILSLYYKLFGLAVATIEILHCLCYIEFVIIFKGF KKIPICFFS
1949	206:341	0.994	0.975	MFCLDLVVLFLFFLFIFYLGVGFLRVFKNSDLV LELFSGIVAALT
1950	70:205	0.953	0.685	MRATLAASLFSWVLKYQNGGLLWEDTLESME ELFHITQDSGDPTT
1951	299:434	0.931	0.85	MISFLFIFVGSSEALFVFNISYRIHDLTGINGVY IVTWSLSDCF
1952	515:650	0.983	0.639	MCIRAYMFSRLRIRTHSLVSFGLESYYMGIFFLS FFLFFFLKKRGL
1953	114:249	0.953	0.805	MMGIRCPGPAWCLSWMLCRWGRPCWLRAG AQARAVGWLSLHKLH
1954	66:201	0.991	0.876	MNNYFLACFLVSFCAHLLFSSLSAFLWEFGIS

				CFRNRHCLNPSA
1955	154:289	0.955	0.834	MCQLLSLASFITLKVCFFPRFDSLRRNNVETFREE YYEWWLGLLFQP
1956	238:373	0.937	0.762	MNHPGSFLPFTLLVLASVIFPPRTKSTSLPILG PQPFCEPFLIA
1957	381:246	0.992	0.922	MCLPLQLSSLFLCVCWAGAVEAAGRSGQGTG RGIQQIWDHNLAML
1958	132:267	0.948	0.718	MGVPSLFFLVLCQIYDHLFWRVACPALVKDPQ KKVWDQSSGTFCE
1959	97:232	0.979	0.799	MHFLIFILKAVLGKGCSSLFGVGLRAWPSELIF QKSSSLCGSCWKA
1960	243:378	0.951	0.878	MKARRYTWLFFHCCNLVASCITSGKILNFIPSL SPKIRILHRTKK
1961	159:294	0.931	0.609	MGPSAWFIFFKAMIKPVICLEHDNMQNPCVLR TVFMSSFWFSVQQ
1962	554:689	0.984	0.866	MGIGCWRNPLVLLMALACQASWGLSKGGRVL PNLCPKKMFXTLFF
1963	702:567	0.943	0.788	MCLRTMVMLVVKTPVTSSRLGGHRGSRPAA WRVGTMLPLEAACF
1964	184:319	0.912	0.785	MTSIKDLKIVLLVLTQVATTIPLHLPLPYFHFPP PWSPGKVESS
1965	233:368	0.971	0.925	MRQIAVFQRFMFPLLPWLSCIFSSSQNSIYYV STFIKCLALKSI
1966	318:453	0.954	0.859	MSGQAIQSTWLPVSVLLFAFKSTSYIITALTK KHSLKARKVRVR
1967	376:511	0.966	0.607	MIDLFAHTLLVSWKRAKQKTVMRATLWALT RNAILLFSKIAALF
1968	108:243	0.94	0.818	MVLEVTMMLMTGLLGMELVASGATDGPTGM RATNRNFDISIWNRI
1969	176:311	0.926	0.682	MNWKVRRELYLLLLIANNNLQASATCCHSSL PAKYKSTHALLTC
1970	91:226	0.963	0.909	MPLRLAFFMFWLPGMKTTPLSEIFLDSLFVSYL RQCKLNSSSVLL
1971	273:408	0.888	0.788	MNRSTAFIHFIILIKTLSSLGGLETDFWSSPSS PSVAFGIPFAG
1972	310:175	0.935	0.592	MFAKMYQVTGCVLLCMTPETTGDYCPCLLS RPCSGAGRAGTQRN
1973	184:319	0.926	0.655	MLTPGLLKVFCRYFYLMVQVFSRSQCTFKN CNNSILRSYPKSGT
1974	183:318	0.976	0.881	MFHNYLYVLCLESCLCLASLHVPDLGLRMAN GRRSHCVSKLGH
1975	163:28	0.972	0.842	MVNSVLVFLGIWVIGFLVAEKINAFHLIVDSKR MYMRCYFFVAV
1976	348:483	0.953	0.84	MEPLCPLLLVGFSPLARALRGNETTADSNET TTTSGPPDPGASQ
1977	74:209	0.894	0.652	MVLKRACLNLRAAAFFWKKQDSAYFSLGYPY GLCCNYSALLFSCE
1978	2:137	0.909	0.576	MEIVHKFWLTFTIINYILKACSMSSCFFFFKN MAASVCSYSFSM
1979	200:335	0.991	0.701	MNLMRKLRRGVSRILLNDCLDGSLLKLLLLLS FLCCRSVIVVLL
1980	137:272	0.904	0.634	MSVCKYTVYGGFFFAFFYFTKDNIPYKVSLOA FCGFQNISWNKY

1981	26:161	0.983	0.956	MLLLITSLSLPLTLGHSLTQWFQFLNKPCLV TLYMCSFIYVNT
1982	3:138	0.951	0.717	MSYLTITSKLCLTFYQIIFTLSDVTFLRTYSYPYI TEKPEPHGS
1983	531:396	0.998	0.973	MNGRLSASFVFLIFCLLMGFVCSGVLVFLCFN SLDLHFHLIKAYF
1984	275:410	0.985	0.898	MIAFVCILYLMSCLTTHRLNIMIFLNSPFRFS WHQKTCNFLIH
1985	218:353	0.965	0.828	MNQYGF AFLSLLVTNLTWHIITKGIPSIQKHR WIQMSDRGFNLF
1986	603:468	0.907	0.701	MTVKVNLIIKILITPLLEMSLPIMIGIYSVLQVP GTDKHFTYV
1987	276:411	0.991	0.88	MSEFQHLWLWMWWSGRCCCLKWLDSCTPKID LSLTCIICVMEIDN
1988	91:226	0.982	0.932	MCLATLMFRSPIYLILLSAFSLALDSKFLICQFW IECRKLHIKNL
1989	237:372	0.943	0.824	MLLLMLFRNFESFSVRLLCLGDHTPVSR LPC PGDHTPVSHLPC
1990	5:140	0.977	0.926	MGITSRFLCSGFVCLFLNPTVAACGMNGGH PVEPTFIEFQGPPH
1991	43:178	0.983	0.861	MWWELGWCLLLSISPSPGSVGAHWGEHPSL GTEDSPPWPGIMFLA
1992	165:300	0.959	0.816	MCVCWWGAVTEQLLCWWEGMPWAKGFLCI PLSRARWGGLSMGRAV
1993	587:722	0.994	0.972	MWDLFLCLPFFKLLLLTPVGAMCPVLWGS LG CRGNLGXKERPSSG
1994	110:245	0.972	0.886	MYLPRLQQLFSLPFTAWVGSCLVGYSYNIPG RFRYCELEIKLHQ
1995	99:234	0.93	0.839	MLLDCVFSSLIFPITVLSPFHFCFVTWNVSRSR SHCPCLHQTAP
1996	195:330	0.918	0.641	MYIFQFCVSLYIYLFYIFMGQNVAKLPTEYIKL LNLDKILNYQM
1997	169:304	0.978	0.931	MIMAYGLYLLSFWR LAVHLNNCLQLLTHLPCS SIRKSLEDELP
1998	358:493	0.973	0.788	MYVCMHVCIARGMCVLAFL LQIKAEQNVVVFV WYCLNKYQYLLVF
1999	186:321	0.965	0.729	MESWVVS LQLISFCLFRIGLIVQDHSDPMFSSY AYKSHYLLNESN
2000	99:234	0.952	0.862	MVYF SHFEYLFIFLFSLSWPITSKALSICASFPL HCGFPLGYWNF
2001	127:262	0.941	0.704	MTRKTCLFIQQISAEYLLWVLLCARPCPKCWE DMSDQQT KILDLS
2002	75:210	0.889	0.629	MCFFPSTSLGSELGPFVCLA AHMAFFRSEI TCWKNL NITLGQE
2003	210:345	0.938	0.683	MCLELVAAIGFFVSLTKNEAVDLP GTKRVEKL RGGLSPVHPGRGG
2004	179:314	0.974	0.908	MFVAQMLCFVKLFPIKTLTKLLTLFNFCGERPF KIYRTGLPRLKP
2005	88:223	0.972	0.766	MIFNKAADTLGDVWILLATLKVLSLLWLLYYVA STTRQPHAVLYQ
2006	251:386	0.946	0.628	MATLRKITYTTLPAYTLSFSISLVIPYNTHNYL MIICILVNFC
2007	526:391	0.891	0.652	MALLISTCINKAVLRFTLSSMNNKIILSWYSFNV

				ILIFHENVVYY
2008	266:401	0.96	0.884	MFSPCGPASLGLLFLVLC THSQALAFFWGPSSL IGASGFLLQRTSL
2009	140:275	0.963	0.907	MRVTPSLSKQLLIFLPLHLLFGVCYTLLSGDKV EKTTVETPMFDS
2010	210:345	0.972	0.818	MQKYMKVLSICCYGHFLELILFLIISGCFWSS VFITMIDNICII
2011	507:642	0.963	0.783	MLPYVHTQVYLVVIALVLWSMMNFPRAHMQ QLHALESRDHSEL
2012	155:290	0.891	0.721	MLLVCVLQTVLNAAEEARWREGKTREVEDRVH SPIPVNEKKLLTRS
2013	64:199	0.983	0.926	MKTGSLLLTLWFSQTF SFNLFFAPPHSLLQSSI FFSVSSITVHP
2014	123:258	0.902	0.623	MKWWLVWANADVLEQSLGCTLYSLLEGGFF RRLFREAFPGEKLIL
2015	125:260	0.946	0.751	MSFGCLTLLFTSRFCIPGGDKMVTLTMMMANI CSFIHNSYVSGTS
2016	99:234	0.984	0.882	MFVLFLLVLRNHFLVTIKYGVGCGFIISVCLRA KHFNFDEAQFV
2017	13:148	0.969	0.826	MTHLCGVTLCSFWTWIIFRGSMLLECTAMWEH WPTDLVRSSPTAMR
2018	84:219	0.988	0.967	MQNRTGLILCALALLMGFLMVCLGAFFISWGSI FDCQGSLIAAYL
2019	1275:1140	0.936	0.601	MGRKEDIFLNILFVPSLKCINILWFYFNFSFIIS QLSFWVALQH
2020	459:324	0.93	0.688	MQKVLHGLYLFNFLACYLDKNLFR TKLLALYH QSGSVRTPLGESL
2021	136:271	0.973	0.799	MRSPSVRHHSISLFLRLPESLLLAIAAILGFILYS MTIGKLHISL
2022	1245:1110	0.943	0.606	MCLLKAAPFFFFYVPQVGKGNPRPPRGCSAF HPPTHLRPGSCSVA
2023	245:380	0.974	0.799	MCDVIYHDLVAFVMSFFLCFLLLGAPPTGPLW QSGCDTSIVSISC
2024	26:161	0.896	0.771	MWAAAGGLWRSRAGLRALFRSRDAALFPGC ERGLHCSAVSCKNWL
2025	47:182	0.949	0.633	MPCGGLCCTIPALQTLRVVCLPRRVYIDNSQ KPGVQGASIW RPV
2026	153:288	0.953	0.866	MKQAFSLPIWLPPAWSMLLSPCPHPSSSPCL PXGSVFMHALESR
2027	217:82	0.967	0.633	MFPSSLPFLPSSLSLPTYLIFICHEVFGFANDL LDIMPHVIENK
2028	243:378	0.891	0.729	MNLAVLSFPQFLPCFSSIFSDFVNYSISFHRIPI LLKLSRICYFQ
2029	191:326	0.889	0.625	MKLQVFAVNITALKAA RLELFLPGGFIVFLAS ELKLQTSLESVA
2030	183:318	0.915	0.679	MPCILLFPELPTSSFLCLPTWIESSSRTESAITL CSLSLQCPAHH
2031	262:397	0.951	0.723	MSLRLRFFKKIYLLHSWDVLTNHLNTQWGKTV RNFYLLLFKSLWV
2032	82:217	0.953	0.699	MIFLLGISFIKFFLPEIYKVHTSKYYYYISLSLRGY PSLDALSLHI
2033	39:174	0.922	0.565	MPRRTRGGLWLCNAHKSCQKYLSSKLSTLL SPLLVLPFYTPSLK

2034	96:231	0.943	0.843	MNSCRNLILNCFLLCFSLGMNIKNDYQKDWC QIIFWPIKSILLST
2035	155:290	0.937	0.77	MFTHWLGPPVYIKQFIVMIVSILTLFPVLQGM LNFLYLNMIFVV
2036	1275:1140	0.936	0.601	MGRKEDIFLNILFVPSLKCINILWFYFNFSFIIS QLSFVVALQH
2037	231:366	0.994	0.952	MHCSFISAFLLPVFLSLTVSASIFVSLHSFPLSL SYFSFLGSFFL
2038	235:370	0.896	0.623	MILFKLCFPNRKFCAFYCGFSRAPDHHNPFLD FLLAISGMGFDST
2039	424:559	0.985	0.82	MLGFLFACFHLCAVDLAHCSQIPFPALLFVTY DNAILELCTML
2040	814:949	0.96	0.809	MSLMSYLLWRMTVLFVNVHNQDLGLRRGPSP KEFEVSQCVGRWEP
2041	275:410	0.939	0.676	MLAYIILCKKFPPLICVXEMYPLRRSSLRHLE SFTKNSISEFL
2042	42:177	0.968	0.899	MLFTVFLFSSSSFTQSPLKPHLLQDDCLSGA MIAAGSRVQRWED
2043	3206:3341	0.969	0.834	MMGRIFAALSILKLMYSLFPVIESSLCHLEWV AWRHIWPTAGRG
2044	87:222	0.986	0.946	MKPTFFAITLSLILLGLFLSMPAQSLSSRQTLLF ACGSAEVLVSC
2045	165:30	0.919	0.735	MKNLSAFLALGLVMKTITSYQIRVAKRFDFTW SCLLSLVHVKEG
2046	296:431	0.913	0.74	MLPVLTGGWPLTSPGHLCVLLNFFNSPNSYF HFLPLSYHFWSHF
2047	169:304	0.896	0.601	MGRKRSFFFLFLECRQKGLHIPLCTCSHAPRP PLAAPSALILPE
2048	295:430	0.966	0.818	MWDHFILSRVLFCLFVFHSRVLKDHHMASNAYK SALFFTURYLET
2049	533:668	0.901	0.624	MCSCSLHTLQRRFLHFVSIALSKIWQNNAFHLQ VEVSWLSTFVDKV
2050	163:298	0.997	0.916	MPFPFLWLVLWLLCFLAYPPGSDCCEGRP CWILCLTPPLGTL
2051	403:538	0.997	0.982	MFLSLSLTLCLCFSSFFCLYLSLSLYLRSFFCLP FHVSVFLCLFPS
2052	9:144	0.939	0.671	MTSHRGLTSHLSDCCCRFSAPLLLALFTLPIL QSEGDEPCTSLT
2053	160:295	0.949	0.801	MLHWGFFSVALPLSCDFHGYHVGGSERKSPE KKRSLQMPEPVNLR
2054	173:308	0.945	0.679	MDFLSRLMLLRMCKCVTATYQYIRRSFLNLV PLLQTLSILTAHS
2055	173:308	0.965	0.833	MLHTPQTCRPGLCVLASRPVLYTLCLLIPVLC GDTFWASWSLLTK
2056	270:405	0.887	0.708	MRSKIMIHIFLLASFRFKEHVQNNLPRDLLTG EQFIQLRRELA
2057	295:430	0.929	0.81	MLWQVLRDCLPICILSFPFYRLSTFQQVRQVC VCVWGCVGYYLHM
2058	248:383	0.943	0.624	MACETFIVIMIVKSIFWEICIKANWDISIYLICILL RIAVQLNAI
2059	538:673	0.943	0.665	MLWYGLLGYLRPLCKQLWPDWIPGRGQQT ECSVGSASSDLQDHP
2060	79:214	0.974	0.903	MVFNLVLSKILISFLGVSFKSIHWPRVIIGHGV

				SQSVQLPEIPR
2061	954:819	0.943	0.606	MCLLKAAPFFFFVYPQVGKGNPRPPRGCSAF HPPTHLRPGSCSVA
2062	238:373	0.94	0.77	MTTLPSFLLCRLLHIPSTFPNVTWFSLTSLLD HTRMWPFASKAPI
2063	81:216	0.897	0.556	MSYTTILGYICTRVLHHTLLLHVVKLCDYHRTC VYIRNDDMSLH
2064	127:262	0.921	0.636	MCYEWVITTVGSWALLCQRTLWKPHRTYQKL TLNSCPTPIVEGGL
2065	248:383	0.996	0.968	MWVWVTAHLLCSLAASFVKKKSLGKLRVDV CRSPPEGSRTQTS
2066	39:174	0.911	0.657	MLGKFPFLLCSCGAHWLKEPQRDLSRRYVSI NTMISIGIIDVGGL
2067	82:217	0.995	0.977	MLHSWTWAWRQVLLLTVICELPLWTAPSSC LHELAPRPQGRANS
2068	318:453	0.998	0.958	MLPSFLFVLFLLSTFILFFSFLFSPFLSPSPTT SLYFFFIYSRL
2069	88:223	0.952	0.819	MVWYIILIKAILSRLFCNRLRIGSQSGLFQGIFE DWRSVGGSGEG
2070	204:339	0.963	0.689	MFALQKMRLCVLWRVLEEGGITRFGDSHSDS LLFSVTFRIHRDMF
2071	374:509	0.95	0.9	MRHPSPWPFLFFCFVPATLRSFSPGLVWPGC WWEPRASPSSLAPG
2072	219:354	0.934	0.797	MVSPGSEFYLPFRFFLFLPSFTLIGISSVCPHQ LTYRTQSLSSYF
2073	59:194	0.989	0.929	MGASGLCLMPVLLLLWLSLYPRCKTMSSLLFP LLSSRRKVSLSWS
2074	965:830	0.941	0.673	MQEPLTFLQLLRWQLFPLPDSPTFSFILVGLC RMLFAGRIISGL
2075	412:547	0.968	0.932	MFSRLFAVFLILYKLLGKYRGIRFKIVITCVWRY VLGGRYILCSF
2076	304:169	0.966	0.837	MLRLDIINSLVTTVFMLIVSVLALIPETTTTLTVGG GVFALVTAVC
2077	68:203	0.92	0.659	MRRALVNVLTVTSGTCNFLYRPYISDIRKAGP REKYILGYFRAT
2078	416:551	0.937	0.83	MLTLLLLLHKRIFRGNFHILHFHICIQIKKQIPIL ENDLFKMYT
2079	245:380	0.973	0.892	MMLTWVFMTVHLTDRFICHLVRVTCWDGSTT CVPLTLGCLKSGQS
2080	215:350	0.928	0.669	MLFKLQTSPPHYRGAQFILPYFIFLCSTYSLLIY NFLTCCIYCFC
2081	316:451	0.948	0.583	MVCRLPCTLLPWPLKHKQGALLYICPASLPAF NPRNLSVYLLFSA
2082	20:155	0.964	0.715	MLSFVPLLSSWLGTWITDRGAAGSCQAEAPR LAGETAGQRVWERG
2083	171:306	0.909	0.691	MMLCHLELQLPALLMRKMIPTKPGVVNSRQY HKTPSKMHYIQGNE
2084	271:406	0.945	0.891	MGNLGFILLLLEEILALSTMDSVITRLCDLELWA IRPSPTFGEGM
2085	47:182	0.944	0.747	MKAVWAFILQTGTNSSMLFVLPVQPCWEGLG ELPTRRDSCCFGKL
2086	241:376	0.915	0.616	MAMSLRAFSSPCLVPASPRPPHNPLVSGRA GNLLHAAVQPLVS

2087	30:165	0.909	0.657	MVFLSVCHFYGMIKDGAPMRHPPSRRGP GCLAVIVRALWFTE
2088	388:253	0.941	0.616	MINTNILRAGAVRVLLWLQLPYPQKDHDFVRI SCCKDQRATFVT
2089	95:230	0.907	0.67	MRTPSCLIGFPCPYFASSLISYFILLIRLPKWP QIIFPKPQSAH
2090	31:166	0.888	0.649	MIICQLLTGVHVSVCARPAPGLGAHIRCDYFS TASSTQHQPPCQ
2091	235:370	0.896	0.656	MLIFICACCFPADSHWINRVQDKSILEQPFSK CSPWTSVGPRDH
2092	22:157	0.939	0.725	MYPRVRPRVRPRVRLFILFGLFTRGKFFPVRR DKNLKISLNDQVM
2093	259:394	0.904	0.819	MLLVCFVFKIVNSTIHRCECSAKSSYQLCLTV KQVTPDSIDKDL
2094	61:196	0.962	0.66	MFPLLLFYPEHSPPLSIWCNLLIYFLSLSCLPLQ LDFQLYRNRDF
2095	69:204	0.944	0.664	MFLCSSTRISVSLHALCYLLMENVPQLPCLIWA SVQAQCRCHFTH
2096	69:204	0.927	0.704	MTRSKCIGDCKLIITGWVALCMILFSSISYFKFL QCTGIFYSGKI
2097	40:175	0.963	0.894	MCYKHLLPICGLSFLFLCGAFQGTQVLHCTVY VNFMFSLHHYSF
2098	47:182	0.963	0.815	MKMLRLLSLGVFYLCCEIRASVEKIFYISSLR AVRSQGSIEYLK
2099	76:211	0.964	0.633	MALFFCKIICTMKKVLLLTKFSISHSTNTRL SFL HIRLCCSRCCG
2100	204:339	0.964	0.772	MRLHLGFSHFLLWFCDWRL EMTLSIEYLL LGD LPECNDGVNLCQD
2101	25:160	0.98	0.91	MFVYMYILYVCM SVCMYIYLQFSQTSYHSLEL CSHVNHNSNSTR
2102	258:393	0.952	0.741	MPRLFSPLILLHTLSLKS HETFQWSQFLYQNT RDACFTWTYIFPR
2103	86:221	0.907	0.653	MPVLT LVRPGLVLR SAGRRGAQLTRKLN CDEI HTQQAPSQM SWNH
2104	1710:1575	0.946	0.64	MGLLNKYASVIYLYFSLVKSESLFHLMYLPSLF IQFFLGIFSLK
2105	538:673	0.9	0.68	MPVCVLQLN NCLGAYCVISSFFTNTFLL NAVI NFLYLGYLGFSE
2106	206:341	0.926	0.721	MPVPLARICWVSFLHQAPCWELCY YCVLTS ALIGAVNSSILQMT
2107	305:440	0.942	0.799	MEITKSWFVFLWL IKFLENRDTYVSFFADLKKI VREIRCVIISS
2108	187:322	0.973	0.942	MHVLFTLYLVPCCLH FEFIGDLAVKNGTKHSA EVL SRVPKHKKA
2109	663:528	0.955	0.698	MFRNEFSLTFYCFLWGR LAFVVIIDRTQSSSR RVSGSQGRRPAQG
2110	265:400	0.964	0.918	MFSLVII RFLFGVVISDFFRGKKIGNFNVLNEFT FDFTISFHLVP
2111	194:329	0.975	0.901	MWL VVLLSHTFVSHLAEGDSATWVAHFTSG SQLCGVFPLLACTL
2112	187:322	0.993	0.957	MLAAFFLLSLKIPFLLKKLPVLM LSHVGGVKRA FIVGFTCQPFFL
2113	502:637	0.887	0.567	MSLFYPRIPSRSLWC VCPVSLAPPIRIPSRSLW

				CVCPVSEFHTD
2114	271:136	0.883	0.62	MTAQHHSIAVLLLNLEVTCECMEYNKVFYSGS
				FASTSFLIGYCSS
2115	91:226	0.983	0.808	MVSALLCCAVLLYILYMKWRVHRVGTCLKGFSE
				PREAFSKAKARTG
2116	147:282	0.907	0.74	MSLLLGRIIWQHIPCTVSGVYCCLTLVTDWEL
				WLAGTAQHHTKIL
2117	241:376	0.927	0.663	MKSLYRRMSLMLLRKSSFQTTYWVVPFSF
				LYSGCVYVCAHHVH
2118	166:301	0.884	0.583	MKCLLCGRYSGSTFYSLSHLILMTALSLSPNP
				PPSHFTAEEVKVQ
2119	140:275	0.884	0.746	MLAHLSEFERSLILHLIFSGIAVSIKALTKTWMP
				EMGSSPVYKAF
2120	40:175	0.943	0.578	MVMGWHWPQGLGLSLSLCPSDLDGWVSREV
				PLDRPQALPPCVQI
2121	112:247	0.985	0.829	MFYLFLLYFGSFNCYVFTFTDFIIFYSTEQTS
				NKFLISDILIS
2122	62:197	0.934	0.832	MTFCMYFTFFSCLNARHIVYPTLVCSQLYVIGP
				LPFTYLLLVSCP
2123	217:352	0.955	0.786	MTSRPHFFRYLCSLPPLLFPLLXQSQQLPGSP
				LPIALQSRVGSLL
2124	23:158	0.982	0.897	MVVARLRILLFVPLSSMRSLFFINGCVFTGANT
				HLDFELPSYSLH
2125	148:283	0.974	0.883	MLLFLIVITVIYIKHPEFWTACFTCIILFNYQQFIL
				HMNKLSFRK
2126	100:235	0.885	0.675	MALLHICVGHPLLSFPKAGDFSFSQDDPSEL
				TAGAKDKEFSCLL
2127	147:282	0.943	0.671	MQVLLLAYKNLIYLFVFRDNTEPLFLYSVFLKF
				KQSVERHFSSSM
2128	151:286	0.897	0.586	MIFHFTQNKTQVLT KILLPYTTLLPVNAVTSCLT
				AIHLAYHSCSW
2129	323:188	0.996	0.952	MLFFLSLMPFFFLSRSLSLSLSTSLFYSPSSFS
				SSFSSFSFSYPS
2130	10:145	0.926	0.693	MVFDERFLFLTFHFISFYIGCTYTVYMNFAQK
				ILCSCEEKVTL
2131	33:168	0.985	0.9	MLWVIVTVAGRSLGFQAVLAHVSGGSVTQV
				GQSPGLHVACVGY
2132	357:492	0.97	0.922	MITSLPAYLFTLPSCLTPLYLLSGFFCLREASLI
				FTLSLRARLSC
2133	65:200	0.948	0.759	MHGNEFIKHAFCLFASWFGVLWFCCQTQDPN
				RIRILWGKDEAVEE
2134	340:475	0.991	0.916	MWGFSFLLCHWRRAIPLLMRHTGIIHCSRTE
				HARYLLGSSRPMN
2135	131:266	0.989	0.913	MLAWIWWPLCCKMILGTIDQISLSNHYSLPFVT
				CSHCFSCECLL
2136	129:264	0.916	0.719	MYVLDWVAMCAFLFQTGAFGSILRAFVYRYI
				SDILEITKLLGHN
2137	111:246	0.93	0.729	MFRSNPGFFFFCCCKSCILAI SLGEIPRNEFTE
				NMSLRESEDLKP
2138	212:77	0.93	0.702	MLCRVVMISIKCLAVPGMCKHSIPIICLAPWLG
				DLRNTTKLQSTR
2139	31:166	0.951	0.671	MLKTKWSIVDFAVVLPICPIVLLLLHFYEMN
				KYQIECNFFGTK

2140	213:348	0.882	0.706	MEAWKALIGLFLRSSASPFTYHCWEPAQPA HQEFHSTIALRGRG
2141	393:258	0.983	0.749	MFFKTSLCFCLFHCWYLECNLTVLTHGLVINS VLPFRDINIHFLL
2142	262:397	0.966	0.762	MNGNRRWQLEAAWGPVRAVQFVCAFFLVLI GFCAADRQKAGMWL
2143	92:227	0.937	0.624	MCRLYSCARMPFSTVLFNSVYINDFLLQKPE NTTSQPLSNQRVV
2144	148:283	0.973	0.919	MWLTCSRILIFVLQSMACHLVEIYEVYEENLAL HRSVVGKGRSH
2145	143:278	0.913	0.569	MGIQWTCEWPSSSLSPGWKFIACLWFSMWGS RPPLSQAMSHKQWPM
2146	35:170	0.986	0.832	MFAIFSVYFTYASTPFCLLLLLARVWKDLEFRA LSVLFFSWLESH
2147	491:356	0.97	0.65	MYTLFQPYCLSLHPNVSHFFSCLKPLLMLLCH LPRCLLLSLHQST
2148	396:531	0.917	0.782	MLDYQLLSLMLLPVSVTSNFPSTPLTYFLKVT GNLIGIKQKDFL
2149	126:261	0.979	0.758	MSLRIRAARNWARDVQKLWTIVLLVLILIRSA VNLLINSRTEDK
2150	91:226	0.987	0.83	MLLPLRTWCLLEVLAVLGGPVQAKAIHLLAAL QPRPADTMHVLHF
2151	269:404	0.952	0.668	MRVLIILCGERMAIQELLRVSCIATHFSAILSG WVIVFLLIVEN
2152	229:364	0.918	0.82	MGNTDILLLLSLFCFSYELVAGKTKAQFGVPFA EFSVFLILENT
2153	823:958	0.921	0.657	MGPKRGLFFFIFFLDTEPSVLGGGGGGQYGL TRTHLWRQGASYLT
2154	60:195	0.911	0.59	MHSSCCRHQPRVLCCLYSWLMSLRQSRRG GTGPFPHQPLLQATR
2155	1098:963	0.977	0.903	MRWIAFAVMIVLALIRIGHGQGEHPPPLADFS GVRNLFVGVVYSF
2156	955:1090	0.892	0.676	MLGIIPSLRRALLQVHGSLSIGRRPGDTGEA RERGVAPPDSL
2157	146:281	0.959	0.786	MGFLCEIGAIPTMVLALWGLRASSASPPSLN RLPGQGSASFQI
2158	497:632	0.993	0.958	MISWVLLFSLCLSVNYLLAFEPTYVAFYYGNN NIEAMYVFTYPC
2159	61:196	0.996	0.97	MAILFIWLFLNYSISFSLFFSATKLTFFSLPKIIF FTLPILVSK
2160	308:443	0.925	0.654	MLKASLKQDRLLWKLWKLAVTFCQRGFICFLA QSVQTTGSSVFT
2161	216:351	0.956	0.791	MSLNPEFLWLKWFSLLLGRNRNSCLIALKGYH SVMIFHLPLIPSS
2162	106:241	0.889	0.6	MPCFMPNPGAVLGLPPWLLSTQRLTHTRAYL NWLASDRWMRRHWR
2163	107:242	0.989	0.93	MICYFHVLF TAKLLKRCFLLSLPLPLFLEST PSCFCPHQSTE
2164	104:239	0.91	0.816	MLCNLALKLLNCVSAWNMNIIRLKCLLKPKNV KVCSRGLYFIYVM
2165	51:186	0.909	0.666	MVTSGRKPHLLPALACLTFAHFPSAQSLAGRS LPLEFDELKCDFE
2166	207:342	0.967	0.664	MTLLGLAVCQRLCPLGIIRVPAACAMGNRVWL

				APVHRQNRAYHLQ
2167	125:260	0.922	0.806	MFMYVYTYKLAVAMKLNQLLLKSTKYFLSYN
2168	179:314	0.93	0.593	FCPPKNQLLFLNS
2169	110:245	0.945	0.636	MOTWALSLSHSTLIYFPYCACVKGQNFSTAS
2170	129:264	0.998	0.977	MFGQGPWARRPWWW
2171	77:212	0.959	0.65	MQSLVCFENGLGVFDVLGCPGFLFCLMATMW
2172	78:213	0.92	0.72	LVSISLYTEVPFGS
2173	112:247	0.986	0.91	MVCWWWVFAVVLFCFVCLRGPHGSCDMYCK
2174	456:591	0.939	0.721	NKSVLLTMLLTNIQT
2175	456:591	0.956	0.714	MFLIIGEKVRLLLLSFLPTPTRRQEVD RDQIELE
2176	179:314	0.964	0.82	EDSICGLPNKF
2177	186:321	0.961	0.873	MFDCVRLVLTFLNFPLANKPLNTAATLILLPSY
2178	441:576	0.926	0.821	MHRCKSRQFALY
2179	199:334	0.946	0.756	MWVLIPDCTFTFPLLLVLVLCVPCEQGP GTCV
2180	195:330	0.988	0.651	FKRFSASRVVLHP
2181	140:275	0.933	0.771	MCDLLLTLTGTSPLSLGLLPPLSHEKVGLHHL
2182	363:498	0.908	0.72	SKYSLPISLLFRD
2183	228:363	0.972	0.808	MGKKFKICLSLCPLLLSAPSLLEKCGKVLTTLF
2184	123:258	0.991	0.959	VLP GAYWCFSKQ
2185	273:138	0.919	0.774	MWYAILHLKQIFISYLLCISP KQLPSTVIPKDCI
2186	13:148	0.902	0.709	LIRPPNQSHI
2187	44:179	0.977	0.851	MCSGLSTYCYFLCSLSLILPISQCPLACGPQVA
2188	125:260	0.934	0.744	WSLGRGILTQLG
2189	41:176	0.951	0.775	MCALLIFSVTIVNIKNKLPTTVVLINDLRASWFG
2190	546:681	0.944	0.744	QTVYPNFYIPS
2191	134:269	0.907	0.631	MKPLFLLWQFNLLKLPCRGHVYRPLGSHSTL
2192	130:265	0.912	0.796	QLLAYDGT H VSTA
				MCVALRQEHTWLCYKRC SKWGMFSLIFMHR
				AMFLFLFFAIYLYKS
				MHFHCTVFFGSCVNSSCLLVIFYFSLRIIFNLP
				GYLIVFKNYFF
				MMTVITVTIINIILFCRGGNQNQEGLFLSPNPK
				LARFPDPPSMP
				MRVILLWYIEYFFALDPVLVCIYSHVLIVTIFSEY
				YFSGEKILLQ
				MVLWLVLISVIEWLMTCHSTTEMLSFGNLLQL
				EGLAVPHLFLGL
				MLLLSSSLKCGTCQWQVQPAVAGSLEG GEE
				ESMVSALLISALPF
				MLNSISLTNWINIFWCYSMVVFMVSKCVSYTL
				CSIFHLGGV TYQM
				MYYSLQLTIILVDVFWRVLFICLNLKEHLTMFMI
				ETVFLVQINI
				MHQNFLSPRLWVFLMSFSSF EKIQUIEFIPSVAS
				KMNSPAIRLNQL
				MLRARTVGALVGASLTSGLCVLSADSCISSLL
				PPPLIEKEWPCAL
				MKDPSEPLPVFLSPA VLTFLPFLMLRLHLVSGL
				SQLPSDHSACSA
				MISVLHGRFCVFGVGLSHSSPALSFTCCHNLC
				QPPWPAFP SCLCS
				MFLHTRFSQAATLYVFITPFKYDRNSV VFLTN
				GAVYLNIAFSRQ

2193	182:47	0.972	0.948	MVVPILVVVLVTLCIAEPQTHLILTKGSKSGDK DDAELKQRVFLK
2194	60:195	0.958	0.844	MERGAGAKLLPLLLLLRATGFTCAQADGRNG YTAVIEVTSGGPWG
2195	49:184	0.918	0.849	MTQVERVIVFLTSTLSLAKTTQPIFMSYEGQ EVNITCSHNNIV
2196	158:293	0.96	0.931	MAVAFVLSLGVAAALYKFRVADQRKKAYADFY RNYDVMKDFEEMRK
2197	47:182	0.996	0.953	MTKLAQWLWGLAILGSTWVALTTGALGLELPL SCQEV LWLPAYL
2198	469:604	0.998	0.985	MLFAFISLLVMLPTWWIVSSWLWGVILFVYLV IRALRLWRTAKL
2199	301:436	0.902	0.571	MSVGLAGAVGRRCHLALAVLHDP LCHHGSLA TICKQPEVCLFTIV
2200	124:259	0.909	0.589	MQVWLLTLERLRVLPKPRSEDFDFPISHTHR RHPNPRISHVRLP
2201	165:300	0.945	0.746	MPFLLNQCGSLLYLTLASTDLTAVPICNSLAI IFTLIVGKALG
2202	154:289	0.97	0.807	MRLSSPWGSLVSCLAIAAFISQILKDPSTEVG HGLCVGSLSAGC
2203	157:292	0.969	0.856	MRWMVLYFQLVFLPMDECYFCQGFNINSIPCF SPYHINGEKHCLS
2204	126:261	0.989	0.752	MGESARPGRVSSCECPALLWASLLCFFALGF LPTFLNLGHPWDSL
2205	74:209	0.954	0.848	MAFFEVLAPLLDCVFSSMFSSTFYELVTFSTP QFKGMNVFYVLC
2206	127:262	0.94	0.669	MPIHHILLAIEILPCFVTLLKSVIIKVVSKRDTSAT SKMLSTRNH
2207	59:194	0.943	0.803	MWK FVN FVRISLCMVVKSCREKKIHRVISLEVT KEKEGYLAPKRL
2208	12:147	0.974	0.752	MAVLVLGCVFSRRLLLHSFSSAGDLGGCILED CEEPQLLPSSSDQ
2209	115:250	0.988	0.841	MVGILKIIWYLLRTALFIWKHFCSGGWAGFPEV PLYRVLRPMQLP
2210	110:245	0.951	0.612	MRLVFFPFTGVTWRSFCSPTYGSPVQFHSY FPIGAHFPCWHEHF
2211	66:201	0.942	0.619	MIRVCAQCLPVSIFFLHTNVLVNPRLPPPGTES FDSNTLIKIYRD
2212	89:224	0.924	0.772	MSRSGIRRPLILVLSALFEASSANHLMSLGLTR QSQQSPVHIFNF
2213	25:160	0.934	0.659	MYRRLIKGFILFMLIARENKFDSTLKIYRQFFFC VLWKKTSKKKF
2214	980:845	0.947	0.697	MLWRLIIILCEALQRKSRL LADCDHFSFPNRYE RKLLLDFTVRIW
2215	49:184	0.983	0.969	MRVFCVGLLLFSVTWAAPT FQPQTEKTKQSC VEEQRQEEKNKDNI
2216	11:146	0.946	0.82	MFTFLCLSKINTLFLIYAMRPSQNTTTTQTIPLP DNNHRYQTILF
2217	424:559	0.896	0.624	MRSTLLLLLGTGTGNAGALQDCYCTGMDLG QGQVKCHKAFSLH
2218	122:257	0.976	0.779	MLLLQILAFAFFQIHSNLGFQPRWEREKEPISS SSSLKVAQLALF
2219	99:234	0.892	0.556	MLPSFLPQSLGNLIHTLGFLIIHKYMSAFKNRT

				DEFMNMGMQPY
2220	89:224	0.933	0.718	MESLSLHQYIELILKIFAWLGFPWPVSSSELQL
2221	103:238	0.925	0.771	PCANSCVLGLP
2222	7:142	0.985	0.756	MLLPVFLLYLSQDLADSRAPAHCSVNTDLHLK
2223	153:288	0.933	0.641	WGSCLVLSHFQVD
2224	205:340	0.967	0.763	MEPLLQKVTEWFLASLIYVWLDVGRLTRFML
2225	544:679	0.977	0.842	WSLTWLNVCPL
2226	516:651	0.992	0.966	MLFPLCFTALSFSNFIDKKCISHQPYLRIGGKII
2227	184:319	0.987	0.854	NLDTNNKRPET
2228	259:124	0.94	0.815	MMEWWTMGKGTILRLVTLFNILKQRLFYLSW
2229	460:595	0.955	0.747	TRRQHNIAARSVG
2230	212:347	0.952	0.789	MAGRGSALLALCGALAACGWLLGAEAQEP
2231	23:158	0.988	0.789	GAPAAGMRRRRRLQQ
2232	142:277	0.886	0.612	MHWVWMLSCCLSHLTASPCCHSWFLLMYI
2233	116:251	0.943	0.787	KGGGGRGFSGAIDK
2234	34:169	0.896	0.663	MLIQFTFFFPISQRFWFCLLFFFPQTFKCMKFY
2235	119:254	0.965	0.574	SLIEVREGVCIH
2236	198:333	0.889	0.779	MPTLLQVMSWMLSFGTQTLQLESCTCALHIV
2237	171:306	0.913	0.567	GAWKVYPYPLFSRVL
2238	313:448	0.945	0.671	MPACCYRPCLLQPISSLNILLLLMRKPSQEVIN
2239	254:389	0.938	0.611	DTPKAGKWLSRY
2240	2743:2608	0.971	0.926	MIRIISFAQICVSSSLHVALVGYFNWRLKILLY
2241	145:280	0.941	0.72	RWLIHMANKLL
2242	151:286	0.952	0.68	MWLFIAASKCIFLLIVPNFIFVFWRKVFSHDRLNI
2243	168:303	0.891	0.843	AYSFELSSKHI
2244	1489:1624	0.98	0.822	MQVKFILKYYISFLWKTVTANGETVNMSLLYIF
2245	209:344	0.983	0.832	TTMEMRKKSEVG
				MLLGVRAPPLCSAWQGAUGLVLSLTISICKHGL
				SFQQNLVPGKSNV
				MRIVRRMCMWSAGPAPATVCAVMVAAPKSP
				QSPPRWACVYSLIGC
				MWSWHVQLQVSAPLHLLCLHFPPAHRIYMP
				FPSPKRAPAMLNKG
				MVTRTLVTLNLTGMRLGYLPPVTYWPDCSDV
				KRYLCLAFFGWRH
				MSTIFTFLYQPPILTVLSSTYFINPISTAVHVIPV
				TDRSVECEL
				MARSARTFLLSSTWHLTKFPMSAGYFSPCSW
				LAIVIRLIQRVLMF
				MWYRISFPTTVLAHSCLLNVSQGIKNGMCYTII
				KKITVGTLEELT
				MIETWLWLLLLNVGGTGQWSGPTFRRENVLP
				AAHIGPKYGPLLPS
				MSLTITMIYTLFNEISLLIMCLEVTAMANCYKIS
				KYRFSIYEFI
				MKACADSHTQNLSLFLSLSFLLSLSLKNWVG
				WSPMCLLMSFKVGQ
				MKSQQIIYLFLLIVFPGVYVHQSIKKFVRKIYYL
				RDFMMSLCTL
				MRFLLWFILRGRQLVPLRPRRSPLPDNAPL
				PGLGGGDGSTQTP
				MAAPQTPFQGVVCFVFPFLLLAAKWFLSPLLT
				PLSSQGYGLLLL

2246	202:337	0.958	0.803	MSLACLCLMVRSGLLSKTKHPCPPHTKTYSR GVVRTKYIQDEGES
2247	185:320	0.924	0.779	MPFLLFLSVFHRQLSGDMSLSMCITQHSASLA SSVVHVAYSFLGK
2248	12:147	0.92	0.576	MFTVILMSQPKSYFLFFLPLEFYINQVSDTSSI MSGLTAFMAFTE
2249	141:276	0.969	0.771	MKRCGRLWHLVKISSHLWMLPCLTTAASHPG QAHLLHKYIPLTPQ
2250	55:190	0.939	0.746	MVTCSGKGALVTVAGCRALVFFLPALSSRPC ALNPKEPILPLCLA
2251	127:262	0.977	0.784	MFCTFNLRLKALRSVGLFILLGAPVPDTEQAL KRCDTWSSYSLG
2252	64:199	0.983	0.949	MLMSATALAILHLMFYFTMSFIKSPTCPCSYIM THFRALLKTFL
2253	923:1058	0.995	0.968	MALIYVMLLLLGAFLGAWPALCGRYKRWKWH GVFVLLTTATSVAI
2254	72:207	0.988	0.961	MASQSMCFLWLAPVTWCVMFSSRTCYSPPG NFSTAPGRVIFHSWD
2255	193:58	0.961	0.712	MLKLLLYVMYFHSFVVKYEFRELDTREKGIIS LHLLRNCWCPCGP
2256	168:303	0.977	0.809	MGFLIVSLVPTVGKMMCLPWPVAFPPAEVLA YHPVQRRDFHDIL
2257	14:149	0.917	0.567	MVKTDAHLKNPPFAPFRVYTLTSLLLKLSHYS CLWVKKDFKDSS
2258	108:243	0.978	0.927	MLTFAIYLTFLFINIYILCQLDPTPGHPKRGINCIH CTPHYVTIRG
2259	137:272	0.987	0.868	MIVVRATFIFCLHCCCHLCTGLLASYPATYKLL CTQDPERPLQME
2260	562:697	0.93	0.735	MMTIKEFTLLLVSLQFSTFSPSKKFLLETHFLKN SENWLGVAHAC
2261	236:371	0.991	0.834	MKLWLVLVQVLLCHSGSWVLWRIQQDLETWPS PLLGITWMCLGRFWR
2262	79:214	0.899	0.688	MNNSPLALFSWEGWKKFLVLLPAFCITPSQST SFSNIVPTTYQYC
2263	105:240	0.969	0.83	MVMLVLCFPGSSVSCRCDYAPMLHSWLTQT PGLVCIFMGCLSFL
2264	103:238	0.978	0.895	MGTKAQVERKLLCLFILAILLCSLALGSVTVHS SEPEVRIPENNP
2265	145:280	0.977	0.895	MGSRAPCSSWSLLLTISLFCVVDLYVLLFHHLF LTSFAYPVVSPL
2266	970:1105	0.956	0.886	MPSSFFLLLRFFLRIDGVLIRMNDTRLYHEADK TYMLREYTSRES
2267	161:296	0.96	0.763	MYFIHQQLMKLGWWHFLAIVGNAALDVSAQV FIVDMGFHFFWANA
2268	304:169	0.966	0.837	MLRLDIINSLVTVFMLIVSVLALIPETTTLTVGG GVFALVTAVC
2269	170:305	0.937	0.638	MAIVTSSWYAGRLLLLVNYEIHCSHWVPNRTF CFLWDLVKTIKLV
2270	41:176	0.96	0.788	MVLVLVFKAGSQFLHLFIDVIQVSKIRHRIQYQ SGPRRGYKDNKH
2271	226:361	0.984	0.908	MALAIFLSSASSLSFLLFHLFLLLSLCPRSPGP CQFACLVCFRP
2272	1218:1083	0.955	0.705	MYTRELLAWIQGLYTWELLAWIQHLNTWELLP

				WIRRLNSWILLVC
2273	114:249	0.889	0.588	MLTRLVLSAHLSTTFPPWTHAAISWELDNVL MPSPRIWPQVTPT
2274	43:178	0.972	0.946	MFSHLPFDCVLLLLLLLLLRSSEVEYRAEVGQ NAYLPCFYTPAAP
2275	239:374	0.992	0.576	MEKIPEIGKFGEKAPPAPSHVWRPAALFTLL CLLLLIGLGLAS
2276	1360:1225	0.965	0.911	MGLKNVFLPVFLPFLLYSEFLSLPPSLSSSLP FLPFLSLPGHFSN
2277	3:138	0.904	0.68	MLDKLFLESVSTTISLVFAFVLCYLWKNNIGLIT DSVHNFLEDEK
2278	298:433	0.949	0.861	MLLFLFFFKNLYCSKNLLYGQTIPSYQLFKNS FQWIYQNHKYRT
2279	20:155	0.925	0.819	MMFTPALWMIYVGRTARPTCQNIYLPENHRKIC KFISLTLWRKPVS
2280	2337:2472	0.989	0.965	MHHAWFFFVFFFLRRSLALSPRLECSGGISAH CKLRLPGSRHSPA
2281	98:233	0.933	0.716	MLIYLLKIICVQRRFCMNIYIYNAFDALLIELL KALHKALHKD
2282	103:238	0.95	0.645	MWRKHLSSLVLRDFFLLAPRRRDSLTLTHMATL AQKPCGIEKQICF
2283	2361:2226	0.996	0.922	MGGVAFLLWLTVFSAWTRLSIFSRLSDLPSCF LPLAGTVSSSLPE
2284	244:379	0.901	0.617	MKLLKLKGLGGRSPTSLILLPFLPRGIYVCLPA PISTYPAMTTLF
2285	369:504	0.955	0.806	MCHWQNSFLCQSFLTFGSILALLAGKACYPES ESIRELFMWALEL
2286	120:255	0.925	0.753	MKTKYTFLLIQLYHTLCCKWEWSSCVCHALLS SSFNSPLSQSRKH
2287	17:152	0.96	0.68	MQAKLLNCLLSTRMLLFLPSNIEYQHIFYQSST SLIVNCQLLSSGV
2288	56:191	0.974	0.82	MLLLLLPLWGRERVEGQKSNRKDYSLTMQ SSVTVQEGMCVHVR
2289	848:713	0.985	0.892	MAWIPLFLGVLAYCTGSVASYELTQPPSVSVS PGQTASITCSGDN
2290	643:508	0.994	0.733	MLFSTDIDLSTLLFKDFGGWLLFFCCCCFCFV LFLLLIIGKVWIY
2291	83:218	0.927	0.648	MIRCLAQPAAVLSSSLGLAQVLGDSGRDEQVLL RRSFRAEGCVLCL
2292	432:567	0.905	0.718	MNIKQSSSGLCTLVWLTCLKTPLGLLEGVQTP GPAGCTTTLTPLY
2293	14:149	0.985	0.856	MHGCHRLFQTLLPVKSSWLSVPLAVPLVM AVFLISSSYFLLCV
2294	1726:1861	0.984	0.843	MGAGCTPVVLGAALWLWRWFSRWGLGGLC WRPCTCTPCHSASPGA
2295	167:302	0.977	0.675	MLGICLCSICVLRCLCEKSKIFPPRTSDHSLE GSVTPVENAARS
2296	264:399	0.926	0.741	MYVFLCPACGRLMGSTMRLLPQSEPALHN RILRQTEPLLYFKR
2297	335:470	0.972	0.905	MSITRLFPALLECFVIVLCGYIAGRANVITSTQA KGLGNFVSRFA
2298	533:668	0.977	0.829	MMTWASLALGLTRALGGMGSFLLRILGWSWA MGSRSRARWPRGRL

2299	71:206	0.951	0.617	MGQVYSWSAFIVALRVSPGLHSNAHGPDYTY MLAWLFFIYVNSSI
2300	1684:1819	0.951	0.571	MILFPLCPSILSLKPKKKEALPSLSVMGTVFLLV SCSLPSAACG
2301	102:237	0.984	0.802	MWLGGQAFWAWLSFMNRWHSKFLMVRSRGE CGAQRQLLCVFVFRDS
2302	265:400	0.95	0.614	MHLISSCLWCLTCHVQSEGQQPKTAARKLPA NDLRVLEWTF SQGG
2303	168:303	0.953	0.698	MVQAPSYHIISHVSSWVLALWLGSSFASELSF PCGLPHSHFGVRI
2304	145:280	0.989	0.969	MILVSLILIVEPLFASLTPLSLCFECVVFLNVG QHLTDTQTFSLN
2305	8:143	0.891	0.608	MCFSCPLQCLAMGHKHYPVAVGRLAKRSQLA SPASSREWNHGSNT
2306	165:300	0.991	0.84	MSFCLISRLAFECWCFLSSLECHKKADQRE PSIRICFLPPFLA
2307	31:166	0.929	0.779	MVLFWYQTAASVWSWPSYYFQKSSQWVG DQKLKRSMHQFWCNIP
2308	242:377	0.974	0.841	MVFLHLFSQLFFSCAPARQYVGGVLRYSCTF LATVSFLIPISSI
2309	205:340	0.969	0.562	MRSMPGNCLPLWPHLLARPPRELWPDVMGL PMVASVLCFSGFWAF
2310	274:409	0.91	0.595	MVRVLTVAWPSHWCGAQRNRNIPDLQDREIGR GSRRRAQVPNDVLSG
2311	44:179	0.981	0.955	MGSTAILALLAVLQGVCAEVQLVQSGAEVKK PGESLKISCKGSG
2312	27:162	0.976	0.92	MSSWFLRAGHGLIWLFFRIGQAAVGVSAAGP GGSPKAHLGRVASQ
2313	428:563	0.988	0.936	MGWDSKLLFLTCLSCVTTCVSTCFQAPLGS SSFAPSGIHGTLE
2314	247:382	0.971	0.649	MSFFVYVHSTTTALLTLLTSIPQNIVHSYLYFS RYCKGFESESL
2315	329:464	0.939	0.562	MAGHHSNERKKEVAQVTFCIIMVLWHPLIICLM YFMPDALRHMSV
2316	125:260	0.966	0.889	MPWLHGMLKAFIGFVLVLSPPHYPHFTLNSV KGRILFIVEALAP
2317	385:520	0.95	0.671	MFFLSPLSAHSSQRRFLTYFFIALPQAASWSL SSSSLHHCGTCS
2318	96:231	0.957	0.769	MFLHSRFIGASLDVKCLAFVPSLIAFWFGFFI WFFGRFLKNEPR
2319	100:235	0.968	0.563	MLLIIPFSSNLHNWTWPNASYDAGSPELSASP FLLCLFFFLPCIY
2320	25:160	0.992	0.861	MVFLKFGRLPLVLLYIYFLPPLLLFHHFLFFW DSSYTYVRLFGI
2321	236:371	0.97	0.789	MWGRCRSLIHCCLYSSSLPLSDWCLYLAVSL SVIFRLFVLAVSIT
2322	220:355	0.942	0.616	MCMPFRTWGFVAFRLKILEDLSRELQTSADP LVLLFSLGPPENT
2323	268:403	0.944	0.886	MKVVTALILIYLGNCCKFVAHLNTSPSAWHLQ GSQTSFELCRVTS
2324	292:157	0.922	0.679	MCHVHCCWKFIVELLQCVIQGIIRCLYFGNICN GTCFLESCFFGMS
2325	8:143	0.912	0.632	MRSFSVYQGLLGTLLMGILRDPAAASQMMKEHI

				TYFHSNLANRNLK
2326	74:209	0.908	0.704	MGFKAGMQTFCWKVCVCSLLNGGEIPWLAULT RSDSKSMGRFEGAS
2327	234:369	0.989	0.955	MIQFISILALLVAVLASGTALFESGKLQRNDQF DSLYAHCLGKMF
2328	721:856	0.967	0.736	MPVLFFLRLLDPFVLWSKYSSCSFAHSGQC GDQKESFPHMGYTE
2329	109:244	0.951	0.711	MGYVPSTFCFAYFPCLFFLQYLKLMVHTNYRF EGMYFGEGMKGPS
2330	1574:1709	0.994	0.921	MCLWFSIGVVFLTFLPLFGSPNQLRGPKESL GIDTRILCGGGTT
2331	334:469	0.964	0.855	MALASAAPGSIFCKQLLFSLVLTLLODACQKV YLRVPSHLQAET
2332	431:566	0.973	0.59	MDSPSISISSLSWNLNFVVVVVVVVVAHRLN LQLLCTKRKGES
2333	159:294	0.988	0.904	MALICVGLLLVIVSVAWSHPSHFCLTLLSVLFS LIYCSPALLSHT
2334	168:303	0.939	0.868	MELLQVTILFLLPSICSSNSTGVLEAANNSLVV TTTKPSITTPNT
2335	40:175	0.924	0.684	MVVLSCCFYCGLERDVLTVHLRIMCVLENFT QFMCYKVSLETQ
2336	135:270	0.897	0.601	MNLWTFSPCTATILVNSTISVDLVNPTISVDLF HSNCLYFHCCSS
2337	38:173	0.901	0.782	MLLWVFLQLNYKIQAIPTYETVMTFFKSFPENC CFLDRDIGQSLR
2338	508:643	0.993	0.883	MLAMGALAGFWILCLLTGYLSWGWQALEEEE EGALLAQAGEKLEP
2339	79:214	0.92	0.875	MLNLKILVFLYRSPFKFTGSASVHFITYQGLH DLTAVHCFWGP
2340	155:290	0.998	0.894	MVCLWVFLQFLAQVICFLTPLIDSRSEATYQF IGCFGAVTNGNK
2341	198:333	0.981	0.89	MSYTAFLSVCCPLPLPLCDFALYVLLDKFKGG FRQQNSPQSIYQH
2342	245:380	0.949	0.832	MPTFFSFFLFCFLSEVQSNNVSKWGVVRVEDG LQHCLIIWSPHGAQ
2343	143:278	0.959	0.7	MLISFCLFMEGTSLYHLYDFVYTVYISLSPLFLP LAWFRPVLFI
2344	122:257	0.984	0.878	MLKVSAVLCVCAAAWCSQSLAAAAAVAAAGG RSDGGNFLDDKQWL
2345	660:795	0.953	0.771	MRSYKPNPLLPKQLILFTSYLIFTLRYLPGV FNILFKTVLLV
2346	1359:1224	0.981	0.837	MSYVEILIPVLLCLHAFFPSSRRHVAWFLIFICK FFKFCILIKFI
2347	340:475	0.953	0.727	MLGPCVFIYLLAKPGGVLALKWVGKGSEGEAF GCEGLEVLCVKGGS
2348	502:637	0.981	0.958	MELKGFWLCLFLRFVKWFVNKGMLCTLFYNL IYSLYNMCWTVLW
2349	189:324	0.97	0.858	MHVSTVMQTLAVRACALPVLCSLSLDTFKWE MVPFYLKPNNFTHL
2350	185:320	0.96	0.886	MIYHICATNLILKILLFSIESFCFIEFSISTHNLK NLPQYNYK
2351	228:363	0.948	0.652	MRFVTLSSACLPCPLGPCWTRHPSYGNLHE ASTSLPPRHWTGAR

2352	539:674	0.961	0.654	MTLERFSPICTECHRLPLLSALLAPLCTWAAS RVWPDGCPNRA
2353	668:533	0.981	0.852	MGGVNSFHFFSLFFLPFILLFEKLYYIILICLAMR AGGFFLLYYF
2354	112:247	0.962	0.745	MCVIQAPCLTWLRLAACHGCPEPANLRSPNL SPLGLESPLLPLCL
2355	39:174	0.968	0.903	MVLXKXNSTFFFILYMMLLMQPKVIFAFLRTIT DASCADEFIAS
2356	178:313	0.957	0.658	MFLLPFPVFYSILLSGEDGYKAGGVSSCLFCL HLLILHHLSHVIF
2357	432:297	0.978	0.699	MLSPIVPLYMKTCCQEVFIYAGFTFPLLFLVTL SFHHVLWLTCSA
2358	280:145	0.986	0.881	MLRKNAFIVLPLYNYLYWFSLLFLWIQVTIW HIHLVVKKITSK
2359	316:451	0.953	0.772	MDLYVWIFWLVIYFSTYIITYIKGNVGLCFQILFQ LSFERRPKSV
2360	1621:1486	0.977	0.925	MCSLPRHLLFLIIFRAYSLAVDLSTHSLTTAKFP SPIVLPTLYRS
2361	231:366	0.992	0.943	MSFPIHLRFFSLFFLHWLLSGFSSLLPWASAF VQYSRCPEHTPS
2362	36:171	0.911	0.745	MIGDILLFGTLLMNAGAVLNFKLKKKDTQGFG EESREPSTGDNIR
2363	208:343	0.98	0.817	MSIAWLVISICHLLKVKYTLALLDSVTGHFRSS NKSQVFGYCFQS
2364	294:429	0.983	0.904	MSLTIWTVCGVLSLFGALSYAELGTTIKKSGG HYTYILEVFGPLP
2365	103:238	0.984	0.926	MSVFWGFVGFVLPWFIPKGNRGVITMLVTC SVCCYLFWLIAIL
2366	177:312	0.983	0.847	MGFAFLCGACFYFSVLPPALPLASFYYYYYYY NEVRLKEPLGANE
2367	103:238	0.986	0.639	MKEDHSPSSGTSVFLVSPLCIDSSAVLMLLFW LILLSCLHHLFCQ
2368	81:216	0.887	0.706	MGALCAHCRILAFCPYGSISLVPYLLICLRGR NIHYATTIPVLV
2369	135:270	0.963	0.874	MKNLLMVHLWGICTLYLEFSAVSAISFLNHISV KTYFPNSSFYR
2370	41:176	0.907	0.59	MSFLVGNSQFIYFLSVASPMCLPEAFNLCSPS KEERLNGLYTPNL
2371	115:250	0.986	0.947	MMANMATSPWVLLIFIIILVDCIFCHYLMSSSSH NNALFPQSLFC
2372	193:328	0.884	0.636	MRIMILLMSIFEKLCPPSSSTNTSLALGNVTPFFS LAQTAGVTTKM
2373	222:357	0.948	0.827	MSATPVIPLPLLLLIISDSGWVQWAKYTQKIEP KIKSLLPTLLGI
2374	197:332	0.96	0.897	MVKWEVRHPLFSCLMLLFSILSCSVGELNCPG SLPACFSIIPSE
2375	139:274	0.947	0.8	MGQRSLGAGTFGLFFFSLAILTKQSFDTHTFPI KLLYIFFQQLPA
2376	129:264	0.922	0.643	MLIYFSKLRISITYLLLRTQVIIPQHLMALLRVQR LRWSFHHPG
2377	217:82	0.969	0.916	MPKHIYILFYFIWFFIFKVSGDYFGLCKLVSSP SSPPPFNALPC
2378	209:344	0.947	0.809	MWSLHIVLMRCSFRLTKSLATGPWWSLILILFSV

				QYVYGS GK KYIG
2379	231:366	0.896	0.566	MLGWQIWRLRPQLLSFHTQDRCHWSITSQCS KPESQESFLSTIHL
2380	207:342	0.969	0.848	MSLLCLKFFSGLWTITFSKGAKIIHWGRSLFN WISMCKRMKLPDY
2381	60:195	0.948	0.67	MILPNLSSPKLFHFIFILMNIYSYKGIFWLLQFLL PLLSPSQIKQK
2382	141:276	0.942	0.759	MRETGILLCFLSALNYITLVTSQKLILSKKMHVN HYLPKKTISKF
2383	345:480	0.938	0.72	MERTIHFVSLFASMWLSLQTKSFFFKNWSRD SFSKLRKTFSNSFQ
2384	71:206	0.974	0.811	MENINSWGRRGSLILFLSLAAIKWALGALSSR QNSRSYTLYIMM
2385	160:295	0.892	0.721	MKCKLIPVCPFLRLNTQPLLIISYGIFLHIFRDFS YIHRVRERHS
2386	118:253	0.953	0.593	MRNVSLLIYRRLMTVVLLQRTEDLRTEVEWGD SLFTVYLVVPVGF
2387	77:212	0.903	0.663	MLFLHIAECSFLRLKVAFPSSSLNFQPLAQFLAH ILEV FYKCLWKK
2388	99:234	0.924	0.679	MYTVVFFCFPNLMCSGNIGRNQALLVMFLKTK FQPLMLTISKKFI
2389	55:190	0.98	0.811	MKQLIYWFSLFFCCSCCHLNRHGNRLHTEIF PSLFLVCCADPL
2390	146:281	0.986	0.929	MSILVVSAFLANLWLLMTISTSQMLNMTKITYL VFLHLHSALRIG
2391	19:154	0.926	0.775	MSPLLPLSYKLVLCFPTPNGVVTHTGEQNASST DIEHGLKTILIKP
2392	176:311	0.989	0.899	MGWLCSGLLFPVSCLVLLQVASSGNMKVLQE PTCVSDYMSISTCE
2393	110:245	0.948	0.84	METSSAFTNPLLVCFLALLHSMVNITYTPPKKK NENCSKPLILTS
2394	191:326	0.972	0.584	MFFLLTSTSIYVTTYRLFLKCPRGTSICPKSTL PSARKTWSSSH
2395	145:280	0.989	0.969	MILVSLILIVEPLFASLTPLSLCFECVFLNVG QHLLTDQTFSLN
2396	74:209	0.965	0.693	MTYFVRALQNC LAPLLVFVLQNQLYGKMKSP SIGVMRRGQFLSI
2397	213:348	0.942	0.852	MYISLAPTTFLWPHGPTHCLLNALHIFLFQC LSIHNLLFLISA
2398	10:145	0.972	0.84	MTWQVTELLPCFTILLIFFESIKPFFFRKSVSLK EEPETRILEQV
2399	940:1075	0.989	0.945	MALRFLLGFLLAGVDLGVYLMRLELC DPTQRL RVALAGELVGVG
2400	139:274	0.973	0.924	MLLFSLNFFFWKIVMFHKNVIFILTCNGFIIVTFK WIDKFILNIS
2401	242:377	0.987	0.899	MQAMVLKILLKFPLSLTLLSVICRQKNLHSFK EGNYKYHNL FLE
2402	135:270	0.921	0.62	MKDVKLAIFTYFRMKNVKFLFLYL VILLHFKTSN NLIVTMSKQQLM
2403	41:176	0.905	0.578	MCYLRSFEEVLPVCCFVFLMWSQKGTKRLG WSLEATENFCESLSV
2404	111:246	0.918	0.719	MLLFGKFLQPTAKLLAFNAGVSKDWFS SLEGL FLMRAHSCPQSMQ

2405	144:279	0.887	0.608	MAISWLGTWLLQSHRHWSEPLCRLPARHHL INLNFMAEGIGDR
2406	168:303	0.985	0.777	MFLVPRSLTVFILAIVYSPFFCCVHFLIELWDLS CKKPIKPFSYF
2407	1530:1395	0.994	0.982	MVWVLLSLLCYLVFLCRHSSHRGVFLSVTIL IYLLMGEMHMVD
2408	106:241	0.975	0.702	MWKVFTFTKVIIESWSLLMCPFLKGVCRLLS LYNHIHIYCYLFH
2409	347:482	0.934	0.753	MPQFPVAFGIMFTYFTLAHKVLHSQASACLFSI ICFFPTCTLHFS
2410	276:141	0.964	0.745	MSCSFSRRRLMIFLAASFSLWSRCIDKWGA RATDRRCRKSSPW
2411	269:404	0.971	0.815	MQLKFSQLTTSSLSFSSALWLLAFSRVFLLAD SNLFVKPSSDLGS
2412	88:223	0.969	0.937	MQKLVLWLWLLTAKACGAESGRERTGEAGP KGNFQTPLVGPQG
2413	135:270	0.949	0.818	MLKWQSNWSWIRGRMGLTVWLMVSVQGAV VSMEFQSAGVSLFWKH
2414	38:173	0.967	0.902	MSLWFCRLSLPRLLALESPLGSLDKETLPTRY TCCTEKQPDCLFK
2415	1929:1794	0.956	0.866	MEFGLSWVFLVAILKGVQCEVQLVESGGGLV QPGGSLRLSCAASG
2416	206:341	0.992	0.861	MAKPCFFLIAFTTFTIILFFMCWFLFPTEECNSH EDKNYSFLFSV
2417	13:148	0.916	0.841	MEFGPSWVFLVAILKGAALCEVQLVESGGGLV QPGRSRLRLSCTASG
2418	45:180	0.948	0.81	MQLRTDLGLGSWLSRCFWLLHWSPPFAASQ HQEELIWGPVQGC
2419	160:295	0.921	0.663	MMKSFAFILKIMLPYWEVALVKFKSHRFADCAIL LLTQLETGLRNV
2420	105:240	0.976	0.864	MVLHWVTAWVVVLCTDWGERGGSTSVERRD HGSTFEHTEFEVSIG
2421	43:178	0.945	0.852	MESGLSWIFLLAILKGVQCEVQLVESGGGLVQ PGRSLRLSCAASG
2422	96:231	0.978	0.889	MCPGALWVALPLLSLLAGSLQKPLQSWGRG SAGGNAHSPLGVP
2423	1560:1425	0.938	0.784	MERGNALVLRSLWPGLTFYHAPRTKNYGY VYVGTGEKNMDLPF
2424	673:808	0.979	0.887	MITVQFSYTAVKWLLNCFVLILYVILSILFQVSQ KNSSKLGRFKN
2425	187:322	0.922	0.619	MFGMIKRRVRRVAVFVGRTVLCGSCNSGIIMHR GKTPPLKMVCRFE
2426	22:157	0.962	0.763	MGFLFLDSALMQTWVTVIDVSLHHVEIKAPRI RLMWSLPLRRQK
2427	173:308	0.978	0.88	MVYCTFAGFVLLRSLHFVWQAISSRICEMRT SILKISCSFWLHI
2428	37:172	0.99	0.773	MLATLACMAIPWTHLGCSCLLACLPFSHHLGL SEDIISSEKPSVT
2429	298:433	0.925	0.85	MVSPTFSLSFVLHLQILSAFPASPDAGYGWG DKMGMHKVPSGSKL
2430	16:151	0.933	0.657	MSLRPCRIWTLPLSSFPLTSKVSYYHPSAYFS LAPMVFLRAATYQ
2431	85:220	0.902	0.759	MHTPHLPNIIVYFILLYICSQYLYLLTIRHNHLTQ

				SLFYNKLLSV
2432	295:430	0.981	0.94	MREWWWVQVGLLAVPLLAAYLHIPPPQLSPALH SWKSSGKFFTYKG
2433	243:378	0.904	0.696	MHGLFGQCFQEALGFLLPRFPQSSQMLKFL KVDVTGSLTTNKLA
2434	777:912	0.932	0.687	MFSRFYLSHILVPFLPGLYHGEGIPGFYTKKQN FWFWPPLFPGEG
2435	144:279	0.939	0.721	MLIVMTLKYTIPIRLSLSSAILLTHDENLPTGRK ALSHGKHLVCH
2436	186:321	0.982	0.924	MCFS DINLCVTWILLGLVLWSSCLDSHSSCLS SRVFTWLSTSVVD
2437	201:336	0.979	0.871	MGKWDGVACVKLLWKLLYLKFWFTAFIGLSV GANKGKPPKLVLLS
2438	607:472	0.91	0.753	MILLKVCSAASLLGEGFMNQVTSTNKASLSLL SLTMKVAVNKGKK
2439	133:268	0.934	0.728	MLLTPVVLIASLSPFSSGDGGPAPASPPHSG GPFNRLTPGHASP
2440	187:322	0.922	0.604	MPVTPDPSAVSLFVTPWPLLLCLPWPVRVPG QSHPGHLSRAPVHR
2441	108:243	0.946	0.804	MPQWLALQRQQALLTLLSGAGTWAGMRPPS QCWPQGPSTGNQSL
2442	193:328	0.983	0.877	MESFIVWFLVQSVLFFMLQLKSGPKWQHSSA GQNRQLQILFLIYA
2443	9:144	0.932	0.645	MSWYTCQCLFFLSNTLRNGATSWHYCSPD DMQMVDFFSSTYERIF
2444	294:429	0.986	0.905	MHCIFSCLLWCILPSMLSVLKTQPSKNHPLW PCKYAYNIFFLC
2445	184:319	0.942	0.878	MPHSLVSLALLMCGGAFSRAPVPVSQVYPDY AGNGFLLLPVGVGG
2446	92:227	0.95	0.79	MYASRISKCLLVFSCCNLLVPAHSCITEALCKH MAWMHLEIVIHG
2447	212:347	0.98	0.945	MSDLLSVFLHLLLFKLVAPVTRHHRYYDDL RTLYKVQNECPGI
2448	52:187	0.987	0.804	MARVLGAPVALGLWSLCWSLAIATPLPPTSAH GNVAEGETKDPDP
2449	637:772	0.891	0.55	MQPIVAKALVLLLEVHPLQDQAESGRLGHVHL LCAPAAALQHALRG
2450	3740:3875	0.993	0.957	MYFFLLLLFFNVQRLAFPFIPNDPMLWSEGQ SHLCWRSPLIPSA
2451	398:263	0.945	0.671	MARSARTFLLSSTWHLTKFPMAGYFSPCSW LAAVIRLIQRVLMF
2452	238:373	0.948	0.732	MPPSSLLFYFLLGACMFTREVNPETSIGQKE NVLKLTQHSRVEK
2453	222:357	0.992	0.833	MAVRVLWGGLSLLRVLWCLLPQTGYVHPDEF FQSPEVMAGKTPHV
2454	63:198	0.949	0.817	MSLAQSPNSLITQLVFLVWLATIPSHLVSINSG NPITQEIPRIS
2455	79:214	0.966	0.885	MSFICFLNFVPTSAIPLRLWNYCGMNSPSRS WDCLCTPLSRQSA
2456	493:628	0.981	0.783	MLCFQAYTYCYVLVLAQIFLPWPCTVHHDFR KSLNNRQRKEIPK
2457	99:234	0.951	0.78	MNCRLGLALWVGSSFPWLPGAQYRMADSP RLVCRPQHLEGHMVA

2458	216:351	0.947	0.669	MAGPELLDSNIRLWVVLPIVITFFVGMIRHYV SILLQSDKKLT
2459	679:814	0.996	0.893	MSCHVASMLLRFBKIIIFLLFAVMSFSFLGTLF IFLHSSFFDPV
2460	151:286	0.934	0.787	MTAKIFCCSHFPGLLGLFCSPNPLCFTDGWLR PWEVAGSGSPNVH
2461	262:397	0.987	0.922	MLLCFDTNLCFVLLYSTFLFLLNYLTLFAKNGV LGEANTEIELGG
2462	285:420	0.973	0.832	MLFVVLPLLIIVFNIPMREAVDFLFMIKIIKVLKV FYCIACFII
2463	1:136	0.963	0.759	MRVPWLLAHLPLGSGWTGVTTGVGLFRSDLPK PELAASHLYLVSP
2464	198:333	0.992	0.842	MNTGLGPPCCFSDCLGLSLCLCSCCFLHLFLL FLVCTPCFALGSL
2465	148:283	0.962	0.764	MKMLCVKLNVRTPIFLLSFPSXCNWPLHQLL MKKYNADKRTTCI
2466	179:314	0.991	0.879	MVWRRLLRKRWWLALVFGLSLVYFLSSSTFKQ EERAVRDRNLLQVH
2467	62:197	0.973	0.766	MFVKLFLWHLGHMPAGICFQNSLTNYNTPCF SRSVVVLVGAFRTA
2468	24:159	0.897	0.648	MGQLTIASPSRFVYDCYFLVLLRMLLVNGICL DTDFGGEVISLQ
2469	198:333	0.917	0.718	MTFSSYTLTFYLISYSLQLSALGYLPPKGLKDL GPLEALLSGPSK
2470	277:412	0.933	0.597	MVTYFIKCFHYEVSFLLWFAVVRNDVDRPVSL SLFSSYSLFSTYP
2471	532:667	0.971	0.779	MQLIRRSHNRHWFRSAITFLMCKGITLLWLWK LLTGNDCEIYIRK
2472	232:367	0.968	0.936	MHWKMLLLLLLYYNAEASMCHRWSRAVLFPA AHRPKRSSSLPLNP
2473	818:683	0.942	0.621	MRLLFSSQVNSKRLTASRAFLVLVPAHLSYLL ALPSIPATRGFWF
2474	236:371	0.96	0.885	MARGQVTLILLLLKVVYQKGCGQSADHVSI SGVPLQLQPNSIQ
2475	176:311	0.971	0.843	MTFEFHLLQIYLVRLTIFFHFSIALALPSRFLG SYTSYDYLKRN
2476	172:37	0.953	0.862	MTDFFLCIHSFYLCVLLQASLDMLSVKSFSFKV LCLMKAKEKPNT
2477	572:707	0.958	0.776	MNLFCPLPSFSVAYILWLGSHLIQSATLLRVYA SFIFKPSSLLLF
2478	6:141	0.912	0.761	MTARFLICLFQTTMYAEFNLGQRRWQTRNAP NLSGWLGLAGAAPW
2479	352:217	0.936	0.554	MFSPANLTCLLCWFSSKNNPTIRTNIEHIKTEILC KLIRMKVLKSY
2480	47:182	0.925	0.632	MSLSYGVYIFPCSLFLINKEILIGGFAESPHHV SLKCNQFPKIC
2481	114:249	0.982	0.761	MGKTWALKLGLTMVGGIWPCLPFLLSSGVVG RKDKAGGNRPLSG
2482	176:311	0.99	0.899	MPKSWLNLLRLWVLVRFIMRSQTGAFLMLSP NILHQDVFPENSDL
2483	277:412	0.952	0.626	MLVIKLLPLGSKSTLLHLLWDAGSRTLVSIFLH CQLARCQVLLTG
2484	157:292	0.988	0.879	MCAMLLFWFVAYDQTLLSSTTCVGLPSFPGE

				FTSSWQNALCVGGV
2485	19:154	0.899	0.655	MANPERWTDLVGLVIRLLMKICLPNLPSSKS DILPELNIALTA
2486	709:844	0.95	0.819	MMCRMCACVCAPVCVHMGLAPAPAIWIEQ FWVENFFSPFLKVS
2487	256:391	0.97	0.901	MAVPIMLFYFSLLYKSLAFFESYSFAEYHPPTS GRQGCVKDILKR
2488	108:243	0.935	0.878	MTSLVSLWKTTLCCGELLGLKSTAEKEPAFLIC VQGEAHYKCPGP
2489	212:347	0.914	0.666	MTTSFIFLQTFSGCGCTKMYPIILCPKMESYKV YCYFYGSITCHI
2490	84:219	0.968	0.805	MGGVHILMLRAASGLFLIGIWSSSVFTEEDKN SCFCRKESLNLN
2491	297:432	0.951	0.834	MRHGGCVMFEVWALLALLSKLGKPPFFTAG KASAWAPQVVEQSM
2492	320:455	0.888	0.573	MLIVQGWYCCNIILTSFPSANAKALLRLLSKDL LEPFLSFCFKHF
2493	56:191	0.99	0.947	MLRLAGTRVPLLGWAVLLWLGLVSVLPPWVG VTRVQPGFAFSTVT
2494	95:230	0.926	0.786	MHFSPRHSLWGRWVKWVCPCHQLVTLTLRV HCPLAVLRTSVHHGS
2495	745:610	0.993	0.864	MSPVAFLVQVWFCPAFPTLFLILPSKLFCSLC LNTFQSWELCCR
2496	107:242	0.908	0.728	MVSASGTSFFKGMLLSISWVLITMFGQIHIRH RGQTQDHEHHHL
2497	412:547	0.977	0.907	MAVKNALVITWAYGFVKVTLSSLVFCVYCMY VILHLRMYITHKG
2498	413:548	0.899	0.554	MQCPPPFLGQWLLCPAARQWGPAGSPGPV LVPAGRRRPPPRSGP
2499	211:346	0.881	0.645	MPLPAYLSLWVGGRVCADWPSNGGLGFGIG XXXXXXAAVQFKRPL
2500	125:260	0.984	0.954	MSVWSPLTLLCPFLCITDAAIASSPLIVTIKLG NLNGLQSVAF
2501	103:238	0.98	0.901	MIFMRVLMLLCCMDSLGSLDTFQWLSRVLCF TENLIFELNGYELN
2502	460:595	0.939	0.681	MLTPFFFRILLKYHLISGTCPEYPYKIATTIPLYF LSHLSFCVLL
2503	334:469	0.906	0.769	MKFQLFLSYVFITQVFSRPFQSNLGSLTASS QIPLQLPKALCVR
2504	778:913	0.987	0.956	MFGVSGFCLLFTFLELVLLGLGRWWRTWKHK SSSSKYFLTSESTR
2505	8:143	0.923	0.785	MATNSLLYFIKYFFSACCLYDFDFNIIKFCFMD CGIRRHPPKLQ
2506	3740:3875	0.993	0.957	MYFFLLLLFFNVQRLAFPPGIPNDPMLWSEGO SHLCWRSPLIPSA
2507	32:167	0.922	0.576	MRHISALTYTIWRLEYISHYIGTYIALTMLITGGA LLMWCDILER
2508	662:527	0.957	0.827	MEGVWRHLLVSM TIPSLFMCIAFSSSYSLLP YYFQGAFFCHLSA
2509	187:52	0.906	0.593	MHTCQIYISTNVTLFFVLDVRACSYVRYLHK LLHYFFLCNTFL
2510	15:150	0.896	0.791	MAAARCWRPLLRGPRLSLHTAANAAATATET TCQDVAATPVARYP

2511	141:276	0.976	0.572	MFILLIKMSLGNYFIEDRHHKSIHVNIWSFILV PWFFLGVVILN
2512	78:213	0.915	0.669	MRIWSRAVGDGPAAVCCPLRSWCLLLWALDS LDPAAVTTHASAML
2513	680:815	0.971	0.877	MGLFAIHSSWLLRACFLIENFESVLYISNTHPF IYMGLHRFFS
2514	16:151	0.973	0.745	MLSISYFSNSLMLRLVPLAAYVLSYLICSVLLHI NQTTVTTYRGR
2515	1203:1068	0.995	0.955	MSWWRNFWIILAVAIIVSVGLGLILYCVCKW QLRRGKKWEIAK
2516	254:389	0.914	0.658	MGKNGIGGWGCRNHLPVVFLLIKALGVLGVL LDGAGEGGVPACV
2517	85:220	0.961	0.815	MLPLHGLVVCWMVWPPGRALLEKLNHKTPPS PKLLILWFFKKQ
2518	226:361	0.943	0.698	MWRRHISLARTFLLSSEVREVLSFCLEVYM DCNCLIYLNLTFS
2519	85:220	0.975	0.87	MFKVVFCFGLVWFCFQRAHKPIRFEKHNTIN EGNLFSMNIPVT
2520	112:247	0.99	0.919	MNLYLFAVLFFYVFLHIKIFCFATKWHNLSKF SYFCILHVKA
2521	218:353	0.886	0.649	MPPVATRVMHVLEAALSCYFLDTYLVANTDIE YLLFLTREFILDE
2522	78:213	0.887	0.553	MFHLSFLQYNILLFKAIKHLMRYIFGGSSIKNGH LKMIASVVLPO
2523	53:188	0.993	0.934	MRLSVCLLLTLALCCYRANAVVCQALGSEIT GFLLAGKPVFKFQ
2524	142:277	0.958	0.673	MYSLSLQLPVLCLVKSFKAYSLLWGVSTGVKE GFAGRTIVNHESY
2525	212:347	0.887	0.62	MSYKLTRQCPATLLYPPILIFSILRLHVSNAKFS TPEAGRKSNAC
2526	223:358	0.923	0.779	MPGSILSNLHVLLKYLFTFAEVFLVPGPFNVLF LSRLETLTFFV
2527	235:370	0.955	0.885	MYVLYKHFAFFKLTFTVSSLAVGINLTLMPTCR HLSENVLMSFHH
2528	127:262	0.946	0.753	MCTLFMHLLFCHLQSIQLKQELRLNYLTLTQF WQRCYSEMIFFCL
2529	103:238	0.955	0.818	MLCWRSQPKLKLCPALLVSWAHVAAQGLGG EGGVMCESAGAALAR
2530	322:457	0.895	0.624	MLSPKVFMFISCSMALQCGRDGVGLERSAVT TSHGASHSRLRGWD
2531	1401:1536	0.988	0.945	MFATTLGVMGLWSGIIICTVFQAVCFGLFIIQLN WKKACQQGALK
2532	596:731	0.915	0.796	MERWLGLIQTLWLPASGSPLGRAWVVPRTS GHYWGGKGTNEGGQ
2533	62:197	0.986	0.94	MLLLGLCLGLSLCVGSQEEAQSWGHSSEQD GLRVPRQVRLLQRL
2534	136:271	0.969	0.818	MWRGPPGLCLFVLFLLSRRAGSRARAASAR SPEWLQGDPLLGRK
2535	89:224	0.994	0.924	MPQLSLSWLGLGQVAAPWLLLLLAGAŞRLLA GFLAWTYAFYDNC
2536	250:385	0.964	0.872	MFQKGLFLICVTCLILRDEGQCLDRNPTPFLPT TKLLISFIYLF
2537	175:310	0.976	0.908	MACCLFLNGSWLSMALKFFNCWGGKKIKRIIFY

				VKIMKFKFQCPQI
2538	123:258	0.955	0.874	MTLVSGANWAWWLTVTRAMCNQGQDLHCG
2539	212:347	0.935	0.693	ARDRVQGGTRAQCVHS
2540	553:688	0.966	0.857	MLSEGFSPFLLSTRFLLPSPLPNFFLRSSLE
2541	49:184	0.993	0.956	STPDAFSLSGIV
2542	238:373	0.953	0.68	MQKVTLGLLVFLAGFPVLDANDLEDKNSPFYY
2543	232:367	0.886	0.677	DWHSLQVGGICA
2544	229:364	0.983	0.848	MAVWSLLSARAVTAFLLFLPRFLQAQTFSP
2545	104:239	0.963	0.866	FQQPEKCDNNQYF
2546	1906:1771	0.989	0.918	MCFTLGASFFGFCPLVRNSYKICSSHVNTCLD
2547	157:292	0.895	0.688	VFSSMQDTCRIL
2548	119:254	0.955	0.842	MLAIFPGNPWEIALIFTQLWGHLCFVSSHIF
2549	119:254	0.924	0.572	YCSAKVIALSSV
2550	134:269	0.96	0.821	MQLEVHIWIHIFSIAFFLALLMYNILLFCIHSPF
2551	199:64	0.95	0.739	DFSPNVIYHL
2552	24:159	0.89	0.556	MWLRGFLFSGILTSYLGKAEWAMFTFPLS
2553	111:246	0.965	0.796	GDINLSRMGGFPPN
2554	167:302	0.901	0.707	MGSACIKVTKYFLFLNLIFFILGAVILGFGVWIL
2555	2046:2181	0.964	0.86	ADKSSFISVL
2556	157:292	0.993	0.888	MFSAPSVLSSLLIQSLLGAQKSNILLPRSSVVQ
2557	272:407	0.987	0.937	GFMATDYPPRAL
2558	181:316	0.976	0.854	MQTFCFFAFWRLCYSFYQKKSSFHCLLNKFM
2559	569:704	0.972	0.816	FIVYVSAKHYSMS
2560	290:155	0.939	0.627	MIVNKIAANVVLCLQCCLTFLDIRSFSYNEHL
2561	458:323	0.989	0.937	VTPPLILWNENQ
2562	230:365	0.914	0.576	MDSLYFLFHHLPGVLWLHLIYLIFKGLAELERA
2563	158:293	0.926	0.742	ELPGVGVDYKS
				MILSVVLTSSVWEYIICVKNQMKTATFRISIPK
				GIDGYVQINSY
				MISRRHLLLRTFQVAPEGTKPLTDREERMAG
				HDTNGDTNGVLDK
				MLSCLLVITLQNFPKFLLQGLQCRCGSLKVI
				SSTMKSQAEDLG
				MGISRCPILLSFIHTPIGVCFFAAKLQLGWGPLI
				RHATFACLNCD
				MTLALAYLLALPQVLDANRCFEKQSPSALSQ
				LAAYYYSLQIYAR
				MWQFTILIVLCPYWLDLSFCTLTLSSLSCITLGK
				SLNLTKPRLLC
				MFLKFIHLIVISCSFSLNLSILFFKYTTVCLLIS
				AESFFFLKA
				MHLTSLLLFSLHFPTYIIRVNFCLVSNLFQRM
				RSTKLLRLIDL
				MWFLVSVVCLYGIGEGNFFSLASVFSLLSLC
				LHLLWKRADFRT
				MRSEWFYKWWFFPPFALHFSLPPCEEHVC
				PMCHECKFPEASPA
				MEFFSYILTHLSILLVAFLFIVTTFTLKLSTMPS
				PTLERCPISY
				MCRQILWPCLPKTCRIYSLLSLSHSASGHP
				VCPCTIAGALARV
				MGLTPWLLRTHQRLWASHYACLGALGLCCFS
				ECELWVCAGEGEKT

2564	101:236	0.953	0.782	MGXXFXFXWXVCVLP PPQILAGAHLP GWLS SRAFFFP PHLCYT
2565	3269:3404	0.958	0.836	MWYFWTLNSVPVIYMSTLMSIPHYFDYCCFIV SDIMLPEITFST
2566	355:220	0.946	0.898	MILLSLKFLHQEGFLYTSHKFFLSCISFPFPP QPQISHWLGGE
2567	849:984	0.969	0.916	MVKSVIFLSFWQGMLLAILEKCGAIPKIH SARV SVGEGTVAAGYQ
2568	175:310	0.905	0.774	MARQTLFEACLIWPLAGMYSEIFFKWK RKHRT QFSKYLQPSKKSL
2569	116:251	0.968	0.769	MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIA LPRESNITVLIK
2570	36:171	0.982	0.747	METLSPVPCPTCLAWLWTPVGGMWVRSPL ILAGFLHPCGVERLH
2571	2767:2632	0.971	0.926	MIETWLWLLLLNVGGTGQWSGPTFRRENVLP AAHIGPKYGPLLPS
2572	65:200	0.908	0.781	MAPRALPGSAVLAAAVFVGGA VSSPLVAPDN GSSRTLHSRTETTP
2573	539:674	0.958	0.637	MQPLHWRRIQCQVAGPLASLILNPARTYLQG AHFPRRASLEGG
2574	35:170	0.918	0.575	MLLVXXXXXXXXXXPSFLLPPPCSLSRLSLLAE KWREAETFSFIR
2575	70:205	0.968	0.753	MWSQIAFVRIPFCFSLLSHSNAWFVQKAASQR QASISTACHCPAE
2576	1195:1060	0.887	0.64	MPSLMMVLEARFVSSCLIFPSRAMPLL SLLA SKGSSVNVLVKVL
2577	71:206	0.987	0.824	MFFIFFCACIYMYVVCVKAISK TALINGVNESLN QIFRQKSEKYP
2578	443:578	0.989	0.714	MMWVG NFPGICWTLLCCCLDSL VQRHSAW NFPDKLADGLGIQET
2579	258:393	0.932	0.75	MSISNNILTSILRKLF LSTTLCSISV NKVLVTEI MIVLYIHCV
2580	155:290	0.971	0.866	MILFTRAWFELVTLVQFIIGSQMLYPYLHIEEFV IRKLPVLLYRK
2581	102:237	0.966	0.655	MMIFLLKVSNSLGLMASLPWADRQDLLMSLCI TQLQETQNLTRTR
2582	112:247	0.975	0.867	MFSALLHFLLLPPHQCSSFLSERPGFAGRLNI PLLPGTVVKFT
2583	91:226	0.907	0.612	MLGCSECQVCMRAVLLLQALPPCRGQKCW AVSCIEGLSGLLHYR
2584	80:215	0.99	0.907	MGKKVTL LLQKCAWLLLVCC LFTGIKYL NKCFI TDRELLRDVHNA
2585	70:205	0.976	0.885	MEFGLTWVTLVAILKGVQCAVQLVESGGGSV KPGRSLTVSCTASG
2586	178:313	0.917	0.647	MGFPPNRQLRAKFWVEGPWCILHLLFMPMG T SGLSVQPLDFLNSA
2587	211:346	0.972	0.674	MLKLLSGVFTIQILVLDVGNTYREELNLCSSF TELRLQKVST
2588	249:384	0.956	0.78	MVQLFIPILKFQLGYSVLSLCNHVLEFLFPSSL SGIFSSSLPLL
2589	284:149	0.972	0.704	MSIGLSLVSQAVY PDLCKVNCALLLYFMFLV IFFYTIFNYIAL
2590	41:176	0.952	0.774	MAFTAIGSLCIFA FSLNPMPIQYFKVFQTFPLFF

				LQKQFLKSESY
2591	53:188	0.986	0.874	MLLFLGFFICSLFFSELSTGTTHSLESYQILLSK FFRHPLCTRIF
2592	163:298	0.97	0.861	MGWPPSLWVLALAYCCKAPQRLCSGSSPCR FSSRMSASPATNRNE
2593	108:243	0.979	0.856	MSTFALGFLCFNLLTPSLLRLRSHVSHSFSEL HYLVLLNEQDRKV
2594	481:616	0.955	0.83	MYLLILLSTKFSCISSLPGLDYRQDSMLCQGIS LAPTLIIHFLM
2595	207:342	0.903	0.7	MVGSLILGLLIVTKQYSLLRNSQFKKFKMLKL CNTIYSDLFRRK
2596	148:283	0.973	0.828	MCVHPYVCTCACMHVCVCLCAWCLSQPGGL GGFSEEVTSLPRPRA
2597	90:225	0.917	0.592	MIKPRCFPKIIFLVHLYVCYKVCYMLKIFSFGVR GEFQTALRDVD
2598	54:189	0.978	0.867	MIFWFSVLYKWYLVGLAKQKQDLLPHHHHHH LFPQYLKSHSLPPV
2599	154:289	0.886	0.575	MLFLKKIQFLKCNKVFRLDFCVALPLLFSSSA VLQITPVDTFSD
2600	166:301	0.978	0.916	MFQCLVSIVLTLDIICFCLDCNQITVCVKVYYYK RGSNILGESSS
2601	99:234	0.979	0.559	MLHKGKSQDPSTKGHIKALQTVTSFLLLCAL YFLSMIISVCNFG
2602	244:379	0.941	0.798	MRDARQMFLIPLWLCPFSSFNIIKFPERVLYFLN PLPFLPFTLKGGK
2603	1191:1056	0.994	0.808	MAPWAEAEHSALNPLRAVWLTLTAAFLLTLL QLLPPGLLPGCAI
2604	92:227	0.972	0.902	MEFGLSWLFLVAILKGVCQEVQLVESGGGLV QPGGSLRLSCAASG
2605	277:412	0.889	0.576	MVAVSLLCPWPSSWNRRSCGRSHRNGLFT AFLSVPEFVIFGACR
2606	95:230	0.97	0.808	MSSNLQVLVYFAWTRLSQRWPFPLCWLLLG QLHGCHPGLPLAVI
2607	490:625	0.966	0.92	MKTLFAFFTLVLSRVHSGIFHRLCDVCYHNGL NAEVDTSLOPSSV
2608	120:255	0.906	0.663	MVGLHMKGAFLGKAFAICRNCLTLGSAVLSRV SKAPRRQNIRINR
2609	191:326	0.912	0.641	MRQVVSNNLLRPFLGTACSHGKEHKITMFSAY RVTGMHADEHPCS
2610	63:198	0.99	0.955	MFPPYFSLILLLFTFASKFFLSNLKKSNIWKARI ESTKTVISKR
2611	55:190	0.914	0.784	MGLSLGLRMVPRLAGLWAPQRYVQVHIGFAA GSKEGLLSVTVDLG
2612	157:292	0.998	0.924	MQSVIRKQFTALAGFCFWFCLFTLAVLSLTLLI CKLRIMPFKLEG
2613	193:328	0.977	0.867	MFSLLLGYSTRYFSLCCIGLVGHFSKNKPDNDR NFVVISRKTFCTF
2614	1331:1466	0.978	0.66	MYRPAPPRQNRQLHPYLLASWPKALNCTLCV CVCVCARVCACVCM
2615	94:229	0.95	0.621	MVSAPTEGAQQKGLFLLRFYLVVVEVLYRRVF GKCLGIKGRSPEE
2616	75:210	0.957	0.838	MYKVFNCNWRIFILYILLYVHIKIVAPKSSNLAV GITSSITKTQA

2617	235:370	0.889	0.694	MSHHCAWPKNFLLKMLSTGRVQWLMPIIFLFF QKMGGNMVGSQK
2618	204:339	0.924	0.753	MEFMFLMCVFFFSYDSDIFFISFEVLFQSFLA SVWNIIKSIVQ
2619	66:201	0.978	0.928	MFFYSYPVVSCLLASLFFFSSSFLPTQNSST CNTDPDKTHLYCLP
2620	155:290	0.91	0.708	MKASFLGPRGHPSWPLQLLLLINASGVLPSTPV ERLCGLDPCGSP
2621	402:537	0.997	0.954	MNLITLCLLKALLVFLMLWFWWWHPQVHSQSA SLPLTGCVAFMISA
2622	12:147	0.996	0.84	MSERHGPSSQSVLLSLWFLTLTPFLVLTLLS CMEHTAPAPFQSA
2623	97:232	0.945	0.836	MNSQLLRMTITLSLLPSSILSLNTVHPQRDKFG DPLAYLFHWDER
2624	254:389	0.955	0.726	MAISWKPTGLPWHSMLQVLLAAWLPGPPTPT HSALPSFSPPPSLP
2625	218:353	0.977	0.779	MTLFSTFTLMLIPGCPLPVSLTFRQFQQPVIISL LPSELQOCNEQ
2626	50:185	0.932	0.756	MDLPRGLVVAWALSLLWPGFTDTFNMDTRKPR VIPGSRTAFFGYTV
2627	97:232	0.934	0.674	MKMETQLLLAHSIGFLVWDCVFETSFIYKLQP PSARALQARGHSW
2628	259:394	0.961	0.689	MGLLIVALSPIRIVLFCDFPTIQGYLISCRAGKP HSLIYCSELM
2629	261:396	0.928	0.793	MALNIIINPVWFCHCLTCTIHIDFHILFIKFKHMF FRSLWSSWL
2630	49:184	0.979	0.918	MAIFPLWKGVNVLVCIFSSFIMLNIYCTLLIWKF YSAFFCYITS
2631	147:282	0.988	0.926	MGYLLWLVLVLSILVCTELGLGRLTFPLDSESPRT SYKVRPWVLEA
2632	44:179	0.94	0.709	MNPHHTFLCVLTVGSLPLLKIRPQTSSPYLWV VCSSPEDLGQEQW
2633	96:231	0.95	0.785	MCYQYYWIFCFVPAFLSCVGGQKCTWWAVS REMPTEGSSGLLQT
2634	79:214	0.969	0.675	MLLLINYSLQLYFRICIWHCTLSRRLGNSLLL DHSATILGHLLT
2635	659:794	0.942	0.717	MFKHPALTIGRKVILVRRWFLLTPAPFLELPLV AKTYLGGLIWDK
2636	250:385	0.917	0.605	MVPAIHVGLYCPCITMRCLSFLTQGFCAKWG RARRGIILTEVL
2637	30:165	0.959	0.58	MSLLLLCSNTCSFLQNVCLVWLRDFTEAIKGG HITLVGVEENQHN
2638	695:830	0.95	0.801	MAITGHTLLQMLLHQTLPQHLACCIIISLLVF WDLVPSLAPXXX
2639	429:294	0.954	0.885	MCLSHLVSLFPAATAFLINKVPLPVDKLAPLPL DNILPFMDPLKL
2640	340:475	0.995	0.798	MTVLLRLPSFLFARPQGNLDPLVKKQIQLLLLL LLLLLLLLLLLL
2641	262:397	0.923	0.615	MLLTVGQWLLSPPSLPQRGNCTPITDFPQV RMISQWLSGFPSIF
2642	241:376	0.95	0.768	MKFSPAHYLLPLPALVLSTRQDYEELEKQLK EVFKERSTILRQL
2643	1108:1243	0.989	0.891	MVKSQWGLALAAVTVLSSLLMSVGLCTLFGL

				TPTLNGGEIFPYL
2644	305:440	0.965	0.825	MISSWPFSRVVRFWFLHQMVLCLGQGVPO QNLENPRERKSFL
2645	1953:1818	0.948	0.817	MLGSRLMTLTVAGALARGRTGTCTREQE KGQNHSTLAWPHEE
2646	462:597	0.977	0.89	MINKAIRFILGRCAVCLQFFILCVTHAICRVTL LILPIELEVI
2647	1225:1090	0.959	0.88	MRGSQEVLLMWLLVLAVGGTEHAYRPGRRV CAVRAHGDPVSESV
2648	41:176	0.992	0.913	MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLT TQTQVQREIVNK
2649	295:430	0.983	0.921	MLRALSLLPYLILITACKGLSVLFTDTKLSLETS GSLPVDAANS
2650	190:325	0.979	0.961	MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQ PWQVGLFEGTSL
2651	32:167	0.986	0.916	MAWIPLFLGVLAYCTGAVASYELTQPPSVSVS PGQTASITCSGDR
2652	160:295	0.983	0.94	MPGLGRRQAQWLCWWWGLLCSCCGPPPLRP PLPAAAAAAGGQLLG
2653	232:367	0.985	0.934	MKKCIVCCLFFSFCLKMHALSSLELVGWAF RNPENICNLTA
2654	22:157	0.955	0.827	MHLSQKYRQFPCFLCHILSIFLVVSQSLSLVTK LLLQVWEYQON
2655	170:305	0.917	0.643	MRQCRALMSVAELSLTWPALDSWGSSRQA VLRRHASCLVFCGPS
2656	2113:2248	0.918	0.647	MEEAWQKPKRKVWLLSVPVLWYCESSCPL TPPWLMGGSNCKAAE
2657	128:263	0.961	0.884	MFVILRGLLTSRCLMKSPPLISTTGSNCLRES LKLSVLALIGPS
2658	1576:1711	0.954	0.752	MLVLQILLCIREFILERSLINVKNAVSLAVLAL LNIGKFILEK
2659	44:179	0.981	0.955	MGSTAILALLAVLQGVCAEVQLVQSGAEVKK PGESLKISCKGSG
2660	165:300	0.92	0.593	MYCYLKMLPFYVLVGPESSEMLSPEFSFFMFLF TYIKFQVPNQDSG
2661	7:142	0.982	0.934	MGCRLCCAVLCLLGAVPMETGVTQTPRHLV MGMTNKKSLKCEQH
2662	1355:1490	0.988	0.958	MALLCICLCIFFLIVKARRKQAAGRPEKMDDE DPIMGTITSGSR
2663	785:920	0.996	0.905	MILLAFVCWGPFLGLLADVFGSNLWAEYL RGMDWILALAVLN
2664	45:180	0.946	0.759	MGLGSGVRALLHVWIRPTLFPSCVSAICRCD FQGLCRMGTSCIF
2665	395:530	0.981	0.944	MKFFVFALILALMLSMTGADSHAKRHHGYKRK FHEKHSHRGYRS
2666	41:176	0.992	0.913	MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLT TQTQVQREIVNK
2667	244:379	0.938	0.824	MVLGARAVISFCILSAMPGYMVVPPERTLLAY KSLRMSMSHFME
2668	174:309	0.979	0.707	MSARGWPCEAFVLAQVCWCWLCVRGRLCEA LTLAQVRRHQVCVPG
2669	27:162	0.97	0.913	MKVSAALAVILIATLALCAPASAPYSSDTPPC CFAYIARPLPRA

2670	206:341	0.923	0.765	MRIPVLLTSLVTDKAVLLCPKVPGRRSQGPVK VGSFLENPWGVFI
2671	113:248	0.982	0.882	MQTLFGIKMNFVLALLPLATLFFPSHFFSCVKK RERGPSSHAYEC
2672	224:359	0.975	0.947	MPYTWCLGLLSCFLTSVANTLSRVFPLLSFRP TLLFSPPLQDHDP
2673	562:427	0.967	0.858	MFNFCFSSLSLSSFPMLFTLLPFPWFLFEQPL NSISLWRLPLFFL
2674	16:151	0.971	0.914	MPCLFCFFSLSFPIQGFLVNQLCWLLARVFED HQLTSCSGLWAEA
2675	66:201	0.985	0.946	MIIAIIAIFILRSLVVTAGTVFIGHLCCPGTCFPT TLIGSLAFC
2676	57:192	0.951	0.783	MVYSAGCLLTNATVVLFYAHCVVTSILNLYKS GWVPQAGLENS
2677	3461:3596	0.992	0.926	MVVGIVAAAALCILILLYAMYKYRNRDEGSYQV DETRNYISNSAQ
2678	1179:1044	0.998	0.922	MYCWWCWLCTAMVCSGVLCRPLWEPLSPRL SVFWAGRYLGFWCMG
2679	118:253	0.985	0.698	MAKCCYNWGGNGPFRQLNILLFFPFLPLLSP TLSPFLLEYPEIH
2680	129:264	0.941	0.828	MGSLMPLRPLALHTALGAALNFSLPCEWSTLP SASEAGRLWGPPS
2681	690:825	0.962	0.7	MKATVHLWMCSCIARFWHLCPGPSLTSSCST SCISSVMSASNNSL
2682	186:321	0.907	0.832	MLLLLLAPIIIKDSQIISDIFKACNRKSNPSPTYP TNDAGYTYNF
2683	148:283	0.944	0.68	MTSTYLGCCSLWDVWNEEGKGDVWRPVAVF IGLGVLISIRVPFLF
2684	178:313	0.972	0.886	MVLRVCFLIFVLYHNLGKYIFIIVYRCKDRFTK GCITVVQQSGI
2685	252:387	0.91	0.76	MKILASFILTRLTDMIFPLSFNTHISISYLWKVFT YNTQYIPLRI
2686	265:400	0.921	0.686	MFSLFNKSFMFLIHSDLWIQFLVSLQNFYSYFLD ICKILVNNEIPL
2687	754:889	0.888	0.674	MVMKALFDLAPPLYPCTLPLLTVPARYSGLCAM SQIGCF SRLFPSL
2688	98:233	0.989	0.973	MAWASRLGLLLALLPVVGASTPGTVVRLNKA ALSYYVSEIGKAPL
2689	337:472	0.916	0.583	MCLLTFHMFNSHLLSLSSKQVVRLEKGAEVTA GKEHSIPGWLTTET
2690	11:146	0.919	0.691	MTGPLNVLICTVLYPKLLKLLMTNVFHQTVTYE LSKEICDKGVIS
2691	324:189	0.971	0.886	MSRMILFTVLFRCIESDILYMLVTCIMTNSLSC PPGSSFSYFLF
2692	269:134	0.97	0.921	MWAGSGPGPLCLLFLSSSLKVVLVYKFPCFC FLSYSFLYKFLPT
2693	177:312	0.96	0.786	MKLVLLRKTSLSVFTTLFSVSSSQYPVLSTSIC NTPVFSTLFLEA
2694	240:375	0.963	0.76	MVRFNQVEVCFMRLLHLQAKTLFVHLAFLTLG LSNFTKEILPEQG
2695	212:347	0.944	0.842	MLLYETGLLLFLRSPFLQPPVTFLYCFSNLYQ QSSSCCLPPGPKP
2696	24:159	0.982	0.869	MLGLGLCTLHFSFVSWLPLKVPPVRDTRESLK

				GMGKGKGICCIQF
2697	111:246	0.894	0.83	MCLFVFPVKVLSFMHARFQLPPFSVALKKLI KILISLLHSPLET
2698	203:338	0.97	0.824	MLELTEHLVLLSFTWMSLLLPLRPLHLTLKKLD GGPFLFTQLWQL
2699	1251:1116	0.951	0.641	MLGLHQLCSLLVQLDFYLQYLYGQFQQFSMC LDLNHVHFLMFPSL
2700	1063:1198	0.962	0.792	MRAWEPFFLFPGHFLLFSFITGGKLPKGFGGM PPRTFSTRGCPYS
2701	402:537	0.991	0.94	MAESRGRLYLWMCLAAALASFLMGFMVGWFI KPLKETTTSVRYHQ
2702	28:163	0.906	0.655	MLILLHILKNIKLYLVNMLKTKLCFYKDRGSPEE GIDKEEMKLG
2703	171:306	0.998	0.983	MLLWPLLLLLLLLPTLALLRQQRSDARLSWL AGLQHRVAWGALV
2704	237:372	0.934	0.819	MIFHLVSGLVILQSFKMFNFSCFNSTFIVGEQ VHRGPPVTGGIY
2705	122:257	0.969	0.761	MFLVGNCATVLLSCSLSEGSCHCFGSETSLPH TFNWKFS AFLQK
2706	1108:1243	0.989	0.891	MVKS KWGLA LA AVTVLSSLLMSVGLCTLFGL TPTLNGGEIFPYL
2707	1245:1110	0.943	0.606	MCLLKAAPFFFFYVPQVGKGNPRPPRGCSAF HPPTHLRPGSCSVA
2708	853:718	0.992	0.926	MAWTFLLGLLSHCTGSVASVLSQPPSVSVA PGKTATITCGGSN
2709	73:208	0.994	0.849	MMLFLVLSLELAYTLRLRQLFLLMASLICLYF PSQHHCLYPGHS
2710	273:408	0.993	0.955	MCKAYVLCHWFLPLATVLTGIFYPLFSALGGS NHACSIYLPQENI
2711	8:143	0.939	0.73	MACVWLYVWDKFLEVILLGQRVLDTSVDDY HQIAIYRVIPACIS
2712	125:260	0.994	0.881	MALQWSILWQASFLLLLGHLIFFYLDVKKIPSL SWRFRNFTRMHL
2713	238:373	0.953	0.915	MNRTMLKFILCFLLMTYSQHSQLSAFKSGSSL QLHQATECFSVLL
2714	34:169	0.988	0.946	MVMRPLWSLLLWEALLPITVTGAQVLSKVGG SVLLVAARPPGFQV
2715	1119:984	0.985	0.908	MILQVSGGPWTVALTALLMVLLISVVQSRATP ENSVYQERQECYA
2716	1631:1496	0.954	0.673	MIFVLGQAEGILIMLMTALTVRREPSLSTCQ QGEDPLDWTVSL
2717	25:160	0.993	0.962	MGSSFILALLAVLQGLSAGVILLEQSRAEVKK PGESLKISCKASG
2718	1670:1805	0.99	0.971	MCVTCVVCMWCMCGVCAMYVACVMHVCE VYVWYVCDVCAFGHTG
2719	31:166	0.977	0.892	MAPRTLVLSSGALALTQTWAGSHSMRYFFTS VSRPGRGEPRFIA
2720	381:516	0.886	0.663	MLLAKRYAKYFIYFIFFNPVLIPIQLRRILRLGEI HIAGQCRAGS
2721	760:625	0.992	0.977	MLLCLHLIIICLVFCIISAIPWVLNQCLIFRLYFLC QKKLAMSLE
2722	372:507	0.989	0.83	MRAF CYLVFWLRKFLALSICKDVITQCTHLM QLFFREKRCRCKS

2723	234:369	0.985	0.935	MNLGLLLFLRQLARCLVLSVEGAGETLRRKEI YLLVPREASVAHG
2724	184:319	0.909	0.763	MLIGSGYLCFCALQWTELGNVCVCAHICRCH MQVSGITSPVHVH
2725	140:275	0.924	0.582	MHLLVSHAFLPFPLHGYSGRQRGAKQWRCH PARASRERPSEDNLS
2726	230:365	0.984	0.754	MKIFKCYFKHTLQQKVFLFLTLWLLSLLKLLNV RRLFPQKDIYL
2727	21:156	0.991	0.972	MLLLLLLLGLAGSGLGAVVSQHPSWWICKSGT SVKIECRSLDFQA
2728	577:442	0.984	0.919	MFLWKWPLWVLQYVVCSLKDKIHKFFYIERVV GELRVLPQGWMA
2729	245:110	0.965	0.726	MLPLFHFMAKIRSTVVLTEFFLLFKSTEHYIR PLNTNLQVWKR
2730	215:350	0.965	0.873	MTWTKCPLPLGPAFFTQCCLIGLLVPLLWGN QNTQWYPTSKMPD
2731	193:328	0.968	0.825	MYGMLEWPISMYFVAFLHCFLCSGGNLGDSF QALPELCANCSSSP
2732	276:411	0.951	0.756	MCPPNLFHGRMLRLLCNLIWLNTAHTHTIGLS DQIQATQYNLNR
2733	58:193	0.932	0.584	MASSYSLLPLQIIVTFTNFGIEMGIYMSDSDVR VFLFAAMAFMS
2734	120:255	0.982	0.843	MLLLWLDHLSVHNLFSMFYAFLFFCSSTTF FCIKYFLAQHLN
2735	497:362	0.964	0.739	MWLHENLQFLQLIFHYWTVPPWRDWCKVI QQARDRPGPNPLLP
2736	30:165	0.984	0.835	MCESLAFLLQFGYFALISFVNSILYSFDRRAY CNKVKIIAQKIL
2737	91:226	0.951	0.811	MRANCGVSRSLKVLATLCLTVIRLQMMEASD LPATPSGLLCMR
2738	160:295	0.949	0.633	MCLKQLFAKQVPVTEWPGAKALLSTLLLNVF GMWEKLVTLGLPS
2739	134:269	0.992	0.956	MSVGLHLGFLAWFLPFLIPTSPPLLFQLGALP NESLALYAWLRD
2740	58:193	0.929	0.588	MSSPCFQCFLCCTIKVWPLCHHLQKAFPDF SIHVFESDLSSFC
2741	94:229	0.993	0.849	MLYIECKSHKLVAPLAVFFALFFLLIFFWVAFSY PFELLFLQLRS
2742	677:542	0.95	0.837	MIRLCVRRCFQVFWWETAISLFCFCDYLPVP MASFIVFIPVHSA
2743	44:179	0.96	0.694	MLLSFPRCLIPAWGRSKRQGWQSCVLGLSRA LACVPLWLLSSPAV
2744	149:284	0.906	0.714	MHTKYFLSFHSTQICLALRVCRAALLFGDAIMKG IKITAGGPLLP
2745	86:221	0.932	0.752	MGPWSSYFSFLELIFVICTMRVLERISLWFLDR QCINSHTYLQAH
2746	97:232	0.955	0.771	MITFKVPGNKSFITLICLLLSLRDLRSRCCNGF PPCVGTSGVLV
2747	68:203	0.927	0.743	MIKLCHQLYNVYVCFHLLVLDIAIDYIIVPNIS YLSISIPFVV
2748	290:425	0.961	0.565	MFYENKRREYLQDMLLSYRLLVAILVLLKKLTE LNTITLICKSII
2749	133:268	0.898	0.587	MNLINHNTFIVIRGILGSWRAVLSLICAVFTYP

				CEGGIGIVNRG
2750	109:244	0.927	0.578	MFGKRMELTNCILFTVCVLQSMDFIDLSSKS LKNNFEDYMKFG
2751	142:277	0.958	0.856	MIIAIFLVVLVSQNLATSHQEMGSTALAFESRQ DKYNTVEARLLA
2752	112:247	0.968	0.808	MNIVFVILLFKDMQVLEVFLVLLNVLTTLTIIAAGI LCTSFCCKPF
2753	215:350	0.932	0.634	MLSYPGLAGSGPWGTELLYPFLTMLWSRALM NVFWTRSGLSTLGW
2754	141:276	0.942	0.696	MRAGKLVVVWLKSVNLCLEIREVTNWDRLR VESIRKKEEWPQPR
2755	58:193	0.93	0.665	MIRFALPWFSQIWLSKQTWTRLTHLAFLLQEC NSMFYPKVSRTTV
2756	101:236	0.923	0.702	MSVYFLSPFPVFFMNEPTFLSTKTCFYCRQS KDHSLRNTDLECA
2757	534:669	0.977	0.808	MLALFFHRFGSLLSFLLSNFESWTTVYLSKP SGLLKFFYLPLTL
2758	233:368	0.971	0.925	MRQIAVFQRFMFPLLPWLSCIFSSQNSIYYV STFIKCLALKSI
2759	95:230	0.945	0.711	MLTPLLCFSAISKSFGLIPFSRISLVKSSDHLIC CFYSFDTNIPS
2760	10:145	0.99	0.744	MLILYPLSLLQNFLFLSILPFFCHKVRIVSLDH SAVKRDALVIQ
2761	207:342	0.891	0.643	MLSLVGSSRGLGITGCLVLSLVGRLGRSGWA YNSTQGS DITGVYM
2762	50:185	0.928	0.749	MLFQRHLAAACSSIFFFEITSSKFTSLDLHVLVY SIVLQVTILPN
2763	126:261	0.939	0.659	MLGLIPCVIGSLVFLDYKQDNLT PFCVWGS LY LRSLCERESDLHH
2764	30:165	0.957	0.848	MTNFFHLLLPLPSLSPSSKTHSFNIHKIIILF FNSIFLYPR
2765	220:85	0.992	0.958	MGFRFLLCFVFQVTTGCTILVASRNISAWNEY FLCKSNLQTYNYH
2766	111:246	0.967	0.605	MREHAAVTACTALRSPCFRTGQRPRPWRAA PLLLTSLLAATQALR
2767	55:190	0.996	0.915	MCKTLWWPVMVCVAMISGVGVCFGVCDTA VGLQDSALSPSCGKR
2768	26:161	0.914	0.582	MNRLICLCVSCCASDAKIQIASVCLSAFSSRER FFLSFCACFTLE
2769	117:252	0.906	0.573	MSSSRVGLRLAACLLNVSEAGRKYIVENIAKA ALLDKNGKKHPQV
2770	230:365	0.952	0.589	MAPTWRCRMAVGILPVFLHGRKGKYAPMETR ITDDHMAYILKLG
2771	132:267	0.918	0.698	MYQCESGIQVFNFFLILFHYTTLFHFTIPPILLH YIILSYWNLDV
2772	79:214	0.935	0.802	MNICNFLNLWIVCIAYLIEQIWGHGWSEMGCP SVTPPLGSGAQWG
2773	1091:956 ¹	0.976	0.866	MLYLLLFPGVSYLRSLFLGRPIGPGITSDFTLIL FSNLLDSWPLS
2774	859:994	0.98	0.902	MRMQLCAAFALLAPRLVQEIFVELSLCQVYIL SVLDHQRKSTLY
2775	141:276	0.99	0.702	MLWLFFKKPLLVLIRFKLTMVLGDTQAWQNLS EFRAKFIAS TSPF

2776	203:338	0.962	0.807	MFLQFYLLSLGFFIPIKRMKCPIETKHYARFLLLI LQKSLFFCIE
2777	56:191	0.985	0.81	MCIFIRTTFWQVTVKWLFLIISIHHTVFYRVKIK MLRKGCLHYSC
2778	500:635	0.919	0.632	MPCSVPETLFSLLWLAPSHHSGFSSNEASLRT DLLFATAILYSLW
2779	84:219	0.983	0.845	MLFTSFVYGLIFILDFYFLSFVERDVKIFNCNG EIVLFPFNSVH
2780	99:234	0.947	0.678	MILNLSSLTLVFAWNYPLHLMISLNVSCSCYS DISGIYRSVLRQ
2781	82:217	0.93	0.824	MCLILVIWKIHYAELIMLNKRVVNKCRSCLIQKC LSTCHSTVIVL
2782	269:404	0.966	0.771	MLAPCPILMALVISGMVVTIEKESYSFYAQLFRI FLKTEGFTVVL
2783	26:161	0.884	0.652	MLMICFVFNVSNSCHSIYLSTVKKRDQLRTIS DLISSCYPFWS
2784	151:286	0.994	0.808	MFALSFIFAFSHCVVIYLSICLAPLIDYRSLQDK VSVLVSLSIKG
2785	167:302	0.964	0.731	MSWLMPETKLISHLFWILSICTLFLHKYRIRNV GHPRLSDLTAN
2786	36:171	0.974	0.909	MNLKRLLLFLAKMFAIFSLPHSHFPISIDN IGHWPQSPKVR
2787	116:251	0.935	0.767	MHLRRFRMSLTISYFLWESVWVPAWNARSVIL QSDCRPCHWVPS
2788	132:267	0.975	0.645	MIMLQLFFFHPLQHFYLTQSLLFPSSTSCSKPC QQYRILSISSSL
2789	389:524	0.948	0.752	MAGSGPGRSCFAGMCCLLPGLPIRFALPFFLT PMFPQYHPHNMLG
2790	165:300	0.978	0.936	MAPLPSLTLRPWCVLMMLDLWAAFGTITPSLK HFHHLPSGTQHS
2791	322:457	0.936	0.708	MFLDLCLGSLSVFIDTHPCMHGGFKCSQDW CSPAKLLLSAFTKT
2792	1064:1199	0.887	0.677	MALNSIYLVFETWCTCMYLYKHLLHLKSTTGK QSVLSFVYKFGVY
2793	204:339	0.967	0.875	MWVAFVFMTHFHWSIAWDLEHITCQSLTFLF TNNAVDNSTSQR
2794	925:1060	0.897	0.657	MADRGRGLGWSGLLRVAPXFFXWSXWVGGR GRWGGGXXXCYARVGR
2795	182:317	0.96	0.878	MLSLVKLLLLCIHDHSINFCIAIQVGLLP SAYRV PGIVLSLENT
2796	69:204	0.972	0.779	MPKALMSLMFSFFGILLNVSDQVEAEAEKVV KVQSTKECILRKR
2797	378:513	0.942	0.711	MHLFAFISYVFKVIRHSFYKTSYLLFFLTALHIL QRITEMGKGE
2798	1031:1166	0.977	0.771	MVNTWLAACCTVVTWFPKMSMLPLPPSKPSA RSSWLWIGAPLASRL
2799	212:347	0.894	0.696	MRSRVQSTWHQLGTQMLILLSSSQLVALHPS HMYLGCPVADAEMI
2800	85:220	0.966	0.764	MRALALVLRPVCSHLLPPSLSFSLLLKGWTP YSFKASLITTAPH
2801	98:233	0.989	0.875	MRPLAGGLLKVVVVFASLCAWYSGYLLAELI PDAPLSSAAYSIR
2802	1608:1743	0.98	0.893	MLPFCHLWVPVTLVAAGAAQPAASVMFPHL

				PALHHHCPHSHRTS
2803	204:339	0.943	0.68	MRQKFLKPLLILLHRLKLGSLYTPSSVARYDSS
				VNENRSVNSSAY
2804	386:521	0.98	0.909	MNPFCEGFLVLLSCCLSLDSQLHNIALQITC
				FKDVEIPNFFCD
2805	83:218	0.91	0.701	MLAGSLLAFERGAAVSSVCRVKKRGQSSEE
				MNPSRKGCCLTSRRE
2806	113:248	0.985	0.906	MCILWAITCTCVRLGMICTNQKTMNFCFMSLK
				FYRNNKRKGHLYW
2807	130:265	0.969	0.884	MRSILFLSSSVLLAKALAQGPITFCPLYLVHE
				DTMRDFVSLAK
2808	78:213	0.966	0.849	MGSTPAATLVTFSCVALSLWLHPSGLASSPLK
				GSKIYVYWRLLSSK
2809	216:351	0.978	0.877	MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLL
				ELLSKYQHNEHS
2810	152:287	0.919	0.614	MVITRAPAASISPLPRLGCCLPALSVPAPLLL
				QHLWLHTEMATS
2811	1074:1209	0.983	0.952	MLLLLLLLPLLWGTKMGMEGDRQYGDGYLLQV
				QELVTVQEGLCVHV
2812	209:344	0.947	0.809	MWSLHIVLMRCSFRLTKSLATGPWSLILILFSV
				QYVYGSCKKYIG
2813	265:400	0.922	0.769	MRSSQSHLASFLPLTLLQPSWPPCSLSDMRI
				SLRPLHCLSLCLM
2814	237:372	0.93	0.745	MSVWSDPCNLSLCSWHTVLLLWPWSLCCVNT
				LRFNPSRCLGGENS
2815	42:177	0.934	0.761	MTFTVSVLLRIVLYSNCKRAGSFPEVIRERRG
				RKLVGVWQWFWSS
2816	515:650	0.951	0.843	MAALLPALLPHLLSTAKPSAKTDTWGFCLPHS
				RGLLHMSGTSDHW
2817	8:143	0.894	0.552	MGSWLKRGSWAELPLLIGPLHLAHRREPGPV
				ASDSPLPLWQHFA
2818	251:386	0.953	0.705	MDCGWLVEKVPWCAFLCPLWILPELSTSEAC
				FTFRLPGQDMQLLQ
2819	143:278	0.961	0.934	MLVLSVPGVVIAAILRCGSIVPSFPFLPDVGT
				VRSAARCHHLGA
2820	100:235	0.945	0.798	MYYTLCNFVFFTLHMILFPKSLNILLSNQIRSAI
				VHLKQRTSCIK
2821	19:154	0.889	0.569	MGSITCLTGTCTLETQLCFWGS LTGTCTLETQL
				CFWDSYDCGHHWA
2822	280:415	0.899	0.581	MLTSSGCEKHLASVSSLSLFCVCCSSCQLL
				WENECERGSQRGW
2823	197:332	0.931	0.635	MYGWTMTSTISCVFWACPQRKKGLCKREGV
				GSSILIHSLAAFVMF
2824	223:88	0.945	0.776	MSRPMMTSASWTSVWSVFVMIYLYFERKYVL
				PLLGVFYTIISND
2825	328:463	0.893	0.708	MFWMVKILTPKASTFQVTTSVSVPLTSATGAA
				CSGSCFHSTGCAG
2826	79:214	0.969	0.828	MQTHLGASCLSLVIRIALFLVQRDGHLSRR
				EIYAIFTKGSLCP
2827	99:234	0.907	0.63	MQLWITTPGPVLAHSAWAPSAFAVCMGSTFLA
				KPCGEMSEAGASLP
2828	24:159	0.955	0.84	MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYI
				RTVIYICASSR

2829	85:220	0.977	0.81	MVCWAWVASGALLSVVRELRRKLSYKMIGRG TWRAQVHMNGHSVK
2830	442:307	0.993	0.912	MFDLAMWNWLLGIFHIVCVSVCTYDMQGKH PIQNSSTLWPSVSP
2831	4:139	0.955	0.732	MCHKLFGYTQIVWIASYFLLLSTIENIGCEHVQ VFLECKILEVQV
2832	278:143	0.989	0.939	MWVCGRPWVMCLFLLTSFVLLNNVACFPHLG AWLRPSSHKALKEL
2833	113:248	0.988	0.94	MLMKLVGRAAFKLFLHVTIVICLLGGDCLG VTVCALSTGSQP
2834	565:430	0.953	0.625	MAPLFFPSEPQTILTKFYLNLIIFLLSPAHLVS SAMLFPSSVQ
2835	135:270	0.914	0.657	MQVSYETNQFLLVCMWNFPVRFAFWHYNVL CSHKQSLLRLSYQK
2836	162:297	0.899	0.682	MHCRQLKEVLQLPLTCSSCCVCTMTVAFPSV QQVWMETVLTGGL
2837	265:400	0.931	0.648	MREARLPQGALPFCQLSPGRIFLRGFWILFLS HLSVGRVPNTMP
2838	90:225	0.984	0.933	MELWGAYLLLCLFSLTQVTTEPPTQKPKKIV NAKKDVVNTKMFE
2839	230:365	0.958	0.806	MSPSEILVFNLSFLILLPAAFLLSLDQDKDQSG TQSSISSPLRVP
2840	280:415	0.93	0.741	MLIGKPGLLKLGVFPFLVGLQTPSVPLPVPSP ALLAQAPSSWVC
2841	39:174	0.979	0.884	MVCLRLPGGSCMAVLTVTLMVLSSPLALAGD TRPRFLEYSTSECH
2842	131:266	0.931	0.785	MSLSCAFLTLLHAKACYANSTQYSKHFINN YINRVYKLFITYLL
2843	54:189	0.922	0.765	MMSPSQASLLFLNVCIFICGEVVQGNVHHST DSSVNIVEDGSN
2844	124:259	0.928	0.794	MRTWSKVIPSLWLKFSRGFIILRFHFLMIWPDI PSSMYICMSFI
2845	159:294	0.95	0.779	MGLCVPAVTTSFSLGLEWDLNVRLHGQHL VQQLVLRVTRGYLE
2846	116:251	0.936	0.598	MGQSLIPSPFFSHKFFKMARFSFKFCFKFCL FLFKTESIYTQT
2847	113:248	0.942	0.761	MKFSNVLCTCLLILQVKLFYKTVHENSFLPC FSLIPSPQRNL
2848	274:409	0.946	0.658	MFRAALSAALQLFFPWKGNCRYELYPASLCDI KAFYHSMACSSSE
2849	182:317	0.994	0.958	MKSSNIFSLFLVTFIFLTISIILFSSWCPFSLI KCNQDLYYS
2850	35:170	0.986	0.965	MLCSLFHILIVTLLAISFGMSSRNTLNMVNSKI KEHSLHRKLEI
2851	408:543	0.965	0.875	MWIIQISALFLCYLGKSQKQISSIPNKDKLGIN YIIHIKILAYC
2852	233:368	0.951	0.879	MERLRGKCLLIILMTPLCTTTISSSCIEGSANF FCKEPGSNCFV
2853	956:1091	0.947	0.7	MQGMKTQLIQLSTLLRLDLSGFCSYLESQDSG YLYFCFRWLLIRF
2854	830:965	0.984	0.822	MQR LGKAPGTWQAISKWLLLLSLPFSQSIII SLRAGTMSYLP
2855	336:471	0.993	0.934	MPRRGLILHTRTHWLLGLALLCSLVLFMYLLE

				CAPQTDGNASLP
2856	384:519	0.951	0.767	MTAGIMPLGLCPCSCLCCLHSRTGAFSAVHWS PVEGTPDPSLREVI
2857	437:572	0.968	0.934	MLIGLLAWLQTPPAHGCQFLPITSVTATVYHLP VHQLKGRSRVQK
2858	86:221	0.975	0.886	MAVSVRLTLVLIAPGFCWMGNLYVNSRYEPDI LQQLCGKGKVVVA
2859	1295:1160	0.914	0.754	MVVNTMIYFFIFTYTLAKRARVHINKNGNKALA EKNMHLTNHVNS
2860	2618:2483	0.987	0.79	MVGFDLLPLFFPFFPFFSLIFFPFFSSPSPSFQ FLPHQEKSQHV
2861	416:551	0.988	0.801	MTLFLRWWSVCCVSFVGKVQCAIHKQLVLE DSFRYRLNCLGT
2862	528:393	0.947	0.787	MSKPILLMTLFLLPNDLSFKNWDRDAEAVTS QRLVRNSGTGLGG
2863	115:250	0.916	0.61	MSIVSRLWSSWLPYPGIESPSYKQAGLRTVG PRIFTLLYLCRASA
2864	1328:1193	0.97	0.802	MYLWVVRWKWCLQKLGRILLHSLHDFIAN MDDKGLCYRGLRAP
2865	383:518	0.989	0.839	MRSLLLIQVFAFSGLFFFYEIFTAEVLFKFKQAQ WGEGLHARISAS
2866	6:141	0.987	0.886	MFWTLVQGMSSLCLTDVFQALPSICIANSEIYY TVLTLMQFNCLW
2867	1054:919	0.993	0.881	MSSGRNFGFCFQWLPWALVATWASVTVLMS SHSSSVGSGLCPMDF
2868	264:399	0.956	0.806	MNQISLLFVECFLFMARRVLTAFQKGKYCIINR MFQRKKQKLST
2869	301:166	0.983	0.884	MQFSCHCFLISFCCCFVILLPDSSTFCVSLLP HLYCLSSPVHRL
2870	87:222	0.882	0.584	MVTGKSPNTHCLLIALYPLLPNSCKWVMRSS YQHSLSYCKVLT
2871	147:282	0.987	0.891	MGLGARGAWAALLGLQVLALLGAAHESAA MAASANIENSGLPH
2872	14:149	0.961	0.731	MIFPLVGYLKFLAGNFIYIKVLGFQPIMNIR DKITRVIVSGE
2873	204:339	0.922	0.809	MYLKPLIYFSILIFLSQRSKLSLPYNVHNCMNIG EDRRPQKVQLL
2874	263:398	0.887	0.607	MLPLALIVDLIYPWWQVRGPEDPNHGTTERKR EEVTCLGAARLSL
2875	208:343	0.916	0.634	MLTLPLFEGLWMCSHRQLVKGSLLNIKEEGCK KKDADVPEEVT
2876	47:182	0.94	0.804	MVYWLWNILRRWVVIENKTCSLNHLRIIFLRV KTEQEVTPVGFA
2877	194:329	0.95	0.817	MLMTLLTLRLKIYICAYDYGEKSSRLRKKNIKL LDFAVHSPVKR
2878	169:304	0.964	0.79	MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLH AWPSSVVEAESNV
2879	218:353	0.97	0.908	MSSVLSDLAFVLLCFTSLSFFVALPSSATLSF FGLQVFPRFLKT
2880	158:293	0.926	0.55	MHLWIRYLPFLVGNERQLCGSGWRTEPTARS VFWLCTLCALAEK
2881	327:462	0.933	0.769	MKSLWEELGKSLWCVLALVLQVDSHAGLVSP SVSVSESESCSR

2882	114:249	0.982	0.959	MPLLTLYLLLFWLSGYSIATQITGPTTVNGLER GSLTVQCVYRSG
2883	103:238	0.993	0.97	MPCARLCARLLYLILFFLRFIMSAVPSFWLLSHI ALRGCTSVSAH
2884	856:721	0.992	0.95	MRLSLPLLLLLLGAWAIPGGLGVMAPLTATAP EVDDEEMSAHMP
2885	352:487	0.968	0.819	MQLLRAVLKVSCLFSFCSHVYTASTDCDTVYE GEKKSFCFLFLF
2886	15:150	0.992	0.903	MLLGFGNVFILLILXTAILWLKGSQRVPEEPGE QPIYMNFEPLT
2887	193:328	0.975	0.895	MFPYHFLVSSLCLCIIMVAVPEGNQRFFDDSK LIFYRIQERHWRE
2888	64:199	0.929	0.692	MRISCPWCLWNLSLEVGGTVATTAQQHIAEV CRSSQAGRGFLHCL
2889	120:255	0.928	0.652	MVLLKRGYVLRLLKCGPPSAVPFNVGQCTE HMVIEIISKCGFIV
2890	403:538	0.957	0.858	MIISLVLEIFYGALIFAQQGYLGHQQGTEGW EMFGILQTAPPP
2891	34:169	0.989	0.945	MRIRLLCCVAFSLLWAGPVIAGITQAPTSQILA AGRRMTLRCTQD
2892	134:269	0.912	0.735	MVRESRPWWFFCFLVKAGMAESPYLLVPRAK LLSRLLSSLTVIPQ
2893	76:211	0.98	0.75	MSICQVFLSSLTALPIAAMSWQCKWSMPKVE LPPFPKPNQIPNY
2894	391:526	0.937	0.836	MSQQSWFTVYLFYLLRSNIWLEMGIKYVKEV ELRSLDFTSNYFS
2895	54:189	0.989	0.834	MFPTIASGGVCKTLWLKAITLLMWVILKIAFR FYLLDCLFSTN
2896	174:309	0.889	0.626	MALKEELTLRLRFSFCGVIRVTYKKRATGTAQ LDFSQALHDTLQ
2897	99:234	0.971	0.904	MKVHVKQLWLWGLGHMWGLGAALSGQCKS CFFFRVRSADVSPSPG
2898	258:393	0.985	0.938	MAFLALPFLILPSQLLFQSLTNHLCASYCASC WQYCSEQNKLTAY
2899	46:181	0.974	0.858	MDWTWRFLFVVAATGVQSQVQLVQSGAEV KKPGSSVKVSKASG
2900	104:239	0.947	0.799	MACRWSTKESPRWRSALLLFLAGVYNGAL AEHSENVHISGVST
2901	193:328	0.968	0.825	MYGMLEWPISMYFVAFLHCFLCSGGNLGDSF QALPELCANCSSP
2902	91:226	0.984	0.951	MRRRSRMLLCFAFLWVLGIAYMYSGGGSAL AGGAGGGAGRKEDW
2903	133:268	0.973	0.905	MACPGFLWALVISTCLEFSMAQTVTQSQPEM SVQEAETVTLCTY
2904	197:62	0.956	0.783	MMGFLIKCHWFPQYVCGLATVSSFCHQFHNN SLEMLSIYYASALC
2905	164:299	0.95	0.632	MVLRLPWWGVLAYGNDVGFGFYSLCYQINP PTCPILWLWEVLTV
2906	372:507	0.881	0.711	MTPNLCIRFLLKFYKAVLAHYLLSQLEPFSHDR LHLHSAFMKSRF
2907	268:403	0.957	0.889	MERPLCSHLCSCLAMLALLSPLSLAQYDSWP HYPEYFQQPAPEYH
2908	83:218	0.977	0.908	MGSLQPLATLYLLGMLVASCLGRLSWYDPDF

				QARLTRSNSKCQGG
2909	158:293	0.884	0.634	MNVIPAFTILLRSPICYPTLCFLRNTRNG GRPPKTLPFHKL
2910	2131:2266	0.982	0.919	MQGLCISVAVFLHYFLLVSFTWMGLEAFHMYL ALVKVFNTYIRKY
2911	120:255	0.938	0.688	MFRERLGGLPRVSWLCTSSLLVASQANDLSA TLCGFCMISVHYEM
2912	232:367	0.942	0.606	MTANTGTGNIVCFLPLLPGHGSFFPEACLSGT GAVLIFQLLCTMC
2913	959:1094	0.992	0.896	MEFLGPCGLRLVGARPLLPYWLLVFLAALNAL LQWLLRPLVLYAP
2914	316:181	0.955	0.808	MEPLTTCRLCPAALAWLLSERWTPSASVHGIA LCVNAPWLILFSY
2915	715:850	0.944	0.763	MGMGRLLPMAWVLAGIPTGAQQSWRRPWS GSAPRCASCGSAWRCC
2916	52:187	0.975	0.815	MIASCLCYLLPATRLFRALSDAFFTCRKNVLL ANSSSPQVEGDF
2917	60:195	0.921	0.725	MSPHNSLVLCFFFGAIKLPATGSFPCPRLPLSL RLSHPTALWETG
2918	52:187	0.938	0.824	MPVWLMVKGISFCPLPLPPQLGWERGGGRR QEGGDNAKRPRRYS
2919	62:197	0.99	0.921	MMCLKILRISLAILAGWALCSANSELGWTRKK SLVEREHLNQVLL
2920	52:187	0.921	0.577	MPRPRRVSQLDLCLWCFMKNISRYLTDIKPL PPNIKDRLIKIMS
2921	266:401	0.925	0.709	MRSLPQPGYPSGNYFLFCFFCIFLLTFNPVSR YSTPCRKYSSLE
2922	411:276	0.944	0.644	MLSRFLYCRIFMAFYMQIYSESVRVPKLNCR TFSCGVWFICLLG
2923	332:467	0.97	0.857	MFFGSAALGTLTGLISALVLKHIDLRKTPSLEF GMMIIFAYLPYG
2924	264:399	0.953	0.73	MCSLMFGSSVFCFPVPLPAPHSGGPPHR AGRSVFSAMKLGKX
2925	122:257	0.984	0.878	MLKVSAVLCVCAAAWCSQSLAAAAVAAAAGG RSDGGNFLDDKQWL
2926	1003:868	0.988	0.844	MSPPTPISLFFLCRSLLLTVILPSCFLCGEMG GGRKYKHICIDL
2927	313:448	0.954	0.798	MLLLLLPLWGRERAEGQTSKLLTMQSSVTV QEGLCVHVPCSFSY
2928	71:206	0.969	0.846	MNFGATAQLLHVAISLFFLIYIFKNPSISAFENKI FFCLLGKLN
2929	15:150	0.929	0.579	MVYGGEHRVLLCVGLVLLGRRRPGKQEVDS FTGKGTQKGVIRGR
2930	195:330	0.986	0.692	MFQIYFSFCQLCFIWSCFFNSRETFNEIYKFFL KSMVRKIFECH
2931	220:85	0.973	0.96	MSLNVLALFCLLLAKERTTTKRCISCLPFSTFF SFGPLQKVTD
2932	295:430	0.959	0.84	MALHCGCFLLPPWTCTELSHVSVCLGTTEEG SMKDAEVRPFYCPP
2933	48:183	0.965	0.645	MVRLLAFVCSEAMSSVLCWVSGWEAMIPNTK NSNRQDFKRKRNS
2934	1642:1777	0.986	0.953	MYFSLIFLVFFFLSLPLSSSSSEPTSSILGFSSS SLSSSSFSPPS

2935	506:641	0.959	0.782	MLFLSFFPLL SKKVTWQLPSACPTIVFWVCVG QVICLLSSRNEIE
2936	24:159	0.881	0.735	MKLLQFQR FCCNLCAEIVATSIGSLMCQGLSK RSTFINSANPQNS
2937	38:173	0.933	0.742	MRAMLGTCALGQFFLIMGNTQRCDDFPTESP PAKTNVSRAGLSPP
2938	590:725	0.954	0.696	MLFGLALQLILDKLTTVNQRES DVARVATAEE YSKKGLLGQETL
2939	204:339	0.975	0.913	MGTFTAILFLLCYSTSGVLGADNCLLALGCWT TGSIFRPSKKDC
2940	520:385	0.987	0.865	MIWALSSSLIPFLIALCFVHSANSHLQVLVICSS LFLEPPPHNFM
2941	1256:391	0.964	0.697	MVAFFFYFSLKTFLLSSFCHKEEIKHSVFLHLTI NQALFWFSSAC
2942	600:735	0.982	0.883	MWNFQHLLTHAMLFHTFVTLIFFSLPGKLDP NLHCHYPLGKYIL
2943	21:156	0.936	0.651	MLYMPSYYFVVCFLNYNVAGAFHVVYRAPPL CEAYRVFSAGCTLS
2944	326:191	0.985	0.866	MWEELLRGLTAPYWLSSWLCFSWRAATVAV AVAVAVAAAAATAAA
2945	237:372	0.937	0.623	MCLIH FREGMLFLALTHLQELVESH CYVNHSD TRLQSRRFMPVW
2946	231:366	0.975	0.906	MLPRYLVCVLMGTGFQACLCPSSL CGRGQVT SLRSQPLHLSVGAE
2947	273:408	0.932	0.563	MSLKFLKGFKNIYLYFILLKKKNHIVCVLNDLC LTGCLLRSTS
2948	270:135	0.993	0.933	MGMLGVLIWFLVLFIVCPESLSLSTRCLPPS QVPKVSFLGTYP
2949	47:182	0.959	0.825	MCPFCPLL FCLSFISKVQIVSSLLKPFMTLYY ERTSSKLLNLT
2950	226:91	0.898	0.734	MFLFSRISNLMFVNHLKPLMITENKQVSKEEN KATHSHRSSFQS
2951	110:245	0.932	0.757	MHESPLAWASVHLSSPLLCTACSSPLMGNS VLCRAPADMGLAWM
2952	206:341	0.941	0.662	MLKLLCAAEVTNVL FNCVFDYGC PKTFCHPW TIFVLFWSSLEGGF
2953	297:432	0.906	0.702	MVYIFMCNCFHMLHLKTHYNLCFPIFLETRRN NPTIKRQSSLTD
2954	241:376	0.988	0.963	MRSSLTMVGT LWAFSLVTAVTSSTSYFLPYW LFGSQMGKPV SFS
2955	303:438	0.97	0.782	MTVSGTVVLVAGTLCFAWWSEG DATAQPGQ LAPPTEYPVPEGPSP
2956	472:337	0.974	0.747	MCHLMTTLWLLHLQALRPCSRREEGRIRANS SHLLSASDNSSPE
2957	365:500	0.989	0.909	MGAWAWVPTPSLCLCHSTCLEFLLFLYILFYCI FETVSLSPRLER
2958	136:271	0.996	0.952	MSLLSLPWLGLRPVAMSPWLLLLLVGSWLL ARILAWTYAFYNNC
2959	856:721	0.992	0.95	MRLSLPLLLLLLGAWAIPGGLGVMAPLTATAP EVDDEEMYSAHMP
2960	261:396	0.927	0.616	MSRTWVMRKL TGGFKFFLQVLIMETDLLQSRI PNVLGLKLQDIRP
2961	782:917	0.982	0.925	MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETES

				PVRTLQVETLVE
2962	31:166	0.914	0.647	MFLQVHSFIKLKIMFYNFIVCLINLYQSKAAITLK VYPGQGKKNL
2963	97:232	0.909	0.67	MTWTAASIPATLIQRGLLTPCGTGLWPHLSQP PPMKPSTROQPPL
2964	96:231	0.957	0.747	MVALLCRQIISAAFSGEGTPLCSWSSGPILSSV CLLCPLAVLCPA
2965	273:408	0.984	0.854	MWVCIYLALLVFYSLDISLSQNNNYILLWYNAIL NRKILGLYML
2966	248:113	0.977	0.664	MLLFGLIYCLGHQVSLLLKASGARTLPSPKPHT QLIYIWREPSVW
2967	740:605	0.973	0.943	MKTLPLVLVLSLTLLTVFSETSPILTEKQAKQLLR SRRQDRPSKPG
2968	222:357	0.924	0.803	MKRDVLITETFCILFWLCAFSMNDYVFKPHVL YIDCPLKRLDSS
2969	364:229	0.917	0.724	MLQPMFFTLSTHLVGLSQISYLSFPLISLHPAQ VVKRQSSLPRLM
2970	314:449	0.926	0.652	MSTIIFQWPFMLVSLHRCRKLPRALKDWQAFL DLKKIIDDFSECC
2971	98:233	0.946	0.755	MRLLTVFILLNMNIYTFYCRNVNIGYRILFPVP YTVSVPFYFFK
2972	28:163	0.922	0.565	MYISLCKTLTVSHFGFISTWVLNNFVHIDVRV DTNIFQVISTTP
2973	961:1096	0.894	0.641	MTAGTVTMLLWHASNWDVQLPSQPLVELTPV RDLDTSGLTAFAR
2974	36:171	0.995	0.94	MLMIIAMILVLMILLTALPRVLNQLRSLVHAA YLHEVFFRGG
2975	977:842	0.996	0.979	MFTRFGLFLFKFILMFFLLSFISYFCLFPCSNLP KVIAIFNIVL
2976	968:833	0.981	0.859	MLFWLIKVSCSFSCSDETSAAASWGFGAFSFSF LLLGISCLMRLVP
2977	98:233	0.912	0.722	MLTAWAASVCPVPSRLALGSWTTVKRPAVMP LFYLNTPACLRSVS
2978	940:1075	0.989	0.945	MALRFLLGFLLAGVDLGVYLMRLELCDPTQRL RVALAGELVGVG
2979	89:224	0.991	0.803	MLVTDTEAFWQPQPWFVVLTATGALLLLALG WLLGRLLQGLAQL
2980	64:199	0.969	0.702	MLPIPLKSIMLKKAFFVLLQRECPLLFFIFVYL PETHFTTPHWF
2981	133:268	0.95	0.846	MVKRKSWTKWCGWLTVVRFLARGFEMHLKS CSRLLFSELAFAFF
2982	229:364	0.972	0.867	MWVDCPVLCCLALVLQSTGSQAWSSTGITLT LEFSSPLSALTKI
2983	90:225	0.98	0.818	MPCSFTLPFTYLLFLQSRMPFILLMPRKLHLIL QYRAPVPPLLLL
2984	349:484	0.982	0.812	MAPFIIFSLCALCFERFCLLNKLHLLSNNIFIFN MRHTSLSMNK
2985	30:165	0.944	0.858	MACLWLTHVSAFSWAGGSKMASPSRLGPWR CVSAGVPQTSSMWLL
2986	247:382	0.942	0.75	MSLFGFGASLASFSFFSLGGAGGEPSQPLSP TFSFTGITSAAPPP
2987	100:235	0.963	0.922	MGQRWKLVTSLIIFHWLELSLMAKYLMMSGDT EKYSQVVCYGEEK

2988	100:235	0.907	0.707	MAAALKDVLFILFQLSYFCDSKTYIFYILSSRKS HASYNLWQFTT
2989	201:336	0.95	0.596	MTLSVDLCSKSPLLPKCHLTksfvllgqlllsf LSSSSLNVPHYC
2990	89:224	0.96	0.815	MLSVNLSWSTHLLRWITFFYLSIGTAHLYHWL EMRTKMRI MG FNA
2991	112:247	0.934	0.741	MVLILSPGLSILFTKMSETFSSSLLKLSSSICIFP LCINMIICYQ
2992	235:370	0.958	0.757	MVYACIFILVRLTLNPERYSFLYSHLEYALPGS VGCLEGPLeASL
2993	213:348	0.992	0.819	MSLFWGIQPVLI FCLN FLGFLSFCPQVELLPSS RSGSGSTIIVNCL
2994	17:152	0.894	0.619	MKITSPFICSAALKIFAFAISFYDPNNRVRKAG WQSYCPCTHGEI
2995	201:336	0.944	0.662	MSFQAFVFLMIGWLHPDPRMTQRSCGPHPE VDSAQEDHF SHPYD
2996	196:331	0.987	0.919	MCLMKQIIYLLYVGLCSILTAFLTPHHVLERYR YYCPDFREIKK
2997	252:387	0.95	0.596	MKEALLKCSRLARGLLLCLDCANDHRSPVER NAQTTLILHSSLYS
2998	44:179	0.969	0.88	MYMLLQAFWLWQETLKTILLYKFTKPPANTPV LGVNAQVCHSCLA
2999	101:236	0.988	0.871	MIAFLWYPLGMCNIHVAVCLFLNASWSVVPDK TQSPFEGFSVAYQ
3000	33:168	0.913	0.594	MWGLPHGKKIVAATHTCLLA AFHTVVSQQIFM EMNEHMKTIAITE
3001	46:181	0.986	0.949	MLETFLFKLFLFFTLLVNLFITNDQLSVGSIFLS FQLPAFFLDMA
3002	1807:1942	0.985	0.832	MDLVQFFVTF FSCFLSLLVA AWWKIKQTCW ASRRREQLLRERQ
3003	397:262	0.927	0.8	MLSMHSPSWIFLCCFIIFSPGRVCQSKKPAG GHSPVLPLCPFGL
3004	175:310	0.979	0.809	MVLPYLDGYFSIFMFLLVHLCFCLVNLLQGPT NCSKAKALVPIF
3005	339:474	0.946	0.749	MHWLRASAGSLLMVPLMTDLHELALPPASLR TVVKENMCVLPFPV
3006	68:203	0.942	0.764	MTFLLHVLVTALSSHSTGRRGTNCFMLLSSGN HPIPCGSLTPYPH
3007	214:349	0.926	0.747	MVYLPVSLNGLRLACFSYVLAPIKVKPGGGSE TRDGFRIPESTPS
3008	514:649	0.983	0.884	MGAFVTRVALPCSF AWCACILGPASALCSLC MKNFQPPFQVILDS
3009	224:359	0.993	0.912	MLGLRLFLVLLSSYSCIFSLSLNYCFRADEL PIC SNGPKSKEGLM
3010	50:185	0.917	0.618	MTLLNLYYLSNFLLYSKRFEGISFCVQKVSII LC IHYLRSTTIWN
3011	55:190	0.905	0.614	MPKFGFKPECMFCFSLLAHTLGVL SYHHQYFL RFPVRNDSYLQKL
3012	104:239	0.932	0.872	MRNLLQFKLFLLYRSSAAA IARVGYCTPTTGS ATEVIYDRSTSS
3013	274:409	0.907	0.696	MLKAVTLTLCPCWQRAIASHEKAEGPLSCLPL KLSIWMP ELKERT
3014	314:179	0.945	0.852	MLYCLAF AQILKSFA SIVIPATYQPRLLPARSSS

				TLTPISNTVWS
3015	8:143	0.954	0.573	MSARDXYKNEWEISFGVFLLLDGFLWLIFRYL PCFSHFLHYFLSQ
3016	67:202	0.907	0.601	MGWAMACAASTTLGLGHHGHGVHQHCQLPR RRGWALECSYYVNAE
3017	115:250	0.971	0.921	MFMVLMLLISVEAATKHSWCLREACLRCQEH FEKEVLPSMRFKGC
3018	5:140	0.954	0.781	MRLFYCSGTYMLVSYAVCWLSLDPDSQDPVS QNQSHGLTPNQWAE
3019	84:219	0.943	0.81	MKLPHLAQFLTSPVLVWSTGVSGSAGFHQLV PQWECEEVPGCGKS
3020	146:281	0.952	0.702	MVICYTLSITTLIYFVCYNKYIQIRKIERDQNEIY NIFKLLIMV
3021	143:8	0.964	0.847	MFPPSVLLNFLLGITLPRAFWMLSNERLAWNC KISHLPIKNVTSC
3022	296:161	0.969	0.797	MQLCFCVWPSCCFALMNSIPLYEYFPVCIHLF CWGGHLGCFKLRL
3023	64:199	0.927	0.618	MLHQMFKFIGHLIFIVLDPDLSDMKNNPEYDYK FVKWMTKHKVMF
3024	6:141	0.957	0.844	MWVFWSYEFCIFLFDLYSXSHLYVYCAVHTLT RFLKMRNRHFLEE
3025	145:280	0.939	0.693	MQESNIYFLSICFKTSWCLFLLATGHLYCNS QTLWQYTEHCYDS
3026	52:187	0.982	0.909	MPFHSISLLWFLFPLLLKKGLGYTRVFIFPPRP ALNENGKEKPLF
3027	51:186	0.956	0.825	MISAFSFGASPLTLNCFFICALLGSIGYWVRKM DVTVISLWTKLP
3028	153:288	0.915	0.655	MNVTAIWLHRDKLFCWLVISYISEICLSECWIKI AVFKNSLFKNV
3029	155:290	0.918	0.745	MPVSLTFWYVLGRGCLYDQPTIQTGLGESLSS FPGREPFRVTA
3030	174:309	0.886	0.556	MAEDNQRRCGNFCLVITGVKWPVCCLVLPR NCCTCCSFAYALT
3031	447:582	0.989	0.947	MPTCFLRYPFLLIFFLAQLLYIWTSLYCPFLSN LSLPYSSALSP
3032	63:198	0.882	0.558	MVLCSSAFLTQWGGGEASDNIYLAIFYFSVCGF TISLTLTPSRHLK
3033	169:304	0.908	0.592	MLFILIQMIRTMGYSLHYVLHCSLGACCPYMY KEESNFLNKLKRN
3034	158:293	0.963	0.889	MHFPVNCFFKSLHIFLLQVFLATFLRKKLSKV AFSCLVEFFYYC
3035	76:211	0.91	0.773	MSVFFLSCLLPQPGPIAAGVRCYSWTPPLVR GDLAGKVACDVHP
3036	74:209	0.939	0.857	MSSWPRMLAHCFYLLKALSSSYLIKEMTIMPG TLLSTLCILTHLN
3037	115:250	0.947	0.805	MYTHFFSIWLLGILTKIENCPFSVRYGISCHTDF LRLYIQLCLEV
3038	207:342	0.976	0.875	MHCTFLSVLALPVIVRILKSWSSCLWEGNLVH VKCLKFPVLSHGS
3039	71:206	0.925	0.666	MPEHLCFEICNTLLNFFSFLLLCVTDHETTFD SGWKASGSTVTC
3040	85:220	0.912	0.653	MPYFLCFYRENSCLLVLTGWYQCQPVTTWCS LIEGFAPHWWVLVY

3041	59:194	0.916	0.752	MITVMWMFVYMTSMGASRLKKTNTKNSKGY SHNHMQVVVNTAGW
3042	86:221	0.909	0.711	MWCHMQCLIMTQLFPNVRCTGLSLHTEASYLI LVLK CERSSCWAQ
3043	417:282	0.965	0.911	MKCFLFVCLFVCFSEKLDLGASFFSLSAPLAF GVRFSWSCLPRNS
3044	60:195	0.918	0.57	MWQDLLVSLFICAFQKYFHYGSSQIKSKCSER WIWSDFLEALEFC
3045	122:257	0.985	0.956	MGRLFPLVLLFPVTNSVSPTALLVLVTTGGS GPATMVLLPAPVM
3046	207:342	0.897	0.604	MTQVHQRVLVCTVADLGFISCLDLLHYQQSES LRSPGQEISEASL
3047	107:242	0.913	0.564	MSEAQLKNPWTSSFFVIFQFAFSRACCMETRL MGANNEWSSELGK
3048	86:221	0.97	0.804	MVSKFKLHYIQFSLWGALACIILETILCLKEESC YTVTSFRESII
3049	109:244	0.922	0.718	MMYLIVLSAVSSPWILRRESPPKFYDVFGGP VFQRCKFVNIPWK
3050	31:166	0.991	0.812	MLTFLVWQAELVLLPTLPFPIVTIYRTSHCCLL CVASASLPGRSR
3051	56:191	0.985	0.943	MCCSFLLEGLISLFSLQLFSVQLVLLFFLWIVSY SKKQIKDTFAK
3052	468:333	0.974	0.884	MPFLSRFMLKLWSLSLGHKPICLGEKIKEGK KKEFRARNSQQPA
3053	466:601	0.984	0.959	MTQILAPSSLLLFLCPIFLPYFLCMFTLPCRRI KLAQILLGTRW
3054	416:551	0.943	0.59	MFIFFNPAFSLIIYPLKKSCKTCLSLHKRIFPAS LFIMWKIRWN
3055	347:482	0.995	0.928	MSSLFILAWTPILFCLGIRHCSVLLAHSFLYCH LVLYNSPALDT
3056	254:389	0.943	0.886	MTFIFIVASWSSIAAGAPAFPATSQAGSRRKG WGRGKKDITYHLSI
3057	31:166	0.919	0.689	MKIGVLFIPRDSFILLLSASCTPRFWKRLTNRL QRQPTLLVTET
3058	133:268	0.992	0.968	MLVPTFLSLVCDLSLFLVLLLGCLSFLPPHLP CTSFPLHLWRLL
3059	182:317	0.906	0.697	MIYILCLSVQPHLCHSWLTVSQLGEFFKHSRV FSAIPHQDLCHFS
3060	71:206	0.945	0.638	MLPLFKHSPVRIFLCLNTQHLSVRNRFVFN VSPGILPISLCLA
3061	95:230	0.964	0.709	MKPILLVLSSITRALLQISSVSWQSCMWRAM PDCLQTDYPISLG
3062	13:148	0.919	0.81	MRLININVLLQLVLGITRQPENYPAGPLSFVPA SSSLFHTPVSSF
3063	197:332	0.902	0.678	MCLCWLSGCSKAWCND CQIPLCKKTAQNPAL CQLESSSQHVHMIS
3064	188:323	0.938	0.648	MCRCVQYILTCSHVPLLCTRLFITGSDDQQW PMPIIRYFQVKPQ
3065	180:45	0.897	0.625	MQSPRAPPGSSIITLVHLCFITPWPLLCALITS INPFHFHTPLQ
3066	45:180	0.944	0.636	MLRITTAWLPFAFPCLSPASSLGGEQRCLPIL HIGKLRPRGNGDS
3067	302:437	0.934	0.727	MIFWLNLSHLFSSYYISSSLNNFILTSCLILTLF

				SLSLIRYTSR
3068	54:189	0.988	0.787	MLWAWVICFAVDCPGSLVFKWIGKREEYCPR YKGAAGSGGRIKE
3069	187:322	0.912	0.552	MKCGPGLAFNCFSLQLRWFPFTFIKCDQLPSLS SLVCCMDTLYSPL
3070	28:163	0.922	0.604	MMGGLAPSIINFFFFRICLIFKNRLGVSSKILHL AIPFYEHNHS
3071	255:390	0.973	0.877	MFALFEGISNKLVLFPLLLFFPFMKMVIHSSAL QRAGTGHSCGS
3072	408:273	0.913	0.597	MCTNIRCWPLPQLLAIHLTNPSPCSASKAGSH RQWALAAAALLVK
3073	147:12	0.978	0.887	MNFLVLFLTILGFTRGLRAAMMPRRRWLPPPP TRPTRPRTRGST
3074	148:283	0.944	0.8	MWVCSFLIFLPLESISPNIKKSATPHPPSRSA VLLWDCCALIP
3075	394:529	0.994	0.838	MLFPFLLFLPSILKLCWEMVVLVSLHSAKYLQD LPRSPKQPILSC
3076	23:158	0.954	0.838	MGASLALGFTEVVVLVGLFTVKLGAHLTLLPPL GGHLSPYCAAQAW
3077	283:418	0.991	0.753	MPWLFLGGKLFYAVIKWALMILQSYIXVERRKL ASPTRLDSYLG
3078	182:317	0.978	0.838	MCCELLAVVIATLIKIGLVLLYFIKLLIHIEFIKR HSILKCES
3079	380:515	0.986	0.954	MVCLLLLFSYIICKQMTILYLNIIYLRRLTLA LPRNVSLSNM
3080	180:315	0.969	0.761	MDHAKSLFYFLLTFNYLCLQMLLPGIGKEKS REDGIWFLDQNV
3081	104:239	0.947	0.799	MACRWSTKESPRWRSALLLFLAGVYGNAL AEHSENVHISGVST
3082	47:182	0.938	0.588	MRKLVLETTLRVWLDYLSLLKITYDVNQPSEQ KSGIEFGKKQKY
3083	230:365	0.983	0.629	MSNRTRIRTHVNLCCFCRYTTPKMSFSSACVS LCLMLLFCSPPLL
3084	259:394	0.94	0.671	MCLVYAQNSSFQMLLVLLHCSSPECNIRAES RLVQSVFGKEVVA
3085	97:232	0.987	0.973	MPARRLLLLLTLPLPGLGIFGSTSTVTLPETLLF VSTLDGSLHAV
3086	47:182	0.986	0.908	MASMAAVLTWALALLSAFSATQARKGFWDYF SQTSGDKGRVEQIH
3087	314:449	0.942	0.648	MLSIRKNHKEDSLFLVHFFLLYFHYIGFLFLFM GTSNQETDWNKN
3088	802:667	0.933	0.649	MHSCWTFQDLSLVQLCLPLSCPQQGPVGP GFLPVSVQVGPCKPA
3089	18:153	0.959	0.755	MELALLCGLVVMAGVPIQGGILNLNKMVKQV TGKMPILSYWPYG
3090	493:628	0.972	0.841	MFIGLGISFLNCPSLFAHFILFCPLPLFGIFISYW FVRLLSINRG
3091	163:298	0.972	0.949	MMNSLFLMVVLQYLMGLIELLRQQVTFSPF LIDL RDQGSTHTL
3092	1955:2090	0.984	0.843	MGAGCTPVVLGAALWLWRWFSRWGLGGLC WRPCTCTPCHSASPGA
3093	457:592	0.983	0.938	MCAFLLPFKLLFFLEISLAMKSHFPFTLLILSRV LLKKTLYVLKL

3094	92:227	0.972	0.902	MEFGLSWLFLVAILKGVQCEVQLVESGGGLV QPGGSLRLSCAASG
3095	541:406	0.904	0.695	MAYRGQLLAGFTFDVSACLWTSWRTALTECV AWGICPLGWVVPVL
3096	169:304	0.953	0.873	MEFGLSWLFLVAILKGVQCEEQQLLESGGDLVQ PGGSLRLSCTASR
3097	350:485	0.984	0.637	MSWRTRSMHTHISVSFKGKIRPTSAYLLLFLFF FCYGVSLCCPGW
3098	40:175	0.913	0.602	MIVHCTIIPLSFCVHRLRAPLDAYFQVSRTQPD LPATTYDSETRN
3099	43:178	0.98	0.945	MGSTAILALLLGVLQGVCAEVSLVQSGAEVKK PGESLKISCQYSG
3100	20:155	0.977	0.91	MEFGLSWVFLVALLKGLHCEVRLVESGGDLV QPGSLRLSCSGSG
3101	48:183	0.99	0.611	MAHYKTEQDDWLIYLYKLLFVFNFFFWGGA AVLAVGIWTLVEK
3102	92:227	0.972	0.902	MEFGLSWLFLVAILKGVQCEVQLVESGGGLV QPGGSLRLSCAASG
3103	867:1002	0.909	0.584	MRAHPHTPRSAHHILSTWLALGPYLYRTRNC GPLTEEPSLAPST
3104	13:148	0.945	0.861	MEVGLSWVFLVAILKGVQCGGQVVESGGGLV QPGSLRPSCGTSGS
3105	188:323	0.899	0.75	MWPQLKSFFLIPTQIHFNLTNLPWRRRELRL RFVWVSMPELIGA
3106	129:264	0.934	0.585	MFIFKTKGILLPCQKMLQIVFFFLPKNTLSSMFY FSDCIGVHKYM
3107	177:312	0.899	0.661	MYMWSGLLGSKWTLVYSHFLNMAPASFHY QASPLLEHDTLSSS
3108	371:236	0.966	0.825	MAPFFLCFPCFASYLFWHEELGPPGIVYTALSS VLMDSDRPWPASS
3109	184:319	0.971	0.929	MFCRLLWATGAYGFLGDDVEYTSVLPHQK GKEAWVFICQLPFI
3110	948:1083	0.987	0.825	MLCGNTQLLFTVAIILLYVTCLLHWTFLHLEWR VSEGRHHDPLST
3111	168:203	0.882	0.714	MAHMMWGGRFVIPRIGCRQCFVTAIAFGLLVEM EYVTWMACLMPSG
3112	78:213	0.936	0.711	MYVFAGCIGTVWTVTAIVYHLWPNTVISYTCV QVVIPQPYEEDAT
3113	175:40	0.951	0.743	MFSFPHSCRMFFILMITLNMFAQSIGRPRNR DQEGRDHRTDPG
3114	70:205	0.965	0.797	MCLRRTLLWHLHIAPLVNILSDYKPLGRWNHA PALTAGALHKTTI
3115	295:430	0.97	0.804	MLVFNLSLVLSHSLVLEFVMFLYSLDSSHVCPL VVPVTLDLIYLVY
3116	115:250	0.977	0.788	MAVVQALTPLVSAAATASCLTSCSWSLTFPEH SVNYQSHPSETQP
3117	721:586	0.9	0.664	MYRLSSSMLLRALAQAMRTGHLIGQSLHSSA VAATYKYVNKKEQE
3118	50:185	0.991	0.931	MIELAFASFLKCAFSLLILFSFPLWFFLSCF ACSYSFSCLLS
3119	70:205	0.915	0.659	MFCSPLLILQVYPTWKNPNWHLTFHTSVFSF PKGVRSLARGIPD
3120	163:298	0.908	0.673	MQQMMWAGLLCPQLEWLQGRACRPCGLLAS

				DAAALWFRGGISAW
3121	194:329	0.944	0.837	MSVLIWCLIFFPLEYSRPKRGLKVDNVCFSTVA LSTGSRISNWSN
3122	60:195	0.95	0.719	MKRLRFVLRVQMTAFITGAHTITNYSRRLYI SPLSHFFMNSGS
3123	140:275	0.932	0.77	MGLNIPGLWSLSSVLSLTGLTSPVVFLGSREQ NPLAKRLALKELL
3124	44:179	0.925	0.626	MAAAAVSGALGRAGWRLLQLRCLPVARCRQ ALVPRAFHASAVGLR
3125	268:133	0.928	0.601	MRPGVSVHLSGPWFCCCLCNEIVGLLDSPRVF HLILISEEGNGKVY
3126	288:423	0.986	0.967	MRSLGALLLLSACLAVSAGPVPTPPDNIQVQ ENFNISRIYGKWY
3127	198:333	0.953	0.659	MWVVQDLMWPWLGFILEWHEPSFTSCCHYT RIFMDTCRLLTLCRE
3128	21:156	0.912	0.575	MPVPHGPPPVWGYTRLCCLALWVDGETPCV SLTRAGAPHRACRGR
3129	226:361	0.965	0.622	MYVAGYLVANSAICQLTQHSLVKLLQGCFLIG SLHLCICVPMCV
3130	161:296	0.926	0.638	MQLFTSTQALTGLALPLPADPSGSPQKGTTM CQAMKTAKRQEPHT
3131	127:262	0.962	0.811	MGHLLCVWGFTYILPCISLRHSPLQPPGWEGF CRNVSFPLLRASL
3132	233:368	0.947	0.701	MHVLI RTPCSLILCLANSSHASLPGFSASSFLF KESCRLLLNSSF
3133	193:328	0.94	0.743	MLYCTSCFLYINIILSKIARGVRFCTCKVVS NPIPFVDANEDR
3134	280:415	0.96	0.828	MWREIARRGCLFLLGISLLRSCFSRVEVNEILH SPVNYSTYFPAL
3135	572:707	0.978	0.736	MTLLWPHTAACLSVTLYLPASSAKYFKRGE GKEKFIPTNPTTRKKK
3136	38:173	0.915	0.648	MPGFSVLGTILHIFCXXXETVAFYLAKHSFLAS EGLTHPLAFLN
3137	425:560	0.991	0.927	MACFTALSGLPSTLLWWVTFLKTLSSSFCE PSLLLQKPNPSIT
3138	252:387	0.973	0.832	MIAFLFGLKVCLWRVAINSNPAVLWLKRKKS R ECFQCAFHRILLY
3139	172:307	0.99	0.848	MSCILASSLVMLVHLVWKLTLCELLWTDQHAQ STSIYLGEIVGNQ
3140	30:165	0.975	0.861	MPQLCGLLLSVWGLGWLGTEDPKVVDDLGI TWSTPQPELQASDF
3141	49:184	0.924	0.747	MAHISFFCYLPFMYMVGATGPRGIKPLPLSLTT APPALPLDYS LH
3142	78:213	0.953	0.87	MYFLLLP SKTLRSPILICHSVNDPQVLVCKPT FLRAYRTQVVK
3143	259:394	0.931	0.807	MYLHVLYLSHRILLSPYIPSFKSVPPPVFSILQM APMSILDIDHP
3144	69:204	0.97	0.763	MVTSEKLLARVCHVCLCLCLGSLGSCSWWL LSTVTPRVSVSKPL
3145	99:234	0.994	0.956	MFLVFCNIITVITMTSLFILLSCIFILITCCYKCR YISFSFTFS
3146	190:325	0.979	0.927	MTAWFCSFLSSHWWIKLPRFLLLVLPFFWGKK FSLGLISQFFSKA

3147	109:244	0.927	0.569	MFGKRMELTNCILFTVCVLESMDHIFIDLSSKS LKNNFEDYMKFG
3148	145:280	0.955	0.62	MLFPLLARGRSLWFSHVFSEQVHGPNLVCG LVSQNCVRTLQNPY
3149	54:189	0.88	0.654	MAKLLACRQNFLALRLGNNYITAAGAQVLAEG LRGNTSLQFLGFW
3150	88:223	0.962	0.662	MFLAWFRGHQTYWLSLLYSPWPINAIYESSHT ERAAAWSLLKGLF
3151	212:347	0.98	0.945	MSDLLSVFLHLLLFKLVAPVTFRRHRYDDL V
3152	163:298	0.893	0.631	RTLYKVQNECPGI MSWGFYLPYPYSLSYKIFLVYRRKHPSSQPSL
3153	86:221	0.962	0.73	STEGRADPTDSI MARCTLTLKMTTELLRGGSFEFKDMRVPSA
3154	280:415	0.887	0.706	LVTLMHLLCSIPL MLHPITIPRKYTFCFSLTWNVLFFQVHLSYSY
3155	97:232	0.966	0.879	RLRAPLSQNHV MSPLPLKSWRFLILAFFLVIEKLQVQKKDSSQS
3156	102:237	0.971	0.798	KSHTHTPQRQNS MQLWGFLNLNFPCCSLCFWALGSRGFTLVLA
3157	458:323	0.989	0.937	VTPINSTGWAAHLP MEFFSYILTHILSILLVAFLFIVTTFTLKLSTMP
3158	229:364	0.908	0.629	PTLERCPISY MQLCPATTLRSLKVLLPPKLRQVLSLAKCLKQ
3159	169:304	0.942	0.889	GYVYRGSWGWIPI MILTMCLLLWSVDAEPTPKGLLSIQEMVVTKN
3160	142:277	0.953	0.786	APSFCLIPFRS MLMVLKLVICSIFIGKEGHFVISYLPFSLSNIQD
3161	155:20	0.905	0.609	TLKSVHQPCSA MLTQFWLGLLYGYGDDSRYMAIVGISAKSKC
3162	146:281	0.925	0.702	GQYPNGKYTNKGKS MCTVAPEPCPARGSLAAILFLRLPQLSCSP
3163	191:326	0.968	0.728	VPSGAMPWARHCP MGISCKLLLLTRVCYLITPLDLERFPFPNTEQV
3164	645:510	0.933	0.676	TFPERRVSVFLL MRILFSGWLFVRFPGHHCSEKAKKAFLLCPVKG
3165	244:379	0.99	0.905	KDLFLTRKGAIRP MGRRWLFLIACLRASILAWATWRNPVSTKNK
3166	116:251	0.956	0.678	KLASHDGPHLAVP MMASFWEAVVLKLRPWLLWGEERGNKAFLS
3167	256:391	0.92	0.623	KEATQMVFQHNGKWL MILFHCEKLYALRSFDFWFMLELLSTWPRALG
3168	166:301	0.969	0.849	LLCPGLAIEAHEG MQFLMMTESSSLLLYTGVLTEYLWAGYCAE
3169	10:145	0.959	0.859	LSTCRILFTFDT MWLFCAWVSTWGQGCPPGRGQMIYASHHLS
3170	29:164	0.974	0.843	VHTTSPHHWLSAWAL MKTCLKIFTYYFLSLSNIFILTIGLTCASGPLDFTP
3171	79:214	0.959	0.859	VFLLGKGLK MWLFCAWVSTWGQGCPPGRGQMIYASHHLS
3172	103:238	0.962	0.913	VHTTSPHHWLSAWAL MLTACFLLRVSRMPWPSFLGIGLYHCHSNLSY
3173	291:156	0.898	0.746	QRQSPRVQSPQR MIQAVFMLLFQHTHIKLCPSSEALPAEVVALS

				YSVVAVPLRAL
3174	79:214	0.959	0.859	MWLFCAWVSTWGQGCPPGRGQMIYASHHLS VHTTSPHHWLSAWAL
3175	15:150	0.959	0.859	MWLFCAWVSTWGQGCPPGRGQMIYASHHLS VHTTSPHHWLSAWAL
3176	57:192	0.991	0.888	MWPALLSHLLPLWPLLLLPLPPPAQDSSSSP RTPPAPARPPCAR
3177	108:243	0.997	0.923	MLLLAAFLVAFVLLLYMVSPKPLALPGA HVVTGGSSGIG
3178	427:562	0.997	0.854	MDFLVLFLFYLASVLMGLVLCVCSKTHSLKGL ARGGAQIFSCII
3179	106:241	0.973	0.915	MAALTVTLMVLSSPLALAGDTQPRFLWQGY KCHFFNGTERVQFL
3180	251:386	0.989	0.944	MELVLVFLCSSLAPMVLASAAEKEKEMDPFHY DYQTLRIGGLVFA
3181	108:243	0.988	0.826	MVAWRS AFLVCLAFSLATLVQRGSGDFDDFN LEDAVKETSSVKQP
3182	554:689	0.982	0.913	MYLLCWLYIMGVLGASCNWHVGVFPFGTHW PRSQNHLLWVYNHLN
3183	178:313	0.962	0.724	MMPVTVVSPVCLYILSLASLNSVHKMILCLEIL RYKEWEKTQTC
3184	386:251	0.947	0.599	MPLD TDAILHRTAEWVVLCLITCIFMYVLYVPY LRSILILEYLHL
3185	56:191	0.975	0.846	MMCVSLVLTILRCLLPPTH SFKIVRTIVIVLQC SAIVIQDGGN
3186	323:188	0.936	0.743	MKGLARWNL CVALGQAFSLRGHRSLSALLH MGSEPHFHFLLGP
3187	229:94	0.965	0.904	MWPLLG TIVSLLSTGTAGIPCAASQGAPEYLT ARVGSTPTRKKLP
3188	154:289	0.997	0.798	MASHGGNTLEIVQSMGCM LVLLLWVLVCVL FLDGFLGVLYRAP
3189	1720:1855	0.979	0.691	MWLFRA PMPAPSLCAFLTSQ LLEYEPRSGE QVPLLLKMKRSKLA
3190	12:147	0.983	0.908	MRVDTLALFTTLWWKTFWSLT VLYDICARCSV YALCQAKEVSFYR
3191	88:223	0.903	0.628	MGLPWLGTRQLTRVAGVGSGKRLLTLGILTPL SRILLCNHFLLP
3192	268:403	0.967	0.792	MGLCGMWVLTAF LCEPMGFRHRVCPHRCVR GSGRSGGCECVMWP
3193	214:349	0.927	0.734	MPFANIFSVCNLFHFLNSVFQRAEVLILIKSK LSIFTFVDYAF
3194	923:1058	0.994	0.975	MGVLLVSMVVLFI FAILCIFIRNRILEIVYASLGA LLFTCF LAVD
3195	38:173	0.937	0.779	MALGVPI SVYLLFNAMTALTEEAAVTTPPITA QQGNWTVNKTEA
3196	438:303	0.988	0.938	MLCNLFCYFAILLFLLITSVKKFQ GEMNQTPYL SHCYPDTSELPF
3197	150:285	0.972	0.783	MPPRPPQSHLPALGWLLTYLAELSEGWTFV AVLKGALPASKVLC
3198	55:190	0.97	0.576	MKVSCFQHLSLTMKMSIELCVVVPYDFFIYIL FTVLFMFCLIS
3199	254:119	0.971	0.879	MQCEKYLLILFCLLQKYFQCLAFHSLGVLFIT DTIIFICTIL

3200	199:334	0.994	0.959	MSRAGMLGVVCALLVWAYLAVGKLVVRMTFT ELCTHHPWSLRCES
3201	516:651	0.936	0.641	MWSLWIVVDQHQARLIPSPQVLLLLRETPST AAAVAGWLVVASM
3202	232:367	0.929	0.748	MWICRVKQAWLPPLLSPLGPPTPWDPFYAAP SPPVWVGSGYWYRG
3203	70:205	0.975	0.775	MGLPHSYEDCILFGILAVLCFTVLLMNLAVYSF FNCFYHSPCNE
3204	178:313	0.929	0.673	MWLRCSLGVRAAQARSLAKPLGLIQHLARPP GLGLRCISIRDPG
3205	184:319	0.982	0.929	MVTWLSFFWVSLTVTMGTPPHTHLPNKHTCH KHVCIGLPLDNTLW
3206	1:136	0.932	0.744	MPFIFSLIAVTRTSSAVLNRIVRGDILAFLMDF RVYILLLSVCI
3207	254:389	0.96	0.911	MLLTVCLTFFLYSGYSQEVWCYTLGNIPQMPS APRLVRAGITWVT
3208	837:702	0.917	0.819	MSRNLRTALIFGGFISLIGAAFYPIYFRPLMRLE EYKKEQAINRA
3209	99:234	0.934	0.827	MQAWRSFVMGVEVLMYIVAVRCRAVFATSLW QPWCYTRAGGQFNV
3210	202:337	0.985	0.653	MHKYLCVFEYLSNLSKCMRLYLILLASICMYLC VARRVFLFASVS
3211	83:218	0.953	0.791	MCFLIHYLPQMFFCQSTYVFSVSEFNVKITIEY VLVFWVFCIIML
3212	2021:1886	0.926	0.742	MAGRTTAAPRGPYPWLCCLLVALALDVVRVD CGQAPLDPVYLPAA
3213	300:165	0.973	0.782	MMLGWGWKALLLKSLAFPTQGYPEGYEELLT KVTGADLTWSPGDG
3214	349:484	0.934	0.759	MNWQHSTMYLFFAVSGIVDMLTYLVSHVPLG VDRLVMGCGKYSWK
3215	859:724	0.917	0.622	MAFLLYHLVYHIPPMAPVSFVFETKSRSAQA GVQWHDPGSPQPL
3216	51:186	0.991	0.93	MWRLPHSQFIHIVILPLKVFLFLCFLRWSFSL VAQAGVQWRDLG
3217	47:182	0.983	0.753	MCFLIDFCLHTLFSCAHCLLFDHLLFLFSNLS SSPNFVSENAC
3218	146:281	0.978	0.734	MMSFLWANVHTATCLGLRLTTGMGAVHSPLT TGMGELSGRGDWSS
3219	1296:1431	0.983	0.947	MHLALTTVLLWAWGSLQAFEIVEKENIFQRT CPAFLMFENAYL
3220	116:251	0.979	0.841	MCAHLVCVKWCLVILICIFQNTNEVEQLILCVLL IPLSSSMTDLF
3221	171:36	0.895	0.699	MGSASHALSWGRWVVGWVLGTGEGFACSI SFIASHNSEVGTVSL
3222	324:459	0.98	0.836	MLGMISMLLNALKLLVYLTECCMALEERVHSV LIGWSVSFKRIQR
3223	313:448	0.932	0.709	MFFFNYASSYRIFLTPLGLQSLKFLHSALLQK KNCQLLVYTLQI
3224	169:34	0.89	0.559	MGLISEHFTMTILLTWLSSKRKDMTYSILICKLG QEHRROGIFSP
3225	209:344	0.972	0.733	MLYLFFASIEMIIFLSFIRERGGIILIDFYKGKM SIWVFFLIFQ
3226	241:376	0.946	0.747	MVLHGLLCLNMAALESDFEHAVTGQLLRCC

				SKLGCKKTFDLV
3227	385:520	0.945	0.796	MGLGQPQAWLLGLPTAVVYGSLALFTTILHNV FLLYYVDTFVSVY
3228	264:399	0.975	0.873	MFMWVGRALATWRLVSGMVASPGSMNSL CSGGVSGGLWPARP
3229	21:156	0.968	0.701	MENQPVRRRALPGLPRPPGLPAAPWLLGLV LLPGTLRLAGGQSV
3230	86:221	0.961	0.666	MGSRCSTLSTVGC RFPSSLSSWLLPFLSCPLC LLYPNFSVRAPFR
3231	1208:1343	0.936	0.786	MAPLSTFASLCPVALSDPTLLSLALSSWVTP RMGMAPSLSPCC
3232	42:177	0.972	0.646	MGCDGRVSGLLRRNLQPTLTYSVFFSGLC IAFLGPTLLDLRCQ
3233	170:305	0.98	0.897	MYFANFVGFLTCLQIFSSVLQPFSLSGTLTTQ ILDLLVLVHSAE
3234	118:253	0.915	0.582	MTCFVTVLFCINIRDYVLFKESLRNEQFLDFM RNKTQFSEFCCI
3235	383:248	0.927	0.685	MNIFVQVLWNITFHLTWINTKAWGFWVYVVF NCIGNCQAVVRSS
3236	459:594	0.961	0.633	MSSVNRDNWTSTFPIWMPLISFSCIALARTSI TMLNRSGESAHP
3237	28:163	0.965	0.841	MAGHWAFGPPVSGLVFLLSLAPSAPGIWSWIL GLQRGSPEFRGSG
3238	130:265	0.888	0.583	MRPWLRLHLVLQALRNSRAFCGSHGKPAPLPV PQKIVATWEAISLG
3239	118:253	0.946	0.623	MCKTISFLLSWCATFERRLEEGAFLSMGTCFC HAGEKANLKGSGS
3240	385:520	0.945	0.796	MGLGQPQAWLLGLPTAVVYGSLALFTTILHNV FLLYYVDTFVSVY
3241	1093:958	0.995	0.967	MLMWMLTLWGCASVTGTLRSNTVPWPFST MDHRWPSNMSTWMKS
3242	57:192	0.972	0.725	MSTCHVTAGQALCLACMVLALCREGQGGIGK SLHRSSTGRWQKEA
3243	65:200	0.98	0.785	MDEKSNKLLALVMLFLFAVIVLQYVCPGTEC QLLRLOAFSSPVP
3244	747:882	0.983	0.9	MLAIHVGLVLLFSLSFNCLNLEDLSVIVCHKM YLKIVEVIQKRE
3245	432:297	0.934	0.841	MPLCWLASLRPMPRILGWGAFMLPWAHPPT PRTTNSHGNFASLP
3246	117:252	0.987	0.977	MLVSTLLFFFKIVLAILRPVSFQMNFKISLLIYTK KPTCVLVEIA
3247	199:334	0.93	0.743	MWLGGRGANLSCPFLALGVFLTSECLAFLL KVRVRILGPAVQG
3248	368:503	0.973	0.938	MGVLVVLTVLWLFSSVKADSKAITTSLTTKWF STPLLEASEFLA
3249	44:179	0.982	0.851	MEPLLPKRRLLPRVRLPLLLALAVGSAFYTI WSGWHRRTTELP
3250	263:398	0.991	0.966	MTLVFLVLALMITICILSYHSHLLINSNIPVKY RNFP SILLHF
3251	1457:1322	0.98	0.733	MMMILVVLRLRRLMVEVVKPKQHLLFLGLP FLQYLESIFHLL
3252	244:379	0.982	0.581	MNTHWNILPVERSCPLWISSELSYCSIKLLFILL TLHLPAYLILP

3253	136:271	0.98	0.834	MWGLLIPCILGCMKLPNLLMLFSLETFLTLRFI LDSFYSYVFKP
3254	83:218	0.968	0.844	MMAGIRALFMYLWLQLDWVSRGESVGLHLPT LSVQEGDNSINCA
3255	573:708	0.97	0.864	MCLLCCECLFHLWKRIWWQGFCSFYLLWV GLLSFPPDPPWKSF
3256	330:195	0.982	0.856	MIAIFVLFPALRGKLLTTLKMLSLVGFLWIFFVR VKKYHSVPRWK
3257	548:683	0.997	0.917	MSHCGLLFLVVTWLLSFIFLVCKMRITFLCCLLT VDMKPNKVLYM
3258	361:496	0.953	0.711	MHQPCAFFNVIYASRVWIISLCTFLLQQMSAH HLSKITDKELKVP
3259	34:169	0.941	0.567	MRVLCAPPEAMPSSNSRPPACLAPGALYLALL LHLSLSSQAGDRR
3260	185:320	0.905	0.791	MSRPQDLVLLLVGWPGTAGYSKGTGDSRQ QLQSTPANFSLAKGT
3261	539:674	0.958	0.751	MLLKQTLAKLLSFIFLELGPFAWSHTQPCLR TGCLRVLKSPFW
3262	817:952	0.946	0.722	MLVGAVAVPWAHTLCTQWAQRFLCTCWES LLQVPARLPRNQRP
3263	102:237	0.977	0.756	MCCVICKQYVLLSILLCLLASGSVDFFLLPHS VLADDDGIKVK
3264	382:517	0.885	0.663	MGFVGWACIAPCGASHMSVLLHNRSQCQVQ EAGXMRLRPAGGALH
3265	113:248	0.943	0.658	MANVFVLRNSFLTKMVKISCCVIFVKFYGIAFYI RCVIKLVLIFA
3266	237:102	0.985	0.967	MQAFRLTSLVLHLMYLTGFIILGFYFHLFSHK FLIFILXXXXX
3267	437:572	0.968	0.934	MLIGLLAWLQTPAHGCQFLPITSVTATVYHLP VHQLKGRSRVQK
3268	195:330	0.883	0.619	MRLSISLKFLLQPLKAGAGICWDLMLVKCLLSNI PYCVSMVSWPCN
3269	617:752	0.997	0.911	MQKPRNICSCFFSCSLFGVFCWLFFVAFGWFF LAALTPLDPFDLIV
3270	316:181	0.967	0.886	MVHCLICMWTCWPTGAILHRVCRTHWPRGVS HTHVMMHWPTCVVS
3271	117:252	0.991	0.973	MGVMAMLMPLLLLIGISGLLFYQEVSRWLWSK SAVQNKVVITDA
3272	44:179	0.911	0.702	MRYKCVLSKILWFCPWKYVWKNSSFFNLEGMF MFIEVTCRHYSTCG
3273	106:241	0.979	0.789	MQTKGGQWARRALLGILWATAHLPLSGTS LPQRLPRATGNSTQ
3274	246:381	0.937	0.677	MIFFIKAPLYLLQSMMDCLYARRIPCITDCAMA EIEKLGQKYPVA
3275	306:171	0.899	0.769	MGYKKLYIMVILLSTVLYEKHSGFLSYSCSDFP SKTLKFTFKSNQ
3276	12:147	0.965	0.782	MGFLHQLQLLLWKNVTLKRRSPWVLAFEIPIPL VLFFILLGLRQK
3277	644:779	0.941	0.704	MSVLTHPGQQAFFRRILSPFLCSLSFLAWILDRT VTPIFVTPYALL
3278	177:42	0.955	0.786	MVYEVFINKANILLLLFLRQSLAVLPRLECSGAI SARCNLHLRIP
3279	1208:1343	0.936	0.786	MAPLSTFASLCPCVALSDPTLLSLALSSWVTP

				RMGMAPSLSPCC
3280	323:188	0.936	0.743	MKGLARWNLCVALGQAFSLRGHRSLSALLH MGSEPHFHFFFLGP
3281	988:1123	0.894	0.659	MLSGWVQCPLLQRVHFYAFSVGPFRKIWD VSFPLTFYFKNLQT
3282	101:236	0.936	0.668	MTGLFLHHNPGILLAPSVLDLLFPGSHIFISLF LSLCPCFGDTI
3283	369:504	0.987	0.576	MQKKWREEGKTAGGVVSGTFALAGSWLCLA FVFATSRPLLCMPED
3284	395:530	0.982	0.878	MCALHMLPLPSKFFRALSALLPRLECSGLISA PCNHPIQGSSNS
3285	69:204	0.977	0.731	MYFRYKSFIRYDLQVCSLFILFFLISCHMLTPIF MLSIVYFEEQK
3286	90:225	0.973	0.718	MFQILLTYVPLGTSLQHSCLLFNYLFWINSQ KLNWVWKGCKYF
3287	158:293	0.946	0.778	MLLPGFIAHALCLTTAGERWPQILTYICCLKTP PMGSVTTSMRRI
3288	270:405	0.947	0.858	MHPLLSHTLAFLQWGLCRPTLSSQECWGDQT QHQLGVTKSDGVK
3289	97:232	0.939	0.733	MWGAPALQCIVFFRWTRSKCLPDTGNVCTKT QRKKAAGRLGVAGG
3290	157:292	0.905	0.564	MLTLERSVGLLLRALGSHGRILRKRVTWHNW PWGTFLLSSVRSWG
3291	129:264	0.967	0.856	MSLGSINHFLFFIQLLVKNSYCMLLKMKNKK LKKIMCLLFLML
3292	141:276	0.955	0.657	MLAWRLCPWGPGLPTTTARSGERTERRERV RTASPRKILFKTQP
3293	78:213	0.979	0.929	MFMPGTVLRILLALPYLILTKQVQFFLFSDEIMA WKVVAPGLELS
3294	101:236	0.972	0.768	MPAPPLPGGWNTWGPSLSLPLLLLGAVAMAL GVRPPGQVGLSPIA
3295	133:268	0.92	0.684	MTNYFFFFSNPCISFLGLFSAFLGDFFSAMV NISDDTGHSYLIP
3296	107:242	0.996	0.928	MGTAAALGPVWAALLFLLMCEIPMVELTFDRA VASGCQRCCDSED
3297	484:349	0.928	0.692	MSAITLLPSLIRLSAETESQISCKARCSQYGE PGCSARARPQK
3298	130:265	0.982	0.865	MRRTAFILGSGLLSFVAFWNSVTWHLQRFWG ASGYFWQAQWERLL
3299	333:468	0.994	0.945	MLTELLLCVLVLCVFMSRGSCLFATIREFWPP WVGCGRGENPSV
3300	327:192	0.881	0.593	MVAATPPGIARWALVISFPPVTPTAPHMCAAQ PWGRHGSAEGTTQ
3301	34:169	0.974	0.943	MVWHVRKSSFVWLLQLFSFISCHSVISVSPVH VPWTQCAVIPPYT
3302	172:307	0.969	0.841	MQCAWTTLVIAPALTWSLPYHEGHSKLTYIRS GTNRRILLTCTDS
3303	380:245	0.987	0.904	MAATMVSIAFRFLMSCTLVAFSPSLLLLAAC GSSSPPSPLNPL
3304	174:309	0.996	0.973	MWLLPALLLCLSGCLSLKGPSTGTAGDSL TVWCQYESMYKGY
3305	345:480	0.947	0.798	MVCRPVFPCRRRFCPRPFLVGLVVAICLFYQT LTLRGSRKLTAA

3306	296:431	0.996	0.86	MHMC AFLHVWTCACMHLCVCVCAETGKGVK VLVREPGSFLFPNLS
3307	365:230	0.939	0.683	MAFLLSTLLNHYLACKHSSSELWLQSSLNNGK KKDKAYIFTVLAL
3308	328:463	0.994	0.982	MVWVLLSLLCYLVFLCRHSSHRGVFLSVTIL YLLMGEMHMVD
3309	163:298	0.955	0.888	MLGPTVFNIFVFLITALGALPSSLPHAHSAAW TLLPGPPAQQHS
3310	142:7	0.948	0.809	MNFLKSFLIPWSLLLPRRAGADGPWGWRQE VARKAWQSGSQSH
3311	335:470	0.969	0.883	MGRFLDEQWVYFIILLFFFRDSLALSPRLEC SGAISVHSLRL
3312	5:140	0.98	0.903	MIFACECVLRLLILNVSFLGAVSEETTNALET WGALRQDINLDI
3313	298:433	0.955	0.881	MAVQQQFIIIVLRLVFPVAGTTRAPLHWGAIP GWEWPPGDDAYP
3314	50:185	0.993	0.855	MLWLFQSLLFVFCFGPGNVVSQSSLTPLMVN GILGESVTLPLEFP
3315	99:234	0.993	0.95	MEPRLFCWTTLLFLLAGWCLPGLPCPSRCLCF KSTVRMCHMLDHI
3316	53:188	0.971	0.911	MSPTASWAFSLPLWYWGVLVAGEGRGNAAP VPFQSQAFLCLLSF
3317	113:248	0.959	0.789	MRSSLAPGVWFFRAFSRDSWFRGLILLTFLIY ACYHMSRKPSI
3318	49:184	0.893	0.598	MCECARACAYAALTCRLLSEVFVCTQASELR GPPVLPPLPSEPRP
3319	294:429	0.926	0.701	MPTLSLLCVSLPFYTNARTQGLILNPYPRAATP EPPVPRHMTLTV
3320	148:283	0.986	0.826	MLGAAPNWDGPEVVLLLFIVSLLVIFILVPSLY LFSPPFPNLS
3321	177:312	0.929	0.779	MKFVKRQGPCWRLCMVALEVLAQGCQSGW HRSGCLLCAPQARVI
3322	101:236	0.982	0.939	MPSWIGAVILPLLGLLLSLPAGADV KARSCGE VRQAYGAKGFSLA
3323	66:201	0.982	0.912	MDSPWAGLLWLLPTLWSSFPAPACWPSSSS SSPVCANGAMSASR
3324	76:211	0.988	0.936	MGWAPLLLTLAHCTGSWAQSVLTQPPSESE APGQWVNISCTGSG
3325	551:416	0.983	0.838	MASKASSLLFSPVLGFTLLKSLSFCCSSNWR LFLSSSKSFCCCS
3326	216:81	0.937	0.667	MKQGGGDWTIYWPSTCFFPRLSCLSYLAVQ LLSAEYFLLSEVTY
3327	63:198	0.925	0.606	MFLWVSGTLWDWRPRGMSGKTDLP RPPA QTCCSQTQRLPIRRG
3328	248:383	0.935	0.837	MRTHTRGAPSVFFIYLLCFVSAYITDENPEVMI PFTNANYDSHPM
3329	157:292	0.973	0.85	MLVIVCIFLTLIVQQVIYSHWRRFNRYKRYGVY LSPIMFHSYWLL
3330	228:363	0.939	0.712	MCLTSTLCRVLLGQLRDSVENILTLFKFAVTSV ALGSCPSESALG
3331	452:587	0.985	0.955	MLIAMGALLCLIGMCNTAFRSSVPNNQNWPS VWSIVQVATWWLG
3332	390:255	0.952	0.829	MWGSWLWICWHIGARRIRGCHVSEWGLQEN

				LPEDRSGLCVCWAPHG
3333	383:518	0.921	0.704	MVLYWFMGMFMTSGDTSAWAMKCSRTGFW MPGSFTLSLVPEWPSS
3334	1676:1541	0.972	0.936	MALRHLALLAGLLVGVASKSMентаAQLPECC VDVVGVNASCPGAS
3335	136:271	0.987	0.954	MEQLLGIKLGCLFALLALTLCGCLTPICFKWFQ IDAARGHHRLVL
3336	47:182	0.987	0.944	MLSMRLRTMTRLCFLFFSVATSGCSAAAASSL EMLSREFETCAFS
3337	373:238	0.96	0.858	MRAWCIWLGWVGASRQGWSGDLGIPHSLE CHEGPGFGWCFCPLR
3338	181:316	0.946	0.869	MVFPVMYNLIILVCRACFPDLQHGYLVAWLVL DYTSDLLYLDMV
3339	58:193	0.906	0.724	MGLLGVLWNTTLHMCRMRLQDTGQKIRTGSC ELHGSQSSHSTGNL
3340	91:226	0.929	0.781	MSLVKLFNLLVFSYRRGAVITIKIEVKIKVTYVK CQAHGERLING
3341	302:167	0.962	0.649	MCIVACAGARVLLPLEQAPFPFGYPPSRVGL DTSSLPPEGPGGP
3342	226:361	0.922	0.631	MGDYRNVRLGFSFSISVTISRVIALLSLLQPS GVGILFADSGGT
3343	224:359	0.952	0.887	MIESVATVLINVLVIASMLNLSHLLGDSKGWL LPLEAFCFLISL
3344	645:510	0.991	0.935	MWPGRIMTVTVVLLCCSTASIWPCLSHSASPS RTCPNFVGRSTRS
3345	280:145	0.965	0.861	MGLALRSILMLSFPFLSCREIGMRMFGIFAEFK TNKHTRTVLRLL
3346	81:216	0.918	0.825	MQPALPLYSSSLLCHLSSCMLYSRNIGLTCTP CFLPLLMLFLSQE
3347	123:258	0.987	0.834	MPVFLAFSSICLACLPFGTLWREEMRTDLC HCCFLPTVLFSCH
3348	107:242	0.939	0.685	MPVGQSQHSFLLISIVWTKLLLNQSQIKSALY PTHGPHVMSAF
3349	72:207	0.97	0.913	MLECAFIVLWLQLGWLSGEDQVTQSPEALRL QEGESSLNCSYTV
3350	197:332	0.974	0.799	MSALRPLLLLLLPLCPGPGPGPGSEAKVTRSC AETRQVLGARGYS
3351	228:363	0.961	0.927	MLKVILFFIPILKAVSVSNYSVISPLSYLAPELT SLSLFSISS
3352	34:169	0.987	0.926	MTAGTVVITGGILATVILLCIAVLICYCRLQYYC CKKSGTEVADE
3353	137:272	0.88	0.659	MSMVLGSFRARLLVPISPRKLLGPSHTSLEW QNQLLGQESSVFP
3354	166:301	0.955	0.607	MRAAWGFRPPLWLPBGVSDGTRENMHPG GGGRLRRWYPPRGGW
3355	432:297	0.956	0.738	MTRLLRLMPGLCWSWEQICGGMACWAPSRD ESRGRGGHVQGTWAE
3356	208:343	0.884	0.56	MGPRFVSTLPFSPSAAWCACEAGGGLRREVA HAQRAASTAPTAHM
3357	88:223	0.954	0.626	MGLGTESPPASLPFSRWGPLYLRALLPPAVL CYGTGICLPHLAS
3358	194:329	0.97	0.897	MRLPWELLVLQSFILCLADDSTLHGPIFIQEPS PVMFPLDSEEKK

3359	143:278	0.94	0.72	MSKFLRYMAACVPVASTLLTSKPFTEIPAVSCI EAKHQLVFTSSS
3360	263:398	0.97	0.935	MLRLYVLVMGVSAFTLQPAAHGAARSCRFR GRHYKREFRLEGE
3361	45:180	0.982	0.931	MKVFYRWAQQLLELLIICVVCACVGVHAYAC ILERKGSGLLSKS
3362	180:315	0.945	0.792	MLSNCSLNFVLCPLSLYQQTPVHPSRPSSS DFSLEPLAASLSP
3363	86:221	0.992	0.808	MFFLVSQLISIFSSQNSIGLALWGFVLFSSYFLY CLFLLYAVFYP
3364	448:583	0.945	0.665	MSFTPLHLLTFLINRREWGLKASSVLRRERCL IRVRVTINSNGR
3365	176:311	0.972	0.936	MAPNALHLLVFMALCKALPLSYTRILTNRIOQK GWTQFLRLGYKK
3366	55:190	0.985	0.91	MAMGVPRVILLCLFGAALCLTGSQALQCYSFE HTYFGPFDLRAMK
3367	364:499	0.99	0.89	MTWLLVAYADFVVTVMMLPSKDFWYSVUNG VIFNCLAVLALSSH
3368	259:124	0.973	0.86	MTLEMRLTMTALSSAVTQLTLMCVSNIIDPGS KNGHCLSLATG
3369	140:275	0.966	0.789	MPGDSTVPHTSGLLLIFGWVAAVARENCSL WSTSAPASVVFCE
3370	237:372	0.988	0.857	MLHLVFILPSLMLLIPHILLENFAAAIPGHRCWV HMLDNNTGSGN
3371	188:323	0.937	0.628	MAASWSLLVTLRPLAQSPLRGRVCGGAWA AALAPLATAPGKPFW
3372	14:149	0.978	0.913	MRVTAPRTVLLLLWGAVALTETWAGSHSMKY FYTAMSRAGRGEPR
3373	42:177	0.979	0.868	MRFTFPLMAIVLEIAMIASFGLFVEYETDHTVLE HFNITKPSDMG
3374	249:384	0.996	0.928	MRLHYLLRLLSFAFLWFILRSFLVKYLNFFTLG FFFCFSSTPRNF
3375	86:221	0.914	0.597	MQRNKLCLFSPSIVTILTNTTELKLSHDVERGA KIIFYLLESFSL
3376	19:154	0.975	0.937	MMAAMLTLAVLFLTGSQARHLWRHDEPPQIP WDRVKDLATGYVDV
3377	19:154	0.957	0.885	MKAAGLTLAVLFLTGSQARHFWQHDEPPQSP WDRVKDLATVYVDV
3378	35:170	0.959	0.738	MWHLRLAYLPKLLSQLVLRGRHYPQTPLGLF NKKPWWQAGWLQLS
3379	201:336	0.959	0.819	MPYPFLMRRCLLSYFGPLLLCYPVPRNLHSXI LPRLPFPTLGRLY
3380	177:312	0.945	0.646	MSSTWPRLARSSLCCQVLRMTQTKHITPLTD LPALLVQGTPHPP
3381	89:224	0.959	0.725	MTCQQPQDLRLKAPLQAWLRVGLLVSTLVK VRAGCALEAWSARA
3382	19:154	0.932	0.765	MKFIWVLKSFMLHSSSVLSRECTPASATKLF HIQVCPAPLLEIL
3383	71:206	0.916	0.782	MLEWPLLGLPMPILPPLPALVWVPIGLTHC PWPSPFVPASLD
3384	145:10	0.995	0.845	MSALWLWVYVSCGCSCALCVLVHAQTCTSFSL VHAQAHLVSCDHI
3385	308:173	0.968	0.652	MFVFSVIHTELVPILRPLCLLYCCPDSCSVPRPL

				YSLKYLLLINDF
3386	233:98	0.944	0.733	MKLFFFLSPLLGFSVKNNGQSGRPQVYSLTAA LGTTTRYSDLTILD
3387	32:167	0.984	0.943	MALFFLALNFWKVGMACYVRTSSWNSLLFFS QPYFLGSCFEQYLS
3388	126:261	0.921	0.638	MQSALMIGIPSGVVMCFCLQKSNEAPIGNVTIS YPRGLKIPFLGW
3389	29:164	0.932	0.809	MYLGLFLDFYSVSFCGCLHMLQPQCFNYFNS KDQSRFHCLKHCSD
3390	181:316	0.977	0.884	MKIFFHIFHHKCLFTYRLFITLALILWYSIDIEEST FPPLMRYCPN
3391	131:266	0.972	0.836	MPISFLTFFSFPCALTRPFLSLLANSRISFSNA ASASPPWTIGK
3392	25:160	0.948	0.563	MWRMRLCXLGYPATWLQMTEIGHARSLMKP DWKLSLTFFSELSPS
3393	204:69	0.959	0.798	MAILFSKLLAVSFQKLIFAFDDSSAEPEVVIS WLGVAHAYKKI
3394	298:163	0.945	0.696	MPASQAFLFCKCSWVFCWSRGESVSRTSGD SRSSHDLTLTEEGVQ
3395	918:1053	0.922	0.649	MFLLRVKLMHFVNLSLHNYIMTRILHSTGLEFQH QVEEAKDLQLI
3396	520:655	0.964	0.759	MLAGQLLPMLTLLPPSFPLPHPTLGPRRHASL TQLGPAFWMAWGR
3397	177:312	0.935	0.786	MRLWVLFKPSALANFLRYHHSRGIGSTASLLP GVARSPGSPVSLP
3398	407:272	0.937	0.718	MLFLNLTFNIFPLKRIIVLFDERGNTLPSQNKLL LDSVPFFTDEI
3399	72:207	0.881	0.599	MILCSVCFKICDPPLLVIASAFQCPLSVAEDIF SSALFPPIVPFL
3400	696:561	0.952	0.838	MECGLPKFAGFLFMILCLWNCPEAMECEDGF HCSSVGLLVFASIF
3401	164:29	0.943	0.589	MLRVCRSKRLWLLHFYTGKIRFDRVKDNGG REDVKEIKDRQKS
3402	311:176	0.928	0.797	MYEEKRVYPVWVIVCLLLTSVTAPKWGKGPL KSGGMNLVVVTTDD
3403	310:175	0.986	0.956	MYLFPAFLSTSTCIFLLCRNCFESADPKLQKT CFGSGVWVLAWK
3404	63:198	0.891	0.597	MVCGGGRAQLLWDFALKLRAALLQQKATQGE IQLVLMGEAFRQAL
3405	141:276	0.945	0.803	MPVCICIIYMFYFVLQISRSSFTCSFSPIYYKY SSLLVYTFLQD
3406	69:204	0.986	0.939	MCLSSLLLLQTALQEICTLVSFMCVITYMCRYS PRKKFSEVASLG
3407	134:269	0.975	0.583	MLSSPKTPLMYPPWIPCGSPNMHWISLLLWV FSTLDAPPYPLWTL
3408	180:45	0.959	0.839	MASLAHLALRCVLAGAIGGLDPVGLLFQQATW ACSQGRWAQFKGS
3409	297:162	0.985	0.946	METRWMSLFTILFFFSSVMPAFQRLSSFLFCI LITFFLLLSGLY
3410	10:145	0.971	0.917	MLVLLVWVHHTLLLGQKSTYEEKRNGKWGRQ RRAPYLGVIYIATG
3411	160:295	0.901	0.713	MLNFLTLPFPLRRVPGHISTRPFHSPPP KLCVCVHFNILSS

3412	82:217	0.97	0.831	MDVGPNSLPHLGLKLLLLLLVTLRGQANTGW YGIPGMPGLPGAP
3413	120:255	0.997	0.89	MWISSINFFLIIGIFFCFFVCLVILYYILEIVYKN DSYDYSNTV
3414	454:319	0.977	0.882	MDLIFVKVLLIFAAIQTLSKWQFAFTFSIQTVPS LVINLSWLLLD
3415	261:396	0.891	0.601	MSSSNDSFVPFFFIFISVNFCLTAFVNLSYIM RNGALMEDILLY
3416	71:206	0.975	0.918	MTLFTILFCIVNLGYGFSFLHNTFFHNYLSELL VGHSLENAFF
3417	53:188	0.993	0.947	MLLKLFCPVASLLCIPLSFILWLLGSIIFRSIIV AMMGEKTC
3418	393:258	0.944	0.696	MVPCPLPVMTGVSVAWFLGEPFCSGTLSPLR AGLGLGGGLECAS
3419	70:205	0.915	0.665	MQHILSCLLKGLFLSNGFPMLSGVPKSITHHT GLNRHGPGLYLTA
3420	381:246	0.932	0.616	MMFRKYQRKTLKLLTYFIPLVTNYEVIKTANRM YFLKGQAPFCST
3421	158:293	0.881	0.664	MVSGWITKTQFLLLRGKICMYKCIQLQVRK TDVITTKQINYE
3422	125:260	0.897	0.785	MKFLLTELGILNLPVPSFHLSCYPFHKGCPFVSH DQDGNTSNESFT
3423	133:268	0.996	0.921	MLLWGGVGLFIFLLLLLIIFWKNRHRSPFSGL PRCCCNWGIRGM
3424	28:163	0.992	0.738	MRAXAPTTVQECMPLKAFLLFPFWPWYLILIP ALPYLSNPITCQP
3425	355:220	0.935	0.726	MHVLTMAYVPGTMPSLTHLFLILHPSGSFLS PFSTQLSSPTKSN
3426	412:277	0.959	0.786	MTRLPLGLPYLSFLPWSVLRPPQSSWPSQPT ATHTQRPLLDGCLA
3427	430:565	0.957	0.836	MFFRMQVCEHHGFVVILLLSLKMEIPLAAYP TAEYSSIGSGFTP
3428	293:428	0.93	0.607	MLACLSGVFLFPDYSHSSCGFPNVIWLTFKAI FVSVVLPNSTHQ
3429	260:125	0.892	0.637	MSEACKTFQWLLITLRKKSLLSLARKVLHG PTFQPLIPSLITH
3430	210:345	0.895	0.752	MCLFCSFVNVTLGSTDPMCCPAQWLAQRMP WAFVSIRKAWPLGRM
3431	295:430	0.984	0.859	MRWPWASWAAVLLKLPRRVLPLWPCGHQQH VRATASSRSPMPVT
3432	6:141	0.943	0.858	MRWILFIGALIGSSICGQEKFFGDQVFRINVRN GDEISKLSQLVN
3433	238:373	0.895	0.59	MRVKFHLCTKGWSQGLFYGLVGTGQCGAY FHYCGRNCWCLWQGR
3434	152:287	0.917	0.747	MWLLEGRVIFYFYICVANVSNSFTFSTQRCLI PPFLYSVFSNVF
3435	215:80	0.941	0.757	MINTAFYLDLVFFSIILSYFYLFNSGGEIPFHTKT XQISTLDVRF
3436	260:125	0.925	0.844	MKLSLSNILTSLFLWGS HQAPHAALAWSGPG VTSTLAFCPHWP
3437	405:270	0.929	0.808	MVLLPLQCGLTKASSCLHTLCSSSDQIGYLPV KNTDQLGLQMEVA
3438	26:161	0.949	0.715	MRICFCLYNKLSVTLITFIEEMLILEVTKYVCT

				RYFIYREKQL
3439	5:140	0.948	0.757	MKLLGIVILYLGKMLLGHKVCKYTSNRFYQKV YQRGLVMLIFIP
3440	419:554	0.965	0.597	MKMEMETKRSWRPQSHGHFTFQFLSWT LILFHFVPPFPYLLF
3441	595:460	0.921	0.763	MYLPLLSIQAVFTRWVISHVKCLC NSWARGTLPSIPN
3442	167:302	0.984	0.883	MCSIKACMRLICWATLMAFFEAMGSL TAFGDQSIFCVLC
3443	381:246	0.993	0.975	MIYTALKFMLFLMILLMCIIVLAYNM CPRLHHHDLMGH
3444	405:270	0.929	0.808	MVLLPLQCGLTAKSSCLHTLCSSSD KNTDQLGLQMEVA
3445	281:416	0.967	0.805	MFTFGRLFQIITVVTCLQFIQDCCI ETSSLSRCLEV
3446	125:260	0.946	0.883	MQILVHAHFVCPACCLSAVTTGGQIG AAAPKAETPLAVK
3447	151:286	0.984	0.857	MIALVLTGAFWCLLLAAKGDGKQFQ PLTEGLSSRGEEAR
3448	161:296	0.974	0.815	MLIRFLTGWLIAYVLGLQGHNCATFY QKVITGTTTVAFL
3449	132:267	0.983	0.925	MTFLLKVGILLLLSDSMCWRHWRNYP RDLEVIHGCSQILS
3450	124:259	0.979	0.649	MNFWSFVPAQALCLTLCYVIRS VVLFFSTERGRNTNR
3451	135:270	0.97	0.846	MLLSLYLLAMVWSQQGLGRRSL PGGELAGGPPGSL
3452	45:180	0.975	0.837	MSHAIFGSVHLVFFVILNTIYVFLYL FFIIVNSNLTR
3453	69:204	0.993	0.956	MFALGNHWAGMLLVTLAAVSLTLTLV QKKANTNTDLRLA
3454	170:305	0.91	0.744	MLQACKAAARASVRLPSLLSFFWASS KTEVATFRRLSKV
3455	140:275	0.971	0.92	MVYFLTLLPQFSLSLHLIVEYFRAGSY HWDEKGEMARVF
3456	757:622	0.954	0.727	MGFSLWPGFLPPNLVLPATPRKSGGL VTAPVVIYESLAWT
3457	344:209	0.963	0.71	MQLFLTCHYHIGFIFVALDSFDIMRD KGDGYSWYLETT
3458	355:490	0.883	0.602	MFFILIFSGIELKKFIFSQFLSGTLFR NCILRKKYQAH
3459	242:377	0.889	0.673	MLYHSKFLYSFGIFSSHLPFLWQDYFC SFIVTLPFKSVP
3460	69:204	0.97	0.827	MSFFSWNSLLSGLGSGLLSRAGGMCL GKITPGGLGVGPR
3461	225:360	0.989	0.742	MFLLSSTHLFFCFYDLLSLLAIPNTV HSFFGQMLQKLL
3462	144:279	0.929	0.672	MNKSILSFRLCLLSKRHSLTGVLNLD CGPDPHVRVNFA
3463	470:335	0.947	0.646	MCFKLCLPFYICTVWRRDGE DLSCVSQVTGAKL
3464	199:334	0.986	0.908	MILIVLPSFLIRLKFCFPLQECFSFIC LYANILDWPN

3465	206:341	0.983	0.962	MLFSSSYRCVLFFLLFSFVASDCVFSNSLSS ASPILFSALSVLP
3466	55:190	0.984	0.633	MGLTPGRCSGWKPRQAPLRGRWGRWSWP WLTEVLGWWSPTFWASF
3467	83:218	0.944	0.898	MPLPHQGAFLSLCLWVDAATAATGLERPAR PSKLLGHPECSRGG
3468	15:150	0.948	0.733	MLFLALQSKSLCELLKEGSNTYQVPHGFQG RTVDYCLLLGLDNL
3469	38:173	0.939	0.641	MHAWLAWTQGGLLILDSFIECTRSAHSGSDN RRRAGDTAEIKQSS
3470	114:249	0.977	0.922	MKFTTLLFLAAVAGALVYAEDASSDSTGADPA QEAGTSKPNEEIS
3471	448:583	0.889	0.669	MLELGRCNKVKLILFFVSVIQSVTRGWRWGLG QLES LGESFMKAA
3472	189:54	0.966	0.89	MSLHLVTTLFIIFQVRSMCVNKRKMLVHTLSL ERCYAVRSFWNQ
3473	56:191	0.979	0.827	MGILSLTILYSFLYYGEMFYMWLNLCFVLIGCL PYFSFILPAKI
3474	168:33	0.95	0.807	MDLLYIVMLILRSYLSLRDVS KPLGALLKFSTS SNSFSFYVLLP
3475	298:433	0.969	0.813	MRFPPLFWNSILLALPLPKGYFIYPAKCSKMS TLLHPRQNRSSL
3476	303:168	0.945	0.775	MPRKIWTLVFWLRNFHVLSGRKQRNSWCLR MRKWYRDRLSGPFFP
3477	125:260	0.912	0.739	MISLLHRRTYFPALCYCTVARRAWLCLGLGGC NKREAVPSALLP
3478	38:173	0.893	0.6	MVRASFLCCVHRTLGPWDL SHMELGQLLQNA PSAHRGCLGVWKEV
3479	161:296	0.98	0.783	MCACAVRALSLAGGAVLLSSLCACARAPRYV GGERRVQSPARPAD
3480	186:321	0.908	0.714	MGYYVCKYFREKKLFFLLQLFCMFSTVSNKI KNHMPRNKSDRQD
3481	312:177	0.893	0.552	MLFFKMLFPPWRHCPPPVGSMSSFRIGRAL PDRPPLSSFVTHSP
3482	156:291	0.972	0.938	MIQVRNLIVLCFLVELLNVPVFLYSRGWQTL THGLTQLKTAFF
3483	272:407	0.977	0.831	MCVMLCWHKTLFNAFFLSFGSQCPACQHS LFAVHRLKLQRFSL
3484	278:143	0.882	0.667	MEPWATSCRWRGGWGTNLQVTLLSLPHLP VGGMGMPEVGSFPRA
3485	228:93	0.901	0.624	MGHWGEGKASLLLLVIRECCVRLLSFAGARG SDQHLP GIGVATGA
3486	384:249	0.944	0.886	MAHPSSLGVAILVALLSSVCSWERHAVIDGRG FDATCVNRLWLRW
3487	70:205	0.938	0.644	MLRGMDSLGVIVLPWIVLYPSPPPSSALRVH LLIRSLDAHVSAR
3488	90:225	0.995	0.892	MRLVPVCLLYLCYVMLCYVMLCYVMLCHDML RYESHSHGLPPPIP
3489	282:147	0.889	0.664	MRRSQCVWVLRGVRRSQWWIPRGVRRSEV FVSYGQHPWERAMLA
3490	413:278	0.972	0.799	MASRTLAVMLGRGGLWGQLFWSSLILPQAQG LCSLHFSCAHSLNK
3491	68:203	0.906	0.629	MILLFLLHLSRRPSIKKGEIWRREKIKISGSLNIT

				HFIFFSHSFH
3492	368:233	0.929	0.805	MLRLWASGRAAAILCPSPAPKANVRSERGWG
				SNWRKSYCAGAVRG
3493	218:353	0.884	0.603	MNFFINSLAMLLGISYSNSHVIEWVFEVRFNMN
				KTVSAVTKLTFS
3494	137:272	0.955	0.726	MPAKTGLFGNLAVMFLCWFLERSDEQLSFNL
				VAWNFSMNNSILVL
3495	92:227	0.907	0.605	MLDHRHLLRRQIWMSCLSLSSTWEGILFPNLP
				CCGRNMQLTSCQG
3496	538:403	0.983	0.805	MLFFIYHNHLPFFGLHLLVPHLLCCSCYTLSL
				PYP SVLGHPHFV
3497	179:44	0.94	0.596	MSGGWNFSLKQSFMVLLDFCLCIRKVRRLMS
				LTKFMVAIEQPIIF
3498	98:233	0.98	0.867	MPHPTVCLQMTLALICMASLKLALLATAQNG
				HPTQFTEHVRTQG
3499	311:176	0.923	0.622	MGTHCSLLLREKHLTLNILGLVLSYXRERR
				GRGKALGFLLAT
3500	55:190	0.912	0.695	MMNLGVIFTCLYFSVQIFYSDYKFHFKTKKFLH
				LGKCSEFPHHVL
3501	135:270	0.951	0.657	MSSRAGKGQLSPAPFLGSLLSYLFQVPFCY
				LGLNSTHAQLKGM
3502	114:249	0.985	0.918	MIYFVLLSFLGFRAVLLNRVKNGLMIIRLVKK
				NLVLLWKIPQYW
3503	185:320	0.983	0.826	MVLPPhKTvQLPRLHLVWLWVSQAWVGGTV
				LHWLASQQLCVLPA
3504	115:250	0.931	0.722	MKYFGFVSFGSETVPLALFGLCFLAYISLYPTA
				NICKMARLDLQC
3505	252:387	0.955	0.738	MHCVLEILVSVLGLTHHLLLRDRDHRYRLVRLM
				GDVGGEELKAMW
3506	418:283	0.925	0.709	MVVIYRMCMLQAFGIMPAVNESKQLQLGAAL
				WPLQSGSHLAVLT
3507	322:187	0.922	0.572	MRARVYIAGVLAIFYLQWPDRSHASRRVSRG
				GWHLVIKPNILERI
3508	68:203	0.962	0.74	MHLFFHTLTSLRLGCIIQSLARGASCCYCHH
				MNIRICEWMSAAQ
3509	309:174	0.884	0.646	MLHILSGICLTHISLYHPLFQVNQLLAEADNVSL
				YSPRRFWPFSS
3510	480:615	0.993	0.942	MKFACPAFFSRLFHSFCVPELLILLILPFSFL
				CFWLILGCKI
3511	38:173	0.962	0.638	MFLVCMVLCFICKRYRKDVAETRGGFLVLVCFI
				SFSSTPVASSSF
3512	107:242	0.927	0.787	MCLTLGGCTPTFLPLTQMPLVSAICSALSCLLP
				QPCPKFTFQSPD
3513	306:171	0.935	0.8	MTFYLACYVLIISHCISSHCPVTLTLIGFPCLNS
				LHLVFPYPQNP
3514	355:220	0.934	0.669	MLVSVFAGCLFELSWSPKVSTQTFQLCCSLAT
				KNRRNGGLLWECG
3515	30:165	0.985	0.863	MRIDLSELLIFYLLFLMHKSRLVVCQTRVQLCE
				QEETVSYPDGA
3516	144:9	0.983	0.874	MNSLLWLKLFAAWCFLKDFSLNNRAKTQTAFI
				QNKRKSYPELNLH
3517	162:27	0.983	0.874	MNSLLWLKLFAAWCFLKDFSLNNRAKTQTAFI
				QNKRKSYPELNLH

3518	377:242	0.985	0.922	MVVLMDLLACFLWQVISMQWCLRGLVIPPS ESATLYHVETIPCS
3519	147:12	0.983	0.874	MNSLLWLKLFAAWCFLKDFSLNNRAKTQTAFI QNKRKSYPELNLH
3520	75:210	0.98	0.829	MMNTLLLFAGLLLTWESGQVLGDQTDSDNEL QEMSNQGSTYVNKE
3521	37:172	0.901	0.58	MKQSWLGLGTGPLTPALSLLQTQGSALPAHP PFSQWGPKEWVGVR
3522	122:257	0.902	0.84	MAHHARARLVFVLGPTACRELSLVFLCSPRD GFQFCLGVITDNE
3523	181:316	0.984	0.865	MCFRCLAKQSFLVSLVPGWWFSCCHGLTLL CSVIRKEDVLQYRF
3524	233:368	0.989	0.937	MLLFAIQIFCAFSILSFAHFSYWIVYQSHTYAH MYVCLPYPCVHA
3525	240:105	0.897	0.585	MPRLKPRRSPLFCRLRFVIFSMEKTPPSSVQG MTSYHIVSHPPPH
3526	276:141	0.924	0.621	MCFLVCSFFSGTNRVIIPSYELKDRRLRRIAKL GLLSWIASSSYL
3527	325:190	0.957	0.832	MCHLKLSVLSFIYSFLPLFGKGYWERSVIKDKS VKRKKNCLENKT
3528	59:194	0.896	0.675	MRTMGLYGCGLSCIPLTFACESPYSICDCIWT QSLQEGMKVQLGH
3529	37:172	0.969	0.753	MILNKALMLGALALTVMSPCGGEGIVGECMS EGCSLELKNSKLLK
3530	163:298	0.958	0.629	MMLWQVYPGPSAAVLCLFLHPPWSRSTAVER EKRQKDGGRGQRMILL
3531	11:146	0.981	0.874	MAPVMARWPPFGLCLLLLLSPPPLPLTGAHR FSAPNTTLNHLAL
3532	155:290	0.962	0.845	MATRSKGAFINCYIILLTFLMIRTFYNLMEYYC PTLLIRKLMSN
3533	254:119	0.928	0.832	MQEGKLKVIRSLFLFLYLFVYVECGFSPGCLP WDQISVCLNANKR
3534	430:565	0.987	0.943	MRGFC AFLGSWLVPFAYLTVDLSKSLSAALL TAALLTFDTGCLT
3535	207:72	0.986	0.897	MHSTVINLLTWIVLLSMPSLIYWLKNLRYFFKL NPDPCKPLAFIL
3536	246:381	0.969	0.88	MYSYFRFTIRIFLTMLISIPISVIFLKRNTNKS RELQLTAQYR
3537	127:262	0.972	0.703	MGFLSLTLYLLTSLNKMLFKLRGAQPTTEEDIG GWLNELKTSKYI
3538	13:148	0.891	0.568	MLTCVPERLFQCHHLIRMTCLFMILEFRLFKYD SNLCSHVIINHP
3539	98:233	0.981	0.811	MGVSELLLLLKMIASVIFLYSFISMFKTQLLCSS STSHGILESRI
3540	47:182	0.958	0.875	MLQRMIEVIVDLFFLSLILSSFQSLWVLPEISLG NSSHSFLPLRY
3541	159:294	0.983	0.886	MVTLRFLLCCLQCSCYADSGLAFIVSFVWKN MLISDNAIKLIFS
3542	25:160	0.943	0.89	MNQLSFLLFIATTRGWSTDEANTYFLECTCS WSPSLPKSCPEIK
3543	70:205	0.976	0.863	MVISA AVLSSILCVFLSKVLNMNDECLRLTFWL HCNAKHYRYSML
3544	31:166	0.95	0.847	MNFEILIQRSLLFYFVLALNFPVASLDFFSVKIIS

				AVFVEQKFW
3545	24:159	0.97	0.659	MKLCFFFTLAFCDVYQCVCNPMLSFSLEEG DLCTPHHLRDLANY
3546	53:188	0.981	0.895	MLDYLCFLLWKVIPQALQLCCWASLSEKTASL LLPGKEAQGFTL
3547	199:334	0.976	0.877	MILCHTVLNVPSSLAILGLADLCLTYACLCVD RYWSFCICRSIH
3548	978:843	0.995	0.915	MAMLPFPIFLVLLLRGLVLWTPASSGTIMPEER KTEIERETETES
3549	21:156	0.97	0.762	MAWIPLFLGVGAYCTGSVASVELTQPPSVSVS PGQTASITCSGDK
3550	335:200	0.985	0.958	MSFTVLCMFLAVVHKIMNTCWVSTSSNYHL QTSFGWPELIGRLR
3551	335:200	0.987	0.63	MFSQSVAWLSNLFTGNFTEQKALIWMRSSLLI FPLWTVLLVSRNL
3552	302:437	0.886	0.617	MTFFKKYIYKIFFLCLDSCCTTRCLDETFSEFVLL GVHRICDLMSF
3553	27:162	0.935	0.591	MLVKVYVMGAILKIFLREGNVINQRSGMDIEK YSEHYLAQGVWR
3554	182:317	0.955	0.807	MRCGIFKLGVMVSFICMMWDSCMLYLQLRLCL CLDYRIFLLRVVSI
3555	271:136	0.893	0.555	MKREAMVSPLLLGRPGWALPVLQQRNQSA KSCWRKPQAVSWTLD
3556	263:398	0.977	0.937	MHPQLIPSVIAVVFILLSVCFIASCLVTHHNS RCKRGTGVHKL
3557	85:220	0.952	0.817	MVFTCPHQKPAISILLRLLLLNRSAAAESQW FLLFTKICPPTWV
3558	91:226	0.967	0.863	MCVPRSGILSCICLYCGVLLPVLLPNLPFLT LSMSTLESVTYL
3559	145:280	0.995	0.975	MYAPACLCLSLFLLLLPLFFSVSLWLSVSGLFS LTHLPCISILSP
3560	113:248	0.967	0.918	MELVRRMLPLTLILSCLAELTMAEAEGNASC TVSLGGANMAETH
3561	178:43	0.951	0.687	MACQPSLCVPWFYWSVLSPPRYLNVVWGCF LLRPPLSFPMAANIS
3562	150:285	0.942	0.776	MPLTTAFLRMVSALCGDCRHQPDPAIPWPHN LRGADYQNQVGGLA
3563	483:618	0.99	0.882	MGSVFWHVLFCISGVCLWCAHRMAAFLOQM AVLLPVDCERPAAVH
3564	6:141	0.952	0.879	MDTWLVCWAIFSLKAGLTEPEVTQTPSHQVT QMGQEVILRCVPI
3565	120:255	0.984	0.923	MWLPPALLLSLSGCFSIQGPESVRAPEQGS TVQCHYKQGWETY
3566	316:451	0.948	0.583	MVCRLPCTLLPWPLKHKQGALLYICPASLPAF NPRNLSVYLLFSA
3567	263:398	0.975	0.748	MRIFCLFLSLGIWYPLPPGPLGEDRACPTLSE AASLAQLPGLGTA
3568	246:381	0.982	0.749	MSWTFLTSLIHSYKMCLLTYGCGLLRFQHLQ AWETVRLEYLEGP
3569	153:288	0.969	0.832	MIWTSFKSAMATILVICQVFIVYSKPFKDRDHF SFIHSANA EYL
3570	6:141	0.972	0.932	MVLQTHAFISLLLWISGACGDIVMTHSPDSLAV SLGETATIDCRS

3571	185:320	0.976	0.852	MILISFGKSWPVSLQILFLLHCLFSSHSMTSMIL IGSFLPCPYVS
3572	196:331	0.968	0.859	MCSVTCGVLFALSGLLLYSSPSPHWNRPSRIA VYLMCLTKYCTGS
3573	165:300	0.936	0.713	MFYVYVFKLTQMVYFKTFSLVIMFLRSSCIRGY SLLLLRAEYYLC
3574	108:243	0.958	0.857	MQATSNLLNLLLSLFAGLNPSKTHINPKEGW QVYSSAQDPDGRG
3575	273:408	0.988	0.88	MGIYLTWLGILAFSMNFFIPHLVLQFVITDLLIPA MHKALAIRFV
3576	569:434	0.907	0.656	MLPRLVLSSWPQSIFLPRFWNYRCEPPCLACF DIFYSVLITNSLH
3577	219:354	0.995	0.974	MKPWILLVMFISGVVMLLPVLGSFWNKDPFL DMIRETEQCWVQP
3578	83:218	0.953	0.726	MLPAPTMPWPLLLVRSVSGAHTTRACFPGCQ CEVETFGLFDSFSL
3579	293:428	0.979	0.556	MENVNLKASYLQFSKLMAGKGWALFIALTFSQ RLLPCLAIIEIN
3580	18:153	0.934	0.771	MKGPSKCTCFSSFFCLLFLASEFPRPCQCLS PPCTFMEAHTSFM
3581	17:152	0.968	0.854	MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVD RGHDFRLLDGP
3582	20:155	0.972	0.834	MAWIPLFLGVLAYCTESVASYELFQPPSVSVS PGQTATFTCSGDD
3583	172:307	0.993	0.951	MRWRTILLQYCFLLITCLLTALAEVPIDIDKTKV QNIHPVESAKI
3584	240:375	0.99	0.94	MSCVLLLLLFACIDVVVYTLVLLLSSGHLTGL SSCRVSPAAAGS
3585	154:289	0.961	0.731	MHLHCLVWRFVLQECFSGLAVAKGRKCLSLS VNINFSIYTLIMAS
3586	42:177	0.939	0.781	MYQVVHLNLCMSLYLCYTSTILTNGNLLHND SIVICHGIREYKP
3587	84:219	0.987	0.958	MRLPDVQLWLVLWALVRAQGTGSVCPCSG GSKLAPQAERALVLE
3588	244:379	0.995	0.964	MLVGWLVLGWLWVSCLTARLHVRVGTESHMFP IVSWDVEQAQCLEG
3589	177:312	0.978	0.847	MGLDALVPLAVTVAIFLLLVLDLMQQHQWRTAR YPPGPLPLPGLGN
3590	164:299	0.905	0.637	MAWKLLGCGSLSSAALPPGSWRVLLQPPVW HHTPCPPLRPAGSSR
3591	347:482	0.923	0.658	MLENPIRPRNLFSCVMCMYVFLIVPKWVEVD KLTRSLQSVFPF
3592	132:267	0.883	0.699	MKSIQILFVNNIFICMGTAEKELKKSKEVTLRS LPTILTKYDKL
3593	118:253	0.977	0.67	MLQLFTPIAWLAGACYSSFIPVARSLASRPGA SQPFHSCRLQLSE
3594	287:152	0.913	0.702	MKGWPLTALPPALRAPVVLKDGSPNLNLHVR PSPRKNKFSLLQFM
3595	14:149	0.957	0.769	MTFTLKGLFLFILTDRTKAMMIMAKGKSVGGE NGLGKVSSLKKHV
3596	91:226	0.982	0.95	MRVRIGLTLLCAVLLSLASASSDEEGSQDES LDSKTTLTSDSV
3597	156:291	0.989	0.927	MLSVFFLCFLIYPEFVFIYLSIHEFIITLDALKYN

				NILGPISPN
3598	314:449	0.992	0.941	MWTNFFKLRLFCCLLAVLMVVVLVINVTQVEY LDHETVSATFIDS
3599	40:175	0.967	0.826	MALAALMIALGSLGLHTWQAQAVPTILPLGLA PDTFDDTYVGCAE
3600	286:151	0.997	0.93	MCFWVIAFFSKLVFFCCLFSTMSIYHFNNKEY MFFRVNQVILFL
3601	112:247	0.942	0.866	MPARNWGHINFMVFLLLVNQCKILLNLTPSGS CFVIHRGGRAFYA
3602	119:254	0.935	0.672	MGICLIAYEFAYLFLLSDHFYFLFFLPPHSEF YLFPTMKNLL
3603	235:370	0.919	0.608	MCGRLVHLDRFALYLVLYSIPPPPPKSKPPCC TPSWGAVHSPF
3604	268:403	0.933	0.749	MNLKLSPIFILRCLCSFDPLFSNCLYICICPSPG NTFLQILSFL
3605	58:193	0.968	0.891	MDWTWRVFCLLAVAPGVHCQVQLVQSGDEV KEPGASVNLYLHDNX
3606	335:470	0.904	0.642	MKRREGALSRSRRLRLAPFVYLLLIQTDPLE GVNITSPVRLIHG
3607	516:651	0.957	0.74	MAWGPCFVAQNLWVLLRXYDIKPGHFAPAHL AFTAEPGGGGLVRD
3608	96:231	0.93	0.781	MLASKWWWVICLYKRVSVIRRLPKEQEPKGE MQPTSTTKPKVAQS
3609	169:304	0.914	0.726	MALKVLEQEKTFFTLLVLLGYLSCKVTCESG DCRQQEFRDRSGN
3610	30:165	0.909	0.651	MAGLRRPQPGCYCRTAAVNLLLGVFQVLLP CCRPGGAQQQAIEP
3611	242:377	0.958	0.819	MGMSSSPLWGQAILLCLEHLILPRLSSLISCHS GTLILLSILSCLL
3612	695:830	0.989	0.925	MSPTGLLVFAPVVLGLKAITLAALLLALATSR RSPGQEDVKTTG
3613	174:309	0.88	0.645	MRAVGMQLFWRGWCPGVGAPPTPNGALPEL YQKYLLSIYFVGGE
3614	223:358	0.99	0.914	MPALWLGCCLCFSLLLPAARATSRREGESAS TRKHLSPGLRICLS
3615	236:101	0.926	0.635	MFNVAITRLCAVVHFQSVFILTDDVVQDLGLLK AKSFYRQMKKCS
3616	121:256	0.941	0.861	MLTCSLSFFCKRMLAVLPYHFFSSGSHLRSSV WMFHGCDPRVGEM
3617	141:276	0.92	0.581	MSCSCPPCFFTLFLHSICQDISWFHPQTPTLD SLLNWIDDLIFYG
3618	198:333	0.893	0.717	MLNKKPLQTLIGIVFNLWINLRGFCLLTHKSSII QEHISPWYIL
3619	402:267	0.953	0.906	MPLFVLLFLPHLYHSHPVGSQQDSAPHIWG RASPPFCSWGSELE
3620	218:353	0.993	0.938	MPALRPALLWALLSLWLCCATPAPALQCPEG YEPSPLDRKCAPYP
3621	43:178	0.922	0.627	MAGSFLLPELLWRTFLNSVPTPAWPSRHCP WDQGLPMSVLAAPA
3622	11:146	0.934	0.601	MLAQAYRWSLMTGTCWFHLKPSISLHPKKHS LTTLHELGAVLGTE
3623	195:330	0.963	0.821	MSQLTLAFCFITFLVEAKKQRVLLSSFFPYVPY FRGERGQCLDTV

3624	283:148	0.993	0.932	MKSLGCRGQWWFLFFLVELGLWIADCELTVL LMIFYLQSPAVLST
3625	773:638	0.976	0.801	MAFRPHQFLVKPRGTFXAFSLFGLHLWLSTLP FLQPFAPFPQSGA
3626	131:266	0.905	0.728	MKLILLFLYYRKGNLGSARPSNLPSIIPALKRL PEDSRLLVSA
3627	387:252	0.974	0.819	MGPLWWRRVLRRLRLLALAPCLIQACGEKCG GPYPSPASVAVKGP
3628	49:184	0.993	0.956	MAVWSLLSARAVTAFLLFLPRFLQAQTFSPF FQQPEKCDNNQYF
3629	210:345	0.957	0.808	MKGKHLIQPLCAFLLCCKMGLASQMTGWRC YIGTLDSCQTPPS
3630	190:55	0.978	0.74	MVFLYGFVFIKKAQLIVLLFTDVAQRTAAGRP PTPVLGPSSPEC
3631	170:305	0.981	0.936	MQWVSFPFLSGANLLCYLVASMLFELLLAAL CSIAEAQTCVPD
3632	244:379	0.896	0.624	MSFLSLLRARLSLGGPARRAFPISQIFSGFLR GFFAKTEPRPLE
3633	226:361	0.932	0.771	MKIQKTLIYTKLLCHLLIFCKGNRLELMSLCCF SDTLTFLCYLE
3634	380:245	0.886	0.676	MAKRSPCLLLPTPIYGVHVSGGEEKQAGRL LINKCFLGRYTLS
3635	265:130	0.946	0.904	MSVFLICLVLAWGQHKELAPSEHPDTSQVE PHTSCLQQKAVEAF
3636	52:187	0.996	0.985	MFVWCLALWSHVLAASGSSSLSCGVFVVECG AEGLRGVVVECREA
3637	157:22	0.93	0.789	MYVPQLEVHLKAFLIFVCRVACFYLIWKNEVLP LEVNEIYENDAD
3638	289:424	0.936	0.696	MSSTRAWCCQKRRLARWVLGCLSSSSSLSV APHAVVQHFASATQL
3639	58:193	0.946	0.627	MTFLKSTWVLYIFVQRNGRTWKIYSKPCNYW FQHDDSPSLNIVKY
3640	62:197	0.899	0.567	MSQLRLLPSRLGVQAARLLAAHDVPVFGWRS RSSGPPATFPSSKG
3641	428:293	0.985	0.705	MTLPFFAFPLIWSIRTVIIFFFSKRTERNNEALD DLKSQRKKIL
3642	122:257	0.962	0.783	MPSGCRCLHLVCLLCILGAPGQPVRAADCSS HCDLAHGCCAPDGS
3643	185:320	0.957	0.682	MLPTEVPQSHPGPSALLLQLLLPPTSAFFPNI WSLLAAPGSITH
3644	431:566	0.975	0.764	MLCLCRFACSRRTAMGLFCLASLTLHHIFKV HPSCSVSVPPGFS
3645	164:299	0.938	0.633	MSEAGGRGCGSPVPQRRARWRLVAATAAFCL VSATSVWTAGAEPMS
3646	44:179	0.978	0.712	MYRPDVRARKRVCWEPWVIGLVIFISLIVLAV CIGLTVHYGRYN
3647	274:409	0.99	0.833	MLVTLGLLTSFFSFLYMVAPSIRKFFAGGVCRT NVQLPGKVVIT
3648	296:431	0.94	0.878	MSHVIWFLFNTHLSWAVEGREHFQKGKSGE KILDIFLKQLEGCG
3649	180:315	0.89	0.646	MPLSFHSTYYLLTSLIYTFNMCIDYKSHEDRDL AGVCVYCYFQS
3650	168:303	0.946	0.721	MESLLVAPQSRHLLGLMKVLLFPYMSSAILFQ

				FLFHSSLNHSLVH
3651	245:380	0.943	0.761	MMTLRRQERFPGITFWLLIQLLQQILISYHQG SLTFMENGNCLL
3652	259:394	0.892	0.675	MGSTKHWGEWLLNLKVAPAGVFGVAFLARVA LVFYGVFQDRTLHV
3653	153:288	0.974	0.932	MGALRPTLLPPSLPLLLLLMLGMGCWAREVLV PEGPLYRVAGTAV
3654	87:222	0.967	0.849	MEALTLWLLPWICQCVSVRADSIHIGAIFEENA AKDDRVFQLAV
3655	217:352	0.983	0.848	MGDARWTESLSVAGCVWLCFCLCVILPAVGC EVICTLSCVVMGFY
3656	102:237	0.92	0.576	MPWLLSAPKLVPANVRGLSGCMLCSQRRY SLQPVPERIPNRY
3657	57:192	0.995	0.951	MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRL ELTNHSSCQEPP
3658	387:522	0.996	0.972	MWACWCVLGTPGVAMVLLHTTISFCVAQFRS QLLTWLCSLLLST
3659	28:163	0.953	0.86	MHLVHLVLLMPGLAAGKEGSPNPFIVHRRGD KLRKSNQKGAGHKA
3660	120:255	0.975	0.884	MVAPGLVLGLVPLILWADRSAGIGFRFASYIN NDMVLQKEPAGA
3661	480:615	0.943	0.619	MKVFFLDESWPQWRFAAGLLALSFGGPAWK FLSVQRVIPWLWAAK
3662	210:345	0.958	0.82	MGSKITVLSVIFKLITGLVNNILLQENENSISSEV VLWSFRHFIA
3663	1099:964	0.951	0.7	MFHCYWFRCCLSPQTLCKCFSGKRTDWNCG SARSHSFQSHFFSAA
3664	110:245	0.973	0.931	MRRARLELSAASWCLLFLLSCLSSVYCNPVLL AGPAESYFFSLAF
3665	188:53	0.907	0.652	MVVRRHQLTCFLYRLNLLRSGHPLLLAVSVGS PFHISKGGIFWGH
3666	25:160	0.969	0.919	MLLVLLSEVLLALSSAQSTDNERPGCAVKDAV ENARLNQGGSPAMK
3667	67:202	0.888	0.649	MLLPSIIFYFIYKSSRRWWPVCAGKNTTSELK SRRPFHPRCHCS
3668	318:453	0.924	0.716	MCLATPRAPSPGRSWGLCALLKLFLCLNEVFP QRMGQNLLPEHKL
3669	689:824	0.93	0.698	MMHNIIVKELIVTFFLGITVVQMLISVTGLKGVE AQNGSESEVFV
3670	127:262	0.973	0.874	MALFALCGWTGWMLGHQCHRAVIERTHELC NQTYWFESWICHIMS
3671	377:242	0.921	0.791	MALHTQLSLCEHLLALVTHMVPLVGATLFATQ QEFVFHGLSHAFV
3672	172:307	0.908	0.596	MEVSLWNLHVLCPPPSCLFWVLGSKLFED DLMCPHWPCLECH
3673	415:280	0.987	0.668	MRWVKRDEELTRSHSFTQLLPFLLASRLGFL LFVSGCTFAVTNS
3674	316:451	0.89	0.573	MTNTLCGTQILLTLTETHMVSAVTAPPMAPT VALSHIEWGVVRW
3675	129:264	0.962	0.858	MIFGRTLGLQLFSVFQVALNWEVLTLPHYSTG PRKIFKVTLVTLH
3676	24:159	0.99	0.592	MPTVAIGSITNSKLLSYSQELVIPLTLARLWLLS VAFALFPFSIL

3677	469:604	0.976	0.58	MASTWSLERVGTCLPCGFGTWQSTARWPSC RSTSMVWLVWPSLLA
3678	1195:1060	0.938	0.818	MLIPHQLPLCSPWLQAMLTIEVPWLLGLAHY RLGWHALEGIFWW
3679	304:169	0.961	0.59	MCVQVCMRLHVCRCACVHVCACVCSCVQVC THTGLGEYKTGNCQL
3680	69:204	0.966	0.836	MALAFGLTVLSKATLGARLTTHCAHPARRARA FSSDVMTHSSILT
3681	153:288	0.959	0.771	MSEITLQEGWPLPCVCVCLFLKLVFLEWSEV LRVHSSGLLFRPR
3682	129:264	0.986	0.842	MFLNLI FVTFTILGTLKVISSILKNDFLKAIMRILL RYSFGIKHS
3683	375:510	0.938	0.621	MLRRMAVGLLFDTTFLKKLHMFNL CQQLFYKL TCASIHFSGRVGR
3684	176:311	0.978	0.926	MALMLRLVLSLLKLGSRQWHVFGPNKPVQAL VGEDATFSLFLSSK
3685	406:541	0.975	0.863	MGEASPPAPARRHLLVLLLLSTLVIPSAAAPI HDADAQESSLGL
3686	154:19	0.986	0.878	MVHILTAACLPLATLLSCGCDVRVTSHWFYKD MHWMVFLILAKTS
3687	218:353	0.976	0.931	MLQSFINYCLLFLIYTVMLAFRSGSDNLLVILKR KWWKYILLGLA
3688	14:149	0.923	0.721	MRNALSRLLVGLASLRGARTLSMGTLPERGNI VEFAPCDGLQIEN
3689	233:368	0.966	0.94	MKALLLVLPWLSPANYIDNVGNLHFLYSELC KGASHYGLTKDRK
3690	483:618	0.99	0.882	MGSVFVHVLFCISGVCLWCAHRMAAFLOQM AVLLPVDCERPAAVH
3691	218:353	0.976	0.931	MLQSFINYCLLFLIYTVMLAFRSGSDNLLVILKR KWWKYILLGLA
3692	44:179	0.991	0.955	MWGRLWPLLLSILTATAVPGPPLRRPSRELDA TPRMTIPYEELSG
3693	21:156	0.934	0.783	MESAVRVESGVLVGWVCLLACPATATGPEV AQPEVDTTLGRVRG
3694	140:275	0.969	0.872	MAPSFTARIQLFLLRALGFLIGLVGRAALVLGG PKFASKTPRPVT
3695	328:193	0.963	0.901	MPFLHSVLVLYMLLPSTFRQAQIFPVRKKPSW SIPLQSSLGALF
3696	179:44	0.922	0.639	MRRPGAHLCTHHCEWRMISFLCLIYLSYMAQ GQLGAGWETEEGIG
3697	178:313	0.98	0.784	MLLIPYFLEWKKLWPLAVLSLAWLTYDWNTHS QGGRRSAWVRNWT
3698	295:160	0.97	0.681	MVPCSGLCPLGGSWPFLYSLGCSSWAKLSFL TCCLWVDGSRPGPV
3699	55:190	0.964	0.902	MALTGYSWLLSATFLNVGAEISITLEPAQPSE GDNVTLVVHGLS
3700	68:203	0.926	0.702	MYGEFKWPSRFFCYLLKITISALLVMEHLKSGL GRWQQSAAAKFG
3701	74:209	0.956	0.835	MLTGTGLSVLWPTLGTGDLVWLRFHKGRT YVCLELSFQYLVLA
3702	159:294	0.984	0.922	MKISMINYKSLALLFILASWIIFTVFQNSTKVV SALNLSISLHY
3703	229:364	0.921	0.597	MWGQSVPGATILKYLLTVRFIWSPLKNEMFQL

				WLEYTEQLKYFEM
3704	233:98	0.917	0.554	MICWRTLHLVGGTSYFSFVDCELGQHFQPYKI CIMGIKNTLMKA
3705	141:276	0.923	0.806	MISIWWLAVSILQTNVGETIRVHCNMLQLYRS QQQMYFLLWNTCM
3706	283:418	0.96	0.702	MWRLAWVNFSFLIFKRSNNTVLPYTERQACE VLWKGQCIVLRNI
3707	38:173	0.947	0.709	MAVVIRLLGLPFIAGPVDIRHFFTGLTIPDGGVH IIGGEIGEFI
3708	165:300	0.901	0.588	MKTNRAAGSHWCVCSSGALLSIFLYLYPYPS PNAQIILMKISKSY
3709	105:240	0.899	0.67	MSATTVKIVFNFRYTLTMCSSCYLLINIIVNIYR FIFKKFLNLST
3710	125:260	0.982	0.939	MALVVVALAAVVVGVPWGRREGIGGRAG AQGCDHLHDIGHDL
3711	229:364	0.989	0.954	MAAWGFCFAVSALVACEFTRLHGCLRLSWG NFTAAFAMLATLLC
3712	252:117	0.948	0.587	MGCKGDASGACAAGALPVTGVICYKMGVLVW LTVLWLFSSVKADSK
3713	314:449	0.926	0.55	MHASEGLPALPLLALVSHSHSCPPLPLQPHHL PAILFFLVGHQLM
3714	87:222	0.9	0.794	MYHRALVACLPTSCSVTLGKAIDLTFIARRK RQQPSLPVPFRA
3715	97:232	0.945	0.71	MGVGAVSLCTLYLFIICKHFKRWINFPNPDKGP SRHILLQLSKLR
3716	518:383	0.93	0.614	MCGPFCLLPHVCGPRVCAFLPPSPSQLLRKP PSGGLFQQTAFSVQ
3717	178:313	0.978	0.896	MLLWLLLLILTPGREQSGVAPKAVLLDPPWS TAFKGEKVALICS
3718	238:373	0.98	0.847	MCLQFDLLSHATAFLRLIIAHSVLLCIIDLVC NELIVLDVE
3719	114:249	0.982	0.959	MPLLTLYLLLFWLSGYSIATQITGPTTVNGLER GSLTVQCVYRSG
3720	258:393	0.956	0.665	MATAAQGPLSLLWGWLWSEFWLPENVSWA DLEGPADGYGYPRGR
3721	96:231	0.954	0.873	MERRRLLGGMALLLQALPSPLSARAEPQD KEACVGTNNQSYIC
3722	32:167	0.981	0.888	MAALAAAACKVWSARRLLVLLFTPLALLPVF ALPPKEGRCLFVI
3723	477:612	0.984	0.921	MFLHSVNLWNLAIFYVMVFLATLGLWDVFFG FEENKCSMSYMEY
3724	220:355	0.962	0.91	MHPLPGYWSCYCLLLFSLGVQGS LGAPSAA PEQVHLSYPGEPGS
3725	176:311	0.91	0.644	MWIRALSCSATCPLPWNSAYYLAAIQTINAFY KMRSLCDRVGFR
3726	180:315	0.983	0.939	MFLWLFLILSALISSTNADSDISVEICNVCSVS VENVLYVNCEK
3727	379:244	0.964	0.724	MATDITPEAIGFLSAVGVFIVLLAVLFLFINKKLC FETIGGLPFL
3728	114:249	0.969	0.857	MVLLWKNFILKRRRCIALVEMVLTFLFSAALL ATRSVITINKNG
3729	251:386	0.972	0.887	MRPALAVGLVFAGCCSNVIFLELLARKHPGCG NIVTFAQFLFIIV

3730	114:249	0.95	0.7	MMKCSVRLTLQFFGLGFFFRPQRGISLFIAET RRNKIILQHICQD
3731	51:186	0.935	0.561	MRRFFWCPSPSFCTSVCSFEVPRPSSQKSG GSTSHSPTALPHRRE
3732	82:217	0.969	0.802	MLATTNFFSVEVGLGLVFFLLNYILQNFSEY LRPLNNTSKKLF
3733	66:201	0.981	0.904	MPVQLTTALRVVGTSLFALAVLGGILAAYVTG YQFIHTEKHYSF
3734	304:439	0.954	0.856	MLLLVVCNLHLIRCSKFSDFYMLEVWSNHPYR MLDNTAYCDLLAW
3735	91:226	0.946	0.775	MSLKMLISRNKLLLLGIVFFFERGKSATLSLPA PSCGQSLVKVQ
3736	275:410	0.977	0.914	MTEATFDTRLRLWLIIILCALRLAMMRSHLQAYL NLAQKCVDQMKK
3737	195:330	0.933	0.7	MLDWGFPMQSTFYLLMPFRTVPSGLPSKPR FPEVLGGIDTTVRV
3738	106:241	0.915	0.825	MNNFRATILFWAAAAWAKSGKPSGEMDEVGV QKCKNALKLPVLEV
3739	61:196	0.953	0.6	MVGDTQWTRPECQAWTGTLGLTSLLYCARS SMPICTVSMSQDFG
3740	216:81	0.983	0.929	MLVAVFIILAFNLVLSPATNLLYGSHTLSPSQRL LPGPPSPCSHP
3741	307:172	0.987	0.92	MADLVLRLTVVLGLLVLFTCYADDPKDPDD KPDDSGKDPKPDF
3742	327:192	0.899	0.824	MPLAFLGWVSGSLGTGVGMVEFGKYLLSYDT GPQVPVRVSNHLM
3743	189:324	0.905	0.659	MRVVPIMIIDLCNFMGSLSALGTDIPQNL GLLIVEKKCKRG
3744	168:33	0.905	0.579	MQFKELIFKIFSIFRFSVLRILWMPESYLLKEL YLQIISKHTNP
3745	158:23	0.888	0.63	MVTQRLVRMQWLPGLKPRHSDTLIIHQEQL WYNRTKRLPDALLQ
3746	508:643	0.958	0.856	MIIAIFLVVLVSQNLATSHQEMGSTALAFESRQ DKYNTVEARLLA
3747	223:88	0.976	0.877	MKQSTASVFFLTCLFITAVIISIIITVIYASVSHK LELSSLVQP
3748	204:339	0.974	0.791	MIKNFSLLSQNSGSLFVLTYLITFTVISNLALL LTYPKIACLI
3749	164:299	0.975	0.614	MKREVTGPLEGSASVCQPFLFLLPGALFIQTA LWLLTSKMLYEAL
3750	52:187	0.952	0.768	MLTLPQSLWMLTRRTICFVPTIVSCRGLLPSNP HHELARLISVSQ
3751	359:224	0.966	0.762	MHCWFLASVCPALLPGAYVGSQIPTMSQLAG WVHGVQLTFYFLQE
3752	162:297	0.95	0.669	MKCRAQLLAGHRHAALLRVLLLTQPSSKLPEA SSMKPKMKISQRI
3753	148:283	0.902	0.569	MYLTMISCKPDLHLVNLAPLVLQHYPRAK ELLLIFFSQFSQC
3754	83:218	0.948	0.791	MQFASNEIQIEFCILLPLLVLIPLSLQERIAVLQ SSHCKYKQRQF
3755	216:351	0.958	0.815	MLGLKRVLALLVRGITLHGGEVTPRTTWPGAA EPACWAGTRKPPQ
3756	243:108	0.905	0.581	MGNSCIGRFIRFLCRLSLNLTNSGQLDRGFEF

				TVLLDPDTRWFMG
3757	705:570	0.965	0.621	MCQYQSLPVCAMGYFMRCPQTQLATYTASC FLFTVSWALPPALLM
3758	268:403	0.987	0.763	MFCLWNQWVTAQRLLVSWLSHAQRQPCPL SLFCGRRNPLAWTIF
3759	231:96	0.914	0.634	MLVFMNCQVVLVCKSLSTARGIAHKRSVSHI SYSREERLVAPLP
3760	283:418	0.973	0.938	MGVLVLTVLWLFSSVKADSKAITTSLTTKWF STPLLEASEFLA
3761	199:334	0.975	0.878	MVTGIFMLLVFIFHKMASVTGLERCPPKCLPCF CYLRLMRPLGPF
3762	702:837	0.903	0.631	MSLRLGPAWRHLTCLGTKHKSANSVLASQHA GFFVAQGRWAIHRA
3763	119:254	0.994	0.972	MPCLLSVFLVTLLEYLSLLFMKTNEICIAFLKF RIDILLFEALM
3764	275:410	0.964	0.833	MLFIPHNCNSYRILLILSFCLQPTPAINYWAHLL DLPFLRHFTW
3765	296:161	0.97	0.862	MITRLLILLWHYHLKVISAKNYFRVLSVSQLAL LFILYSNHFIF
3766	252:387	0.975	0.82	MLFFLLGFECFATFPTLGDSACPPSILVWIRKV WASRPDAAQWGL
3767	19:154	0.938	0.842	MCSSHPILMLLFMDVPITIDSIVLCVLRINIKMI PYPMCEIFSS
3768	293:428	0.945	0.796	MGLGQPQAWLLGLPTAVVYGSALFTTILHNV FLLYYVDTFVSUY
3769	30:165	0.932	0.651	MWWACLCGGIDTCLSGWRVDHRAGGRADG AQGSRWEDEYKWCCDE
3770	221:356	0.946	0.752	MKNCLSTVCLLENLLSLQFISSILLIFIASASKDT SCCVIMLPI
3771	331:196	0.957	0.748	MPFRLTLRKLRLPFLSLFYHILLMCIRNYSKTAT DFPPDLYSCWFG
3772	170:35	0.96	0.854	MLSVKRFRAMVMFFMAMVAMMKNKCQQTNE AKFCVHMYLHFYFSS
3773	224:359	0.959	0.754	MWLLILVAYMFQRNVNSVHMPTKAVDPEAFM NISEIQQHGYPC
3774	126:261	0.965	0.907	MCTKTIPVLWGCFLWNLVSSSQTIYPGIKAR ITQRALDYGVA
3775	134:269	0.927	0.741	MTWMNLLFRASSVPFLSTSPFPGPIQSGKACS AGFSYLSFLNQPL
3776	442:577	0.995	0.957	MGFLGGLFVDVAFCLFVLLTVGPLFCRSA AVCWRSTPDVRL
3777	173:38	0.882	0.72	MLLKIKFLYAVSRWFADDLPVVLKKRSYIEVTR MFCLCVWRNIFR
3778	379:244	0.949	0.78	MYSPTNPLSFTLSSFFLYSLILHLLNTYYMLSIF VPRVSKIWH
3779	215:350	0.951	0.916	MPRIYMLFLISQWVTWEWRINSHSNDFISTLL ATHPASTPLTFW
3780	157:292	0.942	0.739	MGRAALPLQALKTLFPPTLHGCQQLVVTIL GPRCPAQLFPCP
3781	157:292	0.942	0.739	MGRAALPLQALKTLFPPTLHGCQQLVVTIL GPRCPAQLFPCP
3782	325:190	0.947	0.787	MAPLYLGNYQTLFLKLISISVLAFLFRNVWSNI GCHFSSWVTMVI

3783	168:303	0.923	0.555	MFLTLVSGQGFPAAPLTPPVESCRRCTGLL WERLGWDREGERHR
3784	269:134	0.93	0.551	MSQKVNLLGFVSHVSVGPFLLSRKTAADNT KPMSLVLFSLSYF
3785	239:374	0.983	0.916	MAVLYIQAFVLVFLLGKVMGKVFFGQLRAAEM EHLLERSWYAVTE
3786	108:243	0.974	0.821	MQSMINMIVSLLGLVATVTLIPAFRGHFIAARL GGQSLGKTSRQH
3787	282:417	0.979	0.934	MAASLLAVLLLLLLERGMFSSPSPPPALLEKVF QYIDLHQDEFVQ
3788	27:162	0.997	0.982	MLLLGLLLLLPLLAGARLLWNWWKLRSLHLPPI APGFLHLLQPD
3789	139:274	0.987	0.958	MSRSHVALLGLSLLMLLLYAGLPSPPEQTSC LWGDPNVTVLAVS
3790	153:288	0.976	0.804	MKINVSRPLQFLQWSSYIVVAFLIQLLIPLSILI YHDFYLRLL
3791	1355:1490	0.954	0.759	MGRRKFLPPPLLSLSSSLPLPICHPPAPLTPG LGIPPCGVVGRE
3792	107:242	0.958	0.782	MLQGHSSVFQALLGTFFTWGMTAAGAALVFV FSSGQRRILDGSLG
3793	592:457	0.914	0.687	MRAVLLQHLFILLDRQTTKKNNSLDIGHVFREA LIFLADLKSQLP
3794	288:423	0.986	0.967	MRSLGALLLLLSACLAVSAGPVPTPPDNIQVQ ENFNISRIYGKQWY
3795	510:645	0.981	0.953	MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIPAIF GVSFQIRKL
3796	56:191	0.974	0.82	MLLLLLPLWGRERVEGQKSNRKDYSLTMQ SSVTVQEGMCVHVR

Table 23

SEQ ID NO.	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to last amino acid residue of amino acid sequence	AMINO ACID SEQUENCE ENCODED BY THE NUCLEOTIDE SEQUENCE OF THE CORRESPONDING SEQ ID NO. (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAANGKVGAGHAGEYGAEALERHFD LSHGSAQVKGHGKKVADALTNAAHVDDMPNALSALSDLHAHKL RV PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
2	A	25	619	EFHRLRENPPWCSSPADKTNVKAANGKVGAGHAGEYGAEALERMFSLF PTTKTYFPFHDLSHG\SAQV\KGHG\KKVADALTNAAHV\DDMPN\ ALSALSDLHAHKL\RV\DPVNFQSS*SQLPCLGEPWAAHLPAEFQP LAVATSSSLGTFKPGLSVEAPLLTFQITFKGWKPRVGHAFALWASPO PLLPFPAPVPPWSLK
3	A	32	476	LYALRNQIKPPPHVTGGQ*QKQERTKPAWRPPRP/GPPPFIALIGFC FSSVPVAVVELRVEPPGGHWPLSPLGEVRGEWRRLSGLAS/VGQWL VPRSPEGGGGWAGSPQVSGGWPPSAHLRNPLSLGDILPAPQHPAL SPGGPKLCG
4	B	3508	3762	MTPGVVHASPPQSQRVPRQAPCEWAI RNIGQKPKEPNCHNCGTHIGL RSKTLRGTPNYLPIRQDTHPPSVIFCLAGVGVPLPV*
5	A	105	1711	VESNTGRKWTEAAGTGDICLAWGSSGDGRGGDPRGRVPAALGA AV VAAMASPDWPAPGPKQPG/LMGRPGSSPALWAQ\PA*PPY/FPGLTP PCPQEVPPQSFPGPG/EQGRVLRGGQNV*GEGRVPPQVCGRRPPCPSL MEPFVYTPASFFPSGQPGQTPGRRQDGEPRLTGGQTGS PGPLVSG PRGRAAKPGGTQGGLVQVPPGEHPTPGEAR I*HLGWVGC*RMGQG NFGVASKPFLDL/PGPMLGSTNCDNLGSFGLS/GPMFPKWPTSTGRL PKGPSAN*GG/PGMERPPGVMPSS/GHQDPEASGPLDLLVRAALQGG *ALGHK\GGAS*TSQKAESLPQPLGPPGGGCGYITQNP LASGPKQ TW SMGRPGSFPALWAQNRLTFLTPRP\SPPCPQEVPPQSFPGPG\PSQGA ERRARLSPRERGGFLKVCGRPPCPSMMEPSCLHTC*PLSLPASLRQ AKEPPSCGLRAP*HLRRPCLTPPFRPQGLLGTSHCPQKPAPDSGLL HSPNLNSPRGFSGQCNPRRLHPQLNPSNRDR
6	A	144	398	NMVLSLIFHIQELPQAVCEILGLQGSEVTT PDSVGEDENVMTPCP TSAFQSNALPTLSAGARNDSP TQIPVSSDVCRLTPA
7	A	46	1069	ESKHGNFFWVIFLCYCTKEERTQLQKQKTDEYFRMKLQWKSISQEQE KRNSRLRDYRSLIEKDVNRDTRTNKFYEGQDNPG LILLHDILMTYCM YDFDLGYVQGMSD\FFSPFLYVMENEVDAFWCFASYMDQMHQNFEEQ MQGMKTQLIQLSTLLRLLD SGFCSYLESQDSGYLYFCFRWLLIRFKR EFSFLDILRLWEVMWTELPCTNFHLLCCAILSEKQQIMEKH YGFN EILKHINEL\SMKIDVEDILCKAE AISLQMVCKELPQAVCEILGLQ GS\AVTTPDSVG*RTKMLVNDFLGPTVCISKVTALPTLSAGARND SPTQIPVSSRCLQD
8	A	190	383	TRMIHITSVYSHPHQAQLRGCEVLRHKAHLVLP A/WSTSCSGIPRGQ QTAQQGYSRCFLAWSLEA
9	A	1130	1379	ASHLRSGVRDQPEQHGETPTL\LKIQKSPGCGGRHL*SQLPGRRLRQE NHLNLGGGGCGELRSHHCIPAWVTETLT KKKKKRRR
10	A	67	373	FCDCHHFILMFKSPHIWPGIFSSWLLCFFWACLHHSLSIALLSCTK

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02/26/02

				RYSGILLYFLCSSFEBITVSSKSSVSF*RRMVFRNQVLGSRACCCC*Q VAAPRPPF
11	A	366	796	AWVEQSKVLIKEGGIQLLLTIVDTPGFGDAVDNSNCWQPVIKYFDSK SQD\YLNAESQVNRQMPGNRV\HCCLYFIAPSGHGPHLN*RLPPSQ RIG*YMFVTTWHCLLLRLKPLDIEFTKHLHEKVNI IPLIAKADTLMP EEC
12	A	105	702	AGSSVSLGFCPAAAAHKPRGGALRLPVFRRRAQQGPDYALAGVARQP AGTCRRRCNRSHCRAEDPQWPTPAAAPAAHSPHMSLGESGLGKLILI NSLFLTDLYSPEYPGPSQRIKKPVQVYILVFLIDDKLE*Y*YTQSTC CNFHYAS\QSQWPAINYIDSKFEDYLNAESRVNRCQMPGNRVQGCY FIAPSGHGPHLN
13	B	7	177	MSVSARSAAAEERSVNSSTMVAQQKNLEGYVGFANLPNQVYRKSVKR GFEFTLMVVE*
14	A	79	534	SSIMTFLESSAVPPHWTGQDGRVCWTGWIPQCQAGSAPE/RS*VFIN SAGQKSADTGWSSSKPQN*HLSSFHQAVVGM IQPSHSQFLMKRKAAS PRKLEWEH/LQPLHPMTLLYR*DGKPPR*VLLSTYTYCSSRDRPKSS GKNARRFPAHGSS
15	C	354	416	MKESPGGELPQTGKKPVFLF*
16	A	3	145	SSSSSDFAGQTL*STQTVQN*FKKVLKPGRLYPVPIATMGIKEPLIS
17	A	214	464	FCGLLLLHPVSADF*PAELINTQEPQERCQLDTGESSRVQHTLPSCP VQCGGTAELSRNVMIGASELKCLHPSPKLEYILPGN
18	A	246	732	SSIMTFLESSAVPPHWTGQDGRVCWTGWIPQCQAGSAPE/RS*VFIN SAGQKSADTGWSSSKPQN*QLSSTGAALPLASLSRERAW\VDDGKHR LTTTPMTVPQRAVQQL*ETSG**DWRQKVQIFQQA VVGM IQPSHSQFL QREDVIMLRPFGLHLSWEENG
19	A	12	288	FGGGYIPTWGKGE GILALELNHDISREFCSAPALASRPPTPPPLLP PT/PPLPAPRSPADATPRRVGGPLR*ALKPRAPGPGWSRRRCRSWW
20	B	103	282	EDTAAQSSPGRGEEAEASAAEAQGGEQAYLAGLAGQYHLERYPDSYE SMSEPPIAHLLRP*
21	A	918	1872	AEKGPPSPGVPSTCLANSP\PPSAGSAAVPHSAPPGAAPRRSSRQRP CSPRRCWQEGAGVRAGQDGLGGSATR SAAQQSHQRQTGP/EGSTGKA KARGSTGRKR*AMGGSAAAGDGA/PHVLGTGQPRAPPPSTGDGARAGN WLAQGSAPTHRRWSTCWEPA SPGLPASSNCC'THTWRNCPGTAPSGT ALPGLPGRPAPHPEPPPPMPPPP/PPRPG/LPLGSCVFL*VERPIWR EVLSVPAPPRACVDTSGE\ASGPS\PVAGTESPRPWLKQPLPCPPQ QPRSWLTRPE/AELHMPPTPLPAYLPGS\GVPQSHS*PPATLLR
22	A	10	284	FKLIAWHSHEKIYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGLART TTGNKVFGALKGAVDGGLSIPHSTKRFPGYDSESSCCYTRESSL
23	A	3	438	LFISLLSISEKIIENCWV*LSAARS*ALRKLAF*ATRSFF*ARDIL GRFHLLF/CNFFLGLLFIDWILSYSSMSFLIHLHPAGQQASTICC SIICQANLHTIFWQFVCIRCADYHIPLYTGISNLNDISVCHTNVHP VIGVW
24	A	497	753	DGVLLLLPRLECNSAILAHRNLRLP/GFKRFSCLTLLSPWDYRHLPP RLAIFVFLVYVGFHHVGYAGLE\LLTSR*SARPRPPKIA
25	B	922	2057	XTQDSPWFMISEKORNFNAESTIGSHIHGPRIVAGLHAPTLMEEDB DALQETVRASIRKEQRNSRHDGCGD GIRKAHAAIPRESRSMKRSRKE VKKRWNRPKMSLAQKKDRVAQKKASFLRAQERAAES*
26	A	238	446	GFVVSLSDR*QWESRSSIHA\VTN*ASSSSSSSSSSS\FSR\VYPR FIEYLHKDIQSTGQKSPDAWVAGG
27	A	244	309	NPKGQKDREAPLSRSVFLKIKIKRAFALLHGRF*PSTPAASASPA SKSPRGSGKALASALFYIVQLTK
28	A	1230	1820	QEYRPSQTPHLALSPERVAPGRRRAAGRLAPEARAPRGSP/LPPHRVS EKTIRVVVFHPGARKAGGTPPRAPRGDTGGAPGA\PTYSTPLMSLHR ARLESSSTGSSFPADSAPVPLAVVSLDSR*QWESRSSIHA\VTN* ASSSSSSSSSSS\FSR\VYPRFIEFLHFDIQSTGQ/RITSRQHPPR/

				DLRDALF*LNSRIPL
29	A	376	612	FPAFWESQVRWIASASGVQDQPDQYGEILFLLKLQKLGGHGG/IR*E DHLSLGGQGCKEPRLYHCTPAWVTEHYLVSKK
30	A	147	766	GALHLIRKGSPLHGQAHKHVAQQGRGILSRVHRPTHVHTQGRKATRL GLCSAHGRAPHPSFLPLVPVCCS/WHHCETP\RPCPLLPCPPSSGA STSRTASSPVLSLTD*PYLSETEEQVSP\GLTHKASLEPRSDSDAKT SSHPRDWPMPVDCAAALSWTQPLWMFCGSRLAFHDAPAPAHMRAIW ASRAIPAARPGPHLGLAAASC
31	A	1	365	FFFLLLILFLLLIQYHYIFYTFLWLRLLLVLTGSI*C*KCKITMNST *IE/TVFKDYEHLYVCKLKNLEKTDKVLTIHNFRLRNQ*EPEVLTR AKMYKIYNDIE
32	A	603	855	GGWIMRSGVRDQPDQHGSETLSLLKLQKLGGHGGACL*SQLVRRRLRQE YHLNPGGGGCSEPRF\GHCAPAWATE*DSVSGKKKKKK
33	A	200	559	KNFFFLEMEF/SVLLPRLECNGVISAHRRRLRLPLSSYSPASSSQVAG DYRACTTTAG*ILYF**ETGFLHVG\QAGLEFPTSGDQPALASQSAG ITGVSHCPQLKKSILHETPKGLTGVT
34	A	2583	3580	DRVSLLLPRLECNGAILAHCNLCLSGSSDSPASASQVTGITGKCHHT QLIFVFLVEMGFHHIAQAGLELLTS\DSPTLASQSAGITGVNHHAWL FFFC/RTVSLCYPGWSRVA*SRTATSA\PGLK*FACFSLPSSRD YRHVPPHPGNFCIFGRDEVSPCWPGWF*TPDLR\YPPASASQSAEII GVSHHTWQPQEVFLFLNFIYLRWSL/DSVAQARVQRRDLGSLQAPPP RFKPFSCSLSPSSWDYRRPPHPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/NFFETGTHSVTAAVQWYTI /GSLQPRTPELK*SSHLILTSNWDYRCTPPCPPNLFYLFYFHRDE GSLCCPGWS*TPELK
35	A	45	819	RSLALSPRLECNGAISAHCKLRLPGSRHSPASASRAAGTTGAHHRAR LIFVFLVETGFHRVSQDGL/LPDL/DDPPASASQSAGITGVTAAP SRACSFKLARGRACPGWDWAEELTGTSHTRRVHPGQALWGDWRRCS CGSRSWQT*LQRCPAVLRGWLACLTAEQEEQIGPYVSVPVPGAAC CFIDVLR*KISDKDVFKAQGRGAQPKTFSLLRKS/LNPVTQARVQWC DLSSLQLLPPRFK*FSCFSLPSRTIT
36	A	2	424	LFWSPTQREPTMVLSPADKTNVKAAWGKVGGAHAGEYGAELERHFD LSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLVRD PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
37	B	44	307	MVAVSCRQRPTSRPAWGKVGGAHVRSMCAEALERMFLSFPTTKTYFP HFDLSHGFCPGLRATGKKVADALTNAVAHVGRHAQRRCP*
38	A	3	203	HASDKMADKEKKKESILDLSKYIDKTIRVKFQGGREGE/GLPLSVP PL*KFQINPATEMMRTHAEA
39	A	132	370	SNSPA*PSGEPGTMG/CRPPCPVNFILRKNGVPPCGPGGPKSPDLR THPLGPPKG/RGIPGGTHCPGPPLGFKKPWPGRV
40	A	25	412	IQARKKQSVLGIKTEDQGTFNLLRKGIMDIEAYLERIGYKKFTSKL DFETLTDILSHQIPAVSFDNLTVLCGDAMDLEAIFDQAVR*NR\G GWI\LQVNHLLYWALTITIGYETTKIGRYGYQTPAEK
41	A	319	1002	IQARKKQSVFWIKTEDQPTFNLLRKGIMDIEAYLERIGYKKSRLKL DLETLDILQHQIRAVPFENLNIHCGDAMDLEAIFDQVVRNRGG WCLQGNHLLYWALTITIGCETTMLGGYVYSTPAKKYSTGMIHLLQVT IDGRNYIVDAGFGRSYQMWQPLELISGKDQPPQVPCVFRLTEENGFWY LDQIRREQYIPNEEFLHSDLLEDISKYRKIYSFTLKPRTIE
42	A	1	818	MAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGSDSEKCS YSQDKAKVNSGNKYNDNFFGLYCICKRYPDPEDEVRELEVKPGVTK ISTEDDGLVRNIDGIGDQEVIKPENGEHQDSTLKEDVPEQKDDVRE VKVEQNSEPCAGSSSEDLQTVFKNESLNAESKSGCKLQELKAKQLI KKDTATYWPLNWRSLCTCQDCMKMYGDLDFLTDEYDTVLAYENK GKIAQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
43	A	46	512	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGSE\S EKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGSHKLFE

				LYTKRIFRC\DCGNSKF*NFGMQLLP*QSK/DVNSGNKYNDNFFGLY CICKRYPDPPEDEIPDE
44	A	275	403	FSHFWPPEFLRD*MWLG/VAHACNPSTLGGRGRWIT*GQES
45	A	2	343	NLCQVFIPFLFHSLLYVFKTILKGLFQASFLGHLLLLPLSGTPGRPG GGGAGGSGRGDPPAAGASRTIPWPLLLQQLSSSSSHFKA/PSKLSSH G*PRALGPPGPYHRPPSPGTT
46	A	105	328	RDLHMKTITSKVY*LT\H*SGSVGRDYELHENPLVGPNIKLGDFVD ISHPNDEYSPLLLQVKSLKEDLQKETIS
47	A	1478	1732	GGQGRWITR\$AVQDPHGQDGEKPSLLKIQKLARHGGRRL*SQLLGRL /RQENCLNLGGGCGSEPRSHPCPTPAWVTEQDSVSKKKKK
48	A	1662	1858	PSFLETEPC\$IAQARVGWHDLGSLQPLPP\GSSNSPASASQVAGITG A*HHARLIFLFFVEMGCAE
49	A	245	616	NPPN*NPPNACVKPEFENQPKLKWSQRGVGGPRREGPPAQAPEGTA GRRADKLVRVGWRPPPATSAQGSASHPPLFC*SSSRGPPSSPCLEAP TPGASPST*TITPPRRARWRACWTWPCSCPTPCG
50	A	96	547	ADPAAPVPWFGPSQPGARAQWPGLLGAAPPPALCSPP*TDSGVQDP VSNAPWVNSQQWWRQ/PAATEKPPATKAPGLLVQEKYKVS*QKGW/ PSTKKAQGYFP*NCPPLQFLLPPLSLPPGDISGQCPHLPKPLIPPP SYPAPCPGFCPR
51	A	702	1107	LQERYSDPGLLASFHGESSQDRLDTVQQEK*NAGSASPPGPPHPNTC QPRDGRGFTRLPCHRMWGTPGIRWKMPQ*AAGP\PHAA*WPGSLMP PCL*PSASAWTRQ**PGSLPTLTSPG*DPGAHILLWRKQSY
52	C	150	467	MMGLRLQLXX XX XXXXXXXXXXXX*
53	C	150	467	MMGLRLQLXX XX XXXXXXXXXXXX*
54	A	644	906	CQHFRPKWADHLRSGVHDQPGQHGE/IPSLKIQKLARC GGAYL*S QLLGRRLQENHLNSGGEGCSEPRFHQCTPAWVTEQDSISKKK
55	A	730	951	SFLKDIGLFKIIYFFFFFETGV\$FCHPRLECSGETMAHC\SLTSLG PGDPPTSAS*QAGITGVHHARLIFFF
56	A	939	1605	GHSANWWLGPEENPALPTPELVSPPRGCRQSSRPSLRHKEEKAK*K SPQPTILRPPAPPTGSLQAPKGGARPPSRPPPPRPAAPNP\RPL PPPPSPE/PGRSSCPAPPTTRTPR\QSQTHRPPP\SSAYEKDAAR APTATGRAPRRPGLRPK\$WMPEQEKEPPTDRSIDRTPVSPYQTREG GRA\PRASSI*GPDSPATRDGSSGPHRSYRPGCVAR
57	A	1	1513	MGPLSAPPCTQRITWKGLLLTALLLNFWNLPTTAQVTIEAEPKVS GKDVLLLVHNLQNLGYIWKQGMKDLYHYITSYVVDGQIIYGPA YSGRETVY\$NASLLIQNVTRDAGSYTLHIVKRGDGRGETGHFTFT LYLETPKPSISSSNLYPREDMEAVSLTCDPETPDASYLWWMNGQSLP MTHSLQL\$KNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPVTNL LQHSWLIDGKFQ\$SAQVFFIPQITKTYRGVYVCFIHNSATAGTNLII KRIIVPDTLRKRGNEKVESSDDIENSNQPF\$H\$PKAFKNIQVQHGY GIHRKLITKLEKWLDSGLPCVISAETSSPRPGCSVSSGFQGHGKSHY YSSLECPWKWLQRNHIYGGKVGWNLEGAHQLHIPAKLPKPYITINN LNPRENKDVLAFTCEPKSENYTYIWWLNGQSLPVS\$PRVKRPIENRIL ILPSVTRNETGPYQCEIQDRYGGIRSYPVTLNLV
58	A	1107	1365	HSGSAGMHWNLFLVHMCQAH*LFDRLLHMM*CNGRGP*FALCTRC SQ*DSGAN\WDK*KNILPLRNF\$WLGFNRLGSRGWVPEV
59	A	582	1303	GACSRAGLWLLGQGLLPRIYQLSEDCVSWSC\HQPLSPQSLIWAR TELSPDTQSGEDRKTSFVGHQPTALGGLQ\$IESLMSSEAEETEERR CTWMQLSETNRTLFLFGVTKYTAGPYECEIWN\$G\$ASRSDPVTNL HGLDALTISSSYTYHTGEV\$PKLSCLIDTHPLAHSWLIGGKFQ\$SA QVFFIPQITKTYRGVYVCFIHNSATGGTNLIIKRIIVPDHSLRSALS LEV\$TGS

60	A	713	811	IPGRPWRL*A*PVTLRLOTQATCGG*MVRASL
61	A	1	1194	MGPLSAPPCTQHITWKGLLLTASLLNFWNLPI TAQVTIEALPPKVSE GKDVLLLVHNL PQLNLAGYIWKGLMDLYHYITSYVVDGQINIYGPA YTGRETVYSNASLLIQNV TREDAGSYTLHI I KRGDRTRGV TGYFTFN LYHTSYLWWMNGQSL PMTHRLQLSKTNRTLFIFGVTKYIAGPYECEI RNPVSASHSDPVT LNLLLKL PKPYITINNSKPRENKDVLAFTCEPKS ENYTYIWWLNGQSLPVSPRVKRP IENRILILPSVTRNETGPYECEIR DRDGGMRSDPVT LNVLGYGPDLP SIYPSFTYYRSGENLYLSCFAESNP PAEYFWTINGKFQSQGKLSIPQITTKHRLYTCSVRNSATGKESSK SMTVEVSEDPYDDTGSHTDKPE
62	A	994	1108	EGPHDLCCVHVL LCGDEPRIQKLPEHGWSAVLSFLLQK
63	A	547	644	IPGRPWRL*S*PVILRLQPQATSGG*MVRASL
64	A	647	885	TGNLQNGRKFSQPTHLTG*YPESTMNSNKFTRRKQTTPSKSSSPQR RTHRQRPWGSSQPLPAHSASPGRGSCSQHHF
65	A	1586	1775	AGGGQLNVNFMGKPLYVKHEPLRTHQNI RHNNRCSNCKPGQQVDDF TLWTVFPKMSEHDS
66	A	275	577	GGWITRSGVQDQSGQHSVDVSL/LKKYKKLTKYGGVLL*SQLS/RL RQDNHMPGGRSCS*PRQHCTPAWTVRDSISKKKKKKKKKKEKK GKKALLEPG
67	A	1016	1461	VSHSHLSSPQFNHNLNRRPTRIPLSPQPK*GPAYSRRPPVWTPAEPEA LRWGRHRGP*KARGSRPSSAHSGWRPRGEAPHRTGTAPPTAVPCR AHLGEDSTPGPPGALGGVGFPSPASP/PVPTPT*TQTGRRPETQLRQQ TPRGAPRA
68	A	241	492	GGQIMRSGY*DHPG*/HGETRSLKI\QKLAGHGGHRL*SQLLRPR LENRLNLGGRGCSEPSSRHCTAAWATE*DSVSKKKKSR
69	A	709	942	SQHFERSGDQHHPGQHGETLSLLKMQKLAGCGGML*SQL\LGRLRQ ENLLNPGGRGCSKPRSHHCTPAWVTQQDSIS
70	A	170	340	TDSALGSPCLHPTALCAVCGTA*SST/GLVALALMRLELILKSSVPA VMAGIITIYNL
71	A	134	452	QSPDSMNAREFRRRRGMEMVDYVAYMEGIEGLLVYPDV*PGYLRALI PAAAPH*LDTCEDIISDA\EKIIMPGLSHWHSPDLFVYFDSVSSYAR MLEDMQCGALDC
72	A	218	428	LSSLPTTISR VFYNLS/CSHL*YSLKHFIYLFYLFYLFYLFIF ETESPLSPRLCRSGISAHCNRL
73	A	702	1282	AVEMYLVVCGTVAISRVRMSAVCVLRTWS\RNAG\QLI\CFTVFQPC SNVHVL/KGPNYVCFPG\YPSF\KYSHP\HNFVKTINAVCGQ\LVQF RFPDTEEGIRKVTV/KCYVKEGDTV SQFDNIGKVQSDKASVT\IASP YDGUI/RKL*HSLDDIAYVGKPLVNIETEALKGTVNLFYQIDYCPFF VIGSQLKVTFK
74	A	743	1233	ECGVFSFPFLFLRQCLVLS PQAGVRWP\HLGSLQPDSPGSSRPSHL TLLSSWDLTGTCPPCLANFRIFVETGF/TCFPRVLVNS*GSSDPPT PQSVGDCRAGSHHTLAVFSF\CFEMGPCSITRAGV\R*HDHSSLQP* NPGLKRSPCLSLPSSGDYWSMPPCLA
75	A	3	300	VFQRTSLQTFAILTLSCQGTQAYEERSIRSFANDDRHVMVKHSTIYP SPEELEAVQNMVSTVECALKHVSDWLDETNGKTKTEGETEVKKDEAG ENYS
76	A	189	442	KTMRSIRSFANDDRHVMVKHSTIYPSPEELEAVQNMVSTVECALKHV SDWLDETNGKTKTEGETEVKKDEAGENYSKD\NG*RTL
77	C	183	350	MYGLPGFFYAHXXXXXXXXXXXXXXXXRHAPALRV TNRSHP TGGRAV PQPWLVMV*
78	A	226	481	CLASHRSINISTCTGAEGHESESFSYWGTRGPSATMACDGLTRTGH SSPSRARSPLLCARSLTKAACQ*AVPVTWCHCWRPQG
79	A	421	899	IASLFLIVKVEEVSQTAIWKKKKCDEYIPGTTSLGMSVFNL SNAIMG SGILGLAFALANTGILLFLVLLTSVTLISIYNLLICSKETGCMV YEKLGEQVFG\PQGFVIFGATSLQNTGGKKNNMLFFT*LEYTHTSF

				FSKWLFVRLLLLSRSEINLLFI
80	A	44	377	TFFLYLENLNTAVRFWKLPYIHCCKNPGGAGLICIAPWLTAKAFVFGS DYSCLVTVRVK*VFKPFLKDVEIRR/FTWTIRQPWDAVFLRVPDYHA LIKQPMDELD*MRLANS
81	A	457	489	PP*ITLG*KTCQSARWLMPVIPTLWKAIEVGRSLELRSLRPATRRN PISTKN/LKISWGRQGSSELRSRHCTPAWQHSETPI
82	A	999	1525	WEMVEIWSYSSSEQEHQLIKLSYQRIKPLPHAHWWPFNPSPGLPPEAS K*PPG*TL\LGIFLGKKA*LQTFPLNYIRLENMQPRHGGSCFVIPTL WKAIEVGRSLELRSLRPATRRNPISTKNPKLAGGARAH*SPGTPE AEVGGSPPEP/GGRQGSSELRSRHCTPAWQHSETPI
83	A	2	450	LHCCPLQLKMCVACRAIGILSRFFAFRLSRGYICRNFTGSSALLTR THINYGVKGDVAGAR\INSTNSKVNTLITELQSQFSQVMNEILSSYQ IRRAVLISSKPGCFIASSDINILTACMTL*EVSHRSSEAQIIVQKLE MTTLSIVA
84	A	247	287	KRGFVLPPGLECGGPIWVNGR/LRLLGLPPFSGLSFGSWDYGGLPP GRVKIWHFLEKRGFRGVARVGSTLLTGEPPVLGF*KPPFF
85	A	2	526	RGGCDRDGPFSSASSPLAMASLTVKAYLLGKEDA\AREIRRFSLCCST EPEAQAEVAAGPGPCERLLIRVAALFPAVRPGGF/QAHYRDEGDGLV AFSSDEELTMAMSYVKDDIFRIYIKETNECLA/DHRPDAHERA/PR NMVHLNEICDG*NGPVAGTLYMCSFCPYIYLCTPFNV
86	A	285	326	NLPKILGHTQKRLQSTRSWKRMMLSLINLQIIYNPVI PFVGTIPDH LDFVS*IVI\RGPVSSDANYIQYDL*NPKNLSLV
87	A	133	394	LITIIYIPENCQPGQHSETSSL/LKKIKKLACGGTHL*SQLLGRLR REDYLSPPGGQICSEP*SYHCTPAWVTGQDPASKKKKKKKKR
88	A	2	359	EVLRMAGTGLVAVEVVVDALPDFEEGYEGPGGREAAAALVEDETRY RPTMNYLSYLTSPDYSAFETDILN\NDSERLAARQP/I*LLTMKLYY LSSPSCGHYFVLLHVYNCLSLYFPSP
89	A	69	342	VGNMSGTNLDGNDEFDEQLRMLLYGDKGDGTLTDAGGEPDSLQGY STDT\PTEW\DLDI*AWFFMISEYFLFTYLVQFMAFLLYCGFMFL
90	A	144	2205	DRRERCHPFKRALMP/LRPAEPRPAFPIHHPPLLQDANE/PG/CWA EAVQGCPT/AEDPPCVSRAAPGGSVPPFC/PGRLL*GWGGPRGKGD EGLADSGPPCELRFEESRPPRVGES\PAEKLAYPP\GPLCFF*PF SEF/PEL*TKSPS*EMTNHMLHSGCGGSWPGSPTSPGP PPGGSLPRA AALPPKTPGQTRAPAGACPHADLAMSPGPTPGSPPVAPTSLVADCS SQNV*HPRVPEPTQAATPVQFPKNVITSPGCQSPPKQP/APVPVPRM YN/MPRVTEPAQAATPESLGHVPELRSTQTVATASGHLTPMKGTG SAREIPEVGTGPPWCPVP\PPSPLPLCPAPRGASAGGLTLPLRASQTS GSTFLLISFPFCKLTSPFPGLGVQGTAPAGRSVCTVVQGVVSEGGT SVGQLLHLPVPLCPPLSKGQ\VMAPLAGL/PIQCSGPPVQWGDPRPT PP*CIQPGQVYCCD/VLPALLCRFPGAAPRTPHEWACPALAECLPC ALRQVPRAGQPG*TCGAGTGPGCWKGGQKEAGGRCEKLPPLNTT ALPAPAGPCSQPLSHGWPG\PPSPH*DSRQGGPDP/ASPSQPWLR KPPNPTMGLRKPRK*LLPASPKRLRKPKAASLPVRHPKASLGCS*EG LIWALP*GW\PCRWGPLGALGGTQPPRHPGPVLISRA*GLQPQPLT K
91	A	122	876	SPLLGLLRQKIFFNWEAGGSIKPKLTPSPARGQGGGPFSSSSPSS SPES*LFPALRTPSRQGSAPISASGLSTPACVPSGSTRNLFHAPHV GRVSLLLPA*KAAGPSKKGPGQVNPA*FRKPGVGI*RSVGPRQLPL E*LHARKNRAGPVPLPGLGKEGPSLQGPRTQLASLLMEGPPTHPTI HDGTTAQPELWPCRGPMQSWGSGP\EHTFGPRQPHPPHSSRHRSD SESSLLQASAHGKA
92	A	27	321	IINTSISLWFLGLSSI IHHYQERFL*FN*FGSYMVFIEIFFGISSAF FVC*WPK/Y/LLYFRYCRCFLILLLLSIFEF/DLCYLVL*IFMFFLF FYMFLCV
93	A	264	664	IRLAEFCEGIFQAFSICNSNIWLLPEIPLLGIIYP*E*NTKTCTQMF TAALFIIS*KVEISQMPI INEKINKLWYIHMTCHTKNKVLIRDTT*M

				NLENIKLNERGOTKKKKKAIYCLSLFM*YVQNRQIHTDEK
94	A	2	605	SHGTPGRPTRPVEFFSFGGSAGSFSPWFPKAKKRAGGADSNVFSMFE Q\TQMQUEFKEAFS\IMDQNRDGFIDKN\DLRDTFAALGEV\N\VKNEE IDEM\IKEA\PGPLNFTVFLTNVWGENLREADPE\ETILN\AFK\VF DP*RPKGCMKA\DY\VSGKMLTHAGRRRFSKE\EV\QDMFAGLPPLT *LGNLDYKNL\VHIITHG\EEKD
95	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLVAFVPI SGWNGDNMLEPSANMPWFKGWKVTTRKDGNASGTTLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTTTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNPPMEAAGFTAQV IILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAI VDMVPGKPMCYESFSYDPP LGRFAVRDMRQTVAVGV IKAVDKKAAGAGKVTKSAQKAQKAK
96	B	52	554	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMI IILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRS GKKLEDGPKFLKSGDAAI VDMVPGKPI *
97	A	1	1299	MPSIKLQSSGGEIFEVDVEIVKQSVTIKTMLEDLGMNDEGDHDPVPL PNVNAAI LKKVIQWCTHHEDDSPPKVYENKEKRTDDI PVWDQEFK VDQGTLFELILAANYLDIKGLLDVTCKTVANMKFETSKYYVSIIDAP GHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTHEHALLA YTLGVKQLIVGVNKMDS TEQPY SQTYEEIVKEVNTYIMKIGCNLDT AAFVLISVNVTTTEVKSVEIHHEALSEALPGDNVGFNVKNVSVKDVVRH GNNAGDSKNPPMEAAGFTAQV IILNHPGQISAGYAPVLDCHTAHTA CKFAELKEKIDRCSGKKLEDGPKFLKSGDAAI IYMPVGKPMCYESFS DYPPLGHFAVGHRQTVAMGI IKAEDRKAAGVGKVTKSAQKAPKPSE YYPLYLPPQS
98	A	36	698	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYV TIIDAPGHRDFIKNMITGTS\QADCAVLIVAAGVGEFEAGISKNGQ REHALLAYTLGVKQL\IVGVNKMDS TGIAILTGDFPSLEPRHVSTWL QHVVTI PTRNWHKCYCVGVVANFLNVSADFLNPF
99	A	62	1548	PLKAKMGKEKTHI\NIVVIGH\VD SGKSTTT\GHLIYK\GGI\DKR TIEKFEKEAAEMGKGSFKYAWVLDKLAER\ERGITI\DISLW\KFE T\SKYYVD*SLIAPG\HQETFIQKHDLQGTSQGLAWFGGPPFWGGSP LIVAA\G\VEGF*SLVSPKNGADPTKHALGLHTGVWKQTKLFGVNK NWIST*/EPPYSPEEDIEGNC*GKVSTYIK\KIGYNPDTSSILCPIS GW\NGDNM\LEPS\PNMPWFQGDGKVTRKDGNASGTTLEALDCILP PTRPTDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVN VTTEVKSVEMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKN DPPMEAAGFPAQV IILNHPGQISAGYAPVLDCHTAHIACKFAELKEK IDRRSGKKLEDGPKFLKSGDAAI VDMVPGKPMCYESFSYDYPPLGCF A VRDMRQTVAVGV IKAVDKKAAGAGKVTKSAQKAQKAK
100	A	404	1074	ARACKIPNTASDRPI IVALQKRSSPKMTQSAAGTCPTSCMIK/IDS HKCGDDRELFAQAPVDQFPGTAVESVTDSSRYFVIRIEDGNGRRAFI GIGFGDRGDAFDNFVALQDHF KWVKQQCEFAKQAQNPDPGPKLDLGF KEGQTIKLNIANMKKKEGAAGNPRVRPASTGGLSLLPPPGGKTSTL IPPPGE/PVCGGIPRPASSCSQFRSTSSQTQPGTGW
101	A	2	477	IVSPEVRWAPGVAMEESGYESVLCVKPDVHVYRIPPRATNRYRAAE WQLDQPSWSGRLRITAKQMAYIKLEDRTSGELFAQAPVDQFPGTAV ESVTDSSRYF\VIRIEDGNGRRAFI*I\GFGDRGDAFDNFVALQDHF KWVKQQCEFAKQAQNPDPG
102	B	118	419	XLFCVD IDECSIMNGGCETFTCTNSEGSYECSCQPGFALMPDQRSCTD IDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECD

				LNPNICLX*
103	A	59	451	CLGVTVKDVNQEFVRALAA\F\LKSGKLVPEWL\DTVKLLAKHK ELAPY\DENWFY/SREFVRNLASTARHL\YLRGGRWGLAPLTKIYGG DVQRKRAFIAPAIFSRG\SKSVARRVLQAL\EGLKMVEKDQD
104	A	583	1526	PHLILQVTKAMCPFESGRESFLVVSICIFYFKPDSSASFSFPDPYSVQ C*PQLEPPPHCSTSIYFPK/PTLPHIPFPPLLTKHPKEDLELAGWT SSGCFYFSLPSTKLGENWSLHPQSHVYRSGDLVGSF*LLSQKL\HR NPSICSLKGPPPREGLNPDVSTNTAPYPRNLP*DLQRTIFSSPSIF YPGPPGAPSGES*NP*ELEGILEVF*LCLCPT/VH*HQPLVFPFP SGLFSSFPFPQKILTHRFLLVQASKPTPLPLRLCPLWSPSHYPSSL APSSSLEFGPGSPQKTLE*PPLPKQTDRHAPGPE
105	A	1283	1648	SSGASVAPTSWTSNRFP*SWVPSSF*RTHGPRPSGPPRERKPRAPG QEPTKGTpresvclndlpcpgllgicrpilqtsp/CHGHHGILSVVN VLKGDKPKSPRSLGLPVFHNHFRDLSVL
106	C	263	304	MLKLSVRNRETFL*
107	A	426	1519	AWRRRRSGTSGKATWWCSGLRRASPTPSRRVQSWATAVMWKPSPPSS PASWE/PALPREPHRAVSEQRQ*GR*PCKPELTAPLCLEPVHRPEGP MGT/YSRCCLSPLHRP/PGPVGTFPV/SPEPVHRPQDPWHIPGVPEP VHRPQDPWHIPGVPEPVHRPQDPWHIPGVPEPVHRPQDPWHIPGVPE PVHAPTGPVALASVGASSRDGLLPAHAACTLHETAGQTRTSRLSPS *GLGLPFCRRSRQPWTPALGHSKTSGEWGGARPGPCGC*CCMLSP TQQPLPGGHPQRRASPRAGE*TSRAYLAVHAAATLWKLPLPEDPP PLLDARISAHRLPCPSGRHRKVSFLTLFSISCEARKIG
108	A	1	539	RRCCCRHTRSPCLALLLEIVSLFSFAVPQSPDSSPLVFITYFARTHDP PPSLLPLPAQLWQRTMTWTKLLDYER*MRWETAAGGDGAEPAPKDV KGSYVS/LSHSSGFLDFLLL*VLPSIVHCAFEHSTHRHECISQAI LGKDALFPALLDIFLTGVFFLTIFSPVLRLVLLRCLFCLS
109	A	1	457	AGGGCSPKGRPEAKSGQRDWELVAGGPPGISRREGTCCSRFP SRLSQ PFRSAQQLQLAASLPANLSNFCQGSEMPPTSRPALDVKGGTSPAKED ARPEKSTLGQ/YSTLLVIDNQVSSKTR*PDESANQYYASDTFIILSR TYNRYILVHLSK
110	A	232	378	FPTTKSLG*DSFTSEFCQTFKAELIPIILS/RLFQKLEQYVTLPPYFY EA
111	A	515	911	LPLFIMNMTVELVWPDTSNLPRNSEILSSPTRPNQLFVCLFLGSPS LPRLEYKWYSQSSL*PQNPGLK*SSPSASYAKTMDCHHAWLIFLF LQTEGL/NYIAQVG/VQTPGFKQSSCLTLPKC*DYRHEPP
112	A	40	351	LKIPMQFLHSGFWFSFFVFFGF*KFGFGPQGGRRQGG\NKTGKEKLPP GSSSLPGPNPQENREKKGPPKTLKKFNLSSSGGKTRGPRGEKNSDP KGTPGQNPNGN
113	A	307	1429	CTATQSGWLC LHRPCPAWRCTWRTTWFCIRYKGEMVKVSRNYFSKLW LLYRYSCIDDSAFERFLPRVWCLLRRYQMMFGVGLLTRGTGLQGFAA CCMSLRPSTDSLAVSECFASPLNCYFRQYCSAFPDTDGYFGSRGPC LDFAPLSGSFEANPPFCEELHGCHGLSL*ETA*ELTGAPVPSSVFIP EWAGNPQHQRSPA WKQ/MPLQTPPVDPACL*A*VPQWLPAHLQEGGN ALQGRPQHGCALPTE/PTLALPSGRRRLTGCRS*VLPTGSPGP/PAT ALVLP HRSYLGGPRTGIRGREQGPKPRASPHLTYSCEGEGAPGVLSL DLLGLGPLGPQDPGCH*HMKIMVLPGLPSLPVPKSSPQTSPKSHVY RS
114	A	161	218	SWDRVLGRSDELTTLSCTP
115	A	116	565	EPTGTASRAATMPNFSGNWKIIRSENFQELLKVLGVNVMLRKIAVA\ AASKPAVEIKQEGDTFYIKTSTTVRTT\EINFKVGEFEFEQTV DGRP CKSLVKWESENKMVCEQKLLKGEGPKTSWTREL TNDGEL ILTMTADD VVCTRVYVRE
116	A	343	528	KTVSLPGIVPHACNPSTLGGRGGWITRSGVQDQPGQHGETPFILKKK KKKICGRKLIPFSEG
117	A	296	631	FKLTSSRNVPPTGPGAVAHACNPQHFRPRQVDHLRSGV*DQPGQHG

				ETPSLLK\IQKLAGHGGVHL*S*LLRRLRQENRLNLGGGGCSEPRSH HCTPAWTTG*DSASKKKK
118	A	74	396	GQILALMPKGGGQGGILTYPNPPLPG*NNFPGLTPPRTGINGLGPPG RVNFGIFKKGKGGFPPGARGV*NPGPRGASSPGFPKGRG*SPPP/QGP FKPLKRFPDLPIFPR
119	A	454	778	ADPMSPSSKSPNMEAVLWIPDTNIVL*SLKVYPSS*TIKSWLGT/CG SRL*CQHFRPRRDHEVKRLRPS*PTWRTPSLL/RTTKISRWWHT SVVPATREAEAGESLE
120	A	133	359	RHCSSGMEIPPTNYPASRADLVAQNYINYQHGTPHRVFEVHNAYRVI MQD\MSG*GHLVSPSSRFFLHSFATSLFE
121	A	3	1671	SSGARWRFRAGSMGLFCQRKHSS/SHPVLQKPSVFGNDSDDDDDETSV SESLQREAAKQAMQTKLEIQKALAEDATVYEDSYDEMOKKKEE NNPKLLLGKDRPKYIHNLLKAVEIRKKEQEKMEKKIQREREMEG EFDDKEAFVTSAYKKKLQERAEEREKRAAALEACLDVTQKDLGS FYRHLLNQAVGEEVPKCSFREARSGIKEEKSRGFSNEVSSKKQNTT REMHSFKLM*K*RENPDADSYFDAKSSPDD\K*KKLELTAEGKRS*R PLRMTSSTTGKTTLGLHVKKEGTVPGTTRKDHERRDMRKGIKIST RSNPETKRTITLTVITGKKGILIGTERPVIEIPIGRGMNRKINQGRG TKEKEVTEYGKGRKIGRNIPKENKKEIDNKMIRTDVPRKERRKRKAK QRKRAYESKGGKVLKLLINTEIEKNER*VFS/ASERNQDQKGKQPKF QGQRINFLTNLDFIQNGETWQRTKERNQEKPSNSESSLGAKHRLTEE GQEKGKEQERPEAVSKFAKRNNEETVMSARDRYLARQMASG
122	A	170	339	IMKLITILFL*CRLLSLTQESQSAEIDLLDNDLFLAEAA\GLYRYI MQIQTNPRI
123	A	23	307	RQTRWCPVRLSHYRTLGGCCHLRRGRGVA*VRGPQSGTISSVENTP PWRRVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYK
124	C	35	91	MSPPQNKGPFPKSPGW**
125	A	50	230	NLKGPLRRPVSGIIHVISLPLYQKCSKNEKKIPWRQMEM/C*NVPS ANNPPLGLLKNIVF
126	A	814	1292	GISPFYIFGQDMGLEKNPTSFPKMCFHCPLESPLSYVGCWKTGNMS CVVCTVNWFLRSVIYFIWFTNILSHFEVLALKRLLAPGGGGMPPRV L*\CCRRTTGHQRVWPSRPPEQTDQTARRPPSWRPTL/CSPLPLPPP PRSGREKGNRARFLKGPRIG
127	A	191	482	DSSGQVQWLKPIIPVLGNLRQADHLRSGVQDQHVQHGETPSLLKIQK KLARHGGACL*SQLLGRLR/QETH*NSGSRGCSEPRLRHCTLA*ATE GDSI
128	A	1445	1778	NLSRNKEVLLFGKNIPWVGWARWLVPGNPNTLGGQGRADHLKLGVDQ QPGQHGEIPSLKIQKLRHGGVCL*SQ\NHLNPGGGGCSSELRSHHC T\CTPAWAME*DSIPKNK
129	A	3	370	PGFPLFSFPEGNGPSKRQTD*IRCLF*DGKVWECSPSSSSSPKKR KKAVIF/CVPVQTKCIVVEGGEETLVGDV*V*P*\GSFKHVAMFPE K/DCLCTLYEASFKTESRRVDGFVCVRVGT
130	A	412	616	VFVCLFVCFETGSCSVTQAGGQWCNHGSLQPQPATSAS*IVG\GVAG VYHHFQVFLLLLFNREDEVLLY
131	A	278	466	YTHILRQLPTLRHEQKSRENCLEEMSLDRFQAAPK\SPTPTHHTYKP TLAGH*KIHAMGLTRA
132	B	639	1718	MDPLGPAKPQWSWRCLTTLLFQLLMAVCFFSYLRVSQDDPTVYPNG SRFPDSTGTPAHSIPLILLWTWPFNKPIALPRCSEMPGTADCNITA DRKVYPQADAVIVHHREVMYNPSAQLPRSPRQGRWIWFSMESPSH CWQLKAMDGYFNLTMSYRSDSDIFTYPGWLEPWGQPAHPPLNLSAK TELVAVAVSNWGPNSARVRYYSLOAHLKVDVYGRSHKPLPQGTMM TSLRYKFYLAFENSLHPDYITEKLWRNALEAWAVPVLGPRSRYER FLPPDAFIHVDDFQSPKDLARYLQELDKDHARYLSYFRWRETLP FSWALAFCKACWKLQEESSRYQTRGIAAWFT*
133	B	1154	2233	MDPLGPAKPQWSWRCLTTLLFQLLMAVCFFSYLRVSQDDPTVYPNG SRFPDSTGTPAHSIPLILLWTWPFNKPIALPRCSEMPGTADCNITA

				DRKVYPQADAVIVHHREVMYNPSAQLPRSPRRQQRWIWFSMESPSH CWQLKAMDGYFNLMTSYRSDSDIFTPYGWLEPWSGQPAHPPLNLSAK TELVAVAVSNWGPNSARVRYQSLQAHKVDVYGRSHKPLPQGTMM TSLRYKFYLAFENSLHPDYITEKLWRNALEAWAVPVVLGPPSRSNYER FLPPDAFIHVDDFQSPKDLARYLQELDKDHARYLSYFRWRETLRPRS FSWALAFCKACWKLQEESSRYQTRGIAAWFT*
134	B	1029	2108	MDPLGPAKPQSWRCCLTTLFLQLLMAVCFSSYLRSVQDDPTVYPNG SRFPDSTGTGPAHSIPLILLWTWPFNKPIALPRCSEMVPGTADCNITA DRKVYPQADAVIVHHREVMYNPSAQLPRSPRRQQRWIWFSMESPSH CWQLKAMDGYFNLMTSYRSDSDIFTPYGWLEPWSGQPAHPPLNLSAK TELVAVAVSNWGPNSARVRYQSLQAHKVDVYGRSHKPLPQGTMM TSLRYKFYLAFENSLHPDYITEKLWRNALEAWAVPVVLGPPSRSNYER FLPPDAFIHVDDFQSPKDLARYLQELDKDHARYLSYFRWRETLRPRS FSWALAFCKACWKLQEESSRYQTRGIAAWFT*
135	A	885	1173	LSQGPRRHSSAVQPPPHSHRGHHDDCASPSQVRQNY\AINRQINVE LYASYIYLSMSYFDHNDVALKNFAKYFLHQSHEEREHAKKLMKLLH FDC
136	A	961	1051	LRVQACTVVLVNFLYFFCRDGVSLCGPDWS
137	A	2	804	SSGFPASTVLGRNPALVPHPGRPPIASPPSPLHRTLGLPQGP RRSS AAQPPPPAAASPLVAAMKTAVPPRKVRQ\NYHQGLKRAAHQPARINP GSSTASYVLPCPMSYLLLTRDDGGL*RTFA\KYFL\HQFSMKEEGNH AEKT**KLAEPNEGGRLNLSFKDIQEP\DC\SDWGERGLNA\MECALH L\EKNV\NQSLLELHKTGPLTKMTPHLCD\FIET\HY\LNEQGESHQ KNLGDHVT\NLR\KMGAPESG\CAE\YLFDKAHPWGDSDNES
138	A	3	402	HGKIFYFILFYFYFFIFLRRSLALSPQVRTADCS\GAISAHCKL/RL PGFTFPS\CLSLPSSWDYRRP\HPRPANFFLYFLVETGVSPC*PGMG LDLLNS/SIPPRGLPKCWDYRREPPRPVETFFLKAENVRVNYI
139	A	210	1641	DPARAGTGVGASFRGATWQQGQGRGSACSCTQCPATCLLTGADAPT SRPWSLLSRLLGHCFSVLTVPAAAPPPPGSL/PEPPRAGPQCP*TRP PLR*PGCSHLAGPHSGSPRPCSLLGASATLYGFRHFLAGPAAQGGGQ AVGSQGDHPTRAQPP*WSSPQTPLNLSAAQEFEPRGTCPTRW*SRP DALPWPRPWEPSG*AEGWEQE*WRLQPQGTAAPRATSSGYSGSSRG QRARPGPARCGDGGGAGRC\GHVGRWRQLGHRP/RGSSAPAVCCGT LSAAPGPQHSLSL*SSAPGPQWCPHWPQSGRQG*/SPLPPPPGP G\RPPCAPCSGSPSA*GGCTPGCPTAP*GRRQGRWR*PRTGRLSPLG HLPGCRSQAASVSHRCWPLLP*PPR\PSGPPPLRSGSSPGG/PLPKG C*CGGERPGQHQEAGQGPAAQQTWLHPQAPGRRPSHTGWGGGAPG G*QRRNLA*RPLLP
140	A	885	1173	LSQGPRRHSSAVQPPPHSHRGHHDDCASPSQVRQNY\AINRQINVE LYASYIYLSMSYFDHNDVALKNFAKYFLHQSHEEREHAKKLMKLLH FDC
141	A	170	737	IVTATCLWGSVLVTHSVFPFQSYFFDRDDVALKDFAKYFLHQSHEER GTCLRNLMKLQNPGR\GLIFLQDIKVNKRS*GCHTSSSGSVRVSEIT *TSNCPYKVMHWAFAFCAFLGLPSKLN*ANSNVPFAKTWWLEMMGL LTSRLVGRDALTYSHS\KPDCCDWESGLNAMECALHLGKNVNQSLLE LH
142	A	1	809	VVGVSFCNSAWTEPGARSPRPAAHSQPSVTSSPHPRTPAPRPPPLQ RREATAAGRRLSLVAAMTTASHLAGCAKNYHQGLKRPPINRQDQPWK LYGLLRFTLSHVLTNFDRMMLAFERTFAKYFLHQFSMKEEGNHAEE T**KLQN\QRGWPEFFL\QDIKETQTC\DWEEERGLNA\ME\CALHL \EKNVESHLLLELHKTGQLDKNDPPFCVTFIET\HY\LNEQ\VKGHQ RIWGDHVTNL\RKMGSAPNLAWAKYLFHDHSTSLG\DSDNES
143	A	776	1115	APGVDPKPRQNE/IPVSTKNM*LGVDCLRLRQEDHLNQEVPGCS EP*CHDQATALPAWATQQDPVSKKKKKKWWREARKGKPQ*GDGEKDS TTHSWL*RWRSLSRITVSL
144	A	1	419	MAAGTLYTYPENWRAFKALIAAQYSGAQGRVLSAPPHFHFGQTNRTP

				EFLRKFPAGKVPAFEGDDGFCVFESNAIAYVVSNEELRGSTPEAAAQ VVQWVSFADSDIVPPASTWVFPITLGIIMHNNKQVLEPSFRQAFPNT
145	A	3	1363	HASGITMAAGTLYTF\SVNWRAFKAIAAQYSGAQVRVLSAPPHFHF GQTN\RTPEVLRKFPAGKGPFAFEGDDGFCVFESNAIAYV\SNEELR GSTPEAAAQVVQWVSFA\DSDIVPPASTWVFPITLG\IMHH\NKQAT* ECKGRK*GRILGLV\DAYLKTEDFCWGANVERLSGITVV\CTLLWL KQVL\EPSFRQAFPNTN\RWFLTIC\NQPFPAVLGGSETCVRR LAP FGA*KVLQRPQPKK\DTPR\KEEGFTGKKKQKQPAERKEEKKAAAPG \PE\EEMDECEQALAAEPKAKDPFAHLPKSTFVLDEFKRKYSNEDTL SVALPYFWEHFDKDGWSLWYSEYRFPEELTQTFMSCNLITGMFQRLD KLRKNAPASVILLG\TNSSSISGVWVFRGQELAFPLSPDWQVDYES YTRWRLDPGSEETQTLVREYFSWEGAFQHVKGAFNQKIFK
146	A	3	454	AVPGPGFGLSPTMTVTLAELLVLLAALLATVSGY\FVSI DAHAEECFF ERVTSCTMGLIFEADGGFLDIDVITLPRD/RKIKPRLKKKQ* TYRSFMDVTFKLCYNLRMSWMNPNI RNHNHLLLSIKFLITQFRSS LSYLSSCIQSE
147	A	90	513	VQGLGVERVPLGSHRGWMPRPLLSQPQERASCLLLLLLPL\VHVS TTPEPR\ELDDDFRCVLQLSPEPQPDWPEALHRASAVQA*ISAGGS HLQSSFLIGRLRLKTVTVLLWPLFVLICVYLSVYLPFRLCLDTLSCV V
148	A	98	440	KDDTNTKWC*AWNCSSTRAH\WKRTLTLG\RLLTMNIPHDSAIPLL GAHPT*MWAYVHQNPQTVMLTETLFIATNWTLHKCPQ**KE*CNGA VTEWSAALKQNKQLQHVTPRV
149	A	535	917	LVSPGKPEEQQQLP*PRCQII*LVSPGKPE/PTGTAPRSQPRLSV CPSTQDICRICHEGDEESPLITPCRCTGTLRFVHQSLHQWIKSSD TRCCELCKYDFIMETKLKPLRKWEKLQMTPRERRKIFCSVTQQRNG SPVWFGLCMY
150	A	116	830	EGFPGRSLSGGLCCRLRRRFPIDGYRPWRRRRWSCCPSGVRPVRMS HKSWIESTLTRECVYIIPSSKDPYRCLPGCQICQQLVRCFCGRVLK QHAWFTASPAMKYLDVKLGDFHQAIEEWSVEKHTEQSPTDAYGVIN FQGGSHSYRAKYVRLSYDNQP\LVILQLTVKEWQMEPLKLVISVHGG MQKFELHPRIKQLL*KGLIKA AVTTGALILTGGRTGVGKHGGDAPQ RTC
151	A	770	950	CHSEHRNYKNNHHSIIKVRPRWRIHFHSNVIS*SLVHISKVFVAYKC NQYFHIRKFRSVT
152	A	1	253	SKLAAEMTANRLAESLLALSQOEELADFPKDYLLSQSQD\EGDNDGE RKHHKLLLEAIISSLDGKNRRKLAEMSDVILMM*EFVVA
153	A	1	759	VVQTQISKTADELISYWGTSFPPPPFAASLTLYELEYCITIDISLWKF ETSKYYATVIDAPGHRDFIKNMITGTSQADCAVLIFAAGVGEFEAVT FAPVNVTTTEVKSVEMHHEVLSEALPGDNVDFDVKNVSVKEVHHGNVA GQISAGCAPVLDCHMAHIAKFAKLKKKTGSTSGKKLEDGPTFLKSG DAAIVDMVPGKPMCVESFSVYPPLSRFAVCDMRQTAVAGVIEAMDKK AAGAGKVTKSTQAKAK
154	A	1	921	KFETSKYYVSIIDAPGHRDFIKNMITGTSQADCAVLIFAAGVGEFEA GISKNGQTHEHALLAYTLGVKQLIVGVNKMDS TEQPY SQKTYEEIVK EVNTYIMKIGCNLDTAAFVLISVNVTTTEVKSVEIHHEALSEALPGDN VGFNVKNVSVKDV RHGNAGDSKNDPPMEAAGFTAQV IILNHGQIS AGYALVLDCHTAHTACKFAELKEIDRCSGKKLEDGPKFLKSGDAAI IYMVPGKPMCVESFSYPPPLGHFAVGHMRTVAMGIIKAEDRKAAGV GKVTKSAQKAPKSEYYPLYLPPQS
155	A	1	424	VVQTQISKTADELISYWGTSFPPPPFAASLTLYELEYCITIDISLWKF ETSKYYATVIDAPGHRDFIKNMITGTSQADCAVLIFAAGVGEFEAVT FAPVNVTTTEVKSVEMHHEVLSEALPGDNVDFDVKNVSVKEVHHGNVA
156	A	3	1371	INIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSF KYAWVLDKLAERERGITIDISLWKFETSKYYVTIIDAPGHRDFIKN MITGTSQADCAVLIFAAGVGEFEAG\ISKNGQTR\EHALLAYTLGVK

				QLIVGVTKMDSTEPYPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPI SGWNGDNMLEPSANMPWFKGWKVTBKDGNASGTTLLEALDCILPPT PTDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTT EVKSVEMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDDP MEAAGFPAQVILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDR RSGKKLEDGPKFLKSGDAIIVDMVPGKPMCYESFSDYPPLGCFVARD MRQTVAVGVIAVDKKAAGAGKVTKSAQKAQAK
157	A	1	92	TSHQSHCSTFLTYSKW**LKTAYCLYHYHS
158	A	232	552	SLH*PRMATQRKHLVKDFNPYITCYICKGYLIKPTTVTECLHTFCKT CIVQHFEDSNDCPRCGNQVHETNPLEMLRLDNTLEEIIFKLVPLGRE QELERESEFWKENKPGNGQDDTFKSLTNRK
159	A	445	673	RECLH*PRMATQRKHLVIDFNAYITCYICKGYLIKPTTVT\ECLHT/ FCRCMEAFPSLLLA
160	A	22	849	WIERDLLNCIKRLK/PTTNMNLNDEIVNISPKIIKIRQGYLLSMILF GIVQKDLTRKLMQGRETKGIEIRKEVKL*KRKRI*ISICRCHE*IW* VPCIKVMQKAFYDIPAKNMENEILKKQCHFQKDPSSA*REKMRILCFE ELYPENKITKEERDRI/RTISKLLLPFKFHLQP*NPROVSLMLN*Q ANF*EFICIFQKS\KIVKAIL*NGQRGLKFLNIKTCTYKAIEIMKVLI WHKD\KKLD*WNSIQSVKVDPRVYHLSFEKGDIEV*WGKGSFQ
161	A	796	1381	SLTSDKRQWALGSMDFKXKHWHICH/PIKMLHLGVGPKGLSVTQQFSS QN*FPVCAFQSSQYIPLPAQKLMYSQ*PVQNRCSNQTIPIVAHPMSG HQVSHHR\PANNPGEKEVPGQEGKN*NKDVNNF*TGQPWTKGNLEIS TWPERNLILALKVPIKAELKRSWASSNCKQT*LRHPQCDDVFISMKE QSMEKCRNF
162	A	3	1118	LNQWQEQTGNPERTHRPSEGSGLLQDPGDFSNTLSAPTAEVEKGD LPKIPPLEELKETHLTHKDSHKLKIKGWKAFLANGHQKQTGEAILI PDKTKFKATAVKRDKEDYIMVKGLVPQENITILNTYASNTAPKFI KQLLIDLRNEIDSNIIVGNFNTPTAIDRSSKPKVNKETMDLNYTL EQMDLTDIYRTFHTTAETFYSTVHETISKIDHMIGHKMSINTFKK IEIMSSTLTDHSGIKLKINSERNLQNHANTWKLNNLLNEHWVKNEI KMEIIQLFELNNNDTTYQNLWDTAKVVLRGKFIALNAYIKKTERAK KTIYSHTSGI*KQEQTPKPSRRKEIKIRAELENEIETKTI
163	A	41	1135	HRTYKTKIHLKKQKQSTQATKSRMNAVPHISILTLNVNGLNVPLKR YRVA*WIRIYQQTICCLQETHLTPNT\KDSHKLKVGKWK\AFHANG HQKQAGVAILTSDKTNFKATAVKKDEGHYIMVKGLDQENITILNI YAPNTGAPKFMKQLLIDVRNEIDSNTIAGDFNTPLTALDRSSIQKV NKETMDLNYTLEQMDLKDIYRTLHPTTAETIYSTVHGTFSKIDYMT GHKTSLNKFKKSEIISSSLSDHSGIKLEIDSKRNHQNHANTWKLNNL LLNEHWVKNIKMEIKTF/FELNDNNGTAYQNLWDTAKAVLRGKFTA LNAYIKKYERAQTDNLRSHLKELEKQQTTPKSSRRKKK
164	A	265	446	LFCLGDTSLAILGYLPTRLVETRSGEPQSDDIEASRMKRAAAKHLI ERYYHQLTEGLWK
165	A	283	398	NWQEKCTFQIIGGRKMSFRIILINFFHN*DRTVCYVP
166	A	283	397	NWQEKCSFQIIGGRKMSFRIILINFFHN*DRTVCYVP
167	A	2	1012	AEALVESFWKAKQHTKEELKSLQAKDEEKNEKAKAACSAAMEED SEASSSTGDSQGDNNLQKLGPDVSDVTDTSIRRVYTRLLSNEKIE IAFLNALVYLSPNVECDLMYHKVYSQDPNYLNLFIIVMENRNLHSPE YLEMALPLFCAMSKLPLAAQGLIRLWSKYNADQIRMMETVQQLI TYKVISNEFNSQNLVNDDDAIVAASKCLKMIYYANAYAVTKNLGLY DNRIRMYSEIRITVLYSLVQGOQLNPYLRLIVRCDHIIDDALVRLEM ITMENPADLKQFY/RGI*RRTRWVAAFWDRASEPKANSIGFGGSQW MPTPVASYT
168	A	966	3172	SVLLEEFLLSSAEALVQSFRKVKQHTKEELKSLQAKDEDEKEKA ACSAAMEEDSEASSRIGDSSQGDNNLQKLGPDVSDVIDAIRRVY TRLLSNEKIETAFNALVYLSPNVECDLTYHNVSYPNYLNLFIIG MENRNLHSPYLEMALPLFCAMSKLPLAAQGLIRLWSKYNADQIR

				RMMETFQQLITYKVISNEFNSRNLVNEFNSRNLVNDDDAIVAASKCL KMVYYANVVGGEVDTNHNEEDDEEPIPESELTLQELLGEERRNKKG LRVDPLETELGVKTLDCRKPLIPFEEFINEPLNEVLEMDKDYTFPKV ETENKFSFMTCPFILNAVTKNLGLYDNRIRMYSEIRITVLYSLVQG QQLNPYLRLKVRRDHIIDDALVRLEMIAMENPADLKKQLYVEFEQEQ GVDEGGVSKEFFQLVVEEIFNPDIGMFTYDESTKLFWFNPSSFETEG QFTLIGIVLGLAIYNNCILDVHFPMVVRKLMGKKGLFVDLGDSPV LYQSLKDLLEYVGNVEDDMITFQISQTNLFGNPMYDLKENGDKIP ITNENRKEFVNLVSYILNKSVEKQKAFRRGFHMTNESPLKYLFR PEEIELLICGSRNLDQALEETTEYDGGYTRDSVLIREFWIVHSFT DEQKRLFLQFTTGTDRAPVGGGLGKLKMIIAKNGPDTERLPTSHTCFN VLLLPEYSSKEKLERLLKAITAKGFGML
169	B	1	2187	MAGKASESWRKVKDTSCMAVTRENEKDAKAETPKTIRSRETYHKN SMWETAPMIQIISQGVPTPTTHENYGSTIQDEIWLCLTNFCLDMLSFV LESCTNHCAVCLNVWYRKRAAAKHLIERYYHQLTEGCGNEACTNEFC ASCPTFLRMDNNAAIKALELYKINAKLDCPHPSKKGASSAYLENSK GAPNNSCSEIKMNKKGARIDFKDVTYLTTEKVYELIELCREDEYSP LIRVIGRVFSSAEALVQSFRKVKQHTKEELKSLQAKDEKDEKEK AACSAAMEEDSEASSSRIGDSSQGDNNLQKLGPDDVSDVIDAIRRV YTRLLSNEKIETAFNLALVYLSPNVECDLTYHNVSIRDPNYLNLFII VMENRNLHSPEYLEMALPLFCKAMSKLPLAAQGLIRLWSKYNADQI RRMMETFQQLITYKVISNEFNSRNLVNDDDAIVAASKCLKMVYYANV VGGEVDTNHNEEDDEEPIPESELTLQELLGEERRNKKGPRVDPLET ELGVKTLDCRKPLIPFEEFINEPLNEVLEMDKDYTFKVENKFSF MTCPPFILNAVTKNLGLYDNRIRMYSEIRITVLYSLVQGQQLNPYLRL LKVRRDHIIDDALVRLEMIAMENPADLKKQLYVEFEQEQGVDEGGVS KEFFQLVVEEIFNPDIGMFTYDESTKLFWFNPSSFETEGQFTPIGIV LGLAIYNNCILDVHFPHGLSTGS*
170	A	270	498	MHFLKAGRGGURL*SQHFRPRWADHE/RSGDRDNRG*HGETPSLLK NTKKN*PGTVAGALVASTREAEAGEWREPG
171	A	2	423	PAWLSRFTCAATYIKMPEE*ETHYQPMEEEEADTFTY/EAKMAPLML *IINTFYSSKEISLRELISNSSD/AK*LINPQSDFGFRVNLGLVNA *INIFC*QALDKIRYESLTDPIKLDGKELHINLIPNKQDRTLITVD T
172	A	1	267	CSAGGPWRAPQPRRFHRRRRPAQLPPPLPLPPLPASPRIHNRFT\PR PSQRTPPPAALGCPEPGS/RSQGRGHARPPGSGEGDPTVSSPGY
173	A	218	431	FDWWWQIQRAEPEFFPPFLAQLGSGKAPLSGLKIAARPDGSDAACLR PRLSAPGPQCSADGPWRAPQPRRF
174	A	9	201	LLWQELLARQPSSSIPAIFFPPFPFFKTALQLWGLQPASGFLTLLVP SFRRGKAVEQLLHSWQ
175	A	1453	1936	EVEKHLCSQ*ELLRAQHNAACRRPRPPAPGPQCSAGGPMPARAPAP QVPPPPPPCSA\PPPLPLPPLPAS/HAHPQPHFRHGRSALLPRPPW AVRSRGALAGPRTRAAAGLRGGAGAAPAPADARFPASSPAE*PKFPQ NSARALTGFPRCTDPTVSSPGY
176	A	5	712	FEALRMIGHLFAKSPYHGKINSKIVARTNIKLMVKVVMWKNGEIID TLQIVYGDNAPKKSVAVYKCITSLRRSKVLDEACSSRPVTSICKGK\ INLVYANISIGSAYTILM/EKLNLSKLSTHWMPQ/PVHPDQLKTRAK LSME/ILNKWDQDPKGFL*KIVTRDRTWLY*YTFEDKAQSKQWLPRG GSGPVKAKAGWSRAKVKA/TTGFWNAQIVLLVDFLEGQRTITSAYES ILLKKK
177	A	1	152	PGAMAVLLETTLSDVVIDLYTEERPRGEA*APLTCRRGPRACLPTFP SLR
178	A	1112	2085	RHSHAVQKKPLSGGGAGAMAVLLETTLGDVVIDLYTEERP/RCQLYG DQASFFAEAEKVPRIKHKKGTVMVNGSDQHGSQFLITTGENDLYL DGVHTVFGEVTEGMDIIKKINETFVVKDFVPYQDIRINHVTIILDDPF DDPPDLLIPDRSPEPTREQLDSGRIGADEEIDDFKGRSAEEVEEIIKA

				EKEAKTQAILLEMVGDLPDADIKPPENVLFVCKLNPVTTDEDELEIF SRFGPIRSCEVIRDWKTGESLCYAFIEFEKGGGAYGKTPATRPFYGS WPFAGLLLTCSFLRYPLILWITVLPPLSELIPLAAAERPASAASQ
179	A	3	492	GGGAGAMAVLLETTLFYVAIF\LYTEKRPRACGNFLKLCRIKYNYC LIHNVQRDFIIQTVDTTGTGRG*ESIFGQLYGDQASFFAEKVPRIK HKKKGTVSMVNNGSDQHGSQLITTTGENLDYLDGVHTVFGEVTEGMD IIKNINETFVDKDFVPYQDIRIN
180	A	1	451	MGFRHVGQAGLELLTSGDLPASAYQSAGITDVSHCAQPASPLSYFLQ ALKHEFVVRHLTPGHLDTQTPDTKKPGHPDTQTLDTQTPSHLTSRHP DTQTADTQTPDTQ\NLTPGPPDT*HPDTWHLTPDTQTPGHPTLRHPD TQIPRHPET
181	A	143	647	LRSRCVQIQGSPATEPVSGSHCADTGLVIRGGALSAAHAPGQRLSH ALHTASAYINSGRMWDTVHLPQKRCVRPRPQGRVTRPRTRATH/NRV VGARRGTPQRYTG/WGRD*EPSLSQLPQNGDLLAARRREHPACSTGC TSGARVRSRVWRAGQALVPGCAGCAYILH
182	C	225	335	MLARLGSNSWTSSDPPTSASQTAGITGVSHRAGPLT*
183	A	1108	1627	PMDQVMCRT*KG*MGGQRDVSPTASEQVSTARPGPRAVIDYSKADAW AVGAIAYEIFGLVNPFFYQGKAHLESRSYQEAQLPALPESVPPDVRO LVRALLQREASKRPSARVAANG\LHLSLWGEHILALKNLKLDKMGVL APPKIGRHFVQGTSQEEVVVLETKNEDALFG
184	A	56	335	TGFCFFSRVKCNGTILGPCNL*IS/GSKYFSGL/SLPSKWDFRFPAPP RPGNLF**TRFSPVYQDGFDFLTSICPPLGLPKLLEFRGAPPLPS E
185	A	523	818	SQHSVGPQADRLRSGVRDQPGQHGETPSILK\IQKLPGRGGACL*S QLLGLSLRRENCLNPGGRGCSEPRSHHCSPAWMT*DSISKNK*INKN EIKKK
186	A	49	1357	RTPERCLREVGKATGWPECILT*QTIIPRP/YPSVGTAAADTKKKKI NNGTNPETTTSGGCHSPEDAQVQTIRILTCQKTELQMALYYSQHAVK QLEGEARDLISRLHDSWKFAGELEQALSAVATQKKKADRYIEELTKE RDALSLELYRNTITDEELKEKNAKLQEKQLVSEKSEIQLNVKELK RKLERAKLLLPQQQLQAEADHLGKELQSVSAKLQAQVEENELWNRLN QQQEEKMWRQEEKIQEREKIQEQUEEKIREQUEEKMRQEEEMWEKEE KMRRQEEEMWEKEEKIRELEEKMHQEKIREQUEEKMRQEEKIREQEK RQEQEAKMWRQEEKIREQUEEKIREQEKMMWRQEEKIHEQEKIREEEK RQEQEEMWRQEEKIREQEEIWRQEKEMHVRTDEISVCSI FQGFISVG FLCKFAYPFDCFTL
187	A	1	408	ASDRPESRATHASGKSPVFSDESDLDLDFDISKLEQQSKVQNTGHGKP REKSI IDEKFFQLSEMEAYLENREKEEERKDDNDDSVKSSRNVNK DFFDPVESDEDIASDHDELGSN/EDDEIAEEEEAEESISEI
188	B	1	1995	MSKETRQSKLAEAKEQLTDHHPQTNPSVGTAASDTKKKKINNGTNPE TTTSGGCHSPEDQKASHQHQEALRRELEAQVHTIRILTCQKTELQM ALYYSQHAVKQLEGEARDLISRLHDSWKFAGELEQALSAVATQKKKA DRYIEELTKERDALSLELYRNTITDEELKEKNAKLQEKQLVSEKSE EIQLNVKELKRKLERAKLLLPQQQLQAEADHLGKELQSVSAKLQAQV EENELWNRLNQQQEEKMWRQEEKIQEWEKIQEQUEEKIREQUEEKIRE QUEEKMRQEEEMWEKEEKMRQEEEMWEKEEKMRRLLEEMWEKEEKI RELEEKMHQEKIREQUEEKMRQEEKIREQEKMRQEQEAKMWRQEEKIR EQEEKIREQEKMMWRQEEKIHEQEKIREEEKMRQEQEEMWRQEEKIRE QEEIWRQEKMHQEKIRKQEEKVWRQEEKMHQEEKIREQEEKMWR QEEKIREQUEEKIREQUEEKIREQUEEKIREQUEEMQEQEEMGEQEEKM QEQUEEKMRQEEKIREQUEEKIREQEKIREQUEEKIWEQUEEKIREQUEEM MQEQEEMWEQEEKMCSRKRRCNRRRKVVFARI IQRVYLLNHIIRN RKSVQILVLSCDLNSKNSHLLPDTLMLEDKAYLQIESCLIPNEE YQYLAE*
189	A	386	1321	RTLERCLTEVGKATGWPOCILTAYARRSLAPVLLGSH/HGRGLQTPGK LWSWGKSEEQCEEDGSETETGQGEDLEDLQEEEEVSDMGGDNPVEG

				KKARNSSKFELRKSPVF\SDEDSDLD FDISKLEQQSKVQNGQGKPR EKSIVDDKFFKLSEMDLYLENIHK\R*EERKDDNDEL RDSPPQTSP SVGTGATDTKKKKINNGTNPETTTSGGCHSPEDAQVHTIRILTCQKT ELQTALYYSQHAARQLEGESRD LV SCLHDSWKFAGELERALS AVTTO KKKADRRQTGAESA AVGELGDTGDTV GSEHWT
190	A	792	1061	GGSV*DQPGQHGT PSL LKIQKLAERGGGHL*SQLLRRLRQENHLNP GGRCC\SEPRL LHCTPAW/VNESKTSSQTNKKISQEWVCVPIVL
191	A	2	343	LLFFFFFFEMESC SVTRLECSGVISAHCKLC/LPGFKRFSCSLPSSW DYRRM/PPRLANFLYF\ VEMGFHRVAQAGLKLSSGNLPASA/F/PK Y*NYRRDDASLAACSTFLGLGLLWV
192	A	2	449	KEEIIPIL*NLFQNIKAEGILRISFN E ARITLI/PKPN/RAITRKIN PIDQSLMDRHA EILNKISAN*IR*RMKRIIPHGQVRFS*GMWGWFI RKQINVIHHTSHLKKKNHMIISINAEKEFDKIRKLLKL RNIYKRG I* LT**VMVRNS
193	A	128	365	VHTWMLSSP*GPQPGVFHAQIRGCPFLSP*R\CQFQVFSLFYFDLLW VFTILFFFLEAEYHFVARLECSGLISAHCNLC
194	A	233	598	PLLLPLTRRLL LQHGLACQ RAGLLHGPGR LQCQLHSHGHCHLDQSGP AVAGAARPRLLCGPIADQSPSPFRSPRLRWGLLQGWRCEDHRRPS AEHWQEGQGGTVISRRRREKENPKGKE
195	A	38	1222	EPESCSVTRLECSGVISAHCNFR/LPGFKNFPASASQVHGTTGTPHH AQLI\LYF*VEEQGFPPMLAPGWILGSP*PLMDPAPSLALPQSAGDP QP*AHPPHGPSYLF LFKERENYERPKII*LNPLPLAQGKKMEFALI\ WVMKHTQ*IRNNHIFSKRQK/C*DL*SYM VAYFWVGKK*EKNITSLT GNDTF**KILLSFPTRMIHCKAKI IY/IAKFFFWRRSLTSVTLGWSA VWHNLSSLQPPPSGLKRLSHLNL PNT/WDYRPPCPANLCFVVVVVVL LFVFW*RWGF\TMLARLISNS*PQ/CDPPTSASQSABITGMS/HPCL AMGFVFHLLT*KPPFFKDYMKSFQFFKYLIQG*CSLV*GVYRSSL IFFF/CFFETESCLVTQAGVQWRDLGSLQS
196	A	526	835	FNLNFTVSLRTHSPLIPFSSNERIKPGKSTIDGPWTRRTRL*RKNL WMIQ*LWDFLF/VLFETDSSSVARLECSGAISVHYNFHLP GSSDSPD SRSMPIVDRO
197	C	7	276	MQWRDHN YC I FXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXLARPFI*
198	C	2	28	MIDHTPS*
199	A	780	889	NKRNGSSRVGTHL*SQLL/RRLRQENHLNPEGRCGS
200	A	224	552	KVLRVARCGSLLSRPSTLGGQGGRLMRSGVRDQPGQHSETPSLLKM QK\LAGHGG/RAL*SQLLGRRLRQENHLNPGGRCSELRSRHCIP\SR VTV*DSISKKKRRKKVL
201	A	41	320	VRGIPVTDQGELEKERE PKIQR LVT PRVLQHKRRRIALKKQRTKKNK EEAAEYAKLLAKRMKEAKEK RQE QIAKRRRLSSLRASTSKSESSQK
202	A	80	518	VGPLTPNSVLPRGSV/LPTEVGLDALGEG LKGLCGPNPVVETTNQGF PMKQGVLT HGRVR*ET*QSTQDSASCYSTCPAAQTAA YCSE/ASSV PRKIKKRLQNMLNFWPRE*RLRRSARNKLRRDADFLCELLLSLN PVRNKIF
203	A	63	552	VGNQWNAQPRFPHKQGVLT PWP CRL LLSKGPSLSRPKETEP RRLG PKRASVRKLFNL SKEDDVRQYVVRKPLNKEGKKPRTKAPKIQRLVT PRVLQHKRRRIALKKQRTKKNK EEA EYAKLLAKRMKEAKEK RQE QI AKRRRLSSLRASTSKSESSQK
204	A	1	69	SGVKNGRGYVVGISGGTTNKVSP*SRVS*PMAVSACY*VKNRGYV GISGGTTNKVSP
205	A	379	540	IKKVRNLGPXHPRFSVLLLHVSCSTNGGVLL*RSSVPRKIKKRLQNM LNFWPRE
206	A	287	449	IKKVRNLGPXHPRFSVLLLHVSCSTNGGVLL*RSSVPRKIKKRLQNM LNFWPRE
207	A	263	525	IKKVRNLGPXHPRFSVLLLHVSCSTNGGVLL*RSSVPRKKNKEAAEY

				AKLLAKRMKEAKEKROEQIAKRRRLSSLRASTFKSESSQK
208	A	68	280	LDSLEVEARREESLRLFAICSWRFSLASFILLAKSLAYSAASSLFF LVRCFFRAIRRLCCRTGVTRR
209	A	465	1444	KKGEKDYSWTDLILTVPSPPGPQKELARI\GQTFPISLKKMMSASML *ESPLNKG*ET*GPKAPKIQLVTPTCSSSPNGGRIALKKQRT/TR KIKKRLQNMLNFWPRE*RLRRSARNKLRRDADFPLCELLLLWPCPP ATE
210	A	87	904	GGWVAPETPSDPWFPVQRGVGDASVPGIGKNVCEKAATSVDAFRMV TASRYYPQLMSLVGNVLRFLPAFVRMKQLISEHYVGAVMICDARIYS GSLSPSYGWF\DELMGGGGLHTMGTYILDLLTHLTGRRAEKVHGL LKTFRQNAAIRGIRHVTSDDFCFQMLMGGGVCSVTILNFMPGA FVHEVMVDVPLLYLKGMVYMQALRQSFQGGDRRTWDRTVPVMAASF EDGLYMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNL
211	A	217	625	GDELVKREAGMKMLPGVGVFGTG/ELPPEVLVPLLRAEGFT\VEALW GKT*GGRRKALLKEMNIAF\HTSRTYDILLHQVDVLCISIPPLTR QISVKALGIGKNVCEKAATSVDAFRMVTASRYYPQLMSLVGNV
212	A	858	993	LKSPQRPGMVAHACNHSTLGARGGWIT/R*GQEFKTSANMAKPHL
213	A	1	126	FRAWTRSRSERRRRRRKRSSSGSEKFDK*KNSSRKKQHEE
214	A	90	945	SPLADTFLSSGLGRTASPRPKAEARGTGRVRLRRRAVRASPGRMGRS RSRSSRSKHTKSSKHKKRSRSDKERVKRKRSKRE*\RNR RRESRSRST/RHWPCPGASGTGSAPRPRPTASTSSGARRASAGSL DEKQKARGGGEESGVPSGSEKFDK*KNSSRKKQHEE*KNW*QKR VEEELEKRKDEIEREVLRRVEEAKRIMEKQLEELERQQAELAAQK AREEEERAKREELERILEENNRKIAEAQAKLAEEQLRIVEEQRKIHE ERMK
215	A	739	857	IIPSPNSNQLNPP***FPGNYY*YFNITQINKDNYKTE
216	A	263	425	FAFQKFYIYTF*KHTL/WLGAHAGCNPSTLGGQGGQIT*DEEFET TLDKMKVS
217	A	2	660	FVTRPDAGVMRLPLVLLAVLLAVLCKVYLGLFSGSSPNPFSSEVDK RPPAPLVTDKEARKKVLKQAFSANQVPEKLDVVIGSGFGLAAAI LAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIG RFILDQITEGQLDWAPLSSPF\CIMVLEGP/KWPKGVPHVQWRESLH SGPQG/GSFHRRKLSLTSI*SWLRWYPVEPLMPSC
218	A	151	416	ERERESVCVCMCVRVVCVCLRERERQRQDKRLCGEMRKIQYVKNL HYI/SKLYIYKYVILQT*TFIHYIYLYK*ICIHTQMYAVY
219	A	4	328	HGVSLFPRLCNGTISAHNLRLLS*SDSPASASQVAGITGMHHHA RLIL/YFLVEMGFLHVGQAGLELPTSGDPTLPWPSPKWDYRREPTS PGPQTYIITQSKSSP
220	A	436	777	IYSYGKTGPV*KRKNCQSRIKEQNPIICWLQATHLKCKETYKLK/MR KICQANTNQNEEIGIL*NSRLYSKNYYQG***KGSILQEDMTILNMY APKNRSGGYMRQKLIHQGE
221	A	212	275	FLILNCNSF*KIYPKYKSLIR
222	A	770	1573	NHLEIVNLCNVGISQSFPQI*LKAQATKEKINCIPILKKTFG/TEKY IKNVKRQYIE*QKISANH\LSDKRLVFRIYFLKTITVQY*KDKPII K*VKDLNR/HFSKEDT/YMTNKYMKRC*KSTIREM*IKTTMR*TL HYRWNIKKTDNNNC*GCG*TGI\LIHC\WLECKIMYP/IFRTV*Q FPEKVKQHYPDAAILLLGIYPRNMK/SKCLPKNYTRMFITELLIIL KK*KQLKC/PIN**W/IK*NDKMW*IHKYYSIAIKRHRVLINA
223	A	86	428	SPQIRKQEISI/SLTDGTILYIENPKESPPPCLKVIFKNKATRFK INMQKSUVFLHPRN/QFENEFKILSFGTEPS/RSEYLGINITKEV* NLNTKNDIVEKMKELLSKWKDSPC
224	A	35	397	FLTGTQWGK/DSPFNTWC*DH/WNIHRNLDLYLIPYIKINLKQLTGP NLRAKTIKLEQNIGENLCDL*LSRERYSTKSITIRKL/DTLGF IKKNKCISKDTIRKR*ATDWEKIFANHV LKG
225	A	832	1043	LLWWFRLRSSPCGTQQGPWHLVCVGYAG\GWAGPPWHTCPWDPSHC

				PGTE*CPWCVWFCFFCNTYLLVPN
226	A	764	1016	LLQAGAHACNPSGFGAEAKAGGSTDLRSGDQPGQHGETPSLLKVQKVA *RGGAPL*SQL/LRGGGGCSEPRSHD*IPAWMTEGDSV
227	A	748	1488	RLTKRPETFPRRHPKPLPTLKTVPAGATPLSPSHPDWPFVFNPIPLTNR T*PPLQLQLRQPSRSCPETTQGPASSEAEPLVRSPPPPFRLFPPTPE /PGLSRQWP*EVEGTSRTPFFKAEGQK/EGKVKEGKTEGPCSPSRRT RILPPYSRLESGPVHWGEQGNRKS WPPNLPDQGF*QEREAMGHI PSPPGIRQRHRTSVQE*GSEIKPK*CPEPGKAFNPRPWGLGT/TRP LPLHSQKSRQDS*NTG
228	A	34	478	LSPRLECSGAI*AHCNLRPPGFKQFSCLSLS\SSW\DYRHAPPTPQL IWFYFYK*RPGFQLVLVQAGLEL\LTL*IPPASASQKC\WDYQV*AP H/WPALYKVS*EKWFPIMFFAPFSWLSLGTTEKFRVKVKVAGLGTLP TGWALCSLWKY
229	A	28	359	KGKIPWLCGI*PQNEKLM*HSKSLATVFCIYR/TN*KNKRIISINAE KAIDQIQHTFMNPLKNF/MKTVRKLKMDGSILNIKEICERPVTNM* DGELDDDFPKIGDEAQRPP
230	A	1216	2019	HPRGAKYPETNPGFVTLVSYPGPPDSRQLTHSRPSRSENACGHRPGEL NWLNCSGCLLVPRGKRVWTETCNLVWKTEASGPPPGDPLPSLSSPIT HTQARPT/DTQAHCPAPCPPH*PLALNPQQNFCEESAAQVQGQED RTSRGWVHGSQPQVGAGK*PLSTGSKAQGARLTGGGVPSPRLR*EQA LVRCRCRLCRLGSCVRSHSLKFIDEAGEAPSAAGLDGQGTGRAPGAP EARCPRPAESGEGPGSGQAPAEQDPQAPRAALRA
231	A	5	399	DGVSLV/SPRLEYSAGISAHCKLRLPRFK*FSCLSIPSSWDYRHVPP PPANSVFLVKTGFHHVQAGLELLTSGDLPTSA/FPKCWDYRC\DHC AWAKD*KFKCVSVGRRGGPGGEAVHQNNSRLSYWWEDGGKGTG
232	A	481	527	AAGTYSL*IGKE*VKLSLSDSMILYIDNLKTLPRKTLTDDKFSKIS EYNIS\VF*CINDEKAEKEIRKTIPTTIIKR*NTSDLTKVKGLYKG NYKTLMEINKWKDIPCA*IRRINIIVYPK*T*FKAISIKILLSF VTEIE\KIKPKFI*NQKRIRIAKATLSCWNLFPMNSWHNRC
233	A	20	129	SAALHLFSAPCSMGAGPSLLLACDSVDLPVAASKGL
234	A	16	370	ACRIAARAYLDLLRTWVFQVGSSGSQRDVNCSVMGPQEKVVVYLQK LDTAYDDLGNHGHFTIIYNQGFIEVLNDYKWF AFFKDVTD FISHLFM QLGTVGIYDLPHLRNKLAMNRRWG
235	A	1	1125	MASRGVHAEDWMQDPWWHQCADEQIVTDCHWVIKGTTHRSEPSSMKVK RIIPISTNWFYRIQTSSLLNKLWKDSDEVLNCRAFEKGPQEKVV VYLQKLDTAYDDLGNHGHFTIIYNQGFIEVLNDYKWF AFFKKEEGS KVTTYCNETMTGWVHDVLGRNWACFTGKKVGTASENVYVNIHLKNS QEKYSNRLYKYDHNFKAINAIQKSWTATTYMEYETLTLGDMIRRS GHSRKIPSKYYKHLAKKLENLEEMDKFLDAYTLPRLNQEEVGS LNR SITSYESEAVINSLMKKSPGPDGFTVEFYQRYKEELIPFLKL FQT IEKEGLLPNSFYEASIIILIPKGRDTTTKRKLQSNIPDELRRKKSQ
236	A	426	2173	MRAQTHNRAVDIALGTAGAHLEDPGAQQGQDRCSWQVCRSARRRRR EAAGRRRAARRAQHPCCREPSGNQSLSAHLHTGATKGPASSLLHEHL WKPIARSARLPGNSSPLFSAPCSMGAGPSLLLAALLLLSGDGAVRC DTPANCYTLDDLGTWVFQVGSSGSQRDVNCSVMGPQEKVVVYLQKL DTAY\DDLGNF\GHFTIIYNQGFIEVLNDYK\WFAFFKYKEEGSKVT TYCNETMTGWVH\DVLRN\WVFTGKKVGTASENVYVNTAHLKNSQ EKYSNRLYKYDHNFKAINAIQKSWTATTYMEYETLTLGDMIRRS GG HSRKIPRKPAPLTAEIQKILHLPTSWDWRNVHGINFVSPVRNQAS CGSCYSFASMGMLEARIRILTNNSTPILSPQEVVSCSQYAQCEGG FPYLIAGKYAQDFGLVEEACFPYTGTDSPCKMKEDCFRYSSEYHYV GGFYGGCNEALMKLELVHHGPMVAFAFEVYDDFLHYKGIYHHTGLRD PFNPFELTNHAVLLVGYGTDASAGMDYWIVKNSWGTGWGENGYFRIR RGTDCAIESIAVAATPIPKL
237	A	3	463	GTRFLHSFLSSLKHGCGPSLLLAALLLLSPGDGA\VRCDTPAN\CTY LDLLGTWVFQ\VGSS\GSQRDVNCSVMGP\QRKKK*VVYLQK\LDTA

				\YDDL\NSGHF\TIIY\NQGFEIVLNDYKWFAFFKDVTDFFISHLFM QLGTVGIYDLPLHRNKAGY
238	A	12	362	DRVSLLSPRLECNSAIPAHCNPCLP/GFKQFSCSLSPSSWG*RCLPP RLANFLY/SLVEIGFHHVGGAGLKLTTSCDPPTSA/FPKCWDYRHEP Q/WPDL*LTSE*GYRYEDSFDFLPKVP
239	A	3	155	SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFTDRANLGLTRGYYNQ SED
240	A	3	423	GSTHASARMAVMAPRTLTLSSGALALTQTWAGSHSMRYFYTSGSRP GRGEPRFIAVGYVDDTQFVRFDSDA\ASQRMPEPRAPWIEQEGPEYWD QETRNKVAQSQTDRVDLGLTRGYYNQSEDGSHTIQIMYGCDVGPDR
241	B	1	540	MPVNKHKRHDTIAESLITPNVTTDSVKDCIKELGNRLFLWTQGCSSH VATVAPPTAPRGLRVSRAVRPLPLGGWAAAMEGEPPEERRRLQEE LNEFVESGCRTELEV TASLGWDLSDLPGEAAAAELHQIRCQESWEF ASSPFCALKLDTSDWDSNSRIIKGCHQEVVTGNSCGH*
242	B	232	387	MEGEPPEERRRLQEELENEFVESGCRTELEV TASLGWDLSDLPGE EEAAE*
243	A	1124	1396	ACDDWNRMDKSHLHPPPPPPFRDPDYVGSPGTRSPPTSGSRSPRN RSAPPAPPAAPPQVQARPP*H\SPDKRKRPNCRTRGSPWFRS
244	A	171	514	CTVGVRCTVFPTEHKLPAVESHLIVSRSESVINKI*ANQIWEH/IKK IIHHEEVGFILGMQGWLNIRKAPTEIYHINR/SKOKNHMIILT/D*E KAFDKI*HYFILKTLDKLG*GNF
245	A	1	293	FLRWSLALSPSLECSGAISAHRL/RLPGSTNLPA\STSRVASTVGM ATAPGLNFCIFSREG*VKHVGPGCLELP\TSSDPLPLVSPKLRDYRP EPLCLA
246	A	466	744	LNHAVQEMIVKIELTQHMYINFHGIKLEINKGKKFGKLIHLWLKLNNT VLSDQ*VKAETQKGNKEIVLRWNKKEGMMYQNT/W/DVAKPVLRA DAW
247	A	243	935	IPVGELYPLLEDGIAAFIEWNPHEALWEPQEQQETQGPCKKHGEAP VGASWPFRRGFGEARPPPPVRPTLIHAWKSS*PICLPSLRHCHQALP GGTLDKWPSPPRG/GCSPRTPGVTQARRLSPHRVAG*QSSSGACPW MSRSSAPFPFLTSPQSPRAA\L*VRKTKSPGTGEHRLWTGLGAGGVS ARPVVKHSAGPGGIHGRAPGAEQSRGLWKAGCWGVSVRASAPGP
248	A	56	247	QEONPQISILTLNRNG/LNATLKRYRLNLIK/SFCKKDQTMCCLE TYLTCKDTHRPKVK*KN
249	A	1	372	RALAVSMLGAWPGPWALDWGPYSMTARHGTFSL*APYDPDPCAPGPP APRQQGKAPSGCGGRSICSGRLPSVWPLMPAWQRPS*/GGGLHSAP NARKAQAYPGCLPFYLP/LPGLLSGWSAGFLC
250	A	13	475	NGSSLRSPRLR*SRITPQSS*VAGITGAHHHARLIFFFFFETESC RVSQAGVQWRDLGSLQALLPGFTPFSCLTQSSWDYRHPPPRANFL YF**RRGFTVLARMVLIS*FRDPPASASQSAGIIGVSHRARPRGRLL APSYICNRNGLEG
251	A	986	1401	LEQGCNLFHLKHS*LGEVFFVCFRRSFTLVAQAGVKWGDLSL/HK LPSSLSLPSSWDYRHPLPRLA/NFFVFLVKMGF\TVLARMVVIS*PR DPPTSASQSAGIIGVSPRAGPVAGILMFCRWNISNPKGAVIEKKK K
252	A	303	551	QEGIKSKSDENSGLAPQHGGETPSLLKV\SKLAGYGGAC*SQLLR RLRQENCLNRDLGGGCGCSEPRSCHCTPAWTTEQDSV
253	A	3	403	STFGFQGTGWETRWGPT*PGVSAWSLVPSPVLETPDLERGKRAHLGV ATAGGPAGPYRLSPHTLSSRKEGKGEAASKGTEAELMTIGIENSTCQ SCLSPSFSHYFWSPRGAGPKAMWLVGDRKGATKNDKRGY
254	A	1833	2126	EKRKKRGFFKTKPLKCPGPWGESRFWGPCKGKSQV*G/HI*MGPNL GERWKKGPKRPKPKTKGPPFGVHPPKRNPHLG/WPGGPTLKKGK NNLGFC
255	A	70	380	YSNNPKDRKGETGINEKTNNKMVDLSSYTSVITLNF*ML*/D/KIN* KFVKSP*KKPTLCCLLETYFKYGIGGLKVKRWKI*HAHTIGKKTIV

				AILITKHTSELS
256	A	225	353	RWGFQTQLLRRLRQENHLNRGVGGCSEPRLC\TPAWATE*DSVL
257	A	238	514	HMYVPNLRTSKYMKRTLIELKGEIDSNTILVGDFNTTLSTMGRTR* DISKETEDLHNTVDPMDLTD/SAELSTQQQONTLSSQAHGIFSRTE
258	A	167	409	DRRITRSGVRDQPGQHGETPSLLKIEK\LAGHG/GQAPVCGGRSYLR RLRQENRLNPGGRGCSEPRLRHCTPA*VTVRDSVS
259	A	660	1200	LTVGKKNRKQQQHQPSPHKGPHLKGQQPSKVQIEDKFLGR*GKELK NPFTTQKGQSGFVYSKLIHNTSYRQGHSPGWRLRWMN*KQ*ASEGG* *QTSL*STL*PNILERIPELKDWFSEKIR\RQK*KRIKRKEENLQ* VWGYI*RPILQITGIPERRVEISMHWVRACSFSSVKVIP
260	A	1	682	EQCRSPARARLQPPDPASTEAEERRTPYPGSIGAPAGEGKVPGLVIY LLWPWQNDQDEALSCLPSEAYSLSRQHGLPLAVNTMSAGGGRAFAWQV FPPMPTCRVYGTVAHQDGHLLVLGGCGRAGLPLDTAETLDMASHTWV ALAPLPTARAGAAAVVLGKQVLVGGVDEVQSPVAAVEAFLMDEGRW ERRATLPQAAMGVATVERDGMVY/VSGGNGP*HGPPGPGT
261	A	1	403	RTRGQLNRGVYGPRRSLSPSTLAGAPLAGRLDETSGEEQTLTLCGG KMSGPTQPPAEGTEGTAPCGGAPVPPPNMTSNRRLQQTKAQVEEVD IIPVNGDNVLGRDHKLRELDERS\DALQARA*PFESSAAS
262	A	72	276	AIQFSVYICVPGICISPDREKRDRGKDGGRHRTRWRQGE*KGEVGR ERRRGRER\DRQRDRRIYSPD
263	A	166	398	PQIPPPPGIPRKRENLSREPGG/PNPWGG*A*FPLLEKFLGKKNLGP PPGGGPTFPFPFNPNLLGGPKGGDQKAGKKP
264	A	3	413	SSYRWSPFPIKTCRGPMAFSLSPGSLSVPLPLHHPCCPT*L KAAYPNCQLWPFLLASVAPDTAPPECPSCFLLQRAQA/PPFLDLFP YDC*GLCCT*PHQPRGNPLTPRQGLWLGLKTHCMGTAKAGPGIPR
265	A	646	1333	EPGMWQSPPSIGCPHRTGQASCA\SPSTGLS*IPAFPGWRPA\WH LHPLLTSPCTC*L*SLGVFPVPPQWSTPSQDLNDIFPVPPSYRW PSFPILKTCRGPMAFSLSPGSLSVPLPLHHPCCPT*LKAAYP NCQLWPSSASVAPDTAPPECPLLLCFRGPSPILLTSPICLLRTLQ LSSPASGESHYPOGRAVGWAEKPSAWSTRSLALGFPMNNEN
266	A	268	926	ASCTPFPTLPVRGRLGYNPDSPGTSNAHWAGDNEMSLVGLGPVTKPY PHGALPQGWGWSWVRGLSRTPAVTLSQGLCSCVLETWGPGEAWFL SPQSVMCDESPRSPADPDQDGLGVYGLASSWTNVQPTWNTSRIGSA CQA/RSEFNKSHLFIFLEGET*GPQKGGVPPKPHYKAPMQSPGPIL WTQPRAPPTGAIYFFLQMGPPWRFSLFGVGG
267	A	599	1420	SHLPSLSLLPRIPEVIVGSERGVPVFPVPCWGLSRTPAVTLSQ GLCSCVLETWGPGEAWFLSPQSVMCDESPRSPADP/RGWKFRVY GLASSGQMCNHLSESRMLVLARHSELISPTYSFFEGETEAQRG*GIP PKPHSRNAEPGPYTGTHTWPLHTGTFTFSSQMRGPSGLLDGGWIK TEGDKEKAPGLMGLKDRDTGTCYGCVCCKCPGQLQAGGVLYLAQPP ALIRLPNGPRPARARERRDWHHREETGFLLEATLLKARP
268	A	1755	2524	VPWGNPGSESVGLPGGRGLVTAPAVFLPPKPAPGFGAQHVRSRK/PS RRGQLIRAAWLTGSPVRPGQEMLGAGRGGASGRAG*GPAPYRKLSSA SARGAGHPESGNCSSSGSGSTWSSWGSWSGSSWGRGLSQEMVEEV L/HFIQGGAG*AGGTLQWALVSNLGFVVRQDDIVVVTILIGLHGSIE DGAGVQGRSEAMEPRQAG/RGTEGWLGGHSETPHPPAGTSFCNLRP TVSREAAPAGRRGAESQTSLPSTSA
269	A	3	389	GVSPCWPGWS*TPDLK*STRLGFPRCWDYRLLEVDPCGTGHSLYL*KD PPVLPPLPAEGCDYQKEYALSSCCDKSYLLPDYRTKFLCCHPERGTW KLGTVGGCYAPIQSFGIADEQAWLQHGSGAVYLC
270	A	555	1182	RGPMPERPKQMTAVHCQHQRGDSEIRNFRCHGPNISCTRWGSPPHASA SFSTCL*NKPKYFPWGISFLSFFLSRRSL/DSVAQARVQWCNLSLQ PLPPRF*QFSCIRLLSS*DYRCMPPCA/NYL*F**RQGFTI*ARLV LNS*PRDPPVLASQSAGITGVSHQARTFFLFFETTFSH\VAHAGVQW HDLSSLPPPPPRFKRLSCLSLSSS
271	A	80	600	SIQEKRSLGGEQSPTFLKELQEGTSWLLMAKLYEAVTFKDVAVIFTE

				EELGLLDPQRKLYRDVMLENFRNLL/SQWGINHAMEILSTS*GKEK LWVMGTSSQ*ERNLGGKIQTOMET\VPEAGTHEEFSCQIWEQIASD LTRSQDTTISNSQLFEQDDNPSQIKARLSTVHTR
272	A	1321	1913	VEMRRNQCKNSSNSNGLCVICPSNNHTSSPTRVL\TWMNCLELHKYN V*IWIGKKII*TQENGKTQSEENKNNIKVLQELKDKVAGIICKNLTD LNAPKNTLLEFHNAFTSINSRK/DKSDERISELEDWVSNIRWTKVN* NEQILHGGWDDIMRPILQITGISEREVEKSNLENVVDIIFESFPN LARKANSIQIE
273	A	193	310	WSLSVLGSGRRKRSQGTEELLCQSHTLLGDTGNSISHSH
274	A	831	1102	HFGRPRQVDCLSSGVQDQPGQHGEVQSVLKL\KKLAGHGAHL*SQL LWRLRHENHLNLGGRGCSEPRWCHFTPAWTTEQDSV*NNNNNNK
275	B	53	403	ALVTEFQETHSQDAIEHVLNLANFAYDPSNYQYLRQLQVLHLFLDS LSEENETLVEFAIGGLCNLCPDRANKEHILHAGGVPLIINCLSSPNE ETVLSVITTLMLSLPGRSFLP*
276	A	842	2432	SLISCSEGSPPKASGPSS*EHCPAKPLPGPTWPLLTGPESGGGG\ P DVGLR\GQPMNAAPV*SSPCL*N/PGFLTPSGVSSV*MPVLLKEPAF QMAEKAPNGAVCAP/SFPASTSGLWSPAVGVPRSRSLHGSALPWGHA PRQ/SGYPGQSAPAGCGPRPPGGGSRSPGRSVPGSGAWRWPRGRSE ACTAPRAWRSALGESCPAGSGA*AW*WQTAPSPHWGIGS**VGH LLRAGCAPCWPCLTGTCTGLPSRSGHKSLSLSVQQVQWLIRFFFLS *M*KPAACLPS*RERPSCAHWTAGGVMGFLSV*SVIR*SLSHCLAAE SSPHPGAPGQGTATQIGGGGSRVQRG*NHRPCRS*PIQRPCGQAGS GGRVASTWCAQ*QTPPGSHSPPTANREINPGAAAADTRSCWGHKRS WRGWRGLAPWRLGFGSPWNSRDQGPAGIPAARRGGPTFGFLAHGPR* RRTPRDGREGGKGAGAKPSETLTRSPPVWRGKRGSAANGFLSWVQILQ YFAAGNGIWEMGRGLRIL
277	A	721	1027	QHPCQPGPAHVPOARDQPHGQPLGEGELPDGRAHCRAGQAAGAPAA RHSEQGFQVLLASELLPQHPPHAEQSWAQCRRGFQREESALDCRPGGR RGKWESAH
278	A	615	2183	PQVIRPPWPPKVLGLQGLLTFRDVAIEFSQEEWKCLDPAQRTLYRDV MLENYRNVLVSLDTSSKMMKMFSSSTGQGNTEVVHTGTLOIHASHHIG DTCFQEI EKDIHDFVFWQENETNGHEALMTK/YQKVDE\CTERHDQ RHAGNKP\LKMSLDQAFIRICLKCTYFTPKGKLVIKLRLSTMLS/H VSASQRISCRPKTRISNKYRNNFLQSSLLTQKREVTREKSFQRNES GKAFNGSSLLKKHQI IHLGDKQYKCDVCGKDFHQRYLACHRCTGE NPYTCNECGKTFSHNSALLVHKAHTGEKPYKCNECGKVFNQSNLA RHHRVHTGEKPYKCEECDKVFSRKS\TLERHRRHTGEKPYCKVCD KAFR\RDShLAQHIVHTGEKPYKCNECGKTFV\QIHLVMHKVL\H TGEKRYKCNECGKVFNHKSNLACHP*TSIPGRETF\RVMECGQGF\ NRKSNLERHRLHTGKKS*KC/EICKVFRQSNLACHHRLYTGEKPY KCEECDKSFQFQITP
279	A	403	935	QQRWQQGWWQAWGGQPVPQEVGFWFLLSWLLSRLLGVPAPQGPARGEV DPRPGSRGARGGCSASAAPPARASPGRPCCWNGSRPPAQHRRTPAT RVGEAGQGEVRGVRRLPAPLLQAVQPRLSDRSYPAAPARPTATSP/A PPSPAPKAPIVGALS*GTADPGSDSYPPSRSHAPRP
280	B	73	207	ELGTQLRTCTTSLGLASQVEAHHSVLVSHLKTLLWKKISNTKYS*
281	A	276	565	WTSSVSTGQSDQA/GPAPALIQQMRPCCGSPVPGGWLE*RDGQAGM GAAAAPAWVLLCIPAGQGPLPGPRLPFHIPILKPCYCGILVEKKEPR GCF
282	A	1466	2353	RNVHLNLLIHFILYFKINVFHIDFPLGGEKNSGVLGFQAVQKQPRGS FFL\PRIPQ*QNLRIgi*KGRRGPGSGPWPAGDTQQHPSKGKGLPPL PACPSL**QQGRRCSGPGGRLGS*GCKHPECQWSQRGVRPLSVPLF QP\PPGTGAGPTSWASASGSGAGACQPGS/PLGSVHTGSPQAKSPP SRVK*QECQHPTHVSSPVSRRPGF PKLPG\GNRAGPAAPSPRPDTPA APPPRPGPPSPGSLAQDAPGRSLPPPRTTRPAAQSPRPRSASESEAA RRGPVRRSRTGREEKSG

283	A	134	387	CQIMDGLAIQAWPTPQQVASNGTGLNPNKAVWQEIAPGNTDATPVT HGTSSWHEIAATSGAHPEGNAE\PKIYVKNMK*CI
284	A	305	1129	DICKEYEVMYSSSCETTRNTTGIEESTDGMILRPEDLSYQIYDVSGB SNSAVSTEDLKECLKKQLEFCFSREKLSKDLYLISQRSDSQFPIWT AANMEEIKKLTTPDLILEALRSSPMVQVDEKGEKVRPTHKRCIVIL REIPETTPIEEVKGLFKSEYCPKVISCEFAHNSDWYITFQSDTDAQQ AFKYLKKE\VKQFKARPILAGIKAINFFC*EWSSNNGILESIVHPI *TQAQYASPVFMQPVYNPHQQYSVYSIVPQSVWSKSYTLL
285	A	1053	1404	TFTQDSAGSLVVHSPMTSIWKTAESVDQGHFPIIILILFVYLLFETG SHSVTHATMQWCDHSSLQPQTP/SGSGDPPTLAC*VPGIIGMCHHTW LIFTFPAETGSHHVPRLVSNPLA
286	A	259	506	PGYRRGHGGAAGRQEPAAARHNPAVREDADGGD/RPRSAACPGTSTA PPGT*GS\GQAHRDGARPAPAPRPSHPSAGPAAGPSG
287	A	1	2072	FRRSPSPAASVSLGLGVAVVSSLVNGSTFVLQKKGIVRAKRRGTSYLT DIVVWAGTIAMAVGQIGNFLAYTAVPTVLVTPGLGALGVPPFSILASY LLKEKLNILGKVGCLLSCAGSVVLIHSPKSESVTTHAELEEKLDQS RVGGLPCASLLVMLAAHLLDPCRPMGPPTSWSTSASAPCWADTPCL PPRASGWRPKTSCITTRPVREPSACAWYSWPCSAASSSSSGTRNKA LECFDSSVFGAIYYVVFVTTLVLLASAILFREWSNVGLVDFLGMACGF TTVSVGIVLMRVFKEFNFLGEMNKSRTDWRQSSPLIVAPRDHFHLE RGVQFQNMNSVMGSHLVMVALSPGVDFIPQPDPAALLVTELFANRL VSGYAPATGLQGTILQYGNLMEVMPKICRLPRHECGSPGP\PGSCA PPPSPHSTR/RRPPRSAD/CGPCKGTGTRRERAPGAG*AEAAGPGE GVGAGANAGAGAADAGAGGADAGAGGAGAGAGGAGAGAGAGAGAGAG GAGAGAGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG AGGAGAGAGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG AGAGAGAGAGGAGAGAGRAGAGAGGAGAGAGGACAGAGGAGAGAGAG AGAGAGGPVAGAGGAVCSQTI FTRSHGGLHLWRPC
288	A	1	392	ITLGPDSIIIGIWSGNQHKQDPYIASMEHHTDWNNDIVLCCNGKTLIS ASSDTTVKVWNAHKGFCMST/YKDT*ASSLSGNKDSIYSLAMNQLGT IIVSGSTEKVLRVWDPRCTAKLMKLIGHTDNVKALL
289	A	1	1051	FRVNMQDGGPSPAHSKAEESAGMEARFLGLPDAAGSSGPTPARRCP APRPAGVSVIRDEVEKYNRNGVNALQDPAALNRLFTARRDSIIIRI RVNQHKQDPYIASMEHHTDWNNDIVLCCNGKTLISASSDTTVKVWNA HKGFCMSTLRTHKDYVKALAYAG*\ELVASAGLDRQIFLWDVNTLT ALTASNNTVTSSLSGNKDSIYSLAMNQLGTIIIVSGSTEKVLRVWD RTCAKLMKLKGHTDNVKALLNRDGTQCLSGSSDGTIRLWSLGQQR IATYRVHDEGVWALQVNDAFTHVYSGGRDRKIYCTDLRNPDIRVLI EEKAPVLKMELDRSADPPAI
290	A	1	366	FPNSSRLIWEPCNRIKEESLVASPGSFCKPHLDLALGLGL/GVGLM VELGLKLGLFLGLGFDLGVGLGIGL/GVKLGLSDGY/GLGFRLGLGL *AGLVGLGIRVGLKPGLEIFVGLILCICI
291	A	49	420	FMINPPNQVGRYRNIINLTNNIYQKPLAPVIL/HGEIFKIFLTGIGV TQRYPLSPLPFKVFLAALDRK*REGAGEEVNGIENKRIKLSFVSDMI VYVENSKEKNGQLELMRGICKTATKLQKL
292	A	5	377	FMINPPNQVGRYRNIINLTNNISQKPLAPVIL/HGEIFKIFLTGIGV TQRYPLSPLPFKVFLAALDRK*REGAGEEVNGIENKRIKLSFVSDMI VYVENSKEKNGPILLELMRGLSKNATKLQKLI
293	A	346	490	QLQAMAI FEYLKKTFLRPGTVPHSCNPSTL\GGRGGWIT*GQELEAS P
294	C	140	172	MTVXLRTNGDF
295	A	2008	2438	WSLHRPRGPPLLWHMPRVPPPLTGL*SSPHDSVGPQPWKSPPTSFNS PDPPENVQNHGPKPVAKSPFVPQRNGH/PPKR/PTWGSSTCWGEVIR SGSPPPT\KPVWPTSCFGSVLPPEDETVPF\PHFPVSLILFAISF ALVCGD
296	C	165	290	MCHRAGPASLSAGQFIHIFLVTPMAAPRISAVCGPESRHQG*

297	A	883	1097	GSGV*DQPG\QH GKPPSL* LQNL AERGGGHL* S QLLRR LRQENHLN PGGRCC\SELRSRHCTPAWATRAKL
298	B	191	494	MKLKRGAGSCKKPGSSGWGPVGEFHSVQNICARREYQRQDYMDAMA EKQKLD AEFQKRLEKNKIAAEEQTAKRRKKRQKLKEKKLLAKMKLE QKKQEGPX*
299	A	2	478	SGRLPWLAQPPPRCDHRGPRKSRSSSPMRREEQKLKLERLMKNP DKAVPIPEKMEWAPRPPEFVRDVMGSSAGAGSGEFHVYHRLRRE YQRQDYMDAMA EKQKLD AEFQKRLEKNKIAAEEQTAKRRKK/RPQS* *KKNLLAKMKLEQKKQEG
300	A	72	409	VCSETGFILYCRN/DCKWDAPILETVWFFVRS*T\LDMNCTPAIPFL FIYPLEMYGHAY*MTCTRIFMAALFIIAT\NQKSPKCSINSIHATKY YIAMKLIQLYPYVATWINKVF
301	A	92	617	DRVLSLLPRLECSGSLAHNCVCLP/GFKRFS\CLSLPSSWDYRHTP PCP/V*LVLVEMGFRHFSQAKSRTL/TGDPPASASQKWNRYRRNL \AWLASALNKVINLLKSEIPSFLLVQLSGFSRTLLQGFNFNYHTL VYSNNLPIMQTFQTQDFGRISGKPFPGIMILCNREILYIM
302	A	367	620	ETRCRGHPPRDREPPPS*PGIQSSPGVP/PSRPSNKAYPRLPIRPOP PGLSFR\STPPRPSP/KPPCPHIGRHVQPTKTSAVSILS
303	A	2	520	FPLFLFLLLLLAFVALTTTRRIQGVPTLVLOAKRVNTSRPHPD/G S/QPPTSASFNLPTTNTSTPQLRSHVASGYVG*KQM QYPH/PPQHA PAPPQPCPWQVDTFLPAPTRPLLGS GPGSPSRSPGG\PPPAGKGPA PGPECPTAQRPTT/RQYLGPLFKGDPNSPREKPRS
304	A	444	920	NPSLRCLWGLSPGKLAGARGRTVHVGGPEGPCHTSTSTKMAKRHP EVSTGGGGKAP*/SQGIRGQAGQG\GARGSVAGNGGGGARSRLRLS PAAASATA/SGPEGS\GPGSGRSRVPVEAAPPCPRSDVVPARGAA AAGPGGTWLPASQVGPSPGW
305	A	504	935	AYLQSSMIAQSRATRTGLATWHQH KALDRHFPRLSSRHPLFETCSSP PCKRWGEKSHFRACKEGRESAPCGIPRPRFKVHTPRGKLRLM\RPVP RRFGGSRLLGPRSRKRRTKQPR*PAAPRDSPGAPAAPPTPRPSAARN GGG
306	A	163	389	IRQKKAIFVIVAFKRRGLRKT/IYYYARGG*FVKNKYRGFIIELGT TCGKYFLFCTLAIDPSDSNIIISMPEQT
307	A	131	395	LWAARA VLTSLPTGSPSAALSGCCRPGGQGRYSVAACRGRAAGGV APVPAHT*AAAPLGHFSFLLGIVSPAPEPHFELGHYYSGLS
308	A	327	598	GPARNPAQCRWAGTAGGPSTLSAAAGPGAKPLMPGAA/GAGQAGWLL *VQGPSPRPPGTLAQARHTALVPARASPSTPPCKLRGGLRP
309	A	1	630	MKPWTFTVSVTVLKDGVSGVCYFRCSVDVSGVSYFWVVRGLADFRSEA MDLVASVTALNGGVDPKRTGFGDKFKPVIGTWDCDCLVQNKPEAIK CVACETPKPGTCVKRALTLTVVSESAETMTASSSSCTVTGTGLGFGD KFKRPIGSWECSVCCVSNN AEDNKCVCMSSEKPDFFGGVEHLAQGW PCSM TWSDTKGFPQTQGDSLRLW
310	A	101	520	RRLQKPGCLIWTRGST*CPLTLLPSRGAGLGTG/KPAMPEPPTHSM GTCAARASPTSTTPCST/CAQSHRPGRNKQPKG*GMRAHGAGLAGSS TCSPGVGSTG*SQGL
311	A	411	640	ADIDSRGPKMSLQSSS*SRGSWMSGN*WSFSSDPTYSGSGGSAPSPI \PTQGAEECGRTAPGLAGSSTCSPGVGSTR*SHFRPTHPSLENLEDI ALTINV LQNR FVRAEPASLKSPVIALLCMSDLTVGTTVTQLQHLNTMG VIGSQDGRDQVAALNHQKQGDLPFPRTVLWRKGIDQTFWGLLNTG *SELTLIPGDPKCRCSPPVKVEAHGCQVINGVLAQIQLTVGLVGRPV PSTTQGAEECGRTAPGLAGSSTCSPGVGSTR
312	A	375	519	GMLFPKQITPQSI*VE'NAKNV*GGDIASFMSGSTHALFEPDSSHSA
313	A	640	975	VPWEAGGSMSCIFYPRQSEQSHNIVKSKRPVTFQQNRCQKGGHSAD VSSTCQCFCQSHREQGFAKPQFSYL*NGGSNSFYLTGCFDNLITSVF CSVRFIHGPKAIKGYH
314	A	22	297	GKEKLSHSAWAPKSNSSASSWSNQSAQPRFKGED I/ESHLLM

				GREALS*IQS/GRLVYLQSLs*T*RFSTASPEQLDTECRLVHSQTLs
315	A	152	437	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGG\KIR\TRRCHQ GPIKPYQQGRQQHQVWDPDAAVAWRVKGKLGWRGRAVRGPGAPRGADR RA
316	A	3	611	GRARGARGCSGGGAAREGPPKAERCAASGRASAANMSDTKVKVAVRV RPMNRRELELNTKCVVEMEGNQTVLHPPPSNTKQGERKPPKVFAFDY CFWSMDESNTTKYAGQEVVFKCLGEGILEKAFQGYNACIFAYGQTGS GKSFSMMGHAEQLGLIPRLCCALFKRISLEQNESQTFKVEVSymeIY NEKVRDLLDPTGSR
317	A	1	949	MGSCAARASLTSTTPCSTAPSPINHPKAEECERTTAQDWQAAPPAAP VRDPLGEPsWAPESGGDVESLYIYLRDCKYTNQHPVFSSRFVNPPID TLYLAALVGPWKTFMSSSGIVNTPIGTLYLAQVTVPPPLHTRFFALS PRQPRSFKNGLLFQGTGTTLNPLSGYSSDYKGFGRFRNHPQTGFSPAG ANQRGPLVATLSGPGGEGQSAV\PVSLVKRKTTLAPNTQTASPRALA DSLMQLARQVSPTGKRAVSATAINLKVCKHTSQHPVFSSRFVSAPID TLYLAALVRTWRVFMSSSGIVNTPIGTLYLAQGL
318	A	1	4425	MASGAGGVGGGGGKIRTRRCHQGPIKPYQQGRQQHQGILSRVTSV KNIVPGWLQRYFNKNEDVCSCSTDTSEVPRWPENKEDHLVYADEESS NITDGRITPEPAVSNTTEPSTTSTASNYPDVLTSPSLHRSHLNFMSL ESPALHCQPSTSSAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSQFS SRASDKDITVSKNTSLPPLWSPEAERSHLSQHTATSSKKPAFNLSA FGTSLPSLGNSSILKTSQLGDSPFYPGKTTYGGAAAARVRSKLRNTP YQAPVRRQMKAKQLSAQSYGVTSSSTARRILOSLKMSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDsQYPPVQRLMTPKPVsIA TNRsvYFKPSLTPSGEFRKTNQRIDNKCSTGYEKNMTPGQNRQES GFSYPNFSPLPAANGLSSGVGGGGGKMRRERHAFVASKPLEEEEEMEVP VLPKISLPITSSSLPTFNFSspeITTSSPSPINSSQALTnkVQMTSP SSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAEsGSSS TLEPIISSAHVTTVNSTNCKKTPPEDCEGPFRAEILKEGSVLDI LKSPGFASPKIDSVAQAQTATSPVVYTRPAISSFSSSGIGFGESLKA GSSWQCDTCLLQNKVTDNKCIAcQAALSPRDtakQTGietPNKSGK TTLSASGTGFgDKFKPVIGTWDCDTCLVQNKPEAIKCVACETPKPGT CVKRALTTLTVSESaETMTASSSSCTVTTGTLGFGDKFKRPIGSWEC SVCCVSNNaEDNKCVCMSKPKGSSVPASSSSTVPVSLPSGGSLGLE KFKKPEGSWDCElCLVQNKADSTKCLACESAKPGTKSGFKGFDTSsS SSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDS GSINPMSEGFKFSKPIGDFKFGVSSSESKEEVKDSKNDNFKFGLSs GLSNPVSLTPFQFGVSNLGQEEKKEELPKSSSAGFSFGTGVINSTPA PANTIVTSENKSSFNLTietKSASVAPFTCKTSEAKKEEMPATKGG FSFGNVEPASLPSASVFLGRTEEKQQEPVTSTSLVFGKKADNEEPK CQPVFSFGNSEQTKDENSSKSTFSFSMTKPKSEKESEQPAKATFAFGA QTSTTADQGAAPVFSFLNNSSSSSSTPATsAGGIGFSSTSSSNPP VATFVFGQSSNPVSSSAFGNTAESSTsQSLLFSQDSKLATTSSGTGA VTPFVFGPGASSNNTTTSgFGFGATTSSSAGSSFVFGTGPSAPSAS PAFGANQTPTFGQSQGASQPNPPGFGSISSSSTALFPTGSQPAPPTFG TVSSSSQPPVFGQQPSQSAFGSGTTPNSSSAFQGSSTTNFNFTNNS PSGVFTFGANSSTPAASAQPSGSGGFPFNQSPAFTVGSNGKNVFSS SGTSFSGRKIKTAVRRRK
319	A	160	747	VLNGSGRPSQSKKHFPKPGTFGGASVHQMFIMSLPA/GPDLSGFDE DDKGWPENQLDMSDYSSSYQDVACYGTLPRDSPRRNKEGCTSKTPHA LTVSPFKGIFSSATKVFQAPNACKRGA*GKG*PWEGKASSKPGRDFL REGRKMSWKLFNRKLISsQPYVPVGVCLTSVFTIASLGEQGMVFPLK VDLFKLTG
320	A	1812	5065	PNKTGGKTVSDGLHHPsQLHsKLENDQGFYNVDSSSTGFHNKTNPVGP FRKSPFLVMGVDWAETRRSMMMQMRRAPMSDDILARDRGsRLSRGNR RNGGGGCRDDDDDGAGAVRTGEGATEELPPVGGRVVRPQHRGELFV

				LSSAGDLHRDRDTHRGAGSGGGSAMASGAGGVGGGGGKIRTRCH QGPIKPYQQGRQHQVSSSRPDLSGFDEDDKGWPNQLDMSDYSSSY QDVACYGTLPRDSPRRNKEGSGCTSETPHALTVSPFKAFSPQPPKFF KPLMPVKEEHKKRIALRPLLSQESMPPPAHNPQCIVPSGNGSS SQ*NTIANVRRRLTLRRKKMSWKLLTGS**VHSLMYLSLLTSVFT MPAWRTGNG/LSSKVDLSNSRVLEKEVSRSPTTSSITSGYFSSASN ATLSDMVVPCSDSSDQLAIQTKDADSTEHSPTSLVHDFRPSNKBELT EVEKGLVKDKIIVVPLKENSALAKGSPSSQSIPEKNSKSLCRTGSCS ELDACPRIKISQPAKGFCPRELKVCKHTNQHPVSSRFVNPPIIDLTYL AALVGPWRTFMSSSGIVNTPIGTLTYLAQGSNGSSMPVEHNSKREKKI VSSGTISVILPGGPQLASPSGSGTGATGGLACQ/CSRSAPALLSPWA VHGTRRRRAAGGGACRGGSGRAGAGGGGGGGHS*QGYRIC*EYCARVA TKILQQE\EDVCSCTDTSEVPRWPENKEDHLVYADEESSNITDGRI TPEPAVSNTTEGGHNENAAAGPHDSHSCASGRSSSRSPKAPTLSPVHT HHKKGALPEGTHRIGF/TYG/IPVLESTL*KP*GPPVCSTWGAETSI RPSPPAE/CSPPARPRRRWGPIPDVAVRAGFASPKIDSVAQAQTAT SPVVYTRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNCKI ACQAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGTW DCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAETMTAS SSSCTVTGTGLGFGDKFKRPIGSWECSVCCVSNNNAEDNKCVCMSSEK PELQVFSGSNS
321	A	819	1244	KAYASLSLWQAPSGESRPAPAAADLRGSSG/RPP*TFPNPPCGPHTG CP\AGSFPIISFQPRCLLVAKSKPGMPVSDEAAYESPWKGGAGAPALG LLGALSSEVADRALQAAPAWAPRDAGRDLPGQDRPQGPAGASLGPS RS
322	A	2	375	PRVRVRVDLVSGWGGKMVDLFLVLTVKRV\IDYAVKILVKPDWTGVV SDGVKHSNLNPFCDIAVDEAVLLKEKKLVKEGIAVCCGPAQCQETNRT ALGMGAHRGIIHVEVSP**AQRLCPLQVARG
323	C	303	395	MYSQPQANLGSLEHKLGRHLRILGHGSGRL
324	A	268	393	DGRRKEKWHKVERRHRPYLLSSLSQHRW*TVTNFGEISGTIAIEVDE GTIHALNNGLFTLGAPHK/ERIALKPGYGKYLINSDELVV/GRSD AIGPREQWEPVFQNGQEVNRNGGPAEMGEEKRNGTKWREDTDHTSFPLF PSTGGQPKAHSNWRKVCH
325	A	1	67	RHEAYVKSTKL VHKGTKAKRFA
326	A	163	552	AGFSLSAQKSPGAMA*YSYVKSSKLVLKGT\SKKKKSKDKKRKREDE ETQLD/IVGIW*TVTNFGEISGTIAIGMDEGTIHALDNGLFTLGAP HK/ERIALKSGYGKYLINSDELVGHSDAIGPREQWEH
327	A	289	818	EPSRGVWPHEDARINGSKKKKSKDKKRKREDEETQFD/IVGIW*TV TNFDEISGTIAIEMDEGTIHALDNGLFTLGAPHK/ERIALKPGYGK YLSINSDELVV/GRSDAIGPREQWEPVFQNGACAAVFTVIGSEKQSE CSLLRESRAKYHGCETHGQISSSLKQHPRWYSHQEDLV
328	A	213	905	YVQSLKQILS/GCI*ESIAIKKKKNKDKKRKREDEETQLDIVGIWW TVTNFGEISGTIAIEMDKGTIHALDNGLFTLGAPHKEVDEGPPPE QFTA\VKLSDSRIALKSGYGKYLINSDELVVGRSDAIGPREQWEPV FK\MGKMALSTNSCFIRI\HEAEDIEAKSKTAGBEEMI/KGSPNLC QTFTFMTLPYLPEHRSLLLKIRSCAERETKKKODIPEEDKGNIKQCE
329	A	133	482	GYGRRSVKVRWARCTGFSPKTPNPWVNSQHFGRRLRWADHLRSGVRD QPGQHGETLSLLKIQLPGCGGRCL*FQLFGRRLRQEN*I/RLNPGGG GCSELRSHHCTPAWVTEQDSVSK
330	A	27	201	LQE*SRPSRSEADLHGECYSS*GSTSGVVCSSRWARGLAGLRSEA ADLRSEYYSS
331	B	396	809	MAGCRSRALPHGEAAKAQRKVTAAGPGAKHLTAWGWQGLATPSVG PAEPTHTQNSHPASAVCSPSSRLRLSLHTYPQAEAGAGSLGQPRKG LPQCSSRLKGSSSAKVGAQAEVPRASEACEGCQHAVTSHKY*
332	A	130	249	GAPPAPWRPVPSTTQGLRSASAQRGTGRQLHLQPGCGIHI
333	A	1	3408	MSEAPRFFVGPEDTEINPGNYRHFFHHADEDEEEDDSPPERQIVVG

				ICSMAKKSKSPMKEILERISLFKYITVVVFEEVILNEPVENWPLC DCLISFHSKGFPLDKAVAYAKLRNPFVINDLNMQYLIQDRREVYSIL QAEGILLPRYAILNRDPNNPKGVKLQTFVSVTALKVARLELFVPPG GLLVLLGSGVKLQIFAGCRWSCLPVTRRVLALLSPWVVDGTGRRGAG GGARWGGSGRTGAHGVECNLIEGEDHVEVNGEVFQKPFVEKPVSAED HNVIYYPTSAGGGSQRLFRKIGSRSSVSPESNVRKTGSYIYEEM PTDGTDVKVYTVGPDYAHAEARKSPALDGKVERDSEGKEVRYPVILN AREKLIWVKVCLAFKQTVCGFDLLRANGQSYVCDVNGFSFVKNSMKY YDDCAKILGNIVMRELAPQFHIPWSIPLEAEDIPIVPTTSGTMMELR CVIAVIRHGDRTPKQKMKMEEVLDIARQLLMELGQNNDEIEENKPK LEQLKTVLEMYGHFSGINRKVQLTYLPHGCPKTSSEEDSRREEPSL LLVLKWGGELTPAGRVQAEELGRAFRMYPGGQGDYAGFPGCGLLRL HSTYRDLKIYASDEGRVQMTAAAFAGLLALEGELTPILVQMVKSA NMNGLDSDSDSLSSCQQRVKARLHEILQKDRFTAEDYEKLTSPGS ISLIKSMHLIKNPVKTCDKVYSLIQSLTSQIRHRMEDPKSSDIQLYH SETLEMLRRWSKLEKDFKTKNGRYDISKIPDIYDCIKYDVQHNGSL KLENTMELYRLSKALADIVIPOEYGITKAEKLEIAKGYCTPLVRKIR SDLQRTQDDDTVNKLHPVYSRGVLSPERHVTRLYFTSESHVHSLLS ILRYGALCNESKDEQWKRAMDYLNVVNELNYMTQIVIMLYEDPNKDL SSEERFHVLEHFSFGAGKCEEDKNLPSGYGYRPASRENEGRRPFKID NDDEPHTSKRDEVDRVILFKPMVSEPIHHRKSPLPRSRKTATNDV VSENANYLRTPRTLVEQKQNPVASTALRSSPIMRKKVSLNITYTPAK ILPTPPATLKSTKASSKPATSGPSSAVVENTSSRKNITSKTETHEH KKNTGKKK
334	A	3	443	SFQGGLEGEAWAGTGAAPGACGPAPRVPGRRRLRGPRTRPAGPTGPGQ *G/VLAPGPAAAVL/RELTGP*LPSRSRARDREGLQLHS*SQRDHEP TGRN/GTTPDAPP*EL*HSPRRSAASLCPQAPVSPQGSQVPALSGN SPQRLLLT
335	A	2	306	PCGGIRGGKEMNEIKTQFTTREGLYKLLPHSEYSRPNRVPFNSQGSN PVRVSFVNLDNQSGNGDRLCFNVGRELYFYIYKGVKGSLSSSSQAS SPGETVV
336	A	243	748	PCQSFQPSGFGKDRPTSLEQRSQRERQAAIFAVSQPSLVIIPGTGKS EVNADRSRPPAYCSNLGRYSGPGPPSLVIIPGTGKSEVNADRSGPPA YCSNHPPSALP**RSSMRSLSLQQTSAWTCRHFHTSFETIQ/RGGSQI LTLAFCAPAGPTPRGSHVLGLAPSEALT
337	A	514	967	APACCPAAVSPFLCEPTLIHPPHPPDLKEDTGQKHGAQSHPTLAGA GLAGRSSKQSPSAISIWHSD\GTSSCDRRQOCDRDLPSALLSPHLR CSQPATROLESS*T\PPGTADLFLASSGPNPRAFSNARSVRKCKATS EKSKPKSYQGS
338	B	1	456	MKLRTLAVSATALKVARLEFVFPDVRMCSEFLSSGVKLQTFVSVTA LNALRLELFVPPGGLMVSLASGVKLQIFTVSVTAHKSSVDPKTLGWS MGLGAVEQGAALIGEAWAAQEPMEGVGGSGMGACRSRALPRGKAAGA RREIERSAGH*
339	A	1	1519	MAPELSSKEQPGSEWKKACQMEGTVCACAQRDLDGFDQNADDDMDN EIQAEVMSDGEELVGNWSKEPTTLGAATMGLGTEKQLGMGWAGRKG PIEDLEPLPQAACKLHAVAHTTWEAVQCGSLPRRNSNLLLEQGVLE ETRNLQEHGGEIDLEKKRWLGTVHTCNASTLGGRGVKLQFTFTVSI TAPKAARLELFVPPGGLVLLASGVKLQIFAVSVTAHKSSVDPKTLG WSMGLGAVEQEVVLVGEAPAAQEPMEWVGSGMGAGPGALPRGKAA KARREIEHSAGLYKLLPHSEYSRPNRVPFNSQGSNPVRVSFVNLDQ SGNGDRLCFNVGRELYFYIYKGVKRTIP*G\CRTEILISVLTEAADL SKPIDKRIYKGTQPTCHDFNHLTATAESVSLLVGFSAGQVQLIDPIK KETSCLFNEEAFEGRYATFFTI/WYECSHGKLHISALLGLVFFGGDI SYSLSSQPAPLEGASRDSGSRGHELWSESSRKNRNKRH
340	A	759	1034	IQRFTSTPPDSGAQLASPSGSRTRAAGGAACQSWCRAPALLSPWVVD GTGRRGAGGGRRGGSGRTGAHGVGGRLRHGGQLQVPSAPREGS

341	A	587	1097	QKIINKVVPITGRQCCFVRLSPLES LKFQSKEEIRNTSHRANVTKRNSANRKTDAI LATPGPPPAQPHGA/PGGYAPRLPQHAPAGCFPKCGNPAPRPWYGPFSGPLLRKEQKRNPRKGTG*MQGVSPVFPPT*NAGPLP GGSLGPPISGHHFLVSHTWPPPPRSPTAPP
342	A	462	1238	SFYETKLLISGSETLDSKDQYRINKYNHYFQTLHYTHLKFSSGLS SATQ*KLSWSKNG*GERPVSPPLMAPSGQLLAIHVWSEVKS VSSC FLSCQQGHVLTSPGSSFPQCQPAQCYLIPCSEKYTNW/PGPIPPS LGIQSS/SSPGS*SGPISSSKYSGDAQVCFSSPNLFPSFRPVTGCIQ SPPNISPGAEGCGLQPIPVHSFLTPTSTFSPVSP*I*RSRSTHPETH SMSSSSQSSPQAPSALPPSISLPLSP
343	A	2	384	LREDDRRGHRVGS DSRASCKMLLILLSVALLALSSAQNLEDVQS EESPSLIAGNPQGSPQGGNKPQGGPPPPGKPGQGGPPQGGNKPQGGPP GKPGQGGPPQGDKSRSPRSPGKPGQGGPPQGGSPQ
344	A	2	624	SDSRASCKMLLILLSVALLALSSAQNLEDVQS EESPSLIAGNPQGP SPQGGNKPQGGPPPPGKPGQGGPPQGGNKPQGGPPPPGKPGQGGPP QGDKSRSPRSPGKPGQGGPPQ\GG*LQGGPPRGGIKPGQGGPPGKPGQ GPPAQGGSKS QSARAPPKPGQGGPPQEGNNPQGGPPAGGNPQQPQAPP AGQPGPPRPPQGGRRSPRPQ
345	A	85	194	FVEPIRRQRTARSPASRLQCTRARTGAWARCCETS
346	A	617	712	RRRSSTRTARSPASRLQCTRARTGAWARCC
347	A	2	343	SSVRAVEFPEDASGGSSPSGTSKSDANRASSGGGGGLMEEMNKLLA KRRKAASQSDKPAEKKEDESQMEDPSTSPSPGTRAA\TSHLTQRLA GSPGSGATRWRSLCPRFCPG
348	A	2	2355	WCDLGS LQPPPPRFKQFSCLSLPRHS*TSQ*PQPPKTQLNFTVAIDF TASNGETRMSEKVGGNLQPTSLHYMSPYQLSAYAMALKAVGEIIQD YDSDKLFPAYGFGAKLPPEGRISHQFPLNNNDEDPNCAGIEGVLESY FQSLRTVQLYGPTYFAPVINQVASNSWSSVTLGTDSEPAVEVPQYVG IRLLVEGFTIKKPMAMCHRRMGVRPAVPLLTQRGSGEGKDSGTPHS LHTKAQLPSPHVLRHQGVLRQHSKLVGTALSTTGKALRTLPTAK VFISLPPNLDFKVAPSILKPRKSIREDRNGRSQKT VHTEGDMMNLIK KIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSHTRHDM LQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQADGTVA EYNGYHVVFALAGSPKADDDTSIYMFYQKVGDNIDS WKNAGR VFKD SDKFDANDPILKDQTQEWSGSATFTSDGKIRLFYTDYSGKHQKQSL TTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGG TNFFRKESQKLQSSAKKRDAELANGALGIIELNNDYTLKKVMKPLIT SNTVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYV SNSLTGPYKPLNKTGLVLQMGLDPNDVTFTYSHFAVPQAKGNVVIT SYM TNRGFFEDKKATFAPSFLMNIKGNKTSVVKNSILEPGQLAVN
349	A	1129	1822	AWGSGKQRRQEAQCEVAEFTPARRAPDTPAPLVLEPARA*HTSPK KHPPMWCRRFFFRQSFALVPQIGVQWRNLGSLQPLPPRFKA\FSY PQ PPSSWHY\RHVP IFVFSANFCIFNKRWGF\TMLAKL\VLNS*PHEI HPPGPSQSAGIMGVSHCTWLV\FSEKVVLDYFFEKPPN*GNRFEFY FYLFETGSHSVNQAGVQR/PYHASLQPQPQAQVSLPSSWDYRHVPF
350	A	325	609	LMPCNPRHFERLRQADHLRSGVPRPALVQHGETLSVLKIQLGGHGS TCL*SQLLRRLRQKNLLSLGGRGCSKLRSHHCTPAWVTEP\DSVSKK K
351	A	3	220	RGSGRGEKKKGCSCGAAPGYLPWRHRGRGPWRMAFL LATCGGLDSGFV PSVQDFDKKLTEADAYLQILIEQLK
352	A	319	1981	VPGVPAARPERECRAHPASFPPPPGLDSGFVPSVQDFDKKLTEADA YLQILIEQLKLF**QASK\RKEDEQRKKIETLKETNSMVESIKHCI VLLQIAKDQSNAEKHADGMISTIKSCRCNIPA*SLGTCDQAQCLPRL PYLQNPLSCVSQSSVHLS*QVGPVLSYLTSSDSNTQIVPGSGNFTN LAASLTPSQAMSTLSPNTVPEFSYSRQ*/EDEFYDAD/ENSIKVGSS PKRLIDSSGSASVLTHSSSGNSLKRPDTTESLNSSLNGTSDADLFD

				SHDDRDDDAEAGSVEEHKSVIMHLLSQVRLGMDLTKVVLPTFILERR SLLEMYADFFAHPDLFVSI SDQKDPKDRMVQVVKWYLSAFHAGRKGS VAKKPYNPILGEI FQCHWTL PNDTEEN\ KELVSEGPVPGVSKNSVTF V\AEQVSHHPP I FSLFMLECFNKKIQFNAHIW\TKSKFLGMSIGVHN IGQGCVSCLDYDEHYILT FPNGYGRSILTVPWVELGGE CNINCSKTG YSANII FHTKPFYGGK KHRITAEI FSPNDKKS FCSIEGEWNG
353	A	27	750	STCCFQELVTL*GCKLCTFHPGRKWETRL\ EPLPQRDPSPYRVMLGE LRGIVFLT GIVSPRTENDQEISEDTRSHGV\LLGRFQKDISQGLKFK EAYEREVSLKRPLGN SPGERLNRKMPDFGQVTE\RS*PPGEREA/R KYNDFGNSFTVNSNLISHQRLPVG/DTRPHKCD ESKS FNRTSDLIQ HQRHTGEKPYECNE\CGKA FSQSSH LIQHQRHTGEKPYECSDW GK TFSCSSDLILH
354	A	69	378	KGGSLLGAPRVEGPNFGL\KDSSSPKKREFFALPPPGGNG/KRAGPP CPGKFGFLKKKGVP\GGKRLNPRPQGDSSS*PPKGGGITGGAPRP GKKRSFSLQKIL
355	A	213	660	KPVILGYAEPPAPGQFSRGP/WSRAE/WPGTASPLL V/SCATSALL* SIPKGPDSHRGHQHGTPKTPSKPEKGT AHGQLSRYITPQEKEIAPLN PPALKSPSKENRDPRDLTGPGQTSRALT VAPGCALGPQVEPMKALRR QMGAVFPLGS
356	A	629	1007	KGT YIKQERLENLRTNHL DKYYPMPKQNYQKLCQKGMASRTHREES R*MRGNRCRLRITRNA*FEGENLQNK\AQGENLEKKPEPATYI*EA* ESKRDKGV*KS YCVSSFPMTQ*KSD*SEYSYG
357	C	1	555	MLYVLIESERARIKKLQEEKTRNLESSRKLEPTIVSEHKGLRTEQT DIDVLGQHLTKEHVSSHSQSPIRDSQWFTLS PQEKYACSYERK DPLI KRAFIIFYHRNAVVS HGGNGPAVVLPISRFVLT PPTFESTLPFLSSR LAWGTSSKDPRIAAGQQSPLEKKILVSKLSSHHTVWNYTEKES*
358	A	4627	5052	LSTKAPRKDTL FNKWCWENWISICRRLQLGSYLLPY*KINQKWIKGL NDRSETMKLLKENIGEM LKNIGLGKDFMVKT SKA*AT\KQKIGRW DY IKLKICTAKKT/IRVKRPTVDGNNIFKLSNRGLISRVYKEHNSTVKK KKK
359	A	1	368	KKQIFLELISIYSRVAGYK\NTQKSVAFLYNSNKQLNL*IK/DTMPF ILAC/NK*KHLPLNLTK*VQEIYEGNYDTFMK*IED/DKQRNISS\ W*KRFIKM PIPNL IYRYNAPPVKISESYLVDI
360	A	241	583	NGPPFFFFFEMEFSLLLPRLECNGAISAHNRNLRLPGSSDSPASAGGL L*SQVAGITRLRHHD*LILY/FLVEMRFHRVG*AGLELLTSGDPPSS ASQGAGITGMSHSAGHYGKIF
361	A	654	942	CHACNPQHFRPRQVDHLRSGV*DQPGQHGETPSLLK\IQKLAGHGG VHL*S*LLRRLRQENRLNLGGGGCSEPRSHHCTPAWVTE*DSVSRRK KKK
362	A	1	2322	MHHGKRELLPKMDRRWHWRQLLLNRLGAVYTEGGFVEGVNKKLGLL GDSVDIFKGI PFAAPT KALENPQPHPGWQGTLKAKNFKKRCLQATIT QDSTYGDEDCLYLN IWPQGRKQGTCTGTGDRLETGPGGASGVTSR SPISVSRDLPMIWIYGG AFLMGSGHGANFLNNYLYDGEIATRGNV IVVTFNYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAAFGG DPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ KNPLFWAKKVAEKVGC PVGDAARMAQCLKVTDPRALT LAYKVPLAGL EYPMLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIF ASIDMPAINKGKKNVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESW AQDPSQENKKKT VVDFETDVLFLVPTEIALAQHRANAKSAKTYAYLF SHPSRMPVYPKWVGADHADDI QYVFGKPFATPTGYRPQDRTVSKAMI AYWTNFAKTGDPNMGDS AVPTHWEPTYTTENSGYLEITKKMGSSSMKR SLRTNFLRYWTLTYLALPTVTDQEATPVPPTGDSEATPVPPTGDSET APVPPTGDSGAPPVPPTGDSGAPPVPPTGDSGAPPVPPTGDSGAPPV PPTGDSGAPPVPPTGDSGAPPVPPTGDSGAPPVPPTGDAGPPPVPPT GDSGAPPVPPTGDSGAPPVTPTGDSETAPVPPTGDSGAPPVPPTGDS EAAPVPPTDDSKEAQM PAVIRF

363	A	8453	9757	APCLLGWSLPSRSAKTYAYLFSHPSRMPVYPKWVGADHADDIQYVFG KPFATPTGYRPQDRTVSKAMIAWYNFAKTG*DVG*VQGGGPQPRRA SHHEALFPHLPVEGLWASHLTSPCIGIHVCLMRVTGRAPSPCTCTA SAQYAVRGMVPRASSEGGDGSQVQVESRASAPWESPAPAQPLLTQ\ DPNMGDSAVPTHWEPTTENSSTYLEITKMGSSSMKRSRLTNFLRYW TLTYLALPTVTDQEATPVPPPTGDSSEATPVPPPTGDSSEATPVPPPTGDSG APPVPPPTGDSGAPPVPPPTGDSGAPPVPPPTGDSGAPPVPPPTGDSGAPP VPPTGDSGAPPVPPPTGDSGAPPVPPPTGDSGAPPVPPPTGDSGAPPVPP TGDGAPPVPTPTGDSSEATPVPPPTGDSGAPPVPPPTGDSSEAPVPPPTDD SKEAQMPAIVIRF
364	A	10	548	FRLVLSRLEGIGAILAH*NLCLLGSNDSPASATRVAGITGTRHAP LIFVFLVEMGFRHVQAGHKLLISGDPPA/SASQSAGITGVSH/ARL AALSNF*GLGQVPTPLKQATLLSLDTSPLPAIFFLFFF*DRFS\ S VTQAEVQWGDHCSLHP*PTGLK\ DPPASASRLGTTRTRHHSR
365	A	252	934	LCASRLRLPAPMLSLSHRISPHWPVGVHYGC*GGRSGSDIGSCRET GLCRGFSPGCIKTSTS\ PWAPAG*APSTGPSQGETCTAHSPFIPAPA *AQGLKF*GVTESICAGAAGTAGGTETAVSAGSPAGQAQPGPGAGQS LSAGSQMA*GSDHPGPIWQTC*SVQGAFAALDG*GG*LHPHPP*GPAT LPEGGGGVCPPAAKNASGATREVPVAVLQAVHAPGATWLRPP
366	A	169	459	SLEVLGDHDFQKCRFLEKRERFWKGMFSFCSMAVSGFLAAGAGLKPR SG/WH*VFHSPRRSWTENFKFQRDEVASPLGAWRALTKKGAQPL EGL
367	A	186	372	QIRETS GTGT*YTSASQSAGIIEVSHHARQMFQFYSQKYTL PNCKKL *ILMFKIKFFLTQK
368	A	150	799	QC*DPETSETV*EKLRAGRHQRCHGGQSCFDKSATRALPPPRKWRH RGTRCAATKRTRLGEMAVLGP*E*ROPEEFPRRTSILAEPVLSRRK CRPSEKRGSA TEKGATSAVTENPPLGAAGERANKTL/RCCHRD TDF RTPASDGERRRSHTEGP INRSLAMRMGKGGSIGTENRADWAGPGCKV CESCS/RVLHLCVYGSHHRIWHMEGYQHMLV
369	A	1200	1679	RYKLLSYRKPETAI EQKENIPFQNL SRFSKNLHFWK*SPKETSRLYH ECLQLNSSCLILTAYPVQII/CHLFLDEPGRMSDQRRRAQNVPEMGF HHVGQ/ACLNLS\DRPASASQSARIIEVSHHARQMFQFYSQKYTL PNCKKL*ILMFKIKFFLTQKQ
370	A	1	1107	MTLEATHLLLRVLLVLLASGSLFQSPPVKSIILGVAVTVVLLLLLLL ALLINRYLQKARGRARKPYTEDVSVDKKTETWEWARGESESYHVYDD VQKEKTTDRMIRSSSMCVHKINTSVSMCAQETPNSSKKAKLGQKIPV QGKDEILHKALCFCPWLKGKGGMEPLRLLLILFVTELSGAHNTTVFQG VAGQSLQVSCPYDSMKHWGRRKAWCRQLGEKGPCQRVVS\STTCGLL SFLRRWNWEHSHSQTIPWGGTLTITLRNLQPHDAGLYQCQSLHGSEA DTLRKVLVEVLADPLDHRDAGDLWFPG\DLRASRMPMWSTASPLGR\ AREGR*WEEKPRRSPTRDQPSLHTCHLATRTPCSALARDYSA
371	A	2	1310	EQQDLQDPLEVFHPTVEAAEALHIQEPPGGEPSQPTQLPGGAPNTRP PHPOGALWSV*RAPEQELHQDGRQPTG*QWLRTCSLGWPEAQLPAHL IGQADWPSQRPP*DPE*TPPRPQONPGPSNWRCTCFATPSC TGWA*AT TQIRMIENGKPELPGPPSGEVPLGQQQVGPV\PSGFPGPQAPPGL ILHSNNIHQSGVFNEFLFPWGFGEAGPYNGHSASSTTPCPTGRCK PATFRRRH*PPGHPVWATTKSRGM/TAATAGPQWGS LGNTARHPDGE AEPGS*ARAQLASNPAPHLRVP*PQLRLPHSPFPWVPKGCRTWRP EGMTCYAWAHELRLPALPPQPPRGT*SFVLVHSPACPAQALPPNLYC PGGGWEVEAQHPAQMTVPFLEAPHPHWPTGG*VSPYPSGPAQGGGAAS EVGGCLSIKETPCNV
372	A	475	929	NLVACSLPISPETLSPVPL\TPKPSGLLALSGLAFLSCPLATPSP LP TKPQGTAGPPQPCPSGLAPQTL YLSRRRLGGWRPSI PAQMT PIN RPESQTPVFLEAPHPHWPTGG*VSPYPSGPAQGGGAASEVGGCLSIKE TPCNVKKKKKK
373	A	2	643	PICLFSRPTLRPSRSKVS LIEGRGANMAARWRFWCVSVTMVVALLIV

				CDVPSASAQRKKEMVLSEKVSQLMWETNKR\VIRMGDKFRRLVKA PP\RNYSVI\VMFTA\LQL\HRQ\CVVCKQADEEF\QIL\ANSW\RY S\SAFTNKDIFFAM\V\DFDEGS\DMYFQMLKH*ISAPNFPSTFLQK GKPKRG\DTY\ELQVRGFFQLRQISPMI\ADRTDVQY
374	A	562	767	GKSISRYPLYPFVIFYFYFLETESCSSAQAGVQWRNLGSLQSPPSG\ SSNSPASAS*VAETTGERHHAQ
375	A	23	483	NGVLLSSRLKCSGAI SAHCSLCLLGSSNSPTSASQVAGITGAHHHTW ANFCI/YFF*VEMGFHHVG\QAGLELLTSDDP\SALASQSAGITG/G EHLRLAVTYLNKHERGSFLSSSCLPSAWWKWLCLCSCFWVPKCLALC HFKHYGRRKQVGHTSK
376	A	129	366	NYYYTHLYANIFDTLEERGKFL/DKQNL SKLEQTGKAQGFYDLLKKN **L*SLLTKKASGRGPLLGNSFQF*RKKMTPTL
377	A	67	224	NLYLKFSNSWLRTQIPKWKFN SVFLFTEYTDNALIPKNSSVIVRRI PYWRC
378	A	436	829	NLREFPWAPCPVLHYKFSSKLN LWIPVTL*GGSHILPSATLKKQIYG E\KKLKAADCDLQITNAQTKEEYTDNALIPKNSSVIVRRIPIGGVK STSKTYVISRTEPAMATTKAVCKNTISHFFYTLLPL
379	A	74	380	GCTKDSNIYFIKEHFQSVNNHIKRLISFLIRVM*LKPQQVTII\TP IRMAKI*KAENSKWCQECGAATLMH**V*LPLKSWHFLKLSTCL FYDLAIPL
380	B	1	483	MGQARWLTPVIPALWEAEAGSGRPSAAGLLEFARGPLQTLFAWVSA AVAAEQRIFVNRECCCLIVPLEVLSQRSTRPCEVSVCPYWENAFQLG CSGTVTVGSTTVTLAECKWLTTFQLV SIGLAAMVDVLTGDVWWL LNVAEWN SFVNIPNDLS*
381	B	119	955	MVISRPRDPPASASQSAGITGPALGAEGERA FHRHRVMIVTEGAPG GLSSGHLRDAMDSEAGTDDGCASHVRVVRDLKPSN ILYVDESIGNPE CLRICDFGFAKQLRAENGLLMTPCYTANFVAPEVLKRQGYDEGCDIW SLGILLYTMLAGYTPFANGPSDTPEEILTRIGSGKFTLSGGNWNVTVS ETAKDLVSKMLHVDPHQRLTAKQVLQHPWVTQDKL PQS QLSHQDLQ LVKGAMAATYSALNSSKPTPQLKPIESSILAQRVRKLPSTTL*
382	A	1	662	LGSCVTQTGVQWCGHSSLRPQTQAQAILLPCLSN CWDYKHEPLHLA YVTQFCFLSFFFGGGWSLALSPMLECGGVILAQCKLRLLGFTPFSC LSLPSSWDHRHPPCLANFLNF/SVETGFH\FLAQDGLDLTS/S/I PPASA/FPKCWDYRR\DHRAQPM*CNSDVNSLMLPQMPQVK/AHQSP IGCPRFRHTCRLGCPQTCTSHQLAANLEVPTMPSSSITH
383	A	110	784	AAAAASKVLM*TGGAAPQEQP*TGGVQA*APGSVA/AEGASVEGPGF GDTAPAHQGLSPTRSHGQGGAGRASAHSRDPPGGTGGWGFLKCGPGA LCPERGKD GASASVPRGPYAEAEKGGWALRGLGGVAAPGPPSRAGQA PSGLHTGPNARPAPWPIPGQGGGLRRDQAG*VSSWTGSTEPGAHTAH RAPGHGKGKGSPPQPHQPGPGQIPTHTRMHSCRITAA
384	A	244	315	NPKGQKDREAPLSRSVFVLKIKIKRAFALLHGRF*PSTPAASASPA SKSPRGSGKALASALFYIVQLTK
385	A	933	1511	QVYRPSQTPHLALSPERVAPGRLAGGRLAPEARAPRGSP/LPPHRVS EKTIRVMVFHPGARRAGGTPPRAPRGDTGGAPGA\PTYSTPLMSLHR ARLESSSTGSSFPADSAPVPLAVVSLDSR*QWESRSSIHA\VTN* ASSSSSSSSSS\FSR\VYPRFIEFLHFDIQSTGQ/RITSRQHPPR/ DFRDALF*LNS
386	A	15	468	GVPNNFI INKNKTPSGWLQPLPRWL*APVGGACHYPGLEARTEERAP CPSKYTGEPEVLR IKNQGGTPRPGGGPGPSAPRGSFLWST/PGSCPS ITPHSLPAAR/PLPPTPRHPAPSSPPCTE/SAPSGPSSSQAPGITVA PGISQVQRAAALR
387	A	50	481	FMEYLTLSFIHVLQ*FIHCFVHLFIHSFFYALMKSLIQ*FIHLYSC F/ICIDLLISSCIYSFIYALVKSLANSLTHSFIHTFLQ*FVHLFTPL LICSFTHSSIH*PSHSLTFIQLHLFFHALVSGFIWSFIYLFCKINVF LIDK
388	A	119	1533	KKMNLAEICDNAKKGREYALLGNYDSSM VYYQGV\QQDSRDIAQSV

				QRSQLSKGWPTFRGQELL\EEYEQVKSIVKHFKKVKIDKPSQISP VLSR*THLEIPAVWPTP\VPAEHRAPPQIRR/RQSRKTSEERNGR SRSPGTCRPSTSYIKE*/NSLLQVGTRTIEPEGDDKGRKNMQDGAS DGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEAKLLR EAGVLPWMPDFFKGIRRPWKNDSONLGKPYSAQDDIGMNIVGPLT HGFSSASAAPETTRQPLLFLLLLSLSKVTKFKGVLVMPGPGTGKTML AKAVATECGTTFFNVSSSTLTSKYRGESEKLVRLLFEMARFYSPTTI FI\DEIDSICSRRGTSDEHEASRRVKESELLIQMDGVGGALENDPSK MVMVLAATNFPWDIDEALRRRCFIWVGDFPDVPQEKDTSVSPESCLL TDWWWGL
389	A	293	805	KARDKSPFLGDLCLKDTGQQSLLQCRFFPFLGTKISCFQNVHSWQTI TSDGLSAGDGGFGPKYQ/RSRGQIPSGLNSLPLNSESDDLPTPHFP LQSQGLGSQVAQIDDVKAPPPFAEPQPKRLRSPRPLLGAIESVAV SRLSPSGPTGTDAL*WLSVQKPPTRTIHGNE
390	A	2	428	GLPGSTTASAAAAASAASASSDAPSFQLGKPRLQQTsfYGRFRHFLDI IDPRTLFTVTERRLKEAVQLLEDYKHGTLRPGVTNEQLWSAQKIK/SG YIPFGTPIVVGLLLPNQTLASTVFWQWLNHSHNACVNYANRNATKPS PA
391	A	3	297	ASASSDAPPFQLGKPRFQQTsfYGRFRHFLDIIDPRTLFTVEEGCL CSKNALNKASEEEVALLDRGEEWCILILNGERRGKEEEEKNSGKESM ILR
392	A	1	885	RRLEAVQLLEDYKHGTLRPGVTNEQLWSAQKIKQAILHPDTNEKIF MPFRMSGICQGCLLVATSDAQGGKQEGMRPLSQGSELTRCHVLPRAV SQSKLDDQAEPKSEEINSFCDEAVARRIIKGTLWCHGQCPGQQLSGK CSECYWAVSYDVPGGPSTVRGVVGLLLPNQTLASTVFWQPSPASKFI QGYLGAVISAVSIAVGLNVLVQKANKFTPATRLLIQRFPVPPAVGPL DTDMQQLARETSVDPDMRKGLQELKAKGKLVDCKVSAQKLLSLEKD EFKSGAHVDFYDK
393	A	2	675	SCPLSCTSAATGLWVKEGLRIVSSVLLGLSCPWGSPLAELDLGEG/ RLWRTSFYGRFRHFLDIIDPRTLFTVTERRLREAVQLLEDYKHGTLRP GVTNEQL*SAQKISQ\AIYHPDTNEKIFMPFRMSGYIPFGTPIVVGL LLPNQTLASTVFWQWLNQSHNACVNYANRNATKPSASKFIQGYLGA VISAVSIAVGLNVLVQKANKFTPATRLLIQRFPVPPAV
394	A	485	1044	HLVPLCPCNLSKAGRCTVQERLLVICCSRSWRWRNLM*RWLNYPVS SGHRH*SSLARETSVDPDMRKGPAGAEGKGKAVGCKGVSQETAAYW KRTSSSLEPTWTLTNKPMFFGFRNLFAPTFRHTPEALWLPTPCHRG SPALHIEAFMPAALPSGTASCELPGHWPYQLSGVLCCAPWVIKEA
395	A	901	1215	SQHFRPRWADHLRSGV*DQPGQHDETPSLLKIQLAGYSGEHL*SQ LLRRLRHENCLNPGSGGCSEPRLHHCTPAW/VAEPDSVGGGVGGKEK NNTSNMLQTRP
396	A	110	1014	KTTRGYTLHCAAAGRLETLKALVELDVEDIEALNFRERARDVAAR YSQTECEFLDWAGLNPGTATHDSDEEAAFLTRVWSTGHNDSGVKQR MGQKEIQNATSSNHFTCPSS\TLQRKKG*FVGLLW*FRNVSTLLMK TFLPQARNSPPETPSGTITTQITGKICRMFYWSYMESEGPPESERAE FFSQEEEEEEEEAEPEETGPKNPLLQPALTGDEVLQKIFEDPEN PHHEQAMQLLEEDIVGRNLLYAACMAGQSDVIRALAKYGVNLNEKT TRGDTLLHCAAAGRLETL
397	A	247	496	SLILFFYTFCQVRHFASKQDAPNSQPGSLASPAQTCGPSIPQSQGTG PAGGGFMFCFKQKTQPYFSLQKQKRKPKKIQLNDK
398	A	653	1140	RPFFPPHSESONPPRO/PDSSPTGTST*PADTHCPRPVSQAQGGTAE GL**PRVHGPSPLPHSIGSAPPQCQEGAPAGEWAREPGEDGV\PGAP GQN*GKMEFSGAG/GQVPSRVVEGVQSHLRSEGPFPACPAVPCAEG PD\GRPGNTGRGGPGLRNQRRWEW
399	A	2	510	FLANFLCFIRD/GFHHVQDGLHLLTS*SACLGLPKCWDYRREPLRP TSPLLSPRHQALCCLAFGHSAAATCTCVN/SALAWAGFWNPQAPGF/S VAPAHLLTHTVSLSPMPLWATCSPGAGHEAPGLMLQDPFGPPWCSCG

				PVFHEKTAGCKARAFSGRVCRCKAQAALPETGR
400	A	249	434	IVEYRCMWYRLLFFFPETESCSVAQVGTQWHDLSLQPLSPG\SSN SPASAS*VAGITGTH
401	A	532	986	PWAKLGLSCVPAWQVQVLAICRWKEVGILDFFLVFFFLR*SL/DS DTQAGVQWCDLGLSLQTPLPGFKWFSCPSLPSSWDYRHAPPRSADFCI F/M*RWGFTMLAKLVSNS*PQ/CDLPASASQSAGITGVSSQCTRRNLG IFIDGTSVSDSSRT
402	A	2	992	FVDAAGCPLRCSVVTGIVVLQKSGNRPEDLRAAQLPGRLELLLNFC SAMPAPDAAPAPASISLFDLSADAPVFOGLSLVSHAPGEALARAPR TSCSGGERESPERKLLQGVLTISEKLFCTCDQTFQNHQEQREHY KLDWHRFNLKQRLQGG\PLLSALGL*KAELHRRSFPAFSGIRRIQDS ASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQQQFSLCLPLCP R/LLIRIPQKRQNLRLTRTLQSRGPRDCVVLMAAAGHFAGAIQGRE VVTHKTFHRYTVRAK/QGHSQGAFG/NARGGSPHSAGANLR\RYNEA TLYKVS
403	A	2583	3827	DRVSLLLPRLECNGAILAHCNLCL/SGFK*FSCSLSPSNWDYREVPP H\QLIFVFLVEMGFHHIAQAGLELLTS/SI/PPTLA/FPKCWDYRR\ DHHAWLFFFCSE\NSFTLLPRLE*GGLISDHCNLRLLGSSDLPASAS Q\EPRLQACATTTPR*FLYFW*RRGFTMLARLVNS*PQV/HPPASAS QSAEIIIGVSHHTWPQEVFLFLNFIYLRWSLALSPRLECSGISAHC KLRPPGSS\ILLPQPPE*LGLQAPATTPG*FFCIFSRDGFSPC*PGG S*SPDLVICLPRPPKVLGLQV*ATTPGYFYFFETGTHSVTAAVQWY TIAHCSLELLSSSDPPTSSSQVIGTTGAPHHALIIYLFIFYFIEM RVPCVVQAGLELLSSRDPFAWASQSAEITGMSHRAQLGIIKAPRMS V
404	B	1	336	MGRARWLTIVIPALWEAEAGSREVEEYMGAEAVKSWTSSMFKEWDE KVRREKTSSRRARAACGGVFESPEYVHLLKVFLLEDLDKQQQTNSKA SRRQEIIRAELEIKT*
405	A	2	313	FFFFLRRSLALSPRLECSGVISAHCKLRLPGSR/RFSCLSLSHSWDY RRPPRPANFLYFLVEKGFCVSDGLHLLTS/AIPP/TSA/FPKCW DYRCDSMNFLMVSKD
406	A	4565	5027	LIGYILFCFFFFFFFLLRQSLVLLPGLECSGVILAHCNPR/LPGFK* FSCSLSPSSWNYRHAPARP\VSFVFLAEMGFHHIGQAGLKLLT/SV/ IPPTSA/FRKCWDYRREPPRPTA\FFVLNKFTVLGSNSGF*T*DHRI NHFMRLYCNYTLEYSGSHL
407	A	187	743	TRGTSAARTGRSSGIASMASGILVNKKEVTCPICLELLTQPLSLDC GHSFCQACLTANHKKSMLDKGESSCPVCRISYQPENIRPNRHVANIV EKLREVKLSPEGQKVDHCAHGEKLS\IFCQEDGEGSFCW\VC*AVF REHRGSPHVSSQRRFAREYQVKLQAALMLRQKQQAEELEADIR
408	A	1234	1337	TRGPRGPADSCRKAWSEKAWQRGPSWCPAAGASGCCGPLHPWLW/P PEPWVERATPT*GPCSRTPAPGSPLPGFLRPLPAACVCRPPGSPCSE TVLF*EAE/PT/P*APVRIGGTQPCAVLLPARKVQSSSTR*/VT VTRLPVQKVEVAGGWPGSHEKTL/AA/PAWGLDRKPLQAPRSQKLP PNPQGTAEQGWVHRYKCCFVSLTPCSSQLPVP*DLASKG*PSHT* ILGSF*DLCLPA*PMLQGPCPQPLSAP*VFLFPSL/S*VGALIGPFL ARPFSGQLP*AWATPPWPS*PLAK/SPPDVACSLVPGSPSPSHPS APVVEPHL*APGALNVLSPLDLMCIPSPASYVAAKAQAVNGGSCHT SLPELT*P\PATSCIGILRAGPCSLMGPPRPVKPW*RSACLGLNSQ CLTPQPKTGSVPYGPSPAVAWVP/ERLPPPGSP\PPAPIKVLPLMQAC VDHVFPWPEPPPATGGQLPF
409	A	89	596	IILKTGSSSLCHPRLECSGVILVHRNLR/LPG\SSNSPASGSPVA*IT GARHHDRLIFVFLVEMGFCYVQAGLELLTSSDPPTSASQSAGVTGV SHCARPSFAL*F*KSA*YNLELCLFYHH*YSKCIIFHFLFLDYNCQN LITINIESSLIFSILLISTFYCYLAEIPR
410	A	372	639	RAFVQYFKSLNMFMSFDPAILLIGIYPKEKS*IQK/DTLCPEVSEIL LMVVKNYN*YICHTRNDQAGLIY/HLYSGIYLALK*VCEFFTLKG

411	A	136	251	IHQEKPPNIFSVKKRHYD*PGQHDPLASASQSAGITGV
412	A	118	337	IHQEKPPNIFSVKKRHYD*PGQYGKTLSSLKIQILAGYSGTCL\KSQ LLRRVGREVIQLALKIRAPIWKIECL
413	A	160	437	KRDITTSLGQYGQNP\SLKIQILAGY\SGTCL\KSQ\LRRLRHQN RLNLGGRG\GSEQRSCHLHSGGHSETVSKKKKKRERQQRQIGTCM P
414	A	2	150	WLPSLLEPGLHPSNHVQGPVAVGIDLGTTYSCVPI\GNRTTPSYVALR PG
415	A	1	1786	MCLLVITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSD EGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELETSGLTLQ CESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNL MSYSGLYQCTAGNEAGKESCVVRVTQSTMFQGTLLQGLDGTYS\ CVGVFQQRKSPRLIAN\DOGNR\TTPS\YVAFTH*GWIGDAAKNQ \VAMNP\TNTVF\NAKRSDLDGRF*MNAVCPVLIMKHWALYVWGEMM LGRPQGP*DYKGEDQKAFYPEEGCLLWVPDK*KEICRSPNLGEEL VTNAV\VTVPAY\FND\SQRQATKADAGTIAGLNLRIINE\PTAAAI AYGLDKKVGAEARNVLI FDLGGGTDFVSILTIEDGIFEVKSTAGDTHL GGEDFDNRMVNHFI AEFKRXHKKDISENKRVRRLTACERAKRTLS SSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALR DAKLDKSQIHDIVLGGSTRIPKIQKLLQDFFNGKELNKSINPDEAV AYGAEMRQDKKELLDPDIAEDFLEEVAFDKKRMGFGGF
416	A	1	154	PQRRVARRKRAVLPSTKA*PENTPSTFTSASMEWASRSVHLGHSKRF GNLP
417	A	1	893	PTRPCKMAGEKVEKPDTEKKPEAKK\VDAGGKVKGNLKAKKPKKG KP\HCSRNPVLLRGIGRYSRSAMYSRKAMYK\RKYSAAKSKVEKKK EKVLATVTKPVGGDKNGGTRVVKLRKMPRYPTEDVPRKLLS\HGKK \PFSQHVRLRASIIY/TPGTILII LTGRHRGKRVVFLKQLASGLLV TGPLVLR\VPLRRTHQKFVI\ATFTKIDISN\VKIPKHLTDAYFKK KKLRKPRHQEGEIPDTEKEKEYEITEQRKIDQKAVDSQILPKIKAIPQ LQGYLRSVFALTNGIYPHKLVF
418	A	934	1272	WCILGLCTSLMSRTALFPSRHTFFA/RSHSAASKL/EKKKKKEKVLAT VTKPVGGDKNGGTRVVKLRKMPRYPTEDVPRKLLSHGKKPFSQHVR KLRPSTPG\TILII LTG\RHRG
419	A	1	2607	MAFAWWPCLILALLSSLAASGFPRSPFRLLGVANGIEVYSTKINSKV TSRFAHNVVMTMRVNRADTAKEVSFDVELPKTAFITNFTLTIDGVTY PGNVKEKEVAKKQYKAVSQGKTAGLVKASGRKLEKFTVSVNVAAGS KVTFELTYEELLKRHKGYEMYLKVQPKQLVKHFEIEVDIFEPQGIS MLDAEASFITNDLLGSALTCSFSGKKGHVSFKPSLDQQRSCPTCTDS LLNGDFTITYDVNRESPGNVQIVNGYFVHFFAPQGLPVVPKNVAFVI DISGSMAGRKLEQTKEALLRILEDMQEEDYLNFI LFSGDVSTWKEHL VQATPENLQEARTFVKSMEDKGMTNINDGLLRGISMLNKAREEHRIP ERSTSIVIMLTGDANVGESRPEKI QENVRNAIGGKFPLYNLGFGNN LNYNFLENMALENHGFARRIYEDSDADLQLQGFYEEVANPLLTGVEM EYPENAILDLTQNTYQHFDYDGEIIVVAGRLVDEDMNSFKADVKGHA TNDLTFTEEVDMEKEMEKALQERDYIFGNYIERLWAYLTIEQLLEKRK NAHGEEKENLTARALDLSLKYHFTVPLTSMVVTKPEDNERAIAADK PGEASYQPPQNPYYYVDGDPHFIIQIPEKDDALCFNIDEAPGTVLRL IQDAVTGLTVNGQITGDKRGSPDSKTRKTYFGKLGIANAQMDFQVEV TTEKIT\CGTG\RA\STFSWLDTVTVTQDGLSMMINRKNMVVSFGDG VTFVVVLHQVWKKHPVHRDFLGFYVVDSHRMSAQTHGLLGQFFQPF FKVSDIRPGSDPTKPDATLVVKNHQLIVTRGSQKDYRKDASIGTKVV CWFVHNNGEGLIDGVHTDYIVPNLF
420	A	1	1842	MEKALQKRDIYIFGNYIERLWAYLTIEQLLEKRSHITCRKLSLPPPGF LVIPMSPSGLLQHLAIFWVAVITTGIVSAMVALLNPIENPDLKLAIV MLIVPFFVNGFYQSQVAKPLLDVLDLQYPQDAVLALTQNHKKQYYEGS EIVYLHEKHILHRDLKTQNVFLTRTNI IKVGDGLGIARVLENHCDMAS

				TLIGTPYMSPELFSNKPYNKSDVWALGCCVYEMATLKHAFAKDM NSLVYRIIEGKMILTDSKASCGPWKPDWLGSMTPERASGRKLEKFTV SVNVAAGSKVTFELTYEELLKRHKGYEMYLKVQPKQLVKHLSHTAS YQPPQNPPYYVDGDPHFIIQIPEKDDALCFNIDEAPGTVLRLIQDAV TGEACGLGPGPGSSWEGLGPPRASGRTEQFTIHLTVNPQSKVTFQ LTYEEVLKRNHMQYEIVIKVKPKQLVHHFEAGAQAPEIKKKRPPVKD EDLKGARGNLTKNQEIKSPTYQVMRECGPAAAFELSIGVIDGDPLES HMQACKQDRSSKLVSIMDFADFGTTIKQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLE SGQ
421	A	3	379	SYQPPQNPPYYVDGDPHFIIQIPEKDDALCFNIDEAPGTVLRLIQDA VTGEACGLGPGPGSSWEGLGPPRASGRTEQFTIHLTVNPQSKVTF QLTYEEVLKRNHMQYEIVIKVKPKQLVHHFE
422	A	1	623	MTKRCLDHRGEWLPAGGGGGHTEGTRCLHHPVTVVGVIEVDIFEPQG ISMLDAEASFITNDLLGSALTKSFSGKKPVWLRGRHTPKGNLDSEVL AGLSPCPIPLAGLTVNGQITGDKRGSPDSKTRKTYFGKLGIANAQMD FQVEVTTEKITLGTG\RA\STFSWLDTVTVTQDG*APLQGLQGGQ EGDHSGPQPNPGALSEPVLV
423	A	3	2722	FSDGLCMVALSHLGSALQLGSLCFPRSPFRLLGKRSLEPGVANGIEV YSTKINSKVTSRFAHNVVMTRAVNRADTAKEVSFDVELPKTAFITNF TLTIDGVTPGNVKEKEVAKKQYKAVSQGKTAGLVKASGRKLEKFT VSVNVAAGSKVTFELTYEELLKRHKGYEMYLKVQPKQLVKHFBIEV DIFEPQGISMLDAEASFITNDLLGSALTKSFSGKKGHVSFKPSLDQ RSCPTCTDSLNGDFTITYDVNRESPGNVQIVNGYFVHFFAPQGLPV VPKNVAFVIDISGSMAGRKLEQTKALLRILEDNKEEDYLNFI DVSTWKEHLVQATPENLQEARTFVKSMEDKGMTNINDGLLRGISM KAREEHRIPERSTSIVIMLTDGDANVGESRPEKIQENVRNAIGGKFP LYNLGFGNNLNYNFLENMALENHGFARRIYEDSDADLQLQGFEYEEVA NPLLTGVEMEYPENAILDLTQNTYQHFDYDGSEIVVAGRLVDEDMNSF KADVKGHGATNDLTFTEEVDMKEMEALQERDYIFGNYYIERLWAYLT IEQLLEKRKNAHGEKENLTARALDLSLKYHFVTPLTSMVVT EDERAIDKPGEDAEATPVSPAMSYLTSYQPPQNPPYYVDGDPH/FS IIQIPEKDDALCFNIDEAPGTVLRLIQDAVTGLTVNGQITG\DKRGS PDSKTRKTYFGKTGASPMAGMFGPWEVTTEKITLLEQARCAFFSW LDTVTVT\QDGHFLASSRRLSMMINRKNMVVSFGDGVTFVVVLHQ/V CWKKHPVPTVDLGFYVVDSHRMSAQTHGLLGQFFQPFDFKVS DIRP GSDPTKPDATLVVKNHQLIVTRGSQKDYRKDASIGTKVVCWFVHNG EGLIDGVHTDIIVPNLF
424	A	1168	1629	RAGRGEGHKLNSYGGRRARSQGHLLSSALSPFVSAASYQPPQNPPY YVDGDPHFIIQIPEKDDALCFNIDEAPGTG\LRLIQDAVTG\LTVNG QITGDKRGSPDSKTRKTYFGKLGIANAQMDFQVEVTTEKIT\CGTG\ RA\STFSWLDTVTVT
425	A	87	508	MGCFIGEGEENLIKKRFVSEAL\DVRRKRRQEEWENVRKPEDP EECPPEVYDPRSLYERLQEQKDRKQQLRGTVSNCKNM\VRG\LDED ETNFLDEVSROQELIEMHRIEELIELNEYRIALWNVGISYENYEGR G
426	A	90	549	QGASQTTRETSCLGIAR*TFLGL\FVRIERIDGNLKMHLHIVEPYVT WGFPNLKSVRELILKRGQAKVKNKTIPLTDNTVIEEHLGKFGFICLE DLIHEIAFPKGKFQEISWFLRPFHLSVAHHATKNRVGFLKEMGTPGY RGERINQLIRQLN
427	A	215	870	RAPPNGLTDDQKKGKGLRFRKLESFLHDSWRQKRDQVRLRRLEV KPH ALELPDKHSLAFVVRIERIDGVSLVQRTIARLRLKKIFSGVFKVT PHNLKMLRIVEPYVTWGFPNLKSVRELILK\RGQAKVKNKTIPLTRH /SQ*WRSTWGKFGVICLEDLIHEIAFPKGKFQEISWFLCPFHRLSGP SCYQK*SGLPQGDGHTWAIGVNASNQLIRQLN
428	A	476	821	TFTWPLFVRIERIDGVSTWCREPLQDFALRKIFSGVFCGTPQDSK

				M\LRIVEPYVTWGFNPKSVRELILKRGQA\KVKNKTIPLTDNTVIE EHLGECYSLGVSWGRKPGSLKL
429	A	33	371	ATRSRLGKHTRRSKSSAIQAVRIISQVLRCKQRCMHCPRTIPATLQE HKSVMNPSAQRTKTWSIHTPAPHPH\ PAPH PSTHQ/HPHPST/PAP HPSTHQHLIHPHTSISSIRTRG
430	A	42	334	RRFRAAVMAPPGCPGFCPNFVLVCSFLERYGPLLDLPELPLPELER VLQAPPPDVGNGEVPKELVELHLKLMRKIGKSVTADRWEKYLIKSK RVG
431	A	55	1079	SERRRGPLCLPSDSVLDCSGPPMYCGIAEPSLRRWDPQRSPLASASC RLLGCLAI PRHPNFP RPPIASSSILQIKMATAAAAAAVMAPPGCPGS CPNFAVCSFLERYGPLLDLPELPPPELERV LQAPPPDVGNGEVPKE LVELHLKLMRKIGKSVTADRWEKYLIKICQEFNSTWAWEMEKKGYLE MSVECKLALLKYL\CECQFDDNLKFKN I INEEDADTMRLQPIGRDKD GLMYWYQLDQDHNVRMYIEEQDDQDGSSWKCI VRNRNELAETLALLK AQIDPVLLKNSSQDSSRESPSLEDEETKKEETPKQEEQKESEKM KSEEQPMDLENRS
432	A	1	568	ASGPELPGRFRDRAPWLPARLLRGDLSVWVSLTALGPGSFRRRVP SLAQLGHSEAAPSPDDVRWSRPDRCPEDRDRAWPPPPPSLPPSFR RNMANNSPALTGNSQPQHAAAAAAQQQQQCGGGGATKPAVSGKQGN VLPLWGNKTMNLNPMILTNISSPYFKVQLYELKTYHEVVDEIYFK D
433	A	1	572	ANNSPALTGNSQPQHAAAAAAQQQQQCGGGGATKPAVSGKQGNVLP LWGNKTMNLNPMILTNISSPYFKVQLYELKTYHEVVDEIYFKVTH VEPWEKGSRKTAGQTGMCGVVRGVGTGGIVSTAFCLLYKLFTLKLTR KQVMGLITHDTPYIRALGFMYIRYTOPP\KDLWDWFESFLDDEEVC QQG
434	A	6	223	TVTNFGEISGTIAIEMDEGTYIHALDNGLFTLGAPHK/ERIALKSGY GKYLGINSDLVGHSDAIGPREQWEH
435	A	3	687	RTQSGNVYFASTSVPPRPGAAPGHILVLSRLQPLRAEVSRSRLLRVE YSYVKTTLVFKGTAKSKKKKSKDKK*QREDEETQLDIVGIWWTV TNFGEISGTIAIEMDKGTIHALDNGLFTLGAPHKEVDEGPSPEQF TA\VKLSDSRIALKSGYKYLGINSDGLVVGRSDAIGPREQWEPVFK \MGKMALSTSNCSFIRI\HEAEDIEAKSKTAGEEEMKIRS
436	A	115	663	AGFSLSAQKSPGAMA*YSYVKS KLVLKGT\SKKKKSKEKKRKREED EETQFD/IVGIW*TVTNFDEISGTIAIEMDEGTYIHALDNGLFTLGA PHK/ERIALKSGYKYLGINSDLVV/GRSDAIGPREQWEPVFQNGA CAAVFTVIGSEKQSECSLLRESRAKYHGCTHGQISSSLKQHPRWY
437	A	1	381	GPPASVRTDSGHPRRRAEGAVSTRTQADPLAPCGPPRPAQGQAYAR LLLQCLLAAARPSSA\DGSA PDSPTSPPLREEIMSNFSLSHNI SLTEHSSMPVENNITLERPSNVNLTQFTTSGD
438	A	3	217	RVMSHRKV\SAPRRGSLGFLPRKRSSRHGRKVNSLPKEDLVHPLHLT CYLEDSPAFADIVRNVYKTGGSAMN
439	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
440	A	37	527	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSASAIMGNPKVKAHGKKVLTSLGDAIK\HLG*SQGAPF AQA*SELHC\DKPAMWDPENFKAPGEMLLVTRFGQSHFRAKNFTPEG CKASWAERWVT\GV\ASALVPSRYH
441	A	68	398	GPASNALGFVVLLETRMVSASVDPPTSTTGSTMCECISIHVGQAGV QMGNAWELCYLEHDIQPSGTMPSHKALWSSDNSFNTPFFRETQGRH V\PGLSVDLEPAVIAQ
442	A	3	400	CFRDMAFNFGAPSGTSGTAAATAAPAGGFGGFTTSTTAGSAFSA PTNTGT TALGGLFSQPTQAPTQSNQLINTASALSAPTLLGDERDAIL AKWNQLQAFWGTGKGYFNNNIPPAEFTQENPFRCFKAV

443	A	1	255	MAFNFGAPSGTSGTAAATAAPAGFGGLETANSTASGFNFGGFGLTAN PAVNFNIGNFGVSTTSATPFNFGNSLASAEKQVLYEQQ
444	A	2	733	YLVSCFRDMAFNFGAPSGTSGTAAATAAPG/GFGGFGTTSTTAGSAF SFSAPTNTGTTGLFGGTQNKGFSGTGTGTTTGTSTGLGTGLTGLG FGGFNTQQQQQT\AVGYSCMPSNKDEGLVVLVFNKKETEIRSQQQQ LVESLHKVLGGNQTLTVNVEGKTLP\DDQTEVVIYVVERS PNGTSR RVPATTLYAHFEQANIKTQLQQLGVTL SMTRTELSPAQIKQLLQNP AGMFLESQSS
445	A	2	683	AREGSALRVAGVTYLVSCFRDMAFNFGAPSGTCGTAAATAAPA/GNT FLLFGGGFGGFGTTSTTAGSAF SFSAPTNTGTTGLFGGTQNKGFSG TGFGTTTGTSTGLGTGLTGLGFGGNTQQQQQTTL\GGLFSQPTQ APTQSNQLINTASALSAPTLLGDERDA ILAKWNQLQ\AFWGTGKGYF NNNIPPVEFTQENPF CRFKAVGYSCMPSNKDEGLVVLVFK
446	A	1	461	HRRPLYPAGIARMTRGDRTRTGCTRPKGSRTGGAVGAAMQEIIGSVD HIKFDLEIAVEQQLGAQPLPFP GMD/KTPDSQAPISTVWGLLLPSLG LRSSLPRIFGPLRLFKESGA AVCEFFLKAACGKGMCPFRHISGEKT VVCKHCLRGLCMN
447	A	1	811	DGTMEDSEAVQMATALIEQRLAQEEENEKLRGDARQKLPMDLLVLED EKHHGAQSAALQKVKGQERVKRTSLDLRREI IDVGGIQNLIEL\RKK RK\QKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKF LADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD CTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHGAVRTGQVE IGEHLFLSLGLENNARNREGDTALH\ DAGRVNRYPILO
448	A	100	1534	EARNWVGAMGKARRSPPGHHRHCEGCFNRHCHI PVEPNTSCLVISCH LLCGATFHMCKEAHQLLCPLQVPCLNSEYGCPLSMYRHKLAKHLQ ACPASVCCSMENRWPVNDSETTLHENIMKETPSEECCLDTALALQD QKVLFRSLKMVELFPETREATEEEPTMNGETSVEEMGGAVGGVDIGL VPHGLSATNGEMAELSQEEREVLAKTKEGMDLVKFGQWENIFSKEHA ASALTNSSASCESKNKNDSEKEQISSGHNMEVEGAPKKKEPQENQK QQDVRTAMETTGLAPWQDGVLERLKTAVDAKDYNNMYLVHNGRM\LIH FGQMPACTPKERDFVYG\KLEAQEVKT VYTFKVPVSYCGKRARLGDA MLSCPKSEHKA VDTSDLGITVEDLPKSDLIKTTLQCALERELKGHVI SESRSIDGLFMDFATQTYNFEPEQISSGTELADLTAATPGGLHVELH SECVTKRHN
449	A	124	602	WATTPFQPKSNSKMAELFMECEEELEPWQKKVKEVEDDDDDDEPIFV GEISSSKPAISNILNRVNPSSYSRGLKNGALSRGITAAFKPTSQHYT NPTSNP\VPASPIKF\HPESRSSDSSVIVQPF SKPVSVSKTIRPAQG SIGCCLSISTVPSYNSGLS
450	A	1	369	ICRFNPYVFLAAKADQLQVRTTOLT/CKSCWLYHCINHSTLQTCNIS TL/M/ILGHIPGLWILINLSEPWDATPVWHFVKKLLTKLTHHACRAS GI\IIFAIVSLVTLITSAVMSSVALHSSVQMAQ
451	A	126	374	GRGTSKILMALQRTSLLLLLLLTLLGLGLAYPSYGHVDVLY\HRVVA DNHGLEETLVM\DRCLSVMILLRIISRDDCERLIGLA
452	B	1	1812	MPSPSPLFFVATIHDCELETTETGTPSDLQDVPLEKADATVFTDGS SFLEQGVKAGAAVTTETDVLWAHALPANTSQAQKAEIALTQALRWG KDINVDTSRYAFATVHVHGAICQERRLLTSAEKAIKNKNPPSSKPN RSSSSLGNNLRPDGSMYMRSGVPAVSVNVNITPSESLNLESSCV TKKLSPEKEIYEMESLQWENMGKRINHHLQYNGLDNMECKGNLEGQ EASQEGLYMCVKITCEEKATESHSTSSTFHRIIPTKEKLYKSPNPSQ DTGYSQHHTRTTFSKRQPKNCERFPVEGRPLTLPAQTSXGYSKSPD VITLLEQKKEPCVVARDVTRRQCPAAMPVDSLIARVGMARGNAITL PVCGRDVKFTLEVLRGDSVEKTSRVWSGNERDQELLTEDALDDLIPS FLLTGQQTAFGRRVSGVIEIADGSRRRKAAALTESDYRVLVGELDD EQMAALSRLGNDYRPTSAYERGQRYASRLQNEFAGNISALADADNIS RKNITRCINTAKLPKSVVALF SHPGDYLVPVQAKGNVVI TSYMTNR GFFEDKKATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN*

453	A	305	1089	NHWPMLVTFRDVAIDF\SQKEWECLDTTQRK\LSRDVM\LENNYNNL GLTG/SDILGSKPVVITLLEQGKEPCVVARVDVTGRQCPGLLSRHKTK KLSSEKDIHEISLSKESIIEKSKTLRLKGSIFRNEWQNKSEFEGQQG LKERSISQKKI\SLKKMSADRKRPSTLNQRIHNSKSCDSHLVQHG KIDSDVKHDCKECGSTFNNVYQLTLHQKIHTGEKSCCKCEKCGKVFH SYQLTLHQRFHTGEKPYECQECGKTFTLYP
454	A	1	2088	PTQSTRRIATVSIAAAVAPLTLFLYRGDGLSSRRRADAAGALCGE VAVKPPINPFTEFMEKAVNDGSHSEELFCHLKTISEKEDLPRCTSES HLSCLKQDILNEKTELEATLKEAELVTHSVLELLPLFKDTIEKINFE NANLSALNLKISEQKEILIKELDTFKSVKLALEHLLRKRDKYKQTGDN LSSMLLENLTDNESENTNLKKKVFKEAHIQELSCLPQSEKANTLKA NRFSQSVKVVHERLQIQIHKREAENDKLKEYVKSLETAKIKNLQSR MNKNEAIVMKEASRQKTVALKKASKVYKQRLDHFTGAIEKLTQSIRD QEAKLSETISASNAWKSHYEKIVIEKTELEVQIETMKKQIINLLEDL KKMEDHKGNSCEEILRKVHSIEHENETLNLENTKLKLRFPKRITESK NMNILIVLDMLCYISSEKTTLAALKDEVVSVENELSELQVEVEKKQKT LIEMYKTQVQKLQEAEEIVKSRCEENLLHKNNQITKTKNKNVEKMRGQ MESHKELERVCDSLTAAERRLHECQESLQCKGKQADQEHITRELO GQVDGNHNLTLKLSLEEENCLIQLKCNLOOKLEADENKELEKKL ANQEECLKHSNLKFKEKSAEYTALARQLEAALEEGRQKVAEEIEKMS SRESALQIKILDLETELRRKQNEEQNLVCKMNSDPETP
455	A	140	511	PTQSTRRIATVSIAAAVAPLTLFLYRGDGLSSRRRADAAGG/APFS LCGEVAVKPPINPFTELM\ENAVNDGSHSEELFCHLKTISQKED\LT RCT\SESHLSWYSHQYQKSKFPILGFPVLSII
456	A	1	1014	MLLKLQCAHRSPGETFKINSDSVGLGEASADSSYKLLVDANVAERAA GLCCRLVVPCHKGMPRLTDL SVKTKDVWEIPRESLQLIKRLGNGQFG EVWMEKADGLCFNLTVIASSCTPQTSGLAKDAWEVARRSLCLEKKLG QGCFAEVWLEIPVYPLKKGSKRFAPSPFPVGEVYPYACRELAVGHGP STPHPNDSSQPSRKEGDWEARSLTTGETGYIPSNYVAPVDSIQAE RAENEAQVSAQGRKDPGDGRNKALQLVGGSVARVLTATHGSGAGGMD TTCRRDIEYEEGRKRKRTKKKRELESQMPRGLCCGLSGGPAVQYGHN LTRETMVEK
457	A	577	2195	IMGCVQCKDKEATKLTEERDGSINQSSGYRYGTDPPTQHYPSFGVTS IPNYNNFHAAGGQGLTVFGGVNSSSHTGTLTRGGTGVTLFVALYDY EARTEDDLSFHKGEKFPQILNSSEGDWWEARSLTTGETGYIPSNYVAP VDSIQAEWYFGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSL SIRDWDDMKGDHVKHYKIRKLDNGGYYITTRAQFETLQQLVQHYSER AAGLCCRLVVPCHKGMPRLTDL SVKTKDVWEIPRESLQLIKRLGNGQ FGEVWNGT\WN\GNTKVAIKTLKPGTMSPEFLEEAIIMKKLKHDKL VQLYAVVSE\EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAA QVAAGMAYIERMNYIHRDLRSANILVGNGLICKIADFGRLARLIEDNE YTARQGAKEFPKWTAPERALYGRFTIKSDVWSFGILLTELVTKGRVP YPGMNNREVLEQVERGYRMPCPQDCPISLHELMHICWKKDPEERPTF EYLQSFLEDYFTATEPQYQPGENL
458	A	561	966	GALCAASVPRCVWSSAGVVALFEEHCAPLVWVYTYECCHYMCSALLS LSCPCPAPSERAAGLCCRLVVPCHK\GMPRLTDL SVKTKDVWEIPRE SLQLIKRLGNGQFGEVWGMRLRLNYSLSIFPVWKIPNTKDG
459	A	46	949	ARRPRPWLSSARTPRRPFWRPSPCCSPMLTTSSETLMMKNIDPSGLE TQPF/YEVLQSNIQHVLVYENPALQEKALACIPVQELKRKSQEKLSR ARKLDKGINISDEDLLELLHWFKEEFHVVNNVLCCKGGQTRSR DRSLLPSDELKWKAKEVEDHYCDACQFSNRFPRYNNPEKLLLETRCG PWCE
460	A	3	284	FSFLVFSSPLLVLFLCEQDCFHHCRLHLLSLVGFSELAFCSDQLILSD GTLQRCLRGCASAPRSCWFCWLPGLDRVLSQTALRVHSHPRKAVV
461	A	420	690	AAEGRGPAQGFHSLQRFLPSVNGIKPKCIIIFLAWATLYQPGSREHRR SRPIPEPFLPKAEPPTTAWACFQDLLEPGAIRQDQLIRTES

462	A	557	753	IIIEIGIMEQRKPWKKICYFICCASHAKGSL/CRRMKRAPVYYGRTVP SPDGSIAHGEYHVLELNT
463	C	137	274	MRKQLLLQKRRVYLLRITKKVEMIPQDNENPGNTNCHDVVLVQ*
464	A	1	2155	MKKKKMKEEEEKEKEEEEEEEEEERRKEEDDFCNRTSPAGGSEGPG QESEQPAQPPEQAGGRPGASPAPDEDAEAAGAEQGGDSTEATAKPKR SFYAARDLYKYRHQYPWKLSQFHSSVSHRRKEIDCKAFKWQDLAFFG ELTRGKRSQHNYLRITRILKSLGELGYESFKSPLVKFILHEALVENT IPNIKQSALEYFVYTIRDRRERRKLLRFAQKHYPSENFIWGPPEKE QSEGSKAQKMSPLASSHNSQTSMHKKAKDSKNSSSAVHLNSKTAED KKVAPKEPVEETDRPSPEPSNEAAKPRNTEKDSNAENMNSQPEKTVT TPTEKKESVSPENNEEGNDNQDNENPGNTNCHDVVLPRSPAPAAAS SMGNLLGGVSFREPPTVEDCDSTWQTDSEPEPEEPGPGGGSEGPGQE SEQPAQPPEQAGGRPGASPAPDEDAEAAGAEQGGDSTEATAKPKRSF YAARDLYKYRHQYPQNFQDIRYQNDLSNLRFYKNKIPFKPDGVYIEE VLSKWKGDYKLEHNHTYILWL\LPLTEQGLNFYAKELTTYEIDESS KTKEAIRFPPWAYKNDARIFWNKT/GLIKLGMFARGVYWQESFQHL NESQHNYLRITRILKSLGELGI\ESFKSPLVKFILHEALVGGILFPI LRQSAL\EYFVYTIRRTGRRKGRKA/LCGFAP/WKHYTAFQGNFIWG DPPSEKEQFGGGGQRPREM
465	A	226	487	NWTKIITSMLCWGNASFGQLGLGGIDEIIVLEPRKSDFFINKRVRD VGCGLRHTVFVLDGTVYTTCGCNDLG\QLGHEKSRKKPEF
466	A	674	1026	LWAEGTLVWGSIREWLQHTPPNGIRDWAKQRMWRTGQPQAPTRVNI SRPSPTFPFRFTTKLMWALGTDPTHTHTSHSFAHIHSCTHA/HVQ EHTYTYSLPHTSRPFLKGSKSTPKP
467	A	153	380	PRSWGQDTPSRGERSPNSSGTPGLPPPGGHPFPSQPVRPQLLPPTP DLGPGPGGQAGIQG\PSGSPTQDGANSRL
468	A	140	755	TAMSSEEGKLFVGGNLNFTDEQALD\HHFSSFGPISEVVVVKDRGT SSGPGGFGFITFTNPEACFKLPMKKPMNRRSLEWSVRSRCWIMQAK SASGEPEGGLLGAHWGLGSQLTFFKVVGGPGLIGELSFAMRAMNGE SLDGRQIRVDHAGKSARGTRGGGFGAHGRGRSYSRGGGDQGYGSGRY YDS\RPRGYRYRY\GRSRD
469	A	2	259	GGI\DLAFPH/HENEIAQCEVFHQCEQWGNFYFLHSGHLHAKGKEEK MSKSLKNYITIKPSTTVTAPCSKLSSCSWGWALSWRTHVPT
470	A	198	353	PRPAGFSTFQETAARLPCMWWTSWCGSGRRSGSLRWPCPRPRGTPG GSSS
471	A	103	484	NTAVSTTVAGSCLASESAGAPLPSALSVGLGVPAPWNKGRSCLPGRP STGEDLGADFI PNPTLGLYIG\NVQVPIRFLGSHVSLRPESLLTQLR LNAFVFSVSHLHAKGKEEKMSKSLKNYITIKKK
472	A	98	1339	GLRAAQAWAPRCRPRWALGGLGGTGLRSLASAGGRGRAWLQPTGRE TGVQVYNSLTGRKEPLIVAHAAASWYSCGPTVYDHAHLGHACSYVR FDIIRRLTKVFGCSIVMVMGITDVDDKIIKRANEMNISPASLASLY EEDFKQDMAALKVLPPTVYLRVTENIPHIISFIE\RIIARGNAYSTA KGNVYFDLKSTGDKYGKLVGEVPGVGEPADSKRHASDFALWKA PQEVFWASPWGPGRPGWHI\ECSC\LASNGIWKVNLDIHS GGIDLAF PHHENEIAQCEVFHQCEQWGNFYFLHSGHLHAKGKEEKMSKSLKNYIT IKDFLKTFSPPDVRFFCLRSSYSRSDYSAMQ\SSCSWGLGSF LEDARALHGRGAAGLRLRQGS DAVGEALQH QEGREGGLGR
473	A	414	833	NVLVICQRNSNSFKKLFKVRDDGEQTQQDFSAQ/AS/SQGRPELVH SRGVQPGWHQPPWVCQNPLAKAAFTALLVLES LREEERTVTAEGAP LSPGGPHTSPSPGRDAGGSLGTFSSRSYQRLFLSSRKLCLNINCKL S
474	A	635	901	PHPEPKGPKLRA\PLSPDFPPGSRLAGSPGA\PPPPHPEDRLHQ SSHPHPIPRLLERSLAQGGAAPLGPPRMPHGAAPQGCSPSTPT
475	A	816	1099	HFGEFFFFLRQSL/NSVAQAGV\KWRDPSSLQPLPPGFKRFSCPSLP SSWDYRRVPPHLANFCIF/MSRRGFIMLARLAQPQ/CDPPISASQSA RITGV

476	A	3	232	SSEMAASGRGLCKAVAVSPFPWRRDNTTEARGGLKPEYDAVVIGAGH NGLVAVSTSLDPTSLALGVWLSAAWEGV
477	A	2	732	FVPGAEMAASGRCLCKAVAASFPFPWRRDNTTEARGGLKPEYDAGVIG AGHNGLVAAAYLQRLGVNTAVFERRHVIGGAAVTEEIIPGFKFSRAS YLLSLLRPQIYTDLELKKHGLRLHLRNHYSFTPM\RKRQVAAKVPRC LLLGTDMA\ENQKQIAQFSQKDAQVFPKYEEFMHRLALAIIDPLDAA PVDMAAFQHGSLLQKRRALSTLKPLLKAGRILGAQLPRYEVLTASI TKVLDQWFES
478	A	161	612	GRRPSPQETPRPTSLSGAPPTPRHSRCPPNHTVSSASLSLPSRHRLE LTYRHCNRFISILLEPSGCSKDTFLLLAIKSQPGHVERRAAIRSTWGR VGGWAMGRHLKTD/GSSYGWHA/RTPTQLMAYESREFDDILQWDF EDFFNLTLKEL
479	A	15	405	GGTGAMAPW/AGGEHSRMNPLRAV\WLTLTAAFLTLTLLQLLPPGLL PGCAIFQDLIRYGKTKCGEPSRPVACRAFDVPKRYFSL\YTISFLW NDISAFW/LFLFLLTLPFLSYLRFLFHSHLASCPLFLV
480	C	80	370	MWAPREQLLGWAAEALPAKDSAWPWEKPRYLGPVTFEDGAVLFTFA EWKRLSLEQRNLYQEAMLENLRNLGSLXXXXXXXXXXLALDLNLGF WL*
481	A	1	1083	MIDFQMLNQLCRTIINPSVIPCLKYCGDQIGPVTTFEDVAVLFTAEW KRLSLEQRNLYKEVMLENLRNLVSLESKPEVHTCPSCPLAFGSQQFL SQDELHNHPPIPGFHAGNQLHPGNPCPEDQPQSQHPSDKNHRGAED QRVEGGVRPLFWSTNERGALVGFSSLFQRPPISSWGGNRILEIQLS AQNASSEVDRI SKRAETPGFGAVRFGECALAFNQKSNLFRQKAVTA EKSSDKRQSQVCRECGRGFSRKSQLIHQRTHTGKPYVCGECGRGF IVESVLRNHLSTHSGEKPYVCSHCGRGFSCKPYLIRHQRTHTREKSF MCTVCGRGFREKSELIKHQRIHTGDKPYVCRD
482	A	3	503	TGTPVSTISWCCYLVCLLLACVRAQMWAPREQLLGWTAELPAKDSA WPWEKPIYLGPTTFEDVAVLFTAEWKRLSLEQRNLYKEVMLENLR NLVSLAESKPEVHTWPFCL\LGFGSQQLSQDELHNHPPIPGFHAGN LHPGNPCPEDQPQSQHPSDKNHRGAE
483	A	138	2125	MRGAGSPRQSPRTLRLPDGPAMSFRRKVKGKEQEKTSDFVKS ISVHSPQKSTKNHALLEAAGPSHVAINAISANMDSFSSSRTATLKKQ PSHMEAAHFGDLGRSCLDYQTQETKSSLSKLTLEQVLHDTIVLPYFIQ FMELRRMEHLVKFWLEAESFHSTTWSRIRAHSLNTMKQSSLAEPVSP SKKHETTASFLTDSLDRLEDGSAQLFMTHSEGIDLNNRTNSTQNH LLLSQECDSAHSLRLEMARAGTHQVSMETQESSSTLTVASRNSPASP LKELSGKLMKSI EQDAVNTFTKYISPDAAKPIPITEAMRNDIIARIC GEDGQVDPNCFVLAQSI VFSAMEQEHFSEFLRSHHFCKYQIEVLTSG TVYLADILFCESALFYFSEYMEKEDAVNILQFWLAADNFQSQLAAK GQYDQGEAQNDAMILYDKYFSLQATHPLGFDDVVRLEIESNICREGG PLPNCFTTPLRQAWTTMEKVFLPGFLSSNLYKYLNLDLHISVRGDEF LGGNVSPAPGSGVPPDESHPGSSDSSASQSSVKKASIKILKNFDEA IIVDAASLDPESLYQRTYAGKMTFGRVSDLGQFIRESEPEPDVRKSK GSMFSQAMKKWVQNTDEAQEELAWKIAKMIVSDIMQQAQYDQPLEK STKL
484	A	1	2580	MKTEVGTGLGEDDMFPFRQVELWKMAVKGKEQEKTSDFVKS HSPQKSTKNHALLEAAGPSHVAINAISANMDSFSSSRTATLKKQPSH MEAAHFGDLGRSCLDYQTQETKSSLSKLTLEQVLHDTIVLPYFIQFME LRRMEHLVKFWLEAESFHSTTWSRIRAHSLNTVKQSSLAEPVSPSKK HETTASFLTDSLDRLEDGSAQLFMTHSEGIDLNNRTNSTQNHLL SQECDSAHSLRLEMARAGTHQVSMETQESSSTLTVASRNSPASP LSGKLMKKSQGFRLPILQHTSCSYVNLGHDFFFLGLQLLSESRI GAAVIAAVALMLPGSRRRERNKTKQPRGFPLSLIRIEQDAVNTFT KYISPDAAKPIPITEAMRNDIIAGPAGGYANRHRPPDGLAGSPAPVH EVGGTETSGVGSVRLKAARICGEDGQVDPNCFVLAQSI VFSAMEQ HFSEFLRSHHFCKYQIEVLTSGTVYLADILFCESALFYFSEYMEKED

				AVNILQFWLAADNFQSQLAAKKGQYDQGQEAQN DAMILYDKYFSLQAT HPLGFDDVVRLEIESNICREGGPLPNCFTTPLRQAWTTMEKVTQNFK RIKLQEVLLVELIKYKVGKPSRIAQWKLKQSSKVIKSRGLESGLKTV NCKTASDRSFRFPPEGGIVIKGDDGSMRVTAPEDLPVGQDVESSVKK ASIKILKNFDEAIIVDAASLDPESLYQRTYAGKMTFGRVSDLGQFIR ESEPEPDVRKSKGSMFSQAMKKWVQGNTDEAQEELAWKIAKMIVSDI MQQAQYDQPLEKSTKDSKRLTHCTSAQLASASGSHSHQDCPVGEHT PLTTWRQRFNLNAHD
485	A	1	687	YMEKEDAVNILQFWLAADNFQSQLAAKKGQYDQGQEAQN DAMILYDNA AQVSAPRLRGPARGARQRAAGLGQPQPRARADSHAERPERKLGLPRGA RVSEARPGPCRSPWPLPPAAGCLAKRPRRCRARGAVTVTVRAQSRTR ALRQYFSLQATHPLGFDDVVRLEIESNICREGGPLPNCFTTPLRQAW TTMEKVTQNFKRIKLQEVLLVELIKYKELPNSVFLVMEILA
486	A	444	843	EKSIVSLIFPCVFFLPSTWEKEDAV\NILQFWLAADNFQSQLAAKKG QYDQGQEAQN DAMILYDKYFSLQATHPLGFDRCTTIKKIESNICREGG PLPNCFTTPLRQAWTTMEKVTQNFKRIKLQEVLLVELNKI
487	A	77	199	SKSRPIASNKIEAIKSLPAKKP\GPDGFATEFYQTFKEEL
488	A	29	380	SETPQAPTLPQTQGSLLGEERMEDIRTLTVALFTLICCPGSDEKVF VHVRPKKLAVEPKGSLEVNCSTTCNQPEVGG\ETSL\DKVFAGTEQ AQW\KHLGSSNLSP\DTVL\HCHFH
489	A	27	406	HAHLVTLAPISCPGSQSYPSWSPQGTTLTVALFTLICWPRSEKVF HVRPKKLADPEPKGSLEVNCSTTCHHPEVGGLETSLDKILLDEQAHRK HYLDNMYHDTVLQCHFTCSGKQEAAMNINVS
490	A	191	1074	RLPEMSSFGYRTLTVALFTLI\CCPG\SDEKVFVHGEAKGSWAVEP KGS\EVNCSTTC\NQPSGVGLGDLSD*GFCWDEQVQL\WKHYLG FQTFSH\DTVLQ\CHFTC\SGKQ\SMNSN\VSALYQPPRQ\VILDT CNPLLGGFLGKSFHHLKLQGVPTVEPLGQP*PSFLVSVGNETL\HYE TFGKAAPAPQEAATATFNSTADREDGHRNFSCLAVLDLMSRGGNIFHK HSAPKMLEIYEPVSDSQMVIIIVTVSVLLSLFVTSVLLCFIFGQHLR QRMGTGVRRAWRRLPQAFRP
491	A	3	405	SWSGSAAALRMRPVRLMKVFTVTRRI PAEGANLKVISTMSVGIDHLAL DEIKKRGIRVGYTPDVL/TRYHRRTRSLPATYHLPVAGGHRGSEEW W\WTSWKPLWLCGYGLTQSTVGIIGLGRIGQAIARRLKPF
492	A	2	465	DAAGANLKVISTMSVGIDHLALDEINKRGIRVGYTPDVL/TRYHRR RSLPATYHLPVAGGHRGSEEW\WTSWKPLWLCGYGLTQSTVGIIG LGRIGEAPTGPLARPGSHSVVICPGTTCLKAEKTHMSGHFACSRDI SNEGYSFVKHRQIHK
493	A	217	428	TLVNMEADVTTRCLIRSGIRVGYTPDVL/TRYHRRTRSLPATYHLP PVAGGHRGSEEVSRPGAVAHGC
494	A	80	1058	RCSSPAGYPPCRVALARAADCEVEQWDSDEPIPAKELERGVAAGH LLCLLSDHVDKRIIDAAGANLKVISTMSVGIDHLALDEIKKRGIRV YTPDVLTRYHRRTRSLPCSY\HLA\PLAGGL\QGSEEW\WTSW\KP LWLCGYGLTQSTVGIIGLGRIGPGPLLGLKPFQVQRF\YTGROPR S\EEAA\EFQAEFVSTPE\LAAQSDFIIVACSLTPATEGLCNKDFQ KMKETAVFINISRGDVVNQDDL\YQALASGKI\AAAGLDVTSPEPL\ PTNHPLTLKNCVILPHIGSATHRTRNTMSLLAANNLLAGLRGEMPS SELKL
495	A	3485	4056	DLPSRHRVMEACHVCCVRRGCCV/CAC/ICVCHMCSVWCVRVLCV PQVLCVHALCV\CVCCGQCARYVWCMCCVCSVLCMRCV/CVCVPRV LCV\CVCCGCSRCSVWCVCVCRV/CLCV/CACAVWCVCCMC/LCVL CV/CACACVCCVCRVCSVWCVRV/CVCCACSVWCVLWCVC/VCMQC VCYVWCMCCVCCVLE
496	A	1	858	GATLGGMSEHVEPAAPGPGPNGGGGGPAPARGPRTFNLNPNPLINVR DRLFHALLFFKMAVTYSRLFPPAFRLFEFFVLLKRVLERRPQLTVGV EELRLLVLPMAVRPQVAHCTPGIGAPASRSRVTEGPCAPGSLACDF ESDQFFPESLGFHVAVGAPLAQLGPQFCGSGQQVDVTLTRLGGDAWT

				SGWEALFVLFLVLAYIHIVFSRSPINCLEHVRDKWPREGILRVEVRHN SSRAPVFLQFCDSSGRGSFPGLAVEPGSNLDMEDEEEELTMEMFGN SSIK
497	A	106	544	GATLGGMSEHVEPAA\PGPGPNNGGGGPAP\ARGPRHPQFSTPTPLI NVRDRLFHA\LFFKMAV\TY\SRLFPPAFR\RLFEFFVLLKALFVLF VLAYIHIVFSR\SPIN\CLEHVR\DKWPREGNPALWKVRHNSRAPV FLQ\FCD\SSGR
498	A	309	587	NKNLEISFFETESRCCQPR\ECNGAISVHCNLCPLGSSNSPTS/A SQVAEMTGVCHHAQLIFVFLVAMVFHLH/VGQGGLELLTSGGPPASA SQ
499	A	3	451	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAELERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALS DLHAHKL RVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDFLASVS TVLTSKYR
500	A	2	493	GLEFGTSHRLRENPPMAVAVSCPTKTNVKGPPGGKVGGAHAG\EYG\SE ALERMFLSFPT\TKTYFPHFDL\SHGF\AQVKGATAKKVA\DALTKA VANV\DDMP\NGAVRPEATLHAHKL RVEPVNF\LLKPLACLVDPGP AHLPGRVSPLAVALPWNKVSFAFCGQI
501	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
502	A	38	557	APSPDA\MGHFTEEDKATITSLWGKVNVE\DAAGETLGRLLVVYPWT QRFFD\SFGNLSAFCHPWATPKVKAHGKKVLTSLGDAIKHL\DDL KG\TFAQA*SETALVTKLHVG*RTFKLPGEMLLGDPLGNPIFGKR ISPLEVGRLSWAERWVTWSPVALVLPRLPLKLNC
503	A	318	449	ERKKKKMATVQKGM/PHKYYHGKTGSYNVIQHAVGNAVTRNTRGS
504	A	1	468	DHSSSPAREQNWMEN\EFDELTEVGFRRWVITNSSELKHHVLTQCKE AKNLEKRLGELLTRITSLEKNINDLMELKNTARELHEAYTSINWIN QAEERLSEIEDQLNEIKREDKITEKMNSTTVRVAASMOSKLLQGVA EEGPLRLTRSAFSA
505	A	1	1140	MAKGQGESWLLDQEALAEIEKQQQKYKSLEARAVSPVLDAGWTLPSG SLQSAEESAERELNIDHGAARPSLLHDQADHQAFAPIFLDQQSESP KPSYAEVLRRISEKKAARQGLADKIPTFLGQSTWGKVALKRAADLPV QRSNSDTGQTASSGSLTPVYPDWETPPSRGRPCIYHLTQESSGWHL AGAPFGQSFRKEQAAIFAVMQPLLVIPTQTSGGVDLQQTTPVDLKQR ERNINININKKDVLSSETSSDHRLQRSKVDKSTKMGRNQCKKAENSKN QNAYSPTKDNHFLPAREQNWTESEFDELTEVGFRRWVITNSSELKEH VLTQCKEAKNLEKRLDELLIRITSSEKNINDLMEVKNTAQELREAYT GINS
506	A	1	2640	TLQSKSHYMGQARQASGASVWRAGCGHGQQQVLEPKWDERGSSIEEE HEQEHKQARSGMVNRYHDGPSSTPFSGIYSQGPVNVISGADRHLIQK SSSWHLLGALLGQSFQRKEQAAIFAVLQPLLVIPTQTSGGVDLQQT ADLQKRGLTVRGKTNKQKIVATSARTSTQRPHPKHNSLPAREQN WIENEFDERTEVGFRRWVITNSSKLKEHVLTOCKEANNWLLVEFVQ WDLARDGGWKEKLGFLFYPLWCHSSGSDCVPVQVYLNHTGIP FSAHCQEDRHRAFLKDSDPALIRSRQLQVFVKTLDIRQGSQRLNV CGQCPSQEHSSSESWMALTCPSQRACRGARVTGSKVPGPWEELP LEVAMAPQNIHASGRGCGMTRTGETRPFSPAILVLRPLHTQSTACS RRLFSQKNFWEHTEVRISLDPGGTSSYEELISNFSKVSQYKINQK SQAFLYTNNGQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFEN YKPLLKEIKEKTNKWNIPCSWVGGINIVKMAILPKVIYRFNAIPK LMPFFTELEKTTLKFIVNQKRARIAKSILSQKTKAGGITLPNFKLY YKATVTKTAWYQNRDIDQWNRTEPSEITPHSYNYLIFDKPEEKQ WGKDSL FNKWCWENWRAICRKLKLDPLTPYTKINLRWIKDLNVRPK TIKTLEENLGITIQDIGMKGDFMSKTPKAMATKDKIDKWDLIKLSL

				IKLKSTAKETTIRVNRQPKKWEKIFPTYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRRFSKEDIYAAKHKMKCSPSLAIREMQIKTT VRYHLTPVRMVIKKSGNNRCWGGCGEIGTLLHC
507	A	1	714	MDKFLDNYTLRRLNQEEVKSLSLRPITSSEIEAVINSLPTKKSPEPER FTAFFQKYKEELSTIRLVPHFMFRTSPYAPPILSQRLPAKFSTWAL DSNRPAVSLERGLPVTISLSEAQLMNPIKGLLLLNQSMESLPSPVG YAIQDHNSSPARKQNCMENEFDELTEVGFRRWVITNSSELKEHVLTQ CKEAEFELRLHELLTRITSLEKNINDLMELKNTARELREAYTSINS QTD
508	B	1	546	MKQPNRKRKLNMDSKERLDQDGRVLKMSFFVFCVVSSESEHEETO DLMCESEFWVLLHMSLDQQHQHLEDHNSSPARGQHWMESEDELT EVGFRRWVITNSSELKEHALTQCKEAKNLEKRLDKLLTRIISLEKNI NELMELKSTARELREAYTSINSQIDQVEKGYQRLKINLMK*
509	A	1	732	MVIAEQVVFYISKSEISSWFGAAGRHLPGVADRHLIQESTGWHLA GAPLGWSFORKEQTAFVLPQLLVIPRQTGYGVLDQMPADLQORF LTVRRKTNKQKGIYSTKRTSSEGHQHQRRKVDKFTEMGRNQHKKA ENSKNQASSPSKDHNSSPAREQNWMEFDELTEVGFRRSVITNSS KLKEHVLTQCKEARKLEKRLDELLTRKTNLEKNINDLMELKNTAQEL GEAYTSINS
510	A	2	1601	SITHNSQKVETTKCPMDEWINKRQYIHTMEYYSALKRKESLLHADS ENIMLSERSQTQDKSAIAKIYKKKVNSAKEVLNKEPKRRSEGSRSN PLLQKLKLNHKQKANGTWNTSKSEFPTPLERGLKPGSQMVVLVGSHP HRAQQTKIHWLEILAASTAADVDRPGVLEHLGEGAAVRRSFSRLK RPLTALKRAVDLPAQRSSAKGQTASSGSLIPVYPDWETPPSHKH RRPKVDKSTKMGRNQKKAENSKNKNASFPPKDLNSSPAREQNWME EFDELTEVGFKMWVITNSSELKEHVLTQCKEAKNLEKRLDELLTRIN SLEKNINDLMELKNTAWELREVYTRHHTYSKIDNIIGSKTLLSKCK RTEIKTNSLPDHSASKLELRICKLTKNCTTTQKLNLLNDCWVND MKAIEIKMFFETNENKDTTYHNLWDTFKAACRGKFIALNAQKRKQERS KTDLTLSKLEKQQTNSKASRRQEITKIRTEPKEIETQKTLQKI NESRSWIFEKINKIDH
511	A	1374	2220	QAENSHININKDVHSETPSEGHQKRKPKDHSSSPAREQNWME\EF DELTEVGFRRWVITNSSELKQHVLTQCKEAKNLEKRLGELLTRITSL EKNINDLMELKNTARELHEAYTSINSWINQAEERLSEIEDQLNEIKR EDKITEKMKNSTTVLVSTWGSQLEQNNLPHIISPLFHSHTDLNISFY GGCLLQACSSKLLQGLAEGGPLRLTRSASFPAKLCLTKHFLPTMI LIKSRKTPDTPQPRRLYLLQGVVDQTSRKGPTALNIRQKTFAAAPPH R
512	B	1	765	MLAGQQREFPVGVGSADPALGAAGWPQRPQARDLQLAMPEPPISM GSCAAGASPTAPCSKAPSPIDHPRAAECRRRRARDWQAAPPAAPVR DPLGEASRAPESVKDVCIDIMFDGAGRFAAATLGTISELPAPFEE RKSWKPKRQAPGALV*
513	A	594	1300	LGASEPWQPRSQETPKHSWSPH/PANQSKEVPENPNYALKCTLVGH TEAVSSVKFSPN/CENGLASSADRLIIIWGAYDGKYEKTLYGHNLB ISDVAVSSDSSRLVSASDDKTLKLWDVRSKGCLKTLKGHSNYVFCCN FNPPSNLIISGSFDETVKIWEVKTKGCLKTLSAHSDPVSAVHFNCSG SLIVSGSYDGLCRIWDAASGQCLKTLVDDNPPVSFVKFSPNGKYIL TAT
514	A	188	480	QRGVLLKTANVLVPEDLGREMRIFFSVKTWKTFTCIPTKGTNHLFL FYFFFETASLSEAQAQAQ\LGSLQPPPPGGSSDSPASASPIAGITGA CHH
515	A	355	612	SFSISGSFSASIALVCQLLLAVKGSVFEVGGISYCPLNVFLLD\LQV APEEDERKKRRRRERNKIAAAKCRNKKKEKTECLQKVSAF
516	A	3	853	SQARTAQLSSLAARAHPSARAPAVSPRCSPAGQTNSPPDPVPTLAA PSGAWSKMLQHPGQVSASEVSASAIVPCLSPPGSLVFEDFANLTPF VKEELRFAIQNKHLCHRMSSALESVTVSDRPLGVSTITKA EVAPEEDE

				RKK\RRRERNKIAA\AKCRNKKKEKTECLQLQY*QSHRPPLWHHQGF SEEEGLHFPKPSAALPSPIFLSQLDEPRCV\QESEKLESVNABELKAQ IEELKNEKQHLYMLNL\HRPTCIVRAQNGRTPEDERNLFIQQIKEG TLQS
517	A	226	569	TGMDYLQVGVTSQKTMKL\IPASRHRATQKVVGHDHGVVMCFGMKK GEAAAVFKTLPGPKIARLELGGVINTPQEKIFIAAASEIRGFTKK\G KQFLSPFETNLTESIKAMYVKC
518	C	512	739	MAEHHWAFPIPSXASXGFXLQPTKATLKXKEGFKXFXKKKKKKKTP EGGAXGTXIXXPXGGAGXNKPXGXXXG*
519	A	1	760	WQQQKDRERERREEKKREGRETRGDTRGETRGETGEGEREERTKRERG ERDTRERDERERERERERETRHERREEREREREREREREREREREREE RERQRETERETEREKKRERERERERERERERERERERERERERDRERERER ERERERERKREREQRERERERDRERERKREREREREREKEREREREREKER GREREREREERERERGRKRERGDRTEREKERGRERERESTQAMFPQPK TRALAIFFPANVRQINGD
520	A	669	823	MSRGWAASCRIRHEERERERERERERERERERERERERERERAEQCLLLGALRP RASP
521	A	3	108	VCREREHQKVFNMKPK*SYRTVPVTPEGIVLSL
522	A	383	542	LWSP PNSNILDTTAGETPEQDLNREREREKE/RERERERERERERE RERERERERES
523	A	389	549	ERKRPSRKQ/RERNRKNQNERKSRGDWQRANVGAGQKEEMKCLAVEL EIGSQPRS
524	A	1	495	EELVPIFLTFLHFKIEKEGTL PNSFYEASITLIPKPGKDITKKENYRW ISLMNIDAKILNKILANQIQQITKKI IHHDQVGFIPGMQGWFMHKS INVIIHVNRKKNKMHMII SIDA EKAFDKIQHPFMIKTLSK/MGIQGT YLSVIKAIYDKPTANIKOTFQIQD
525	A	219	471	INFKKNRFLFNKQY\WTCVATLEKNKMNSFLMIYPKSNSK*FKNPNV RGKKL*NLFIILYFKF
526	A	1	1423	MNPQEEISDLPERIQETEKEGTL PNSFYEASITLIPKLGKDKTKKE NYRPI SMNIEANILNKILANQIQHIKKI IHHDQVGFISOMQGWFN IHR SINVIHHINRIKKNHMI ISIDA EKAFDKIQHHFMIKTLSKIGI QGAYLNVIKAIYDKPTANI ILNGKKVE\AFPLRTGTRQGYPLSQLFF NIALEVLARAIQENEIKGIHIGKEKVLSL FAGDMIFYLENPKDSS KKLLELIKELSKVSRWELNNENTWTQGEHHTPGPVVGSGEERGIAL GDTPNVNDKPLTGAALASTLGVWENENKFTHLFNIHSQFCLPSQGI FLCGTSTYVCLTTNWTSTCTLI FLSPKIDIAPGNQTL PVPVRAQVHQ HRAVQII PLLIGLGV TNATGTGIAGLSPSLSYHTLSKDLSDSLQDI AKSTLTLSQIDSLAAVTLQNHRLRPPNRRKRWAMHLFRGRLFFHQ PVWD
527	A	31	332	QRRSGCVLRMTWETAAPAVAETPD IKLFGKWSTDDVQINDISLQAI WLLCTGAREAAFRNIKTIAECLADELINA AKGSSNSYAIKKDELER VAKSNR
528	A	27	178	QRRSCCVLRMTWETAAPAVAETPD IKLFGKWSTDDVQINDISLQVR GTW
529	B	110	719	XGRQQHQRWHTPD IKLFGKWSTDDVQINDISLQDYIAVKEYAKYL PHSAGRYAAKFRKAQCPIVERLTNSMMHGRNNGQEAHDCAHQAC LRDHNTCSQAKNLLEVGTAI INSGPREDSTRIGRAGTVRRQAVDVS PLRRVNQAIWLLCTGAREAAFRNIKTIAECLADELINA AKGSSNSYA INKKDELERVAKSNR*
530	A	443	565	QPGFGAGARAPNILTHKHLG/LLEFKTTGAQQQGF*LNESSF
531	A	82	986	TMNTRNRGVNSGLGASPASRPTRDPQDPSPGRQGELSPVEDQREGLEA APKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAELELANLEK WKEQNRAPVHLVPRRLGGSQSETEVRQKQQLQLMQSKYKQKLKREE SVRIKKEAEEAELQMKAIQREKSNKLEEKRLQENLRREAFREHQQ YKTAEFL/RQTEHRIARQKCLSKCCLWPTILNMGQKLGQLQ\DSLKAE ENRKLQMKDEQHQKSELLELKRQQQE QERAKIHQTEHRRVNNAFLD

				RL/RRQKSTRWPRAIWRLLEYE
532	A	122	1342	EAASKTTKDNICSWKDDTIGCKEMPTSENCPSFALHQKIS\DRNHGE CREYGKTLQCDSKPVQHERIHSSEKPNRCKECGKNFSNGHQLTIHQ LHVGEKPYKYECKGAFISGSFVKHGRIHTGEKPLKCKQCGKTI SYQLTVHKSIGHTGKKPYECGECGKAFLVYGKLRHQSTHTGEKPF EECGKAFSTFSYLVQHORIHTSEKPYECKGKAFSTSSPLAKHQRI HTGEKPYECKGKGSFTVYGQLTRHQSIGHTGEKPFESIHA KECGRTFSRASVYLVQHGRHLHTGEKPYECKGKAFSTGSYLVQHORI HTGEKPYECKGKAFISRHLTVHQRVHTGEKPYECKGKAFRVH VHLTQHRKIHTDVKPYECKGKTSRASVYLV
533	A	456	824	DRVSLSPRLECSGVIL\AQCNLHLP/GFNRFSL\TLGLPSRLGITGHA PLCLGQFFVFLVEDGGFHHVG\QAGLELLTSSDPPTSAPVPCRDRYH EPLRLACCSFLKQENIHINCWVRIYIRIFQTN
534	A	1	2278	MDSSIHLSLISRHDDEATRTSTSEGLEEGEVEGETLLLIVESDQAS VDLSHDQSGDSLNSDEGDVSWMEEQLSYFCDKQKWPASQLRQQLS YLKGDNFFRFTCSDCSADGKEQYERLKLWQVVMAMYNLSLEGSG RQGYFRWKEDICAFIEKHWTFLGNRKKSTWSTVAGCLSVGSPMY FRSGAQEFGEPPGWWKLHVNKPPTMKPEGEKLSASTLKIKASKPTLDP IITVEGLRKRASRNVPESAMELKEKRSRTQEAQDIRRAQKEAAGFLD RSTSSSTPVKFI SRGRRPDVILEKGEVIDFSSLSSSSDRTPLTSPSPSP SLDFSAPGTPASHSATPSLLSEADLIPDVMPPQALFHDDDEMEGDGV IDPGMEYVPPPPAGSVASGPVVGVRKKVRGPEQIKQEVESBEEKPDRM DIDSEDTSNTSLQTRAREKRPQLEKDTKPKPRYTPVSIYEKLL LKRLEACPGAVAMTPEARRLKRKLIVRQAKRDRGLPLFDLDQVNA LLLVLDGIYGAKEGGISRLPAGQATYRTTCQDFRILDRYQTSLSRKG FRHQTTKFLYRLVGSSEMAVDQSIVSPYTSRILKPYIRSDPHWTPEP DAPLDYCYVRPNHIPTINSMCQEFFWPGIDLSECLQYPDFSVVVLK KVIIAFGFMVPDVKYNEAYISFLFVHPEWRRAGIATFMIYHLIQT GKDVTLHVSASNPAMLLYQKFGFKTEEYVLDYDYKYPLESTECKHA FFLRRLRR
535	A	750	1053	PSTLSSLI\SRHDDEATRTST\SEGLEEGEVE\GETLLLIVES\EDQA S\VDL\SHD\QSGGISLNSDEGDVSWMEEQLS\YFCDKQKWPASK ELLKSFDLSIPV
536	A	426	634	VFCYSRTNWNKTEINRKKFGKLPSIWKLSSSTLLNNQ/L/VSEENKRE IKKYPDINENEDTTYQNLWNLKQC
537	A	1190	2097	SSCLKILNIITLAKSLLL/CLDISVCYLLDTGICYCLLDISVCYCL LDISVCYCLLDTSVCYCLLDISVCYCLLDNISVCYLLDTGICYCLLD ISVCYCLLDISVCYCLLDISVCYCLLDISVCYLLDISVCYCLLDIS VCCCLLDISVCYCLLDISVCYLLDISVCYCLLDISVCYCLLDISVC YCLLDISVCYCLLDISVCYCLLDISVCNCLLDISFCYLLDISVCYC LLDISVCYCLLDISVCYLLDISVCYCLLDISVCYCLLDISVCYLL DNSVCYCLLDISICCCLLDISH
538	A	163	374	IRQRKAKLVVLA FNRRGLRKP/IFYAGVGKIVKKKYS GFFIELVT TCGKNYLMCALAVIDPRDSNIIRS
539	A	995	1194	IILGNLTACSFYTTSSLNAVWLIKSA MLQLYFIF\FFGDRPSLCHPGW SAVVQSLLTATSTSWAQAE
540	A	77	199	SKSRPIASNKIEAIIKSLPAKKP/GPDGFATEFYQTFKEEL
541	A	212	322	DAFFRTPRVPSVTVPVQCVFGARFKNAPPPFSTPQF
542	A	1	518	MAVARLA AVAAWVPCRSWGWA AVFGPHRGLSVLLARIPQRA PRWLP DLPNLAYKKLKGKSPGIIIFIPGYLSYMNGTKALAEFFCKSLGHACI RFDYSGVGSSDGNSEESTLGKWRK\NVLSIIDDLVDGPQILVGSSLG GWLMLHAAIARPEKVVALIGVATRCRYLSDKV
543	A	3	606	VMSWAFTFIHSLTDS PRATSSPPSPIHEGDQDIIVLKFLKVLGGKN SGAWGRNGRPQGRRRGAR\FLRLNVGGCIYTARRESLCRFKDSMLAS MFSGRFPLKTDESGACVIDRDGRLFKYLLDYHGEVQIPTDEQTRIA LQEEADYFGIPYPYSLSDHLANEMETY/CFKALTD FCDSYGLVCNKP

				TVWVLHYLNTSGAS
544	A	3	533	AEGDQDIIVLKFLKVLGGKNSGAWGRNGRPQGRRRGAR\FLRLNVGG CIYTARRESLCRFKDYNVASMFSGRFPLQTDSEACVIDRDGRLFKY LLHYPSWRSSEFPQMRDTRGRPTGKRADYFGIPYPYSLSDHLANEME TYSLSRNIELKKALTDFCDSYGLVCNKPTVWVLHYP
545	A	1492	1672	KQWHESHDPDYDRSPSQTGEGDEPCSWHRLFAQGDK*YEATACHRNLD WQKATDISCNTNG
546	A	138	257	IFLLYLKKNKVQNK*EIKQHFLGKIMSRDNNYLTWGTEN
547	A	5	960	PTFSRAVATMFSRAGVAGLSAWTLQPQWQVRNMTATLKDITRRLKSI KNIQKITKSMKMVAACKYARAERELKPARIYGLGSLALYEKADIKGP EDKKHLLIGVSSDRGLCGAIHSSIAKQMKSEVATLTAAGKEVMLVG IGDKIRGILYRTHSDQFLVAFKEVGRKPPTFGDASVIALELLNSGYE FDEGSIIFNKFRSVISYKTEEKPIFSLNT\VASC*QHGVSYDDIDA DVAAKITQEY\NLANIIY\YSLKESTTSEQSA\RMTAMDNASKNASE MIDK\LTLTFRNRTRQAVITKELIEIISGAASSVKKENSAS
548	A	1326	1780	YLSKLPYFELESIAAARSRPTAQRHPRERKLKPARIYGLGSLALYEK ADIKGPEDKKHLLIGVSSDRGLCGAIHSSIAKQMKSEVATLTAAGK EVMVLGIGDKIRGILYRTHSDQFLVAFKEVGRKPPTFGDAS\VIALE LLNSGYEFDEG
549	A	20	403	KVQGPASAHASGEGSLTIIPVTRSPATMNHIVQTFSPVNSGQPPN YEMLKKEEQEGAMLGAPHNPAPPMSTVIHIRSETSPDHVWVSLFNTL FMNTGCLGLITFVYSVKA\RDRKMGRRTRPGAQ
550	A	2	431	DAWAMNHTVQTFSPVNSGQPPNYEM\LKEEHRVGCAGAAPTTLFPP TSTLIHNRQDLPCPTHVWVSLFNT\LFMNP\CCLGFQ*EFAYSV\K SMDRKMVGDTVGA\QAYASTAKCLNIW\ALILG\ILMTILLIVIPVL IFQAYG
551	A	137	838	SSGICSAIWPWPALHLTNARKRKLRLKRNRYWRKGEGLRTIPVTRS PLVTMNHIVQTFSPVNSG\QA\PNYEMLKKEEQEAMLGAPQKPCPE CPPVIH\IRSETSV\PDHV\VWVSLFNTL\FMNTC\CRLGFIAFA\YS SEVSGTRKMVGEVTRAQGLLPPPPKCLNIWA\LILG\IFMNQFLLIN HPPPSVGSSRPSDRSGRHHLRPRELCPVEPVSVQVNSIFHSLALPPE ARKFCP
552	A	1	528	MTDNLSDTLKKLKITAVDKTEDSLEGCLDCLLQALAQNILFTSDFL ISEFKMGRKAAETTSNINNALGPGTANEHTVQWWLKKFKGDESDE EDCDVQQEVDFIWQLKSGFYTTGDDQFSDWTKKLQSTSQSQTCTKKR SWSLSGGLLLIHYSFLNPGETIKSEKYAQQIDEMH
553	A	1	1682	MDNLSDTLKKLKITAVDKTEDSLEGCLDCLLQALAQNNNTETSEKIQA SGILQLFASLLTPQSSCKAKVANIIEAEVAKNEFMRIPCVDAGLISPL VQLLNSKDQEVLLQTGRALGNICYDSHSLQAQLINMGVIPTLVKLLG IHCQNAALTEMCLVAFGNLAELESSKEQFASTNIAEELVKLFKKQIE HDKREMIFEVLAFLAENDAIKLQLVEAGLVECLLEIVQKQVDS\EKE GGITELKTGSDLMVLLGDESMQKLFEGGKGSVFQRVLSWIPSNNH QLQLAGALAIANFARNDANCI\HMDVNGIVEKLMDDLGRHVEDGNVT VQHAALSALRNLAIPVINKAKMLSAGVTEAVLKFLKSEMPVPQFKLL GTLRMLIDAQAEAAEPIGERMLKL\ERLVGWCEAKDHAGVMG\EQN RLLSALIRHSSKSDVIKTIVQSGGIKHLVTMATSEHVIMQNEALVAL ALIAAELGTAEKDLES AKLVQILHRLADERSAPEIKYNSMVLICA LMGSECLHKEVQDLAFLDVVSKLRSHENKSVRQASLTEORLTVES
554	A	3	911	GRPPRVPPWLRERRRLEGGHRAAPPAPYDLRLAPPVPHPRGATWQII LSDTLKKLKITAVDKTEDS\LEGCLD\CLLQA\LAQNNTANKCKKSK QVAILQLFASLLTPQSSCKAKVANIIEAEVAK\NEFMRI\PCVDAGLI SPLVQLLNSKDQKVLQTGRALGNICYDSHEGRSAVDQ\EGGAQIVI DHLRSLCSITDPA\NEKLLTVFCGMLMNSNENDSLQAQLINMGVIP TLVKLLGM\HCQNAALTEMCLVAFGNLAEIDAIKLQLVEAGLVECLL EIVQKQVDSKEDDITELKTGSDLMV
555	A	1062	1421	DRVSLCC/PRLECSGMISAHCNLPSPGFKQFSCLSLPNGWAYRSVPP

				CPANFCVF/SVETGFHHVQGAGLELLTSGDLPALASEKCWDYRREHT ARGPVTKPSYFQVLFRLHPFINHLNT
556	A	213	513	GGKSLARRVPKGRMDGLLNPRESSKFIAENSRDVFDISGGARRVAEL LLAKAAGPELVEGWKALHELNPRAADEAAVNWVFTDTLNF\SFWS EQDEHKW
557	A	584	829	FLFYLFIFPETGSHSV\TRLECGDTIMARCSLNFPGSSDPPASASWV AGTAGVLYHTWLSFAFFRRDGVSRVARAGLQLLAW
558	A	442	626	VEEGGSEAGWALRIKCINGVSPKL/VLQLLHFPQIFNGSFVKLNKAS VNTLRIVEPYITWST
559	A	3	398	GGIRRKLLTFLLVAGCWTPEASPIIMATSATSPHAPGFPAEGRCGYY VEKKKRCFRMVVAAGKRFCGEHAGAMEVWYRPTLSRVGNKYPGPVGA GTRPLPSLTAFCLCPLDSPAFTLINPVLPSLRSDYEF
560	A	1	960	IMATSATSPHAPGFPAEGRCGYYVEKKKRCFRMVVAAGKRFCGEHAG AMEEEDARKRILCPLDPKHTVYEDQLAKHLKKCNSREKPKPDFYIQD INAGLRGETEIQEL/CLNSTLTDHIMSHPALHDALSDPINDSATK HLKQQASI\LGNIENLKLGP RR CFVEFGAGKGLSHWVDIALKDAE KVHFILVEKVTRFKVDGKHKRKNVFERLQIDIOHLCLNKIPVLRE EKLPPVVGIGKHLGCMATDLALRCLVETYAASFEERNEEPLAKRIKND KTEKBIYTLAKEGNEKNVPEKWNPVAGIVIALCHHRCDW
561	A	111	350	SLDSDSGCKAYVVGDEY\LPGP\LDLHAQPSLLKEHEEEKMFTLKGNR LPAADVKNIIFFVRPRLELMDIIAENVLSEDRRG
562	A	223	748	CIGKVYVWLGVGWLQKSWGTPLFSPHPPGRPRSFAGKHSPPGIGL VGLGGENRILVIFNLIYCTYLGQGLGEVEGEGSPLSAPPTPFLRR FVCV\GPHPLPIPHCCLDVVLFYRSPFPSPFPSPFPPLPLPFVS CSFLGCTTQLVYTVYTQPAKRKPNGKHFKKKKK
563	C	238	267	MQINSQMER*
564	A	549	848	LFFPHSQSTKVFSTYEQIMCVCVFLFFCFFVFPETGSHSV\TRLGCS GVIMAHCSFNLPGPSDPSTASQVAGTTGVCHHAQLIFKFFVEPGQH TEIPSL
565	A	178	375	ANFIAGVWSQSRFHALALHIIQQGSKKVP*ANFIAGVWSQSRFHALA LHIIQQGSKKVPVIVSKLENDTAARHELFAEWRKQCSEKKAQAKGWR QW
566	A	656	874	VTHLSKKKFTHQPDACKGNGWNNPTGSSTVKKMRRSLSTSSPIRSAH IVNSSGSRRRARGILAKCILMSLVIW
567	A	718	971	VPTNTPPAPEEEATGGRQVTAPCSYPEMTSAQPGTYWMCQETPPGP HPPGRNPASQKEAPRCTSAWESCPPSGRPARQALYRA
568	A	480	683	PHHYAVLLFYRLGLSRIAVSLALAICDWLNALYQRLHFARRSGSTLC NNCLRCIADRHLHYVGNITV
569	A	811	1481	GNGILLMVHHHCDAGTVIMRADRFIPGEDQKNRVLVNTVLVRISRAV DGKHLASAGIRHTVFRICHNACTQHRGLFRGFNVFGEFLRFAYILIV KENADQCAGFVGIIELGEIDRVMQALPDVEQAVTHACVINQAAATGG DARQLVGYLVSQSGFNINGNRHLTTINPVGFPADK*GFPLMLPRVS GRNQHRIS/RVYLPCTATTLLRPGNGPPPSSVRPRR
570	A	961	1627	LPHPAVAVIQNVRSRGRFHGSPTLVVIPGNPRHSRTITLIKLLHGI VIIIGRVKQFQHPGCGQAKFIFFTLRQNKPNVVSSTGRPKGVMVGQT AIVNRLWLMQNHYP LTGEDVVAQKTPCSFDVSVWFFWPFIAQAKLV MAEPEAHRDPLAMQQFFAEYGVTTTHFVPSMLAAAFVASLTPQTARQS CATLKQVF\ADLCREWQQLTGAPLHNGLCVFLMR
571	A	803	1403	FNRRILKINGLTREQTSGVQQQIRQALSALPLPVNRLEEFDNCREAW RKCQAWLKDIESARLQHNQAYTEAMLTEYADFFRQVESSPLNPAQAR AVVNGEHSLLVLGAGSGKTSVLVARAGWLLARGEASPEQILL\GL VAKPLKRWTSGFANGYIPKTLPHARFMR/*ALHIIQQGSKKVPVIVSK LENDTACRHELFA
572	A	3	1642	SAKEPWI LATNLPVEIRTPKQLVNIYSKRMQIEETFRDLKSPAYGLG LRHSRTSSSERFDIMLLIALMLQLTCWLAGVHAQKQGWDXHFQANTV

				RNRNLP LLAFHLGPFRSLADIPRNRVYEDFDPHCRPMIITSLSNLP WHSINSCQQPLGVAITCTCSLNVHDSHLRYAASCTCVLPMSGAQPL STRAVAQLYSPDADAKRAAVPARSTDKPENHAHPHSHFTHQYYKTQY HHLKKTFFPWWLGDVKLTIPLTGLMVAAALTDLDRLAGRLRNLIITL FCFFIASASVELLPWPWLFAIGLTLSTSGFILLGALVQRYATIAFG ALLIAIYTMLGTSLEYHWYQQPMYLLAGAVWYNVLTIGHLLFPVRP LQDNLCARCYEQLARYLELKSRMFDPIEDQSQAPLYDLALANGLMA TLNQTKLSLLTRLRGDRGQRGTRRTLHYFFVAQDIHERASSSHIQYQ TLREHFRHSDVLFRRQRLMSMQGQACQQLSRCILLRQPYQHDSAFLS ALLRILMLRWSGCAITAHPPIYSKHWDNA
573	A	114	5270	SARSASFRPGRPAARRPKCSHPLVPDGVPECCCKCVHPASTNFPRTS TAARHSHNDGSTSTMGRWQI/VGYLVSQSGLPLDTSALQAQLRET LPPHMVPEVLLQLPQLPLNANGKLDKALPLPELKAQAPGRAPKAGS ETIIAAAFSSLGCDVQDADADFFALGGHSLAMKLAQLSRQVARQ VTPGQVMVASTVAKLATIIDAEEDSTRRMGFETILPLREGNGPTLFC FHPASGFAWQFSVLSRYLDPQWSIIGIQSPRPNGPMQTAANLDEVCE AHLATLLEQQPHGPYYLLGYSLGGTLAQGIAARLRARGEQVAFGLLL DTWPPETQNWQEKANGLDPEVLAEINREREAFLLAAQQGSTSTELFT TIEGNYADLSSARSWASTSFPLNHDFGTLAGVCIGLSHNRASDAETV VLENWRQVHEQCLALHSQQOTLQQQDVLAQSLQKAQAQFDTALQAS VFDDQQAFLAALMDEQTLTQLEQLKQNLNQRRAQTLLVQTAECLA QHQQHRPDDGLALTVTVEQIQEELAQTHQKLRENTTSQGEIRQQLKQ DADNRQQQQLTMQQAQMTQQVEDWGYLNSLIGSKEGDKFRKFAQGL TLDNLVHLANQQLTRLHGRYLLQRKASEALEVEVVDTWQADANENQT HAQHEQAPTGTGTHGTTMTHNTEHTERLSPGSGHRRYRHRSTDRNRQ CTGTGNDTHFTRFVNTRLDTDFAFTRSDNAWAVRADHTNACFIQLH FHGQHIQRRDAFSDGDNQFDACVDGFGQNGVFAERCWYSNRSGSASGS NGFTHGVEHRQAEAAVSQFLRAEFGVVTFTQYHTRYVNTHFCYRADD TVSDQVATNDTAEDVNQNGFHFVVREDDFERFGYTFFGCAANVKEV SRFAAVQFNDVHRTHRQTCVNHNTDVTVQRNFPLCSLCFTRI FLRL VTHFAQIRLAEQCVAVSAQFAVEANQIALFGDDQKRKIRKRFMDKVR SFFRHHFFDFHAAFGGKNKDHTTGTTVNNGTEIQLLSDIGRCFNQNLV NRLAIGICLIRYQTLAQPVFCKSTDVFFAVYNFHTASGLFQSSSAND VRYTLTATEMVIAPAGFMDEAISENVLAGNIMSRRALYSYGLLLPHN AQGNVGNGLGVTLATGDPSSIAPTCTIVRTGEMIIDGLEFDFLMT GSEAPAEMHFYIPALKALCTAENATHLHNFYTLRGAKTRDTSKWTE YLNELTDMWGNDAEVLFPHTWVPVWGNKHINDYIGKYRDTIKYIHDQ TLHLANQVYTMNEIGDMIKLPPALANNWASRGYGSVSHNARAVYNF YLGYYDVYPANLHPYQGVEMGKRYVQALGGSARVINLAQEANKQGDY RWSAELLKQVIAANPGDQVAKNLQANNFEQLGYQAESATWRGFYLTG AKELREGVHKFSGHTTGSPTIRGMSVEMLFDFMDRQACHQYNRTRV VDQLIEFLQDQHVNAHLAEIVRHHQPNRAGTSDRHLERYEMSINMQN NEQTEYKTVRGLTRGLMLNMLNKLDGGASVGLLAELSGLHRTTVRR LLETQEEGYVRRSPSDDSFRLTIKVRQLSEGFDEQWI SALAAPLL GDLLREVVPWPTDVSTLDVDMVRETHRFSLRSFHRAMVGRRLPLL KTASGLTWLAFCEQDRKELIEMLASRPGDDYQLAREPLKLEAILAR ARKEGYGQNYRGWDPGGEDRLYRRTAAQ
574	A	1	2967	MKQEVILVLDGATNVRAIAVNRQKIVARASTPNASDIAMENNNQA VFPQGLQIPRRQTMTEIQRLLTETIESLNTREKRDKNKPRFSISFIRK HPGLFIDNKMNTSIPKIDNLPGEYAQLAQLNATQVEIPETTL SALV AEQAAKTPDAPALADARYLFSYREMRQVVALANLLRERGKPGDSV AVALPRSVFLTLALHAIVEAGAAWLPLDTGYPDRLKMMLEDARPSL LITDDQLPRFSDVPNLTSYCYNAPLTPQGSAPLQLSQPHHTAYIIF TSGSTGRPKGMVVGQTAIVNRLWQMNHYP LTGEDVVAQKTPCSFDV SVWEFFCPIAGAKLVMAEPEAHRDPLAMQOFFAEYGVTTTHFVPSM LAASFVASLTPQTARQSCATLKQVFCSGEALPADLCREWQQLTGAPLH

9902

				NLYGPTEAAVDVSWYPAFGEELAQVRGSSVPIGYPVWNTGLRILDAM MHPVPPGVAGDLYLTGIQLAQGYLGRPDLTASRFIADPFAPGERMYR TGDVARWLDNGAVEYLGRSDDQLKIRGQRIELGEIDRVMQALPDVEQ AVTHACVINQAAATGGDARQLVGYLVSQSGLPLDTSALQAQLRETL PHMVPVLLQLPQLPLSANGKLDRLKALPLPELKAQAPGRAPKAGSET IIAAAFSSLLGCDVQDADADFFALGGHSLAMKLAQLSRQVARQVT PGQVMVASTVAQLATIIDAEEEDSTRMGFETILPLREGNGPTLFCFH PASGFAWQFSVLSRYLDPQWSIIGIQSPRPNGPMQTAANLDEVCEAH LATLLEQQPHGPYYLLGYSLGGTWRRVAFGLLDTWPPETQNWQEKE ANGLDPEVLAEINREREAFLLAAQQGSTSTELFTTIESECNVYSDLDL YLGVQRINWTEMFNPGATFAVTFSGLNDTIRNSQYGAMKVDAIVDA FTRKNLPRPNVDRDAPDIRVNVWLHKETASIALDLSGDLHLRGIAI VL
575	A	1882	3404	LDASFWIPPKATQGMTWIFTFPPSSPSYNSS/CYAGWLKGSAPLQLSQ PHHTAYIIFTSGSTGRPKGMVGQTAIVNRLWMQNHYP LTGEDVVA QKTPCSFDVVSQFFAEYGVTTTHFVPSMLAAAFVASLTPQTARQSCATL KQVFCSGEALPADLCRVWQQLTGAPLHNLGYPTAAVDVSWYPAFGE ELAQVRG\SSVPIGYPGYLGRPDLT\ASRFIADPFA\PGERMYRTGD VARWLDNGAVEYLGRSDDQLKIRGQRIELGEIDRVMQALPDVEQAVT HACVINQAAATGGDARQLVGYLVSQSGLPLDTSALQAQLRETLPPHM VPVLLQLPQLPLSAKAGCPAAQVPRVAQVRVCAVLEDLGDIRESEG ERKQEADAVLGTQDTPRVTSQPNGLLLKIEPQENVKIEGQHQLGVWL CVAASPVLRVTREREKKEEKNMRFTSLVLSVLVNI VRALEKKV LDIMFNCRGTGVQAITLSHRRALAIALARYIKSALYDG
576	A	22	413	QVSAPHGAGASGVPPAGESVAPSGTSDGRGRWSGVVEWVEEIKSLLL FGGQFASSQETYGKSPFWILSIPSEDIARNLMKRTVCAKSI FELWGH GQSPEELYSSLKNYPVEKMVPFLHSDSTYKIKISHF
577	A	1	2148	MAEEQVNRSAGLAPDCEASATAETT VSSVGTCEAAGKSPEPKDYDST CVFCRIAGRQDPGTELLHCEVGGDARPGNEDLICFKDIKPAATHHYL VVPKKHIGNCRTLRKDQVELVENMVTVGKILERNNFTDFTNVRMGF HMPPFCSISHLHLHVLAPVDQLGFLSKLVYRVNSYWFITTNLQGNGE ISKEMVKFQSNFEEQVLKGCRESWKHTPSGTITWKYTVLLSQAAPES HASPLTSYQRWETPNHQFTGEEAPPTAAGVSDSEREKRDSACLAE LPLPALQALSLWRLGFGREKEGPSAGRAGARWAAAMALSCTLNRYLL LMAQEHLEFRLPEIKSLLLLFGGQFASSQETYGKVPFLHSDSTYKIK IHTFNKTLTQEEKIKRIDALEFLPFEGKVNKKPQHVFVSVLEDYGLD PNCIPENPHNIYFGRWIADGQRELIESYSVKRHFIGNTSMDAGLSF IMANHGVKENDIVFDPFVGTGGLLIACAHFGAYVYGTIDYNTVHG LGKATRKQKWRGPDENIRANLRQYGLEKYYLDVLVSDASKPSWRKG TYFDAIITDPPYGIRESSTRRTGSQKEIPKGIKWEKCSGFQQQISNI SLIILFGFLDVICGTLGGNLKVFKDDLFSVFLFKPSYLCFVWEL PIHPAESHLYHSVKAPYSPSFKFVCDLILPACWTRTRVSRGQGVKGC HPDSPLSWFNT
578	A	222	666	SLCFCFLEVSLPACQETYGKSPFWILSIPFEDIARNLMKRTVCAKS\ IFELWGHGQSPEELYSSLKNYPVEKMVPFLHSDSTYKIKIHTFNKTL TQEEKIKRIDALEFLPFEGKVNKKPQHVFVSVLEDYGLDPNCIPENP HNIYFGRW
579	A	1664	1846	WQKLLFLFGTESCSVARVGVQWRHLSSPKPPPP\GSSNS/PASASRV A\TGAHLHARLIFVFL
580	A	3	441	PGSTISWDCAAATTDVSGVRGLSRLPSARRLALALAKAVENYGMPPS RTEDGKIYQRAFGGHS LKFKGGQAHRCCCVADRTGHSI LHTLYGRS LRYDTSCFVEYFALDLLMESGECRGVFALCIQDGS IHRIRAKNTIVA TGLL
581	A	1	693	MDQDSASTKTCPGTHRKS GPRSREQHGALGAANAHDTVRDGERYDRW SGPRRREQHGALGAANAPDTV RDGERRSLRRDWRDCAEATADVSGVR SLSRLLSARRLALALAKAWPTVLQTGTRGVHFTVDGNKRASAKVSDS

				ISAQYPVVD\HEFDAVVVGAGGAG\LRAAFGLSEAFDTACVTKLFP TRSHTVAAQLENYGMPPFSRTEDGKIYQRAFGGQSLKFGKGRQA
582	A	306	458	IYIFLLNCIFLIIIIIYFETESCSVAQAGW\QVQWDLGSLQALPPGF TPFF
583	A	47	359	SLLTPLVSPVPACPCPSKSEVSVQEHPLPCRPLFRVWRNRQSRGCP QGVEHYGAGAWGLLPVWKSCPPAKTCKWGLP/CPPCGRSCLHSG\ GAALCLLCGSSA
584	A	1248	1667	TNTGGWGRPHHAFVQHTLELLSLLCLNCGFLVYPFFLSWTVMYGSVN LVNLLKYGFQGIIVFYCYIKKKKIWLCLPRPR\VPWLPTSDPSL RSPSSMVLNQICRVYSATKRGSVTGSWAYPCVLSRGMSELCKSRA
585	A	334	698	IKPEMEAGISVTGLDRNTRVQVGCRELSTKYISGWASCTSIQPSG REL/VCVVGEC\LPLPVVP\NWIGGGYGTKYWSRRSSQ\EWAVCSMD KTRYPEDSQLQCQDGSTRYKITVSSLPAS
586	A	258	384	NKSSESLNPPVCLAEFVKRLRYCEYLKGYFCDCCHSYAESC
587	A	1637	1834	VFSTRCGTHPPVCLAEFVKRLRYC\EYLKGYFCDCCHSYAESCIPAR ILMMWDFKKYYVSNFSKTA
588	A	1	856	MKRSMTLTIHFSERIILRNRPKESWEDIEDFGETHLDFLKQYGD FENGIPVHDTIARVSCISPAKFHECFINWMRDCHSSNDKDVIAIDG KTLRHSYDKSRRRGAIHVISAFSTMHSLVIGQIKTDKKSNEITAPE LLNMLDIKGIITTDAMVNCIVKVTGVFAINGDQORVAEPDSGALCQV RYPGNHRNDQRYLFRHSDSELLHWMVALDAVKRVKCLWMSLHKVYS CIELPELPQPESAG\HSGSQYA*CNRTRPHGQKPGTSAPGSSGVWRI TSV
589	A	148	333	KDQDMRLRFWLLIWLLLGFIHQPTPVINSLAVYRHRETDFGVGVRD HPGPTWQNPISKIG
590	A	311	577	FFLSEILSVSLTFSLFQLLLQVINTLADHHHRTDFGGSPWLHVII AFPTSYKVITLWIVYLWVSILTFRCGILVIANKNKLYKTI
591	A	279	603	FFLSEILSVSLTFFIISNYYSQVINS LAVYRHRETDFGVGVRDHPG Q/PWQNPISHEKLDNLIIGFLRRYTFNIFCTSCLCVSILTFCR GILVITNKNKLYKTK
592	A	66	1474	TAPPPSPSPSSLLSPCNGVHHVSTQPSCPGRGKMSKLLNPEEMTSR DYYFDSYAHFGIHEEMLKDEVRTLTYRNSMYHNKHVFKDKVVLG\VG SGTGILSMFAAKAGAKKVFGIECSSISDYSEKIIKANHLNIIITIFK GKVEEVELPVEKVDIIISEWMGYCLFYESMLNTVIFARDKWLKPGGL MFPDRAALYVVAIEDRQYKDFKIHWENVYGFDMTCIRDVAMKEPLV DIVDPKQVVITNACLIVWTLIRGGPGCAGSPAVPPWSPGNAGSCTAP TWARAKVRLRYEPEVRLEGHATLVTEGTTKERYQGPWKEPGAWLIG PEKVMKSVLTPNVILDASYCWELAYQKIGEGVWVFIYITGGPDKTQ IAVLVQQEVDIYTVKTEELSFTSAFCLQIRNDYVHALVTYFNIEFT KCHKMGFSTAMEEPCIFI VLSKEKVN NVVVTAQVESVLDEGEAG
593	A	379	475	DLQGVNHLRP\GVQDQPGQHGETLSLLKIQNN/LARRGGGRL/QSQL LRLRLQDNRLNPGGGGCSEPRSRHCTPAWVTEQDPISKQNKQQANF LIWEDFPYIPQGTKLIPTAQKLPRCK
594	A	2	307	QAGV**WDLGSLQPLPRLKQFS/CILNPGNLSKEF*STKETKQNI FGHIQSQTSKFAISLIQIHPINMRSGTKTFMMV*GNKQRSKFPITWF KIFPDMLPS
595	A	374	665	GAQGLSLSPRLECNGAILAHCNLCPLGSSNSPGSAS*VAGTIGMHHH ARLMFVFLVESGFHHVQGAGLELLTSSDPPASASQSAGIRGISRRAG LDF
596	A	1	687	EIKYHSLPRLECRGEISAH*NLCLPGSSDSPATAS*VAGITGMRYHA QLIFLFLVET*FHHVGGQWSRTPDSNDPPASASQAGDYRDD
597	A	3	198	GIPGSSFCGLCGDVPKGPV*RADGSC*DGVAPRLLRPRGFRGGRCGP VLDSLQAGRGAESEGCRG
598	B	188	246	MAWLPGSCARVAFPAAGAAAR*
599	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFDSFGNLS

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				SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
600	A	3	496	HSLFGTSEVINKLRSPDAMGHFTEEDKGTITSLWGK\VNVEDAGGET LGRLLVVYPWTQ\RFFDSFGNLSSASAIMGNPKVKAHG\KKVLTSLG DAIKHLG*SQGAPFAQA*SELH\CDKAALLDPEELSSFLGEMLLGDP FLGNPIFGQKNFTPEGCKAFLGQKDG
601	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
602	A	38	538	APSPDA\MGHFTEEDKATITSLWGKVNVE\DAGGETLGRLLVVYPWT QRFFDSFGNLSSASAI\MGNP\KVKAHGKKVLTSLGDAIKHL\DDLK GTFAQADVNTCDK\LHVD\PENFKLLG\NVLVTVLGNPIFGKEFTP EGCKASWAERWVTWSWPVPCSSRIPLKPLCP
603	C	83	349	MRSEAQSGPHRREVVISHRYGTRPPGFKYQLQHXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXQNHTCVPWHACAYVSFNRVPCSC
604	A	295	448	NQTCVCWHACAYVSSNRVPWSIGSAIRSVCCYPLPFPALCAPCL*IS TALD
605	A	43	208	ARTLIEVIGLSHHNQKAHAMLNAP*SSIRASP*RSYG*SSLWNQTS RFQIPAPT
606	C	892	1269	MGQSQEVVRVQGPCVWHRRTRGPRLGQGWATVHLELDGEFAGAKCEA GREEHSALLLCDRLSALPLTPLDLLEKQVLEQGRAAVPRNAVQLQHS VVDDFSSAFSARGGQSVNELISLSSGVASAWV
607	A	187	363	MPLRLPIQDVY*IGGIGTALVGRVESGAVNYGLVGSSVH*AVQSVAL DFRFSWMLYSQ
608	A	514	792	DSRCPGAMACALRAPPRITNPVSAQWDPETGSGVAGEPWIWTQRERNQ SALQRGNVPFCRCRDHEFTLDLGGQGGQIT*GQEFETSLANMAKPH
609	A	1169	1336	NFASDDKFSLP*DYTTFKVNWPGAVAHA*NPSNLGGQGGQIT*GQEF ETSLANMA
610	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
611	A	3	552	HSLFGTSEVINKLRSPDAMGHL/TPEEDKATITSLWGKVNVEDAGGE TLGRLLVVYPWTQ\RFFDSFGNLSSASAIMGNPKVKAHGKKVLTSLG RCHKSTWDDLKG/TPFAQA*SELHCGQACMWDPEELSSFLGKCCWVT RFAWIPFSAKEFHPWRLQGFPGKSRRWQKMTGV\ASALVPSRYH
612	A	251	488	GGWITRSGDRDHPG*HGE/IPVY*KKLAGRGGGRLKSQLLGRLRQEN GMNSGGRACSEPRSHHCTPAWVTERLLLKKKKK
613	A	5987	6461	GVNKSWNHWFHLGVREAEHAGVVRTPHHDLVLLPRGMAACALGACS LGAVALPGHPVAGGVSHGCSSSGTTYRGERHRVGRMRQKNRLNPGGG GCGEPRSRHYTPAWAT\EQNSVSKQNKTKQNKHRLVHWNRRKKWIYL LFALKKYKMSLMLCRKS
614	A	180	347	GLSFHMLKKKVYKYMCIYMYICTHHTHLI*MYINRPSLYDYQFLFY YLSQLDSC
615	A	173	339	GLSFHILKKKVYKYMCIYMYICTHHTHLI*MYINRPSLYDYQFLFY YLSQLDSC
616	A	363	414	FLAHVHGGGLCCVPQR
617	A	540	820	KIGPQPGQHSKTL*TIKKKLARCGGTCLWSQLLGRRLRWEDCLSAG S*GCCEL*SYHCTPAWVTERDLVSKTQKNRAITGKLLLDVLSLLIR
618	A	45	366	HHLHFLQRHKSQMRMTNTGLFEILTMLTTMNLVDIFHEKADVVDMA YNAFDDEYLNCTDRMDIKYVVQLLKEEQASHHH*DTECENA*ARWAA RMTHIFLPMODYN
619	A	112	322	NSLIAGYILVYKTPRTQKEKSFLKVLSTYIKVAKYKV*ILKSITFL

				FTTKEYSKINIKMPFTTPTPN
620	B	180	372	MAKDAGLIEANGELKVFIDQNLSPGKGVVSLVAVHPSTVNPLGKQLL PKTFGQSNVNIAQQVVIX*
621	A	39	462	GVYLLKSINTVGDKEKVRRHHPITTQLOCGIQGHNLWVVTAASEIR SFHLSPSSRRFRFKSIFCHVTRSGKSMQMFTFPEKKNDFSGCPVRP RGRGRGEGAVRSAGRRG*ARAGAGPGGPGRGVPALGRVAPGLVPN
622	A	138	322	GFFQGAQKKRVHPKGPFGKSRF*KFFRAGPGGSIWNPHELLGGPGGPN CWPPGFGQTPNNPG
623	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
624	A	60	548	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLS SASAIMGNPKVKAHGKKVLTSLGRCHKSTWDDLKGTFAQ/LSEL/HCGQACMWDPENF/KLLG/NVLVTVL/AIPFSGKEFHPWR LAGFPGQKDG*LGVA/ASALVPSRYH
625	A	32	452	SRRHGSSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMTGVASALSSRYH
626	A	3	570	HLSGTSEVINKLLVQTAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQL/SELH/CDKLHVDPENFKLLG/NMLLVTVLGNP IFGKEFHPWRLQ/ASWQKQKMAEDGDCSWPVPCCSSRLPLSSLAHDGR VFQG
627	A	62	281	SGVYFSFVQRLKTLTQHLLIFGFLP*EYPTLTTFEGEIISKKHPF LTRKWDADDEDVDRKHWSKSDLCWVI
628	A	1	395	TLTTFEGEIISKKHPFLTRKWDAYEDVDRKHGKFLAFYQYAKSFN SDDFDYEELKNGDYVFMRWKEQFLVPDHTIKDISGASFAGFYIICFQ KSAASIEGYYYHRSSEWYQSLNLTHVPEHSAPIYEFR
629	A	27	121	APTPDAMGHLYED*ATITSLWCKVNVDSDG
630	A	128	380	FNSRPSLRIGLFCITCSLWDCFWCCWIHASLYSVIRSLLSFGTLVCF SLFCVAFLSPSF*VVLFFLLFISSGFFSFVFLVFLF
631	A	1	371	RQGPQGGRAAPRPPMPGPPLSSARHALPLGSWESWCCCLIPADRPW DRGQHWQLEMADTRSVHETMMQASRKEIQSLPKNGSFPTNEMRLRY YSSYNQASE*P*KLSRPGLWDPIGRAKWD
632	A	323	586	SQHFRGRTKPEDSLRPGI*DQTGQPRETLFLQNLKKLAGHGGACLOS QLLGRRLRWEDRLISGV*GCSDT*LYHCTPAWVTEQDPVSE
633	A	1	231	FRGAVRAGLGFSCGFGVPDSGIGGAMSSFEGQMAEYPTISIDRFDRE NLRARAYFLSHCHKDHMKGLRPPTLKRRLE
634	A	1	686	ARAGLGFSCGFGVPDSGIGGAMSSFEGQMAEYPTISIDRFDRENLR RAYFLSHCHKDHMKGLRAPTLKRRLECSLKVLY*SPVTKEVLLTSP KYRFBWKKRIISIEIETPTQISLVDEASGEKEIVVTLTPAGHCPGSV MFLFQGNNGTVLYTGDFRLAQGEAARMELLHSGGRVKDIQSVYLDTT FCDPRFYQIPSRRECLSGVLELVPKLDHSEVPVCCVAELQ
635	A	52	264	GLLVGVGAAVMPGIVELPTLEELKVDEVNISSAALKDACHDYGDEW DKPNVDIML**LEQLHPSMGQAL
636	A	1	380	KHSVCGRARASCSSFASVFLISKMVREQYTTATEGICIERPENQYV YKIGIYGWRKRCLYLVLGLLLMILVNVNITLTIWILNVTWVSSTSTAP HRV*H*NSLCAETQLQLRLPKRGRHVNFVPI
637	A	23	360	LCQSQATLLSIFSQEQKHAKRTHAKHTSEAIESYYQRYLNGVVK GAAPVLLDLANEVDYAPSLMARLILERFLQEHEETSPPFKGIINMMLR YPSQIPDGALAY*VYHGK
638	A	1	77	ESYYKTEGDEEAEEQENLEASGK
639	A	34	421	AVANMSGWESYYKTEGDEEAEEQENLEASGDYKYSGRDSLIFLVD AYKAMFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAWVFGT

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				EKDKNSVNFKNIIYVLQELDNPRCKRILKLCQVKG
640	A	3	347	DAWAWPLNRGFFRMMMDIGAAGVMQGGDSVELLDIPILKLPDGS DIP LPPILLGRLGFHPLKNTVCIIYGHLDVQPAALDGDWSEFPTLVERDG TLHGRGSTDD*VPLAGWINA
641	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTRHALLAY TLVAFVPI SGWNGDNMLEPSANMPWFKGWKVT RKDGNASGTTLLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGVNA GDSKNDPPMEAAGFTAQVIIILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
642	B	52	554	MGKEKTHINIVVIGHVDSGKSTTTGHLYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMIILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRS GKKLEDGPKFLKSGDAAIVDMVPGKPI*
643	A	36	697	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYV TIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTR EHALLAYTLGVKQLIVGVNKM DSTGIAILTGDFPSLEPRHVSTWLQH VVTI PTRNWHKCYCVGVVANFLNVSADFLNFF
644	A	62	1548	PLKAKMGKEKTHI\NIVVIGHVD\TGKSTTT\GH\LIYKCGGI\DKR TIEKFEK\ EAAEMGKGSFKYA*VLDKL\AERERGITI\DISLW\KF EDQQVLMWTIIDCPRTETTFIQKHDLQTSQGLAWFGGPPFWGGSPL IVCCWCLVEFESWYSSKHWGRPREHALLGFT\TG VVWQTKLFGVNKN WIST*GHPTAQKKILKEIVKGKSALT LRKIGYNPDTSSILCPIISGLN GDHMPGAQMPNLP\WFKWK\ITRKDGNASGTTLLEALDCILPPTRP TDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTE VKSVMHHEALGEALPGDNVGFNVKNVSVKDVRRGVNA GDSKNDPPM EAAGFPAQVIIILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRR SGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGCFAVRDM RQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
645	A	2281	2431	KLFFLKNVLLLNFFLPLLSPVLVCCYCCFSFFFLYLCLFFTVVLGSA RNK*KLFFLKNVLLLNFFLPLLSPVLVCCYCCFSFFFLYLCLFFTVV LGSARNK
646	A	203	372	HTDYIPNGPRTNEPTAHELIG*H**PSHFRT*VEQYNINADLKS*YQ HSMRMLSG
647	A	12	357	LFSSLSGGMQSLSLGQTGISEGLN*LTSMAPGNLWHMRNNFLFGSRC WMTRFSAENIFKSVSFRLEFGVKCHNTDSEPLKNEDLLKNLLTMGVDI DMARKRQPGVFHRMITNEQD
648	A	1134	1633	PNPTGTLMLARKWCPDGLQSLPPDVLGS*GEHLLSCLCQERACSSNS RRPRQAWTGSQGSRVINFFFAKVGTC HQPNHQAPKAPGTPPTPS YPGTPSRQLLWQWVQPRPALPASSPCSRHQLYLPRQAMSWLLSPAPS VPLDFSGASPVWATLCFPHRPLPHR
649	A	1	370	QRLAEMSNAIERKHATKMTYQPTNGTLTSGYVADRRVKHHS GGEEPP QAQKQEPHPGTSRQ*QTRVNLHSLPDPEMHEQTYFRGMYRKLGGWKA GPEGTFYDIPRYVTAYTFAHTRPADIRAM
650	A	1	222	HLLLGIMAALRPLVKPKIVKKRTKKFIRHQSDRYVKIKRNWRKPRGI DNRVRRRFRKGQCAVKKMSRQLMCTFSV
651	A	3	556	LPTEVA AISFSLAIGKHSATVFSWAGKPPSRILPHLGPILLPQKASW PPLRPLVKPKFVKRPPKFI RHQSDRYVKIKRNWRKPRGIDNRVRRR FKGQILMPNIGYGSNKK\TKHMLPSGFRKFLVHNVEQG\LEVLLMC NKS YCAEIAHNVS SKNRKAIVERA\AQLAIRVTNP NARLRSEENE
652	A	2	396	PRVRAEHSIVGTRLVSGQLQPSQPSADHGKLTMMRIAGICFCLLGIT CAIPDKQADSGSSEEKHNAESSEETNDFIQETLPSKSNESHDMDDM

				DDEDDDDHVDSDSIDSNDSDDVDDTDDAHQSDEAHH
653	A	1	1055	TDCRVDPVRPRVRVEHSIVGTRLVSCQLQPSQPNADQGKLTMTRIA VICFCLLGITCAIPVKQAES\GSSEKQLYNKYPA\ VATWLNPDPS /QVRQNLGPTGPFPSKVQRKGHPHGMWGWKVDPPC/VDSQDS IGLGTTLDDVDDT\DSHQSDSHHSDESDELVP\DFPTDLPATEVF TPVVPTVDYDGRGDSVVYGLRSKSKKFRRPDIQYPDATDEEDITSHM ESEELNGAYKAI PVAQDLNAPSDWDSRGKDSYETSQDQSAETHSH KQSRLYKRKANDESNEHSDVIDSQELSKVSREFHSHEFHSHEDMLVV DPKSKEEDKHLKFRISHELDSASSEVN
654	A	2	1103	PGRPTRPPTRPGGRAQHRLYQTLQASCSLLSQTPTRGKLTMTRIA VICFCLLGITCAIPFKQADSGSSEKHF\YKNYPDAVATWLKP*PIF RRQNLGPTTEWLCPLKETNGL*TRRTLKSLRSNGKAMDHM\DDMG*W KVDGWTMWDSDSID\N\DSDDVDDT\DDSHQSDSHHS\DESDEL VTGFSTDLPATEVFTPVVPTVDYDGRGDSVVYGLRSKSK\KFRRPD IKYPDATDEEDITSHMESEELNGAYKAI PVAQDLNAPSDWDSRGKDSY ETSQDQSAETHSHKQSRLYKRKANDESNEHSDVIDSQELSKVSRE FHSHEFHSHEDMLVVDPKSKEEDKHLKFRISHELDSASSEVN
655	A	3	267	TINPKLLKNHARGTPEVPNQKHHWSPKQKPLLTKNPKNNLRWPVPI IPPFPEEKPRKFP*TPKRRIP*TKIGPLPSNPGYPTKPPF
656	B	197	404	EQQQLQAQHLSHGHGPPVPLTPHPSGLQPPGIPPLGGSAGLLALSSA LSGQSHLAIKDDKKHHDAEHHRX*
657	A	2	652	LSRVLEFEFQFLQAQYHSLKLECEILASEKTEMHRHYVVMYEMSYG LNIEMHKQTEIAKRLNTICAQVIPFLSQEHQQQVAQAVERA IQVTMA ELNAIIGVRGLPGLPPTQQQLQAQHLSHGHGPPVPLTPYPSGLQPPG \IPPLGG\SAGLLALT\SALDGQSHLAIKDDKKHHDA*HHRGDRPGK PD*DFVLILLQCKVVCIAKESPNLYREQT
658	A	455	1033	GLYFGKVGEVIEQVKAFDELKALIAFFPLSSLSFLAPFVCLLNLFC FRLPLLSCFLSPGCRHLRHCHHYLLLLLLFLSHHHHQQQQQLQAQH LSHGHGPPVPLTPHPSGLQPPGIPPLGGSAGLLALSSALSGQSHLAI KDDKKHHDAEHHRGERPGKPD*DFVLILLQCKVVCIAKESPNLYRE QTMR
659	C	178	360	MERPERKIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXSYYSFKNLI*
660	A	365	801	INVNFLEFYMTDITCFLFSYLSTLMSPIYLDVLLLSLLLFLPHIAGM HILTFINHDI*VVHSFYLR*HAMEITVYEFICLRIRYPFKASKIFS MYNATVLFHI*CDR*LGS*IGILERSVGVCVMVCIVYIRYVISS VDAP
661	A	2	58	AGRCAQHGOPPAAPACRE
662	A	218	342	QPKMKYSGMPLLPVSRVQAILDGSRLRPPKKTCHLKNFGA
663	A	527	665	AGLLQNTAGFLGMPGLLPVSRVQAHIGMGSRLRPPKKTCHLKNFGA
664	A	1233	1706	CLVFWLLYYPGLQLPFHLLPHSLGSGQSSSESAATPSLAEGRREA FRCPAGLARQAWRPHARLPGPAAPLAAPSLAPLPTGRSGRWLPMLC AASC*SPSPAMSVYPQRRLGQGAEDSEGGPVSRGCRAPGPQRPLAA PGEQTAARTQAICLIW
665	A	598	1159	CRQTGVKIYDVWFFWLLYYPGLQLPFHLLPHSLGSGQSSSESAATP SLAEGRREAAFRCPAGLARQAWRPHARLPGPAAPLAAPSLAPLPTG RSGRWLPMLCAASC*SPSPAMSVYPQRRLGQGAEDSEGGSVSRGCR APGPQRPLAAPGEQTAARTQASVYLLPHSPPLLSALHIHLLPPS
666	A	358	644	RRSLALSPSPECSDVISAHCKLCLPGFTPFSCSLSSWDYRCPPPR LANFFFVFLVETGFHRVSQDGLDLTS*SARLSLPKCWDYRCEPPRP A
667	A	55	288	PFKKGGFFNGNLPTTFGKLGKFKPLNLFPGGPPLPHGGKKGPGAP QVPPLFLKKPQTSPP*GLREGPPPLKKFYLF
668	A	2	386	ARGEPTMELSHADTTNVKAAWGWGAHAGE*GADVLVRMVLCLPTIW TYFPYFDLSHGCAQVNGHGKKVADALTNVHVDDMPNSLIGLSELH AH*LLVDPVNFKLLNHCLLGLTADHLLDEFTPAV

669	A	787	896	LLYNIYCGEKKREERKD*PGQHGETPSLQKIQKLAG
670	A	539	787	SIGRLRRVGHLSRSGVRDQPGQHGGTPSLLKIQKFAGHGGAFLYSQVL GRLRQENRLNSRGGCSESGSQHYTPAWVTE*DSI
671	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
672	C	336	728	MGLPKTGHQQHFPOELESSSRIPHAGLSQVQVHFRLGQRCPLRSSQV LLWHLPRKVSTFLPCALTLGVAHWQRQRTGCQSCQRTSGSMGRQPG AFPGFLLQHLSTFTLPHRLCDSSLVLLCEMTHGRDL*
673	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDDKLAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLVAFVPISGWNGDNMLEPSANMPWFKGWKVTBKDNASGTTLLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNDPPMEAAGFTAQVILNHPGQISTGYAPVLDCHTAHIAKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
674	A	1	921	KFETSKYYVSIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEA GISKNGQTHEHALLAYTLGVKQLIVGVNKMDSSTEQPYQSQKTYEIBVK EVNTYIMKIGCNLDTAAFVLISVNVTEVKSVEIHHEALSEALPGDN VGFNVKNVSVKDVRRHGNAGDSKNDPPMEAAGFTAQVILNHPGQIS AGYALVLDCHTAHTACKFAELKEKIDRCSGKKLEDGPKFLKSGDAAI IYMVPGKPMCVESFSDYPPPLGHFAVGHMRQTVAMGIIKAEDRKAAGV GKVTKSAQKAPKPSEYYPLYLPPQS
675	A	659	1601	SRASSSVPLALPSLQVTFHPLNEGTLAVASSMLSSSQPEIGTNATV LGL*PIFLM*VLTSLTISSYLFWL/RGWLSGTTLLEALDCILPPTRP TDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTE VKSVEMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPM EAAGFPAQVILNHPGQISAGYAPVLDCHTAHIAKFAELKEKIDRR SGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPPLGCFAVRDM RQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
676	A	1	1335	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLILRER GKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYR VLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKL NLVAPDQDLLEKCLKNIHRIIDLKTKIQKYKQSVQAGTSYRNVLQA AIQKSLKDPSSNNFRSIPERYKMKSKPLGICLIIDCIGNETELLRDT FTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGG SQSVYGVQDQTHSGLPLHHIRRMFGDSCPYLAGKPKMFFIQNYVVS GQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMS LLEQSHSSPSLYLQCLSQKLQERKRPLLDLHIELNGYMYDWSNRVS AKEKYVWLQHTLRKKLILSYT
677	A	1	811	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLILRER GKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYR VLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKL NLVAPDQDLLEKCLKNIHRIIDLKTKIQKYKQSVQAGTSYRNVLQA AIQKSLKDPSSNNFRSIPERYKMKSKPLGICLIIDCIGNETELCGVR GPAGGQQPLGGWASDEECGIQGSSEARAVHSSPRS
678	A	269	561	LSFVGSLSRLFTAGFAECPRFRFRPAPNPRTPSTRNSAPDSQKGATW ATAVQAAPRWT*ETGSPNPWPTLAAPCSRSPRGPPASFSGGPSASCKL CLK
679	A	415	1094	SKSRMSAEVIHQVEEALDTDEKEMLLF\LCRDV\AIDVPPNVRDILL DILTERGKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPH LVSDYRVLMMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLV VELEKLNLVAPDQDLLEKCLKNIHRIIDLKTKIQKYKQSVQAGTSY

				RNVLQAAIQKSLKDPSSNNFRMITPYAHCPDLKILGNCSM
680	A	551	1706	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDI FT/RERGVLSVGDLAELLYRVRFDLLKRILKMDRKAVETHLLRNPH LVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGGRKISKEKSFLDLV VELEKLNLVAPDQLDLLEKCLKNIHRIDLTKTIQKYKQSVQGAGTSY RNVLQAAIQKSLKDPSSNNFRLHNGRSKEQRLKEQLGAQOEVPKKSIO ESEAFLPQSIPEERYKMKSPLGICLIIDCIGNETELLRDTFTSLGY EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCVLVSRGGSQSVYG VDQTHSGLPLHHIRRMFMGDSOPYLAGKPKMFFIQNYVVSEGPAGEQ QPLGGWMGQR
681	A	76	158	KDKRVGKMYKEVPLSKGSKKYNDINII
682	A	1	2313	MVYRQNQLPSSCAPEMGREDGLRALHPAQPPPPRAQQSPPPPLSAQK SLHLPVHSAKLRPCSPPTVAIILNPSQPHRPPVHSPGSGLGFTQLSP SLEASLGHGLQHARPARHPLPLHMGWATFTLTLSAPWKLRRRRLQ VAGVPHVQRMWPAPHAPAELETTQAQLWGHRRGHWIPDGRACNTEF THPGLEIGARESGSACKGPPPGSLVFPASPPLGSKINGGSCYQILTG SSGKICRINGCSCQNKWSMPTSATASLQTCPARAVPDLGIARRSWSP HRRPSWTHEKSSCPSQKAPQGRAVPLQPGKGGEVPSFWSPGQAPSKA RGRRAGSAAMRGRAAKLLSRSRSTGGLCVLCGQGTGVLQMQGRAAPP APPPAHPLFPRPVSPLDFSASKRALQHPALLGGKDSWRPECGLHNL HLPSGVKDSWGSECGHLNLSHLP SGVKDSWGSECGHLNLSHLP SGGK DSWGPECYVFCMLHRLPEQHDCTFDHMGRGREEAIMKMVKLDRKVGR SCQRIGEGQEDDVVASILVSMQPHSPRTSPHLPYSKFDFSSCNC ARQGWKEMGACVQRPSAVLGGTRPVSQAKQPLPCFLLGASALGSCG TGLGVKDRDIDRIVMSVMKILRGNQRPSGDEQARGQARAREGLGGLG VRRACREQWAVLCPLVHRNWVCVSSFLIASQSNPQQQHNCYANNS PQQEEMVGRQAETFLGGVRNRKPWVGVRGLQGSHQHQHIGAVSS PSSPKKGVSCKREGPRWAQQ
683	A	788	926	PSPELPEGDFEGFFPQKLQ*SCLPTLQKKNNNNNNNNNNNNNNNEK
684	A	242	438	KSCFFCLIRCYDSLPLPLLLNNFFFLGTESCSVAQAGVRWLNLS TSGLPGSINSPASAS*AA
685	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEAL DCILPPTHTPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTTTEVKSVMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNPPMEAGFTAQVILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIIKAVDKKAAGAGKVTKSAQKAQKAK
686	A	73	1553	PLKAKMGKEKTHI\NIVVIGH\VDSGKSTTTGH\LIYK\GGI\DKR TIEKFEKEAAEMGKGSFKYAWVLDKLKAER\ERGITIDISLWKFET\ SKYYVTYPFDAP\GH\RDYFPTWITGDI\RLDWFGGPPFWGGSPLI VAAG\VEFEAGYLPRNGADPERHA\LLAYTLGCETTCLSGVNKNGI PLEPTPTAQKKILKEIVKGKSALTLRKIGYNPDTSSILCPISGW\NG DNM\LEPSA\NMPWFQGDGKVTROKGNASGTTLLEALDCILPPTRPT DKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTGFPVNVTTTEV KSVMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNPPME AAGFPAQVILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRS GKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPPLGCFVRDMR QTVAVGVIIKAVDKKAAGAGKVTKSAQKAQKAK
687	A	67	408	KAAGKRGDFKTEGAYQRQRTIFKNKKRAREKTGRENLRGNYKNMGR GLKTPRGALGGPYLDKKGPLRGKGPFGGTTLLSSSPKIKIQGTL*IR RNYWPHYIRRYNRFKKRQKNM
688	A	10	386	AGAAAIGEPMAR*RGEGHPWSVDERADSTNVNNWHWTERDASHWSTD KLKTLFLAMHVQNEERNGEATEVSKLDGEASINNRIGKLMFFYEWGV

				TLDWTGAS*SGVPYKGVHEIPYLADENCVD
689	A	2	323	REMDLQVHNAMDQLEQVSEFFMNAKKNIPWEWREEQMASIKKDYYKA LEDADEKVQLADQIYDL/RSLELDTPSQPVNNHHAHSHTPAEKRYN PTSHHTTTDHIPEK
690	A	2	495	AKKNKPEWREEQMASIKKDYYKALEDA\DEKVLLSNQIYDLVDRGGR KLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNNHHAHSHT PVEKRKYNPSTSHHTTTDHIPEKKFKSEALLSTLTVRCLLRENTLGCR \NNNSTASSNNAYNVNSSQPLGSYN
691	A	50	392	GSQKIAPVFWSGFECDSERLTDLESWLYILPATQPWSLTIFYFQFS FILTFRLRYDKLFFFFTLTYLNLNLYFFLYVFLFIV*ICIFCYIYLVFI FKCVV*FFIFFVCFMLFFL
692	A	3	548	PAPPGRVFAAWPGSEEARVLVVLKGCACRAGLFKMYPLLPMTVEVCTK SSTVTWFCFAAYESLFETPFSAIGSVLVPWGLTLALS*VCFAAFA *LLASLFSQDPLVSPSAAMWASPACFCAEPSSAAIGVSSPSSSVFTQ QS**GSPLAGSASASAKNMARARSVAPPRNGRPGNTNADS
693	A	3	391	DAWVDPFRFLIFLKTTLTGKTMVDLEPNDTIANAKA*IQDKEGIPPD QQRLIFAGKQLENGRTLDPYIIHKESTLLLVLRLKGGMQIFVKTLTA *TISLQAEPSDTIHN*EKIQDKESIPPDQHTVIL
694	C	70	225	MNIQYIQHESVYQNVRSQRESTGRWSHCCPSQGRSRRIPTVVEIQ QHGV*
695	A	277	396	EAP*HPDFIKNMITGTS*ADCAGLIVAAGGGVFKSWDLQK
696	A	549	709	SQNFWRPMWADHLRLGVRDQHGQHGETPSLLKIQKLGHGGGRL*SQ LVRKLR
697	A	82	417	AFQEMELKRPQEEDVAALPEGMRPHSNLYGFSWE*VICAADVGLFAA LFFLWRSFRTVIRIRIHVGRERKLALMLSGLNQ*KSELLGHCILAQNE YDGYELDE*FVDLRVDKE
698	A	751	1063	FYQDKRHQPGIVAAACNPFGRSRQEDLLRS*VGDQPGQHSESPSMQK I*KLAGHGGAHV*S*LLRRPRQDNPLSPGGQGCSVL*SHHCTPAWAT QGDPGSKSKN
699	A	3	17	ILQR
700	A	3	443	DLEGTkmFQVRNAWAMEWDKKERRKERRKERRKERRKERRKERRKERR KKERTEGRKEREKERERQRKRKKERERERERERERERERERERERER GRKEKKERKKERKKKKRKETKEGKKEGKKEGRKRKRERKNSKECQSSY RLFRV
701	A	147	437	WYVKKERKKERKQERKKERKKERKKERKKRKRERKKER*RERERERGR KEGRKEGRKEGRKEGRKEGRKKGRREGREKERERKKEREISREYDS EK
702	A	505	637	CLLLNSIYRRHQGR*DGKERKKDRKKERKKERKKERKKERKKERKK E
703	A	220	476	HNSLVVYFIEIWSRILFVYSCSIHTSVVTH*SLLSLGHLKYIWAGHG VSHL*FQHFGRPRWENHLRPL*DPGQHSETPSLLKK
704	A	1	554	DLILNHLFFCFVIRQQFSFLFFFPFFHFFFIAMLTQSYVIFLSVYT VILHLDYFISLFLTYDIMYF*TKINT*AKLLLIYENMLIVL*CSAFL SNYTVLIVQIIASLIHSSTK*ISQCANI*IKI*IIILH*L*SSVEINSY L*LFCYLVSATILELVLSQFSYMYILRIQLDFLNEEMHI
705	A	1039	1560	SLVLDLTGLPRPTSPSHERGLDSSSSGPGSLTGP*ECSDPDNPMCPK VLPDPDQRCWNHSTAPIAFPEPVRSR*SGSWTPVPATGATLNPRCQ RGLAIPNSLVSSP*GPAGWRELPSQQAHPHPR*KALRSENROEGP DQCGCNCVVKYGGVRVGVYSGPVRTGCSRASN
706	A	644	931	EGSHGLGVVAHACNPSTLGNRCGVDHLSGGVQGPQGHGKTPFLQKI QKLGHGGTRL*SSYLRLRWEDEGGRCSEPRSRHCTPAWATE*DP V
707	C	185	397	MMVRLSYIQPAGSEESRLQNDAXQPDWIFEWKCSRIYGRTVAPAAK LPRKHRGNPFCCFRTXERRNKT
708	A	3	521	CKMDAGFF\RGTSAEQDNRVSNKQK\KLLKQLKFAECLEKKVDMSKV

				NLEVIK\WITKRTEILGFEDDVVIEFIFNQLEVKA*TKMEVIPC *SIAPSPY*VTAE*VSQCRSDPTPLMMQCVFG\NPD SKMMQINLTGF LNGKNAREFMGELWPLLLSAQENIAGIPSAFLEL
709	A	730	983	GAVAHICKSQQFGRPRQAHQLRSRV*DQPGQNDETPSILKIQLAGH GGTRPLSQLLRRLRH*NHLNPGGGGCSELRSRHCIPG
710	A	108	420	GWGGLLIARPPFKRGKSSGPVGHLPKRGVGGRRG*NVNLCPKSSNPQ GGLGERPRELRDKATVSALANFTARKGC*LRGPEGGQPGPRGKLFK GVPGVQGGP
711	A	274	394	SPFPKEVGGGKFLNLGGQRFWGPFGPLFSAKTKKGTSFLK*GFKNP PAQGGKPPFFLKIQN*PTLGGGPNLPHFLRRLGGENF*TSEGGKFGD PNLALCSPPKQKKGLLF
712	A	59	306	FGTDRTAQTSSSQLCLPWVAQKTYWLLVPSSLLKDLKEKKEVVEE A*NGRDAPANGNAVSVCFAPPEWQLPPHKIFPVL
713	A	171	565	TLAFFLIPCIGSPACPTMSDAVDTSSSEITTKGLKRRRRKLWEEAEN GKRRPCLTGAENEGKWSREA\ DNEVHQKEE*CGEEQEEEEEGDGE EEDGDEDETLSATVTRATEDEDDDAVAPTQKQTRLDE
714	A	1	1497	MSLADELLADLEEAEEEEEGGSYGEEEEPAIEDVQEETQLDLSGDS VKTIKLDWDSKMFAEIMMKIEEYISKQAKASEVMGPVEAAPEYRVIV DANNLTVEIENELNIIHKFIRDKYSKRFPPELSLVPNALDYIRTVKE LGNSLDKCKNNENLQQLTNATIMVSVTASTTQGGQLSEEEERLE EACDMALELNASKHRIYEVESRMSFIAPNLSIIIGASTAAKIMGVA GGLTNLSKVPACNIMLLGAQRKTLSGFSSTSVLPHTGYIYHSDIVQS LPPDLRRKAARLVAAKCTLAARVDSFHSTEGKVGVELKDBIERKFD KWQEPVPVKQVKPLPAPLDGQRKKRGRRYRKMKERLGLTEIRKQAN RMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKARISK LQRTLQKQSVVYGGKSTIRDRSSGTASSVATPLOGLEIVNPQAAEK KVAEANQKYFSSMAEFLKVKGEKSGLMST
715	A	32	3730	NSERRGLMSLADELLADLEEAEEEEEGGSYGEEEEPAIEDVQEET QLDLSGDSVKTIKLDWDSKMFAEIMMKIEEYISKQAKASEV\MGPVE AAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKRFPPEL\SLVPN AL\DYI\RTVKVSAEKELGNSLDKVARAIEEPWQQILTATIM\VVS V\TASTPQGGQ\LSEEEERLEEEACDMALELNASKHRIYEVESRMS FIAPNLSIIIGASTAAKIMQPLSLSEPPLHLPLAEWARSPAWQGHR GIQPELHVKVPSTRAPRQIYSPHSLSSDRPLPPSLPRRCGGGLTN LSKMPACNIMLLGAQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPDDL RRKAARLVAAKCTLAARVDSFHSTEGKVGVELKDBIERKFDKWQEP PPVKQVKPLPAPLDGQRKKRGRRDEKRGGEASSAAAILDRARSASA EPSADAAASLEPRPPSSEQPRAQSNKPTIRHTRRYRDSARARGARKR RRALASPACRDITLLSGGASSCARGSRGAAPSLSPSRSCASFTFLSA SRGSFREPGAPGPARRRLPWHRVGPPEIDRCLKKVSEGVEQFEDI WQKLHNAANANQKEKYEADLKKEIKKLQRLDQIKTWASNEIKDKR QLIDNRKLIETQMERFKVVERETKTKAYSKEGLGLAQKVDPAQKEKE EVGQWLNTIDTLNMQVDQFESEVESLSVQTRKKKGDKDDARVQTSR LFLSKDPGSPSPNPQPDARVLASNLLVCQIQQSKPLTFSSLRMTVPVH KRVLSDSLRSRIGPQRDVSHFLAAYRSLRLVPLGLMSLADELLADL EEAEEEEEGGSYGEEEEPAIEDVQEETQLDLSGDSVKTIKLDWDSK MFAEIMMKIEEYISKQAKASEGETESLTPFKTPGRSSLPPLALRRL CLLPLPDPTGHKMWSNFFLQENRRRGAAGRRRAHGQGRSGLTPER EGKVKLALLLAAAPCAKRPHLGLWKACTKRLWQADVVDRTDCGPAE LPGEANCYFKFFTGENARIFQRTTKKEVNLA AVI AVLGLAVMAL GCLCIIMVLSKGAFLLRVGAVCFGLSGLLLLVSLVFRHRSVRALLQ RVSPPEPPAPRLTYEYSWSLGCVGAGLILLGAGCFLLLTLPSPWP GGGTGPPRATLPPGTTSSNYSLGNFVRLGLAAVIVVIMGAFLVEAWY SRNVSPGESEAFKPE
716	A	3	117	HKRPLMASYLLFFCSFVRVE*TIITCLT**ECHRYNR
717	A	1007	1119	APGPCPNQTLARDSGWVG*KNHQLCTCVCVCVCVCVC

718	A	1692	2123	SQPRFSWTQERLRLFPGMILLNSLIVSQATQGPKSCLGSCLMFTFK KMEPSPMSCSPQCFGKPMGRSLGGQKFKNQAGQYHKTPSLRKS ASHGGVHLWS*LLRRLRQEDCLILGIRGCSEL*LHLCTPPSATQRDP LS
719	A	1	371	HRHCHPSHTVDGRMESIDVATDGG*RTGVLA VSGLSVSLRTAELSTR KLLMNSEQRINRIMGFHRLGSGAVE*RHTQSMQHDSKLNLSLIIPSV SKRVVLVDSVCTGTTDHQGGVLERKVTTL
720	A	3	409	DAWANARSVRLEVAGLRDDL*R/CSERWPLARATPFCFGSAMPYQ EESNLSLQALESRQDDILKRLYELKAAVDGLSKMIQTPDADLDVTNI IQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPGFPPLF
721	A	25	494	PLTVSERWPLARATPFCFGSAMPYQVKPYHGGGAPLRVELPTCMYR LPNVHGRSYGPAPGAG\HVQEESNLSLQALESRQDDILKRLYELKAA VDGL\SRRIKPPRATLD\ETNIIQADEPTTLTTNALDLNSVLGKDYG ALKDIVINANPGSPPLS
722	A	358	445	NSFGRTIFFFY*PFFFFFFFTIQTFKGGPLSPFFFFFFLFFINPFPRF FFFF*TPFLRALAFKPFFFFKIVLAEPYFFFTNPQILMRGGGGFSG RGS
723	A	452	765	LLFSKRAVEKNLSKEDPHMETIKVAFVMTSGERDTGLTEPMAG*RG S*GS**DGPARGHETSLGHRGVSGDGGSGMPSLTANALPSISRFPD SVTDSGSAPL
724	A	209	385	KYETIRYRDSVKGRFTIF*HLTKNCLHLRAIGLGADDSHFYSCANDV ADSGTTLFFDS
725	A	68	362	SLPTIRECIYIHVVHAGDHIGNACWELYCL*HGIHPDGHMPRDLTIG GGEDSFNTFTTETGASEPVPRAAFADLEPTVIDEVTVTYQGYLQL* QLIK
726	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTTTEVKSVMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNPPMEAAGFTAQVILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQKAK
727	A	65	1552	PLKAKMGKEKTHI\NIVVIGHVDNGQVSPLLGHLIYKC\GGI\DKRT IEKFEK\EEAEMGKGSFKYA*VLDK\AER\ERGITI\DISLW\KF ET\SKYYVTYPFDAP\GHQRLLSKNMIYRGHLKA*PGLGGPLFGGVL P*LFAAGVWNLKAGISKNG\Q\TREHALLGLHTWVWKQTKLFGVVK NWIST*GHPTAQKKILKEIVKGKSALTLRKIGYNPDTSILCPIGW \NGDNNASPNA\NMPWFQGDGKVTRKDGNASGTTLLEALDCILPPT RPTDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVT TEVKSVMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDP PMEAAGFPAQVILNHPGQISAGYAPVLDCHTAHIACKFAELKEKID RRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPPLGCFAVR DMRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQKAK
728	A	344	803	KRDPSLSAYPFFKCNLLSTLHFMTAYASLYFIYTEPVFVQHDWLH AL*IPFHISPSTTIPLTMVSQPYTEHYIVTKLGEFQVSKGNYIHKR FCFIAQFTI*LVITQPTMLR*ISDYLDKYIGFCPPQPMQKQERHTYSP PYQGCVSVVQS
729	A	209	373	KRKKILRINKTKS*FFEKINKIYKMLTHLRDRKQKKSEIKKGDITT DTTEMKK
730	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDSFGNLS SASAIMGNPKVKAHGKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGEFTPEVQASWQKMTGVASALSS RYH
731	A	99	641	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR

				FFDSFGNLSSASAIMG/NTPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHF\GK\EFTPEVQASWQKMAED\VTGVSALASTYPLSSLAHDSLSRDRLLFCKQIKI
732	A	154	411	AGQPGPEGIQLG*PQIRDKGDQMGPHPCW*VCGLTTPNTSF*VFCCVAGR DGAPGVKAHFPAAQKPWDGGFPGP*SAGVGPPPIPR
733	A	233	353	STAPGSGRQRTVSEEP*PHSTEDGQRGQWGGTSLQHPAQD
734	A	1017	1882	TLAKWWTRREQRSQSLSTQASSYHQWQVRGACGQAARMRSAPAVIPTRPGEFVHQSLASANSRLQPVSTSTGHRSAPEAGLLTGCVLMPGCSASQASMEHLSWSPCPDGFCTYRVLRSCLNCNSRPDGPKEHNGQEPEAAVRSQPEGPEGGRTRAGRPEPGGGPHLQEPKASETHNPGIPSRGAAAQGHLOGSGTHVRGGKQPSAAGPGRIIARVLSGPPGPRARGRCADGS*ASPRARSSCRSGGRSRAAAPRRRRGGAGAACARGCAGG*AGSAA RGSSGR
735	A	1000	1211	VPSTVLDALHILFCLISFLKNKLWCSGLTPVIPGLWEAEAGGLLESQEFGTRLVNMAKPCLY*KYKKLA
736	A	109	346	PRSLSPHRPAPPPSVSVGFRPRGKRGTOGDKGKCLGYRGPQQL*PHGTPGPQTQRRRARGCYLQPGAWGPLLSPPWECDV
737	A	134	387	PRSLSPHRPAPPPSVSLGFRTRGKRGNGQGRQGEVSWGTGGPQQLWPHGTPGPQTQRRRARGCYLQPGASGPFRLRPPWECDV*ERG
738	A	33	509	VSVSVGLRPPWELQVWVLCVPRGQAKTRLEPAGRAPEAPLPALSVLAGGSDSDSRFRQSLSSAAAPGADSLGARTELRVEPGPSRPRPRPRPSWTTASTADASRAAGARGRGNESAGSGAEVRSEQKVKRESIGNR*K RKNKTHSKRKKTLQKKG
739	A	2	350	PASSIQQGRRACLEVTWSCSIWNPTATGGLDRGSRVHSREGGGEAPVRVQGPGE MIPAVPKSSWTLHKMQLPGHV CSTLGRRGDEKGEAGPEAHAYDPSTLGGRGQRIT*GQEFK
740	A	15	239	RSTISTSSISPSQEVEDRWQNHNTQHAQSALAADWMVSIHTACGSSSRPPTQLSVFSGNTLTDTPRNSTPPAI
741	A	2	311	FQLDTGSR SAPML*CSGVIMAHSAIAKSLQTPGLMGSFNL SLPSRWDRHIPPYLANFLIFFIEMGSCYITQGSHPPTLNGLSLSSLANKIQGNI GSDLVEDTG
742	C	398	574	MLQVAVEELPRRPSRPGELLQTHAAKVLAVDVELLERDTIGIQLVVF XRCWSHSHTCYL
743	A	3	862	RNERHAYDKGTWKTRRAIMTVQ*SGETNVDRAYNLLYQTLTDWTD SYVTC*ENKEIAAGQRNESHSDWTKYQVWEWLQHLLDTNQLDANCIPFQ EFDINGEHLCSMSLQEFTRAAGTAGQLLYSNLQHLKWNNGGHTGISKSCKETRHLFPFFYLGPHTLATCRAVSKRLQPKLQCAVHSFVTPGIPYLDEIGYRARDLREPGQGVAAALLPLSSDGNPRRRPGLPKLKAQRRVRFPSNKGRGGPSSPPFHS AFLNWQHKNVMMVKELSSYLGLQYYPGSF GGAI
744	A	15	404	RNFRVDDLVS PRCCGILWFFTQGGQASCWRPLATLPSRQKPGSSPGKAGC WPA/WDLGLVPHGVSGVSI AASSTPQGQAVCSPSVAAPSTLLLLL RTHLLGAASLQGCQHQILLHHLIGMDLYVAASPSHRFW
745	A	1001	1459	GVYVVPHTLVMMPLQANESLITTGCLREKPENSTAPWRVLP GCDRAS GREDVPMAPPSVGGADNALARAARTACDQPNLRLRLGPWDGSSQGLQLWTS DALPPGKKPPRRLSLPAATKAPSSNSFPTS VAGSTR LAPVEL YSAERTSKRKE
746	A	3	359	LFSPRQKGEGNGAYFLLPGLLKKDSGCGCAAGDKRCNTGAAPDTATPSHRHGPICGSKSISSLLVKVSPVCKDSHSSLDLALLRRHKTPCHSA VAAAASASACAGLSGYAGSRFALR
747	A	461	792	ESLQTGLTFTKSDMDLLPHIGPCR*DGVAVSGAPSSNSFPTS VAGSTR LAKERGDHHLRKQPRWEVHGAVRRRAVHRPFIHLSRKEAACCLFP PPTLLPSRQOTLPLSK
748	A	40	317	LRVTAQWASHTLPDPVVG NPGSGWKEKDRDSEWGWRDLKSKTWVEVEAEGGLSGDTFQWLPQGS SQR PGLPLVNQAGVQETKGAGPL*SPAPL

				PPGSPEGAQASGCSFVGAIGMYPLTGPLPPPPQPRSWISGPSTPILS LCPSPSTRSQGFPPQGLEVCVTPIELLPEVRLKIRECFPSFL
749	A	2	335	QKRGKTLPDF*SDFG*QLNGRHTHFQ/HPVVGNPGSGWKEKETGAG PLCYPPSHSKVWGRGATSSVSEGGSQRAGHLP/TSPAAQQGLECRNT RLPKVRAVAVRLCYPLGG
750	A	444	1001	HSLTATALTLGSLVFLHSSPCCAAGLWASDLPSVSLPLTQRRWLFPF KP*KWLGG*QRGPAPLVSCTPAPWFTQRERMKDGSISHAPSPTLRHP GVGGRSPRPLAWSFVGAIGMYPLTGPLPPPPQPRSWISGPSTPILSL CPSPSTRSQGFPPQGLEVCVTPIELLPEVRLKIKECLSLVS VKK
751	A	172	431	IGRPTKQGLGQWTAVWERMERTNKSRAWPNACEGPAVGNIAWASG LP*MLKTRAARTWVQAGVRESAOGFLNKNRRILEMGLSR
752	A	253	429	QASGVSDLQ*KLCAC*AQSQDLRGGGFREARKTST*QPGFGLLFCLL YSANKLQESVTFKDAADFSWEEGQAESAQRMTVYGEVMVENYQEP GFLGKYLEQTRGGLP
753	A	963	1497	NTALSNEEILVMALVVISFLSLTFFQLMEGTRLNKLWGFIPRTL*F SE*TLSSIKAKLLTILTPSLKFNREVKNEVCHFVEWFWSYHNNLIK VPFISMFTPLNKMKAFTFICKMTVNINNMHQSTIYAKGEEHLMGCY VNCKLRTACFMAFAVKKKLLAFNMYFKIYSCLGENT
754	A	1	363	WRESPHSARPLEPQCYDLSSLQPPGLK*CSHISLPSSRDYSCCATM PS*IFCVFFGVEMRPHHVAKAGLKFPSSNPASGIPKCWDYRCILG QFSSFEAKPRMLIFTLFIICSGHVMMS
755	A	1	433	FFKNFYRINRDSYKAAKFFPVLCISSFHSYCSTLPQAPLPQAWLNL RRSSGVFLLLSIVRADVPTFPQILGLILEAPPSQSYFLPFSSMDGL MLHPNRKVQQLTFSRPGEVAHTCNPSTLGGRGGRIA*GQEFETSLGS LIS
756	A	362	567	PAPTPGTWDRHKSPLANFLYFY*RQGFHHIGLAGLELLASR*STH LGLPKCWDYRCEQHVQPENIF
757	A	204	391	DMGYDVTRFQGDVDEDLICPICRGVLEEPVQPCQTKVICIILGQV*G EAHDYHAPYCEHAFC
758	A	381	1335	DMGYDVTRVQGDVD*DLICPICSGVLEEPVQAPHCEHAFCNACITQW FSQQQTCPVD\RSVVTVAHLRPVPRIMRNMSKQLIACDNAVFGCSA VVRLDNLMSHLSDCHEHNPKRPTVCEQGCGLMPPKDELPHNHCIKHLR SVVQQQQTRIAELEKTSAEHKKQLAEQKRD IQLLKAYMRAIRSVNPN LQNLEETIEYNEILEWVNSLQPARVTRWGGMISTPDAVLQAVIKRSL VESGCPASIVNELIENAHERSWPQGLATLETRQMNRIYENYVAKRI PGKQAVVVMACENQHMGDDMVQEPGLVMI FAHGVEEI
759	A	1	1236	MNKQIQGRTGACSQRDTATLIKTESSDVIHLIMQYLKENGLHRALAT LQEETT VSLNAVDSIESFVADINS GHWDTVLQAIQSLKLPDKTLIDL YEQIVLELIELRELA AVKDVEEEKFPTQLSRHIKFGQKSQVECARFS PDGHYLVTVGSVDGLTEVWNFTTGKIRKDLKYQAQDNFMMMDDAVLCM CFSRDTEMLATGAQDGKIKVWKIQSRQYLRRYERASHSGVTCLSF DSSQILSASFQDTIRIHGLKSGKTLKEFCSHSSFVNKATFTQDGHYI ISASSDGTVKIWNMKTTECSDTFKSLGSTAGTDITVNSVILLPKNPB HFVVCNRSNTVIMNMQGGQIVRNFSSGKREGEDFVLYCFSTATGKLE RTLTVHEKDVGIAHHPHQNLIATYSEDGLLKLWKP
760	A	55	792	GRAGACSLIDTAMSIEIESDVI RLIMQYLKENS LHRALATLQEETT VSLNT\ VDSIESFVA\ELKSGHWDTVLQAIQSLKLPDKTLIDL YEQV VLELIELR\ENLGAARSLFETR PDPMIK\LKQTQPERYIHLNEN\LA RSYFDPREAYPDGSSKEKRRAAIAQALAGEVS VVPPSRLMALLGQAL KWQQHQGLLPPGMTIDLFRGKA AVKDVEEEKFPTQLSRHIKFGQKSH VECAPRAEFVQRRSN
761	A	85	379	KKPKTKKRTGPPVRQNVWRGSLSPGRAPAEGPQGGSTES PPLLVGRC LILGLREPGVPPAAYGRFLRDYMNSIQGKLEKQRPQ*GLPSLTGAAB LIKH
762	A	209	394	WAVYCTSFMLS*CYKI*CKPALSLGI*TTEVKTYVYTNRCCEMSTS ALLIVAKN*KHSC

763	A	348	640	VQKPKWGMGRAVCPAPGPVRLEERPVCCTPCLCLHPARMTPAWGSIH CLPSHGGCPCLPVNAPSWLGQPSWARALLQ*WVVLGAEGHLHTLRT TVG
764	A	746	1280	ISHMELQFGAIFAEILFRGPFHHLNINFTWASCCPHASQPGRQRGS SWNEYHSFREFNQEKEIWRAGESAPLPLAGAAACPWGASNPIC VTGASAAGGRAGGSGEETGSAPGAACSST*ESYEA FSGFSSSPGNS V*TFSTSSTYTASPTSPSPSVSPSPPCYYYSSSSSL
765	A	1	493	KGPVSKEPRSGMNRNSALRVNVRPLRPCQEGGLPLQSCVPPLGLCR VPSRGKQPKHLLPTG**AIAGLPNLHVIDFIPLKLSFGL*GVPQGGP PLGRGPQSQGS LVTQAPMGGGPRKGLPIDRCE*GACTLGPWAAPVP LSSKGPFPPTVGRSLSDSFSAR
766	C	82	201	MKSKHFINLISRQHKYNYLIYTFIRSRDFKTAIFLSILS*
767	A	88	372	QGMDSKRRGVKLNLDGQFMPVLGFGTYAPS*VPRSKALEVTKLAIEPG FRRIDSGHLYTNEEQAGLAILNMIADGCVKREDIFYTSELWATFY*P E
768	A	177	313	WFQNPCYYYLFLETESLSPRLERSGTVSAHCSL*LPSSSDSPAS
769	A	193	363	IPLALSTGNGTLLFFF*DRVSLLSPTLECSGVISAHCNLCLPGSSYS AALASQVAGI
770	A	260	361	SPN*SPNVIDFS*DSPEKTAATVRGDFYVTGDRGMMD
771	A	80	358	GPFFFFFGDRVLLCHPRLECSGMITAHCSLKLLCSQ*PSHNSLLNSW EHRHMPPHLAKFFFHQOTKL*KK*NKNRSLESAPLSVFIKKVTTT
772	A	80	358	GPFFFFFGDRVLLCHPRLECSGMITAHCSLKLLCSQ*PSHNSLLNSW EHRHMPPHLAKFFFHQOTKL*KK*NKNRSLESAPLSVFIKKVTTT
773	A	810	1077	SLRSSKTQPRQHGKTSSLLKIQKISR V*RTLLGLKLRQENCLNPGG GGCSEPRLHHCTPAWATE*DSGSQKKKKGQGRKSCHFSVRT
774	A	499	946	LWLRPRGAGIAGAGICLRREGTWLLPLRSHGGKCEAASPVWSQRLEL LQKPSALWWPLGLLHVHIFWKYTCAGSFLAGKLLRITFNFFLFFFLP FPI SCIFYLFLFLFFFRDGVSLCCSGWP*TPGLKQSSCLSLPSSWDF KCTPLCLL
775	A	56	426	GQSPPGHWGHVAQARELLRPGRLPCWVPDGHTPVRPVSGPEPPTGSR ILSGEESPSRPPSSQAARPQPGQPRDPSSLRIPLLLPRP*LSQSGLA SSGSGLRAGALPRRPPGPALLSPTPCTSI
776	A	3	385	QGFRKLPLKTTTGKEKTHSCIVGLGHVNSGKTTTTGHLYIKCGGFDK RTIDKFETEADKAKGSFKNAWDLDKLKAERERGITIDI SLWKYETS RYYVTIIVAP*LIDFIINMSTGTSTQADCAGLIV
777	A	120	399	DGPGCWGFRRRWPEASWRDSARWHGCRSPGGPGPARPPCPA*GGCA* CGLTARPPQTAYYTWCRTPPAWRSATVTRTPC*GCPGAPAGPSAA
778	A	213	500	SKRCLSLGRGASSLEAAEHLSCCPQADGLSRSPQWASAPRQLLSCP SAGPRGPLQLARSPGSRGPWPVPQGGPPHQHSALTI*APAQRKRKN G
779	A	1	615	MEQVKTAALINGKILPRIPNEQKENADTSLAFSFISSQDGEITMLRE RVRIEIASTHIALQHAIVTGDVGMDDIPQEARQYRHNQAYAYS IQG DGAEDDDERIVRFHTRVTVDSDTLASDAARLTCRHAGVTGYFVHITV RKMLCDKQDTAAIHSRHTTAHRGEHIDYCGYSVLPMAVEQDVLI AVE PVKTYALQANTNPLYP
780	A	140	460	RSSLLPCLGLWTHLIPVKVRDSLGPFAFRGEKADMPVLYDRLLKLME MLYFKSGTIPMFYG*APRRVYIIGERIHYCGYSVLPMAVEQDVLI AVE EPVKTYALQLAN
781	A	595	1060	ARFLPKYQSPTGPHPSFNAFLSLGAMCVLPRPNFHS LAVRSPIVPGG PAPLVPGKE*EGLGVTSQSRPDCSPMSGTPRCRS*LRPAAGRGCS LLGGCPWTVTHPLRTKAGCTLSWAQQPVVLPVGEGGPCASPVAVLG FSPCALCHLDPPVK
782	A	71	237	EQPGMVTHTCNPSTLGGRGGWIT*DQEFKTS LANMVKPCLCWRYKKL AGHGGACL
783	A	236	405	EDGHSGLHSKQKQPAWPSMVTHTCNPNTLGGRGGWIT*GQEFETS

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				LTNMEKPCL
784	A	2737	2915	KNVVHTHQGILYSHKKEQD*LGVAHTCNPSTLGGRGGWIT*GQEFE TSLTNMVKPCLY
785	A	361	711	DLFWLF*MDKFLDTYTLPRLNQKEVK
786	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERHFD LSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLRVD PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
787	A	1	462	MVLSPADKTNVKAAGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHF DLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLRV DPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASTQREPTMVL VSCRQDQRGRLG
788	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWWTQRRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVSALSS RYH
789	A	38	485	APSPDA\MGHFTEEDKATIT\SLWGKVNVE\ DAGGETLGRLLVVYPW TQRRFFD\SFGNLSSASAI\MGNP\KVKAHGKKVLTSLGRCHKSTWDD LKGTFAPQPDVNCTCDKL\HVDP\ENFKLLGKCCW*PVFGNPIFGKEF TPEGAEPLGQKDG
790	C	128	274	MMDR LAVSCTLRNWAFSATTANTNPIYNVTLLGLVAQSARFIRPGGV QL
791	B	72	524	LPAPPGR IKRADLATRPSKVI RVRGRGRKRPVPGATLRKPVHHGVN QLKFARSLQSVAEERAGRHCALRVLSYWVGEDSTYQWITKPVHKKH REMRGLTSAGRSRGLGKGHKFHHTIGCLAGQLGEGAILSSSTVTAN ISKVCKIHT*
792	C	56	289	MNFTNFTYISGSGGAGEYCAFSKLPGESHRIVWWNLWPFPRRLLSA CRCQPQRHLPCALWELVLVNPTGCSRISSE*
793	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWWTQRRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVSALSS RYH
794	A	38	604	APSPDA\MGHFTEEDKATI\TSLWCKVNVE\ DAGGETLGRLLVVYPW TQRRFFD\SFGNLSSASAI\MGNP\KVKAHGKKVLT\SLGDAIK\HLD DLKG\TFAQA*SELH\CDKAAMWIPENFK\LLG\NVLVTRFGQSHFR QKNFTPEGCKASWAERWVTCWVPVALFLQDTTEAQLPMNAELFKDKA FILASNYK
795	A	23	153	APSPDAMGHFTEEDKATITSLWGQCPVLQIPLSSLPMMQSFQG
796	A	84	359	APRADAMGHFTEEDKATITSLWGANVEDAGGEALGRLLVVYPWWTQR FFDSF/GQLSELHCDKLHVDPENFKLLGNVLVTRFAIHRKEFTPE
797	A	1	428	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGT LHV DPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVSALSSRY H
798	A	2	476	VNVEDAGGETLGRLLVVYPWWTQRRFFDSFGNLSSASAIMGNPKVKAHG KKVLTSLGD/ASSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGT FAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQ KMAED\VTGVSALSSRYH
799	A	23	349	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAWGKVNVEDAGGET LGRLLVVYPWWTQRRFFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDA TKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVQPVLCCHHGQP QSOGTWQEGADFLGRCVQGEGRCWRRNPGKAPGCLPMDPEVL
800	A	17	535	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDATKHLDDLKGTFAQ LSELHC\IKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVL

				AIHFGKEFTPEVQASWQKMTGVSALSSRYH
801	A	17	533	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQ LSELHCDKLHVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMT TGVVGQGEGRWRNPGKAPGCLPMDPEVL
802	A	160	434	LISVIPALWEAKAEDHMRSGVQDQPGQGRKTPSLRKIHLARHGGMH L*SQLLGRLKHKNRLNPGGKSCSEPRSHHCSSAWATDQDSVSKK
803	A	1223	1339	RWPLWSFIIETKRRTL*SQLLRRLRQENLLNLGGGGCS
804	A	1057	1354	SQHFGRLWQVNHLSRGAPAQPGQKTPYLLKIQKLAGRDGARL*SQ LLRRLRQENRLNLGGGGCSEPRSCHCTPAWVTKRDSFSKTNKQTENN KKRIL
805	A	831	1084	SQHFGRRPRADHLRSGDRDHPAQHGETPSLLKRQKLASHGGRHL*S* LLWRLRQENHLNPGWGGCSELRWRHCTPAWATSKNSF
806	A	144	443	GYQLPLQDELVLGQFLFQVSKIRFFSARKITCNSHFLLLKFF*FPHI ICK*VSFSSERAAAADRAGASHPRIHNLQRLQENSIRGPKYSSHTV SADAW
807	A	165	1222	QSKRLNAKRYLLTDNVVKLKEFQOKKVAVACNLSGKTETYFRNLKKK LTQNKILKGEILITLLHLCESRDHVELAKNVIYRYHAENKNFTLGEY *FGLFVRLCYQLDLEESAGELMKDQHLRGFFSDSTLFNIMDMFLFI KGKYKSALQVLIEMKNQDVKFTKDTYVLAFAICYKLNPSFKICTT LREEALLKGEILSRRASCFAVALALNQENMAKAVSIFSQIMNPESIA CINLNI IHIQSNMLENLIKTLKNAEENLSKFVKRHFVSEVLAKV REKVKDVPALVAKFDEIYGTLHITGQVTTDSLDAVLCHTPRDRKSH LLLNKRMVSRRTFQPLSQSLLAE
808	C	324	500	MGNWGRSSFLKLQNLFLKMRSDQAQWLTPKIPALWEAEAGGSSE VRSLSAWSTW*
809	A	1734	1910	NWVGQQEGREFFQV*WATDLKSA*GEEIEPDIPKLKPGGQKWETGL RFLHFDKWWF
810	C	226	306	MTTSPPPSALQKKEMEILPVILRVPS*
811	A	168	258	GHLGPRQKQARGL*GHRVQVLHNYVIPM
812	A	229	436	TEELKRCRQTLPSGCGVLPWRARLAVGVS/GRRGRSSPMLTPSAAP CGNPGSLTSNLPAAGCKPSCQAW
813	A	1060	1542	GRDMVAPDASWKEASGCNAPARICPGQAFRANGCSDPTLGIQHQRLF RSRLSPKVLGPVGPWELGGE*DEAPSASFFSHWEVLGRLLVGASGS PSVKQEPAAALERARVPGDAARRQPRDRKGPPGPPCCSEHPAPVRAPL VAGLDAGSGAPRAKLGVM
814	A	166	437	ADHLKSGV*DQPGQHGEILSLLKLQ*FPGRGGAHL*SQLLGRLKQEN HLNPGGGGCSEPRCHWTPVRATVGDSVQKK*KSQDGPRAKLG
815	A	3	238	SGDRDHPG*HSETLSLLKIQQ\IAGRGGRL*SRLRLRQENGVS GGGACSEPRSHCTPAWETERDSVSKKKKKKL
816	A	4005	4346	SQHFGRRPRADHLRSGVQDQPDQHGETPSLLGGRGGRIITKSGDRDHP G*HGETPSLLKMQ/EKLAGRGGRLWSQLLGRLRQENGVSPPGRACS EPRSCHCTPAWLTEQDSVSKK
817	B	1	9234	MGAPTLPPAWQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCP TENEPDLAQCFKCFKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFE ELTLGEFLKLDREKAKNKIAKETNNKKKEFEETAKKVRRAIEQLAAM D*
818	A	1577	2233	SGCLLSPSPVGRQNSPVELGGAGLSRAGWAPQERGRAALLISPGPN VRGGPDWLPSVLQMRGLPLWDLGGRPDVGRMSPGGRPGSCWATQLRF HISSLAPLFSWAGRSGSRLNPSTLGGRGGPITRSGDRDHPG*HGETL SLLKIQKISQACWR/CACSPSYGRLRQENGVPNGGACREQRSGHCT PAWATEQDSVSKKKKKKSGSTIRLKHILHKII
819	A	151	455	FQKIGPGAHAACNPSTLGGRRRITRSGGRDHPG*HSETPSLLKIQ \KLAGRGGCL*SQLLWRLRQENGVPNGGACSEPRSRHCTPAWVTE RDSVSKKK

820	A	1362	1649	ECVHWRTAPRPFALCLAKLTVETCPRLVSDQSLWHRKTWPPKKKFWN WKPDNFGRLRQENGVPNGGACSEPRSHHCTPAWVTEQDSVSKKKKK K
821	A	10289	10708	SQHFGKLRQEDHLRSGVREQPGQHGTPTYLLKIQKLARRSGACL*SQ LLRRLRQENRLNPGGVCSEPRLHHCTTAWTLQ*DPVSKKLKKKYIE RQRYHQHMKHPWSTKIQYVCMG*HRSVEKQIIQTLCMFVFHTY
822	A	662	766	AHFLHIVLVLMPVIPATREDEAGESLEPGRWRLQ
823	A	749	853	AHFLHIVLVLMPVIPATREDEAGESLEPGRWRLQ
824	B	1	855	MDVDPDIFNRDPRDHYDLLQRLGGGTGYGEVFKLFAKCYTCIHTYDA MRVLFMLTKSGSQLPRLKEKGKWEYRTGGRSANVHYIIIVCESVHF LPILLPTLSTKPLSSPELNAAASYVPFPPIIHIDTAASMCYLFHMYV GVRAGGGIGDEIEDPAGDEYELRVVFDITFFFFVIVILLAIQGLI IDAFGELRDQQEQVKEDMETKCFICGIGSDYFDTPHGFETHLEEH NLANYMFFLMYLINKDETEHTGQSRALCRAFRGMRETGLVRLKEL AV*
825	A	65	290	HLVSSLAKGKLAVRQAPFARVPPQHP*VKVKNWDPLLQPPPCRGLAL KVTGCRVLGTEGLPHLKDFPIRAATQPL
826	A	230	653	GLSAPVAADPSLEPTPALHASIRPEADLQP*PRTPLRSWGS/PGVR SPRTGDPSPGVTRLHRAIHQ\PITISSSTWVTCTGPLCSVLISPSQQE SAPKRTVLEEHLRPPPGAHADAHSQQLRAWPGQOREHGQEASQWEQ HP
827	A	108	1102	RMTQCLSECLICKFLSGKVTLGQAQWLTHVIPALWEAEAGRSPEVGR SRPSLAGMVKSRL/VLKIQKKKKKKKISRWWHMPVVPATWEAEAGE LLEPGKAEVAARRDRATALPAWGSQADGK*G*GLSAPVAADPSLEPT PALHASRRPEADLQP*PRPPPLRSWGSQVCEVPGLTTPPGSPASQSH PSTPSPYLPLPGSPARVPCARCSSRPASKRARQSAPCGRAPTSPAAR GSRRCTQRAAQLARSAAARTRTEASAVGTAPAAAGRTGRGGPDKQEFV HGLVPLKQDNGRLQCTAQERAPRARTLRHTARPAAFVGLDLGGNHVL PCQ
828	A	241	1104	QNILLGPKTLTSLGPLQFRDVAIEFSLEEWHCCLDQAQRNLYRNVMLÉ NYRNLGFLGIVVSKPDLITCLEQGRKPLTMKRNEMIAKPPVMSSHFA QDLCPEQSLKDSFQKVIVTRYEKREYGNLELKKGCESVDEGKVHKG YNGLNQCLTATQSKVFQCDTYVKVSHIFSNSNRHKIRDTGKKPFKCI ECGKAFNQSSTLATHKKIHTGEKPYRCEECGKAFNQSANLTTKRIH TGEKPYKCEECGKAFNWSSDLNKHKKIHIERKPYIVKNVTDLLNVPP LLISIR
829	A	95	463	PAGIRRVARTPGPPGSLEMGPLQFRDVAIEFSLEEWHCCLDAAQRNL YRDVMLENYRNLIIFLGIVVSKPNLITCLEQGGKPLTMKRHEMIAKPP VMYSHFPQDLSSEQSIKDSFQKVILRKI
830	A	2	648	FVKMAAPAGGGGSASVSLAPNGRRHTVKVTPSTVLLQVLEDTCCRQD FNPCEYDLKFQRSVLDLSLQWRFANLPNNAKLEMVPASRSREGPENM VRIALQLDDGSLQDSFCSGQTLWELLSHFPQIRECLQHPGGATPVC VYTRDEVTGEAALRGTTLSLGLTGGSATSQVCHEVLRPRGRPPQEA WARQRLARQPPALHFPWNLGSSAAAT
831	A	90	401	AGMLPAVGSVDEEEDPAEEDCPELVPIETTQSEEEKSGLGAKIPVT IITGYLGAGKTTLNLYILTEQHSKRVAVILNEFGEKSALEKSLSVSQ GGELYEEWP
832	A	276	490	TNFLSKTMYFKRAARFPVLLTGAGKTTLNLYILTEQHSKRVAVILN EFGEKSALEKSLAVSQGGELYEEW
833	A	186	537	IWFPLRRRKARQEEKSGLGAPRSPSHNYPGYLGCLGKTNTS*TYIL DQSNIGKRV\AILN*ILGGRKLRLKSLSCQPKVEELYERVAW/IP *KPGCLLLSVKVRNVFDWCTWVY
834	C	79	405	MIGGTPQMFFISGAKQWSPSLQPPPRHRSSPWAPSSKSTSGGTAA LGSLSKDYFPRTGDGVVELRRSDQRRALPGCPTVLRTLLPQQRGD RDLQQLRHHELRL*
835	A	1	321	MDLLCKNMKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSSETLSLT

				CTVSDVSITSGNYFWAWIRQPPGKLEWIGSKFHTGTNLYNESLKSR VTFSIDTSGSTRP
836	A	101	290	FSSEHINQACEMHPPPCPSYFKPSVVHSTVCTTSLFKHSSVFLAPKQ IWVRFVYAETTYEEGP
837	A	21	215	PSATPRQTGPATTMNSKGQYPTQPTYVQPPGNPVYPQTLHLPQAPP YTDAPPAYSEVLVPCQI
838	A	158	955	KMTSSSEQEEDKNNQSATPRQTGPATTMNSKGQYPTQPTYVQPPG NPVYPQTLHLPQAPPYTDAPPAYSELYRPSFVHPGAATVPTMSAAFP G\ASLYLPMQA\SVAVGPL\GSTIPMAYYPVGPIYPP\GST\VLGGK GGYDAGARFGAGATAGNIPPPPPG\CPFNAAQLAVMQGANVLVTQ\R KGNFFMGGSDGGYTHLVRNQGHLCAREKTSHTLQHFSQCNCFSHINL KLQFRHMLLGLCSGAQTFRHFSNLIRNHVMVAVPP
839	A	217	491	LQVVVSNRVVTSPPCIVTSTYGTANMERIMKAQALRDNSTMGYMAA KKHLEINPDHSIIETLRQKAEADKNDQSVKOLVILLYETALLSS
840	A	1789	2411	KTYWRKKVEKVVSNR\LVTSPC\CIVTSTYGTANMGENH*KLQAL KETTSTMG/YMASQRKHRGIKPLTSLIIEYLKAKRPEGLIRTDKS\ VKDL\VILLY\ETALLSSGFQSWKIPRHH*QVSYRMIKL\GLGIDE DGPYLLDDTSA\AVNLKELPP\LEGDDDTFTHGKEVGLILLGLRGWT LPVSVLYNSSDNIFQGCFFPLFLVNI
841	A	225	338	RSSSSPSLGLCTCAAGDPPLMFNEDYQKSLLEQYHL
842	A	610	834	ISIPQGYLYCRGLQVPSDLPHHPSALCCCPSPGSIGFSLLTQTRQV PASGLAWLLAGGWGNSCSTCSLTSTFYTC
843	A	36	353	APRPGAMGHFTQDDMATITSLSGQVNVEDPRGETLAWLLFVYPWTHR LFDSFGTLTSASAIMGNSKFKAPGKMVLTSLIDAISHLDDLMGSFYQ LIELHCDKLPV
844	A	3	259	HEPQTQREPTMVLSPACKTNVKAAGKVGGAHAGEYGAEALERMFLYP RMTRTYLWYFCLCHCCRQAWGPGFNFWTTCDGQCQTRRH
845	A	3	663	EGKWLAWKHNPLSLFEFVLSSFLVPCDSRPTCCDVCRGRNWSATQPG SYHSLDMTEALQWARYHWRRLIRGATRDDDGPYNYSSLLACGRKSS QIPKLSGRHRIVVPHIQPFKDEYEKFSGAYVMNRIRTTKYTLNLFVP RNLFEQFHRAANLYFLFLVVLNWVPLVEAFQKEITMLPLVVVLTIIA IKDGLDYRKYKIDKQINNLITKVYSRKKKK
846	A	33	382	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQ LSELHCDKLHVDPENFKLLGIK
847	A	21	371	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKA/HPENFKLLGNVLVTVLAIHFGKEF TPEVQASWQKMVTGVSALSSRYH
848	A	24	474	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQS FGNLSSASAIMGNPKVKAHGKKVLTSLGDATKHLDDLKGTFAQLSEL HCDKLHVDPENFKLLGNVLVTVLAIHFRKEFTPEVQASWQKMVTAVA SALSSRYH
849	A	24	415	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDATKHLDDLKGTFAQ WPVPCPPDTTELTAHDAELSRIGFILQAIQIINLFC
850	A	24	432	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRF FDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVHFGKEFTPEVQASWQKMVTGVSALSSRYH
851	A	323	737	QAACGLWGKVNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGVSALSSRYH
852	A	24	589	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQ LSELHCDKLHVDPEVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGVSALSSRYH

853	A	100	684	MWKMLEEKPWEGSWLSTHGPRGSLTALATCPLPLPSWATPKSRHMAR RATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLSSASAI MGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPE NFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGRRNPGKAPGCL PMDPEVL
854	A	135	851	APSPDAMGHFTEEDKATI\TSLWCKVNVEDAGGETLGRLLVVYPWTQ RFFDFSFGNLSSASAIMGNPKVKAYGKKVLT\SLGDAIKHLDDLKG\T FAQA*SELH\CDK\LVDPENFK\LLGKCAGDPFLAIPFSAKEFTPG GCRLPQGQDG*LGVGQCPGPPDTTEAQLPMNAELFKDMALFLQAITN NKSISAKRSNFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGVAS ALSSRYH
855	A	40	505	QPQTVSILHLTPEEKSAVTALWG\KVNLEVDVEALGRL\LVVYPWT QRLLESFGNLSTPDAMGNPKVKAHGKKVLGAF\SDGLAHLNKLKGT FATLSELHCDKLHVDPENFRLLGQRAWVS/LAGPITFGKEFTPPVAG LPIRKL VAG\VANALAHK
856	A	41	536	APSPRRPWGHFTEED\KATI\TSLWGK\VNVE\DAAGET\LGRLLVV YPWTQRFDD\SGNLSSASAI\MGNP\KVKAHG\KKVLT\SLGDA\T KHLDDLKG\TFAQA*SELH\CDK\LVDPENFK\LLG\NVLVTVL\A AIPFSAKEFTPEGCRASWAERWVTWSWPVPCSSRYH
857	A	241	435	GARLQKAGSGFEAVAGEALRKSEIEYYAMLAKTGVHHYSGNNIELGT ACGKYRVTCLAIIDPGD
858	A	243	451	FCYFLKALTTLTVKEVVTFSLSVTWYRIYLFHAFGSQRKSEIEYYA MLAKTGVHHYSGNNIELGTACG
859	C	275	397	MLCWLKLGHHYSGNNIELGTAMRENTYRVLHTGLFIDPG*
860	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERHFD LSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLAHAKLRVD PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
861	A	73	608	SVMTVPVAPTLLKAAASKSDSSGPHRLRENPPWCLSPADKTNVKAAGKV GAHAGEYGAEAL\ERMFLSFPTTKTYFPHFDLSHG\SAQV*GATGK\ KVADAL\TNAVA\HVGRTPNALSGPEATLHAHK\LRGGPGSTFKLL \SHLPCLGEPWAAHLPGRVSPPLGGCKASLGTNFGFLKQPC
862	A	7	330	LREPYTRKETHQNIKPTGRANTQIKRKNLYVTTEKPPPTTMKNMNR ERKEEMLYKNQKSITKMTGISPVISIIILNTNELNLSLKRYRGAERI FLNDPTTCCCLQEIH
863	A	2	380	APSCQPTMSSQIRQNYSTDVEAAVNSLVNLYLQASYTYLSLGFYFDR DDVALEGVSHFTSACNGPQLLLRGWLLRLRRLQVQKVQMHLQEE LLLLLPPGLCQVCPGLHLQRGVREVQLLCLMS
864	A	3	722	HERGSVSCFNSGWTDHIRGHLFQPPTALRFPLRLQPPGPSSRSPAS GTCQHQLWLAPSCQPTMSSQIRQNYSTDVEAAVNSLVNLYLQASYT YLSLGFYFDRDDVALEGVSHFFRELAEE\KREGYERLL\RMQTQRGG RALFQDIKKPAEDEWGKTPDAMKAAMALEKKLNQALLDLHALGSART DPHLCDFLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFER LTLKHD
865	A	40	264	SGYKLRHSSREWQPPLGPLPSYGSSVFTLLNLATARSSGLCLLRLLEL SFCSLSTTAVCRCYRPAIDSHPGPPLLF
866	A	3	1231	ISLPDLNINSMLEQRREPWSGESEVKIAKNSDGRECIKGVNTEMSSS VKTPIFNRNDFDDSSFLPQEQKVLHREKPYECNEHSKVFVSSSLTK HQVIHTVEKPYKCNCGKVFVSRNSHLAEHCRIHTGEKPYKCNVCGKV FSYNSNFARHQRHTREKPYECNECGKVFVSNNSYLARHQRHAEEKP YKNECGKGFSSHKSSLANHWRIYTGEPYKCDCEGKAFYRIALLVRH QKIHTGEKPYKNECGKVFIONSHLAQHWRIHTGEKPYKNECGKVF NQLSNLARHRRHTHTGEKPYKNECGKAFSEYSGLSAHLVHTHTGEKPY KCSECGKAFRHKLSLTNHQRHTHTGERPYKNECGKVFNRIAHLARHR KIHTGEKPYKNECGKAFSRI SYLAQHWTHMG
867	A	3	498	GHAARLTSKESCWDEKAQKRKRKAYESGMALPQGHLEFRDVAIEF SQAEWKCLDPAQRALYKDVMLENYRNLVSLGISLPDLNINSMLEQRR

				EPWSGESEVKIAKNSDGRECIKGVNTGSSYALGSNAEDKPIKKQLGV SFHLHLSELELFPDDRIVINGCNQ
868	A	1121	1442	RSLLAYPLPALSPGCSVVPLTAHQGSLNSSEKNAPHSVPGAGGLDF YLPSRVCILYRGNCMKNWGGGRARWLTPVIPALWEAEAGGSRGQEI ETILANMVKPRLY
869	A	2380	2714	EETEGQARWLTPVIPTLWEAEAGGSPEVGSSRPA*PPLSAFLYPAFF LRSARFL
870	A	3260	3533	HFKQNRKLGKCLFKRAGQARWLTPVIPALWEAEAGGSRGQEIETIL ANTVKPVSTKNAKISRRAWQAPVVPATREAEAGDWREPRRTL
871	A	6330	6802	RSKGRAKIKSRRAGQVQWLMPVIPALWEAKAGGSPEARS*PAWPIW *NPALHSSL/V**SKALSQKQKKQKNHGDGQHDETVSLLKIQKSAG AHL*SOLLREAEAGELLEPRRQLQ*AEILPLHSLGLDKSKTPSQKK KKKRSQQQGVGVREPQGP
872	A	1	500	MPTLASPGALPLASPSPTWALAEKSGGKKPAECPPLLCGRVRAGAHT HTHACTFPKQEAALCQDRMEFRFPEGVLGLQLYGCMMKKGPSVCAGG WERGASSSAHIYLGPKQNPQLAVLSPATPSLGHIPSLPEPTLGGPGK PASTPPSPAGRPSPSPHGAASKYK
873	A	63	377	QNLCLGKGLMALSLGWKAHRNHCGLLLQALRSSGLLLFPCGQCPWRG AGSFLDPEIKAFLEENTEVTSSGSLTPEIQLRLLTPRCKFWWERADL WPHSDPYWAI
874	A	27	376	DRRSVANMHLVRGEELHTFEVTGHETVAQIKAHLSLEGIAPKDQV ELLADAPLKDEATLRQSGAEAMTTLEVASRMLGRKAHGLARAGKVR GHTPKEANQDWKKSMTGRAKRC
875	A	1	801	MATWRRDGRLLTGGQRLLCAGLAGTSLSLTAPLELATVLAQVGVVRG HARGPWATGHRVWRAEGLRALWKGNAVACLRLFPSCSAVQLAAYRKV VLFTDDLGHISQWSSIMAGSLAGMVSTIVTYPTDLIKTRLMQNI PSYRGLLHAFSTIYQEGFLALYRGVSLTVVGLPFPFAGSLLVYMN EKIWNQPRDQFSLPQNFANVCLAAAVTQTLSPFFETVVRKMQNIQLF LFIGVSISSNIKPSVSLLLYTPVDFDPITAHK
876	A	1286	1389	WQMAAVGLIMQNIPEPSYRGLLHAFSTIYQOEG
877	A	1	1056	MEPSNICKLGLLIRPKADDCRVVLAKQEITRLLLETQKQQQFTEVA DHIQLDASIPVTFKTDEVFLEAQIQNMTTSPMFMEKVSLEPSIMYN VTELSNSVSQAGECVSTFGSRAYLQPMQDTRQYLYCLKPKNEFAEKAGI IKGVTVIGKLDIVWKTNLGERGLQTSQQLQMAPGYGDVRLSLEAIP DTVNLEEPFHITCKITNCRYKILNILGFAGRKVSVTNTELCIVLQEQ PVAKKYSGVTKEQLTREAEQKSLNRRRDNRVHIGPKMEIRVVTLGLD GAGKTTILFKLKQDEFMQPIPTIAVVVFVVDSSHRDRISEAHSELA LTELKELRDALLIFANKQVFAAG
878	A	651	1469	RCETVLNHFQNMMLSHSTVMVCTVDLLEFQPSLKKQYLTWSHTLKEQT NSGNLVMRLTKPTLFTNIPVTCEEKDLPGDLFNQLMRDDPSTVNGAE VLMGEMLTLPQNFNIFLGETFSSYISVHNSDNQVVKDILVKADLQ TSSQRLNLSASNAVAELKPDCCIDDVHHEVKEIGTHILVCAVSYT TQAGEKMYFRKFFKFQVLKPLDVKTKFYNAESDLSVSTDEVFLEAQI QNMTTSPMFMEKVSLEPSIMYNVTELSNSVSQAGECVS
879	A	3	416	HAWQPLRTCESFLPLHSPQLSHAGGGFGACTCTLTSTRRLTLVPL RKDPEGALAEAGEMGNPLSPHTPVASSGMKHTGEKPFECPRCGRHFL KENLLQHDARICMSRSEQVFTCSACQVTFRLKKKLVRHSAHT
880	A	164	412	PQQTSGPPGMASSRAVQVKLELGHRAQVRKKPTVEGFTHDWMVVRG SEHSDVQHFPAEKCCFLHESGTTLLRVYSHPSYRV
881	A	29	490	GEFFHMERASTITYLKGETIGTEPEGKGECEASTGLVNPRFDFPSK VSFPKYRINKRKQKQNTTSLSGTKQNPQILFYTRHEVKSLSSTVSP HGRKASTQSLSRNFHSEASEHAEDGALRVPLPSWRPPSGVETVKSRS HMPEDHQPTTHW
882	A	44	847	IKENSFIWIRASTITYLKGETIGTEPEGK\EGECASTGL\VNPRFD FPSK\VSFPKIPV*TSLHITPL\AIVCPFQNIWSLHGKGQRGKG\QN INKRETKNKTTLFREPKQNPQIPFF*TTQGH\EVKSLSTSVPL*IT

				GRKA\STQSL*QEFSTLEASEHAEDG/ALLRVPLPSW\RAPSGVGTV KSRFSH/VPRDHQPTTHWWPWSMAGRQRPSPTLSHFLSWMTSCLGP SHFRRELAFWKPTFPIHHRTRQSAHILVPLVFKGHFQOTL
883	A	40	431	ESPEAGTGSWLGRTNRQGINTLADHRHRETDFGGSPWIIIIIEFLGR YKFTILFCTIYLWEPFLKTI FWSRNGHDRSRDVOQRAMRSNRCLQEG IKIGPEDICTLWKQAE TKVQAKIRKMKVTKKVNHHY
884	A	122	342	WWSLETRMRTDRVPMKPSWTRTPSFARALKTSTHSWGPLIARVILRV ATTARGYRAMIRAKFRSILPANAIGH
885	A	23	420	WDLSTMEPKKAMKRAGANSNGVSMFEQTQIQEFKEAFTIMDQNRDG FIDLNDLRDTFAALGRGNVDNEEIDEMIKDAPGPNFTAILTMFGEK LMGADPEETILNAFKVFD PVLKRELKADYLRKMLTTQA
886	A	1	598	LARNPGSTHASGGILLGRQCWVLTMAPKKAKKRAGGAN\SNVFSMF EQTQIQEFKEAFTIMDQNRDGFIDKN\DLRDTFACPWRLNVKNEEI DEMI\KEAPGPINFVFLTMFWGRNLKGADPEGKPLNRISKVFDPE GKGVAEGLDYVREMLNAGRRGFPRKEVDQMFAAFP\ DVTGNLDYK NLVHIITHGEEKD
887	A	174	454	ERNPPRGGGGFPRGALFFSPFLRGGFSGGPPKPRAPPPPPFLKG GPPPGGPGGVAPLFFPPCPGGGGGFLKIKPPPSGPPPNKPFLLGG
888	C	60	245	MAXPXGPXLFYSPXLXXXQXGFXPXWAXXGXPPXLQXXQXAXXGXQ XFPVSXXERKTPLGP
889	A	1878	2295	SFSPAWP SRWCASSSWCTDCLVPSTCAALQHPVVFLDKGNHFLIFFY FFFFVILYTSSSHEVED*PCVMFSKIKWYLLE/VRYILVVAYRLSFC KERKKTIKLCQIILLCLAARTWLPCLSLSLPPFLSFLSLCMDFFEKK
890	A	3218	3469	GFTMLARLVSELLTAGDPSSLGSQSAGITGMSHHAQPSMHFFYFFFE TEFRTSCPGWSTMVRSWLTATSTSWVQALLQPQPPE
891	A	618	1238	QORRYSGERDEGRDPLCKDEPQGASSEAPLLVLLFSRGVMMHLHQSC SPSCQSRQGGKAANIWSTSSLENLSAWVVSISRTVISLQHPFAFRVK HFECVENGFLRVRSCLKFLPKHCEEHCKVNWTRSLLDHFINFFIFHVH SPKSGKGVSI VLVNEAIPVLVHDSEGLLKFLDLGLFEHGEHVGVGA PGSLLCFLRCHGGKDPAL
892	A	12	138	TDHIMREYKLVVLGSGGVGKSALTQVQFVHVISVVLYLLIL
893	A	1	1002	MKRDPDVGVLDDNAEAQLDSHMKPKHGRNPLSSLMRKACSRGKAMTE QCMEVRIMNFCRSRTIAGINQESQENPQRSEGSRLLLQDPGDTNPNTGS LRKAARGTGKGHCRRKPPAEVCNNLNRQRI SWPELGGGHESVQTSQ EATSLGKEGEYI I KGTPCGTKESEQQPSALDLP SDKAYPNEKEPENQ LCSPAMPDPNQEEI PDLSEKEFRLVNKLIREAPEKVIAINTKRTYINN FLKEQLIINHSGKLGATNTTCGQAVFQIMACFGLKVGSEKAGTGRAD FFPLALHESYFRVGVGCLALAKSDTPAMGARETAYGDQPFETLRLG EEHRT
894	A	66	295	RLLFRFFCPTGCSLDVVL SLFS*GCGFL*SLHTGFMPSPFEWPGDSL SVQIVTNFSWRFSSAVAFSSASGSFPQGS
895	A	2202	2337	GLPNHASHTACRFSSSFATLKTATLTSPPLPPQPTQHEDTQIR
896	A	343	906	YDKTRLFNTVPLPPPHKKI IKKI IQDIKGEILRAFPPLRTGTHRCPL SPLLNFILLEVLARAIROEKEIKSIQIGKEEVKLSLFADDII IYLES PKYSSRKLQELIKEFSKVSRYEINVHKSVALLYTNSNQAENQIKKST PFTIAAKNKIKYLG IYLTDAKDGKYNKYKTLMEI IDDKNKQKYIP
897	A	1455	1604	LGVLAQLGKNGGLWSQAMEFQTMQAQALLCLPRWLGSLSLPLVCLAP QA
898	A	370	807	CCLSWTFHIVKHVGLLCLGSLSQGATIGVDFMIKTVEINGEKVKEK GGEYHIKGTSCGTKESEQQPSALDLASL TEPTQIRRNQKTNSGNMTK QGS LTPPKITLAHQQWIQTNNKSLIYLKKN SARHQRKAKPDARKSK KQYEK
899	A	1	1548	MLPERVPDPDPKKGFWDLVEERIQGESISCRKRIQRASVEAGGYCKV QSKDDEGQRRGGKNGEKLSDSALLPRLEKLSDIRKKPPRYPLHRA CSVLRPGFDCGTPASGPLRASGVRVPLNRAGSLLGNRAARAGAALRW

				LSPEPARRGRGGQSRGTGGCRARVVVVFEERFGLSRRHPRFQILEEV PGEMDARRKHWKENMFTPFSSAQDVLEETSEPESSSEQTTADSSKGM EEIYNLSSRKFEESKFKRKKYIFQLNEIEQEQNLRENKRNI SKNET DTNSASYESSNVDVTTEESFNSTEDNSTCSTDNLPALLRQDIRKKFM ERMSPKLCNLNLEEELNMKYRKIEEFENAEKELLHYKKEIFTK PLNFQETETDASKSDYELQALRNDLSEKATNVKNLSEQLQQAKEVIH KLNLENRNKKEAVRKLKHQTEVGNVLLKEEMKSSYELEMAKIRGELS VIKNELRTEKTLQARNNRALLELRKYASSMVTSSSILDHFTGDDF
900	A	3	127	VLCQFSKGMPLPVFAQSV*YWLWVRYVPSIPSLLRVFSMKG
901	B	1	1926	MFSDSLTPMHKERIVTLLKREGHVVGFMGDGINDAPALRAADIGISV DGAVDIAREAAADIILLEKSLMVLEEGVIEGRRTFANMLKYIKMTASS NFGNVFSLVASAFLPFLPMLPLHLLIQNLLYDVSQVAIPFDNVDE QIQKPQRWNPADLGRFMIFFGPISIFDILTFCLMWWVFHANTPETQ TLFQSGWFVVGLLSQT LIVHMIRTRRVFPIQSCASWPLMIMTVIMI VGIALPFSPLASYLQALPLSYFPWLVAI LAGLATNSDRFDLNLHV FRQTGNFNARTCREGGVVFGEFGFASGFFDRFYVIQRLTCLCSDVCR YFARFRIYRDLTGDDHIAQINXLYVRPIAAGPAPGTFRLWHSRRAM LLTRADMEDRERFLNARDTLRALLDNNIVPVINENDAVATAEIKVGD NDNLSALAAI LAGADKLLLLTDQKGLYTADPRSNPQAEIKDVYGD DALRAIAGDSVSGLTGGMSTKLQAADVACRAGIDTIIAAGSKPGVI GDVMEGISVGTLFHAQATPLENRKRWIFGAPPAGEITVDEGATAAIL ERGSSLLPKGIKSVTGNFSRGEVIRICNLEGRDIAHGVSRYNSDALR RIAGHHSQEIDAILGYEYGPVAVTMHMYR*
902	A	1	1602	MFFETNENKOTTYQNLWDTFKAVRRGKFIALNAHKRQKRSKIDTLT SQLKELEKQEQTHSKAYRSLEITKIRAELEEIVKQKTIQKINESRSW FFENINKIDRPLARLINKKRDKNQIDAINKDENITNPTETIQTTIR EYKHLIYANKPENLEEMDKFLDYTLPRLNQEEAESLNRPTGSEIE AIINSLPTKKSPPGPDGFTAIFYQRYKKELVPFLKLQFQSIKEGILP NSFYEASIIILPKPDRDTTKKENFRPISSMNIDAKILNKTLTNQIQ YIKKLIHHDQVGFIPGMQGWFNHKSINVIQHINRTKDKNHTIISID AEKAFDKIQQPFMLKTLNKLIGIDGTYLKIMTAIYDKPTASTILNGQK LEAFPLKTGTRQCPLSPLFNIVLEVLARAIQEKEIKGIQLGKEE VKLSLFADDMIVYLENPVSAQTLLKLISNFSKISGYKINVQKSQVF PYTNNRQTESQIMSELLFTIASKRIKYVGIQLTRDVKDLFKENYKPL LKEIKEDTNKWDILCS
903	A	1	972	MPWADKRNPSGAQSLNGYAPPDLIWGPSHRAFRQAQVEYSIGISSIYN SGTHTLPI LNQEDFESLNRPTGSEIEAIINSLPSKKSTGPDRTAE FYQYNKELPLWDIFAKICSIPHPSYHEEQLAEYIVGWAKEKGFHVE RDQVVFQALIHVLVKNMGTGILGLPHRCEERGHGPGQSRLIQLWEQLF SIYGIHVGQMLLTRADMEDRERFLNARDTLRALLDNNIVPVINENDA VATAEIKVGDNDNLSALAAI LAGADKLLLLTDQKGLYTADPRSNPQA ELIKDVYGIDDALRAIAGDSVSGLTGGMSTKLQAADVFRQAQ
904	A	280	358	SHFSCYQONDSPYQGGVFFLTIFHPT
905	A	141	152	QCPPQPRPPGRCPPTQSGHTGCSTGG*GLNPLYYNLCDRSGAWGIVL EAVAGAGIVTTFVLTIILVASLPFVQDTKKRSLLGTQLRGCHHTAG TMGSC
906	A	177	247	SWQEAGARSSGSPNPPTASPRHR
907	A	574	737	AWEGAHVFTTSPSSCHSWVRDYARVGLPPLPLPCPQRALLGLWEVWK GAYSPAI
908	A	221	576	GVGGDTHDTHPNTGREGGPSRSGAHVAGPARGRRSLESPLPGARSSG PSPNPASPPLTQSHT*GFPRPESSCRLSRGVAAWWLWAEYIVF KPAGSSWHCPSWLLAVARGRMS
909	A	1	157	TKTWTLLKKHFVGYPTNSDFELKTAELPPLKN/GRVAAKRLKEGDTMM GQQVAK
910	A	3	484	VRLREDDRRGPSLGTCHKSDPGRPAQSQPPSPGSGTFGLLSFRMVR TKTWTLLKKHFVGYPTNSDFELKTAELPPLKNGEVLLEALFLTVDPYM

0924

				RVVESKNVALPKGTIVLASPGWTHSISDGKDLEKLLTEWPDITIPLS LALATVGMPL\TAYFGLLE
911	A	1	1148	MLLCQKAPSLKTTYNHPPAADSAGTALNLETTVKQTRTQLEYNNVG TDLSPPEKSFNYPLLSSSSGDQFEIQLNQQLWSLIPNNDVRRLVSHVI RTLKTDCTETHLQACAKLISRTGLLMKLLSEQQELRTVSMTAWKPR MNRKSRSRMRQSHFASHAGRWVHNHSTLQFQSPKLQMAELSEARRRS FRMVRTKTWTLKKHFVGYPTNSDFELKTAELPPLKNGGLEFLIAYGM LYFVEVLLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVA LPKGTIVLASPGWTHSISDGKDLEKLLTEWPDITIPLSLALGTVMGP G\LTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGCKVVG AVGSDEK
912	A	214	540	ASGWVRTKTWTLKKHFVGYPTNSDFELKTSELPLKNGEVILLEALFL TVDPYMRVAAKRLKEGDTMMGQPVAVQVIISICPQCLENMSPLYLLLG PVSVHCSYNLFSLCC
913	A	495	686	TDQQNEVTLSHEVTLQPKHVNIHTDITIYPLFGFFFETQSRSLSQP GLQWRNHGPLQPPPE
914	A	1	1911	MGRKQSRKAENSKNQSSSSKDCSSLPATEQSWTENDFDELTEVGFR RSVITNFSSELKMYVRTHCKEAKNLEKRSTQFIKQVLRDLQRLDSHT IIMGDFNTPLSILERSTTQKVNNDTQELNSALHQVDLIDIYRTLHPK STEYTFFLAPHHTYSKIDHIVRSKALFSKCKRTEITTNCLSDHSAIK LELRICKLTQNHNTTWKLNLLNDYWVNNEMRAEIKMFETNENKD TMYQNLWDTFKAVCRGKFIALNAHKRKQERSKIDNLTSQLKELEMQE QTHSKASRRQETTKIRAELEKEIETQKTLQKITESRSWCFEKINKIDR LLARLIMKKREKNQIDTIKNDKGDITDPTEIQTITISGYKHLSTNK LENLEEMDKLLDITYTLPRLYQEQUESLNTPTITGPEIEAIVNSPPTKK IPVSDEFTAIFYQRTNDKNHMIISIDAFAFDESQQHFMLKTLNLKG IHGTHLKILRAVDKPTANIILNGQKLEAFPLKTRTREGCPPSPLLF NIVLEVLTRAIRQEKEIKGIQLGKEEVKLSLFADDVIVYLENPIVSA QKLLKLI SNFSKVSGLRVLNVYGSFQDMETQGLRFFGQNSVPQQLR PYNGASLQTLSEGEKASAPAKDHCLV
915	A	3	1381	KTPFVGQYQHQRPKVDKTTKMGRNQSRKAENSKNQSTSSPPKDRSSLP ATEQSWTENDFDELTEVGFRSAITNFSSELKEHVLTRRKEAKNLEKR LDEWLTRINSVEKTLNDLMELKTMQELRDARTSFNS*FNQVEKRIS VIEDQIDEIKQDDKAAETCNWRWVSESLRQLRASVDAFHARASHYNA GECLEHQLAALNSRLNCAQEMARRDSIGEVPPVPWRTVVGSGIAGEAK LDHLRLVSLIGREVNKENSAPATRWFSPQAGALAGGQIVLQAAKPN AHGQPVVATRNLLNPAGIVAVLKQRPRLVAAAQAFYLRDPIDLRAC RVFKTFLPETRIMTSYYAIEWSLWTLVDVLHAENSESAHMSHNSYDP PSDVARHLTHLPMSPIDYIIARFRYRHRSRVRLTARKLSAPAFMRCS SEIQRYSTMLERGFNGGYCRSTTVRVVTEATRMLSF
916	A	1	1191	MAHACNPSTLGGQKKVNVSNLETLLNNIEIEVGKEEYEDLLNHLPV DENEMVDVNVMDKAKAFTGEKVNVSNLGNELRKMGLVLTDEEHEKL LKTLPIRRPRVNTKKVEIFLENMGTIKIDEELEELITQLPTEERNV NINEKVIYTKTPSVGHQHQRPKVDKTTKMGRNQSRKAENSKNQSTSS PPKDCSSSPATEQSWTENDFDKLTVEVGFRRSVITNFSSELKEHVRTHL KEAKSLEKRLDEWLTRINSVEKTINDLMELKTMARELHDACTSFNSR FDQVEEKVKRATDTYNLGIALLHREKEMNLWQKIRGDLIGMSRNE FYDTFSTYTWSWNVQCELLSPKDLRLYDAYVNRNSSHNSRSSSSSDT SECYTDSGRKRKRKGLKGFQQ
917	A	1	227	GTRDPGVVHSLLLSESQESDQOPLPPPGPRSPELIPMELCRSLALL GGSGLMTWLIACGTDHLPWTSLSLVRL
918	A	1	392	CTSGTMPLVSVFMEADESEKAAREQELEGTEQTLDAEEEEQEESSEA ACGSKKRVPVPGIVYLGHIPPRFRPLHVRNLLSAYGEVGRVIFHAEDR FLRRIKNAYSICRRIIAFYTYDFTNQLYIYIYFIK
919	A	157	388	PLMHILKYTMVYLVCPLLSSSHNLPFTPVKLLSYSLFYPYFHFSRFL RLCCLRLFLSFFYSSSLHSLYSFPFLLSP

920	A	451	593	DQFRPLRPKNPTPPRTCEHTLTATPVTRAATHTHSHPHPHAHPRR
921	A	467	1038	KRCFQVFDYALPPKRWFKDYNADFLQGLQAFQNLVAHKDIA NCLAVREFLCDDPPGPFDSLEESRAFCEETLEETNYRFTERTTWNK RRWIHLKKLLSEKQLHIDTLENRIRTLSEPEESLDVSETEGEQILK VESSALEVDQDVLDEESRADNKPCLSFSEPENAVSEIEVAEVAYDAE ED
922	A	233	346	QLHTLDSFSQDVKIRFHIIMRLFPLLMPIFFTQWQDNV
923	A	1	1386	MDIKKGITDISASLRVESGWEARTRKEKTHINTVIGHVDSGKSTTT GHLIYKCGVDKRTIEKFEKEAAEMGKCSFKYAWVLDKLAERHGI TIDISLWKFETSKYYVTIIDAPGHRDLIKNMITGTSQADCAVLIVAA GFGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSPEPPYSHK RYEEIVKEVSTYIKKIGHNTDTVAFVPVSGWNGDNTLEPSANMPWFK GWKVTRKDGNASGTTTLEALDCILPPTRPTDKPLCLPLQDVYKIGGI VNVATEVKSVMHHEALSEVLPGDNVGFNVKNVSVKDVRRGNVAGDS KKDPPMEAAGFTAQVILNHPGQISAGYAPVLDCHTAHIACKFAELK EKTDHSGKKLEDGPKFLKSGDAAIVDMVPGKPVYVESFSDYPP LGR FAVHDIRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
924	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLVAFVPI SGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTTLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTEVKSVMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNDPPMEAAGFTAQVILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
925	A	36	697	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYV TIIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTR EHALLAYTLGVKQLIVGVNKMDSGTGIAILTGDFPSLEPRHVSTWLQH VVTIPTRNWHKCYCVGVVANFLNVSADFLNNE
926	B	52	554	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMIILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRS GKKLEDGPKFLKSGDAAIVDMVPGKPI*
927	A	63	1545	PLKAKMGKEKTHI\NIVVIGHVD\TGKSTTT\GHLIYKCGGID\KRT IEKFEK\EAEMGKGSFKYA*VLDKLAERERGITI\DISLW\KFET \SKYYVD*SLIAPG\HRDFYSKT*FTGTISRDLVWGAPFLGG/CLP *LFAAGVWWNLKAGISQEWGRTREHALLGLHTGVWVKQTKLFGVNKNW IST*GHPTAQKKILKEIVKGKSALTLRKIGYNPDTSSILCPISGW\N GDNM\LEPSA\NMPWFQGDGKVTRKDGNASGTTTLEALDCILPPTRP TDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTE VKSVMHHEALGEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPM EAAGFPAQVILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRR SGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGCFVRDM RQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
928	A	2	246	VTKELLQMDLYALLGIEEKAADKEVKKAYRQKALSCHPDKNPDNRA AELFHQLSQALEVLTDAATAAYDKVYASMHVT
929	A	318	422	LCGRLWWLMPVIPALWEAKAGGLLKLRSMPCLY
930	A	205	400	QSAVLPRLECNGMILAHCSLHLLGFKRFSCLSLPSSWDYSRLREL PREGREVGAKHTKPGCPII
931	A	234	427	ICKWILPCGLAGSYKIAKWVSGFTLLLTHTMVGAAWV*LSLFGYTIL F*FPKMSSFLTMMKDI
932	A	405	862	DCRMGLRIHFVVDPHGWCCMGLIVFVWLYNIVLIPKIVLFPHYEEGH IPGILIIIFYGISIFCLVALVRASITDPGRLPENPKIPHGEREFWEL CNKCNLMRPKRSHHCSRCHGCVRRMDHHCPIWNNVCVGEDNHWLFLQL

9926

				CFYTELLSCTH
933	A	2	413	PRVRPRVRLILLLENVSGYRFPVIFQLDASPGHKILPDCMIYSITV SLMFPVVDYISTLYGLGLHLGMSLRIVYALIVLNLCSVSYSTLSFYF RSISYYTLTIDYIYITILSVWIWFFFFFYLDLFLHFSLTSS
934	A	110	431	RKLVHIRAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLDRIS VYYNEATGGKYVPRAILVDLEPGTMDSVRSGPFGQIFRQDNFVFGQS GAEPSPQACQFP
935	B	754	1544	MREIVHIQAGQCGNQIGAKFWEPWKASSIELSQCRNSPSKVFRSKEH DGLPVTPTTR*
936	A	1	451	NQMTSKQYTGNSNMPGGLPRQAYTFKTSQLEHKSQMYQVEMNQGSQ GTVDQHLQFQKPSHQVHFSKTDHLPKAHVQSLCGTRFHQQRADST EKLMSPLKQHLNQASETEPFNSHLLQHKPHKQAAQTQPFQSSH PQNQQQQQI
937	A	1	258	SVALNTRKLWSMHLHVQAKLLQEIVRSFSGTTCQPIQHMLRRICVQL CDLASPTALLIMRTVLDLIVEDLQRYFHFALKIFSSNYF
938	A	3	1906	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEKQYTSQTTRL LALLDALASHKACKLAILHLINGTIKDERYAEIFQDLLALVRSPGD SVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISELEQLSNSLPN KELMTSICDCLLATLANSESSYNCLLTCVRTMFLAHDYGLFHLKS SLRKNSSALHSLKRVVSTFSDKTGELASSPFEFMRQILNSDTIGCC GDDNGLMEVEGAHTSRTMSINAAELKQLLQSKEESPENLFLELEKLV LEHSKDDNLDLSLDSVVGKQMLESSGDPLPLSDQDVEPVLSAPES LQNLFNRTAYVLADVMDDQLKSMWFTPFQAEIDTDLDLVKVDLIE LSEKCCSDFDLHSELEERSPLSEPSSPGRTKTKGFKLGKHKHETFIT SSGKSEYIEPAKRAHVPPPRGRGRGGFGQIRPHDIFRQRKQNTSR PPSMHVDDFVAAESKEVVPQDGIPPKRPLKVSQKISSRGGFSGNRG GRGAFHSQNRFFTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRG GQSNFNRGPLPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANS GSGRGKFVSGGSGRGRHVSFTR
939	A	1	585	ECLCVSTAVRIRHELKTMTELLRGGSFEEKDMRVPSALVTLHMLLC SIPLSGRILDSDEQKIQNDIIDILLTFTQGVNEKLTISEETLANNTWS LMLKEVLSSILKVPEGFFSGLILLSELLPLPLPMQTTQVSLPYNMHL INDCSNTF*KASDSVKKQKPSSPFLPKRHKITG*GGDKTETSWSLRK YGGKNFK
940	A	625	2115	YIRGHSTPRKLWSMHLHVQAKLLQEIVRSFSGTTCQPIQHMLRRICV QLCDLASPTALLIMRTVLDLIVEDLQSTSEDKEKQYTSQTTRLALL DALASHKACKLAILHLINGTIKDERYAEIFQDLLALVRSPGDSVIR QQCVEYVTSILQSLCDQSSHIDVVRFPVVIINEVRVIPPVRAHS SLPDNRAYGYLHSHHFLELVTLILLSIPVTSAPGVQATKDVLFKFLA QSQKGLLFFMSEYEATNLLIRALCHFYDQDEEGLQSDGVIDDALFAL WLQDSTQTLQCITELFSHFQRCCTASEETDHSLLGLTLHNLVYITFNP VGRSAVGHVFSLEKNLQSLITLMEYYSKEALGDSKSKSVAYNYACI LILVVVQSSSDVQMLEQHAASLLKCKADENNAKLQELGKWLEPLKN LRFEINCIPNLIEYVKQNIIDNLMTPEGVGLTTALRVLCNVACPPPPV EGQOKDLKWNLAVIQLFSAEGMDTFIR
941	A	180	359	GSLQRDRWPTSSWRTGRQGSSLLRPRWISFLAQLWRV*RIPAGTFVI RIEDGNRRAFI
942	A	1286	2189	HEEKPCSGQNWTPVPGWVWLEVPVDLVKSPQMSAVAGLGCGQGTG APPELGATAGWTRDPPTANCSPPGGIRVEVFPFGGGSRLSPVLAG RTRGFPAAPSFFMYAHVEIDGLALLEAQVQFRALVWVLMGFCFTL LFHPLEMVLQCNIEVKGITSVPEANSNKRPSISIFDADHEVPAGIR HTLHSCARKLIHRGLSKELPIVAALMTVFFIMQLVGQVPAALWVIFG EDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGM AADALGYVLLAFATDMAIF
943	A	1	2537	FRAAATWPGPPCARRAVNKVVYDDHESEEEEEEDMVSEEEEEEDGD AEETQDSEDDEEDEMEEDDDSDYPEEMEDDDDDASYCTESSFRSHS

				<p> TYSSTPGRRKPRVHRPRSPILEEKDIPPLEFPKSSSEDLMPNEHIMN VIAIYEVLRNFGTVLRLSPFRFEDFCAALVSQEQLTMAEMHVLLK AVLREEDTSNTTTFGPADLKDSVNSTLYFIDGMTWPEVLRVYCESDKE YHHVLPYQEAEDYPYGPVENKIKVLQFLVDQFLTNTIAREELMSEGV IQYDDHCRVCHKLGDLLCCETCSAVYHLECVKPPLEEVPEDEWQCEV CVAHKVPGVTDCAEIQKNKPYIRHEPIGYDRSRRKYWFLNRRLIIE EDTENENEKKIWWYSTKVQLAELIDCLDKDYWEAELCKILEEMREEI HRHMDITEDLTNKARGSNKSFLAAANEEILESIRAKKGDIDNVKSPE ETEKDKNETENDSKDAEKNREEFEDQSLEKDSDDKTPDDDPQGKSE EPTEVGDKGNSVSANLGDNTTATSEETSPEGRSPVGCLSETPDSS NMAEKKVASELPQDVPEEPNKTCESSNTSATTTSIQPNLENSNSSSE LNSSQSESASAKAADDPENGERESHTPVSIQEEIVGDFSTSEKSTGELSE SPGAGKGASGSTRIITRLRNPDSKLSQLKSQQVAAAHEANKLFKEG KEVLVNSQGEISRLSTKKEVIMKGNINNYFKLGQEGKYRVYHNQYS TNSFALNKHQHREDHDKRRHLAHKFCLTPAGEFKWNGSVHGSKVLTIT STLRLTITQLETTSLHPSFIPTGHHIGQIGSRQRCVANPENLHLWL </p>
944	A	2	437	<p> RTTAARRAVNKVLFDDHVSEEEEEEDMVSEEEEEEDGDAQETQDSE DDEEDEMEEDDDSDYPEEMEDDDDDASYCTESSFRSHSTYSSTPGT HPAQLLQTPSPPLPSPLAHSCAVHPAPISPQPRLPKQGRNARAHQ VAKN </p>
945	A	298	581	<p> GARAEARAGSGQGAGLGVSPPVRWRGWSDKGAERPGLSPLREVS AGPSG/HAARGQPPGRPRFPFPPGPRPPRRRCPCTRARPGGAAGGGPC L </p>
946	A	377	640	<p> ITSSLLFPSSIFKCRHAHTGLLISKHGDHRVSKESPLNSPASQAGSA TFATTPLTTPPKLQLRAPWQPLHSFRPCPGVTSRKRTARAR </p>
947	A	1279	2253	<p> PLLTSAASSKLLTSSWPTSKCSVVRTSSGPCTSSKDTMQSPERPCLM PLKKWQELSPETSGKRKKRKQMNQYSYIDFKFEQGDIKIEKRMFFLE NKRRHCRSYDRRALLPAVQQEQEFYEQKIKEMAEHEDFLALQMNEE QYQKDGQLIECRCCYGEFPFEELTQGANAHLPCKECLIRYAQEAUVG SGKLELSMEGSCTCSFPTSELEKVLPTILYKYERKAEVEVAAAY ADELVRCPSCSPFALLSDVKRFSCPNPHCRKGCCSPSGFSRNSQR QLLTPRQVAEPTPTCISEPRKSRVSVGSENPAATWGLRCRRPP </p>
948	A	268	369	<p>ELLILTLIFFSFQEFSGYVQVKYAMTRIKAGMP</p>
949	A	15	442	<p> CRDDPRVRLSRSPVGPFLSPTMFRRLRGLDYHNPAAFNCCKDETE FRNFIVWLEDPKIRHYEIEDRGNLRNIHSSDWPKFFKEYLRDVNCPF KIQDRQEAIDWLLGLSVRLEYGDNAEKYKDFRPDNSKTADNGTKNAE P </p>
950	A	118	376	<p> VAVVQIIFLPVFAIEKYKDLVPDNSKTADNATKNAEPLINLDVNNPD FKAGVMALANLLQIQRHDDYLVLMLK\AIRILVQERLTQD </p>
951	A	1	969	<p> AATVLTITIGEAPSRSDSAPARPLAASPVPAPPAPPRFFSPGRGPGD QSEKRWTFRRKLT\SLDYHNPAGFNCKDETEFRNFIVWLEDDQKIRH YKIEDRG\NLRNIHSSDWPK\FFEKYFKRC*TCPFKIQDRQESYLTG FFG\LA VRLEYGDNAEKYKDLVPDNSKTA*QLQLKIAEPLIN\LDVN NP\DFKAGVVGF*TWLQIQRH\DG LPGQMLKANSGFWVQERLDHQG CQFA*GQIKQKRGLPVA\LDKHILGFDTGDAVLNEAAQILRLHLIEE LRELQTKINEAIVAVQAIADPKTDHRLGKSLEDEHLRTSASHLL </p>
952	A	1258	1429	<p> ILFWIIQLNLECSFWSRLRQGRGIMLFFFPFLFFETESHSSVAQTG VQWCDLGSLQ </p>
953	A	189	405	<p> GLPRCASCTACGMLPKLTLEEVAMDITWEKWKQMDTVQKSIYRNMLEK YRNLVLEKPYEYHDWENFQLFR </p>
954	A	51	1702	<p> GLPRCASVQPVCEYQRRWKRWLWDITWEKWKQMDTVQKSIYRNIL\B KYRNLVLLDGKLAAGAKTSRVEQQDISKED*SQRLMEELAKRKSV EEIWKSRGQFKNQQLNKENNLGQEIATCTKIPTRKRDIESNEF/REK FYCKINTCC/MNR*ILWKRIVINMVHVERCSNKTQI*LYKESMMEKK KPCKYSECGRTFRGHITLVQHQITHCGERPCKCTECKRGFNQSSHLR NNQRKTLSGEKPCKSECGKAFSYCLVLNQHQRIHSGEKPYEGETCG </p>

				KTFIQS\SYLTQHQR/TSHTGEKPYTCLECGRLFSQNTHLTLHQRIH TGEKPYECNECGRSFSQTAHLTQHQRMYTGEKLYECNECEKAFHDHS ALIQHHIVHTAEKPYDINTGKTFSYCSDLIQHQRMTGEKPYKNEC GNAFSDCSSLIQHQRTHTGEEPYECKQCGKAFSRSTYLTQHQRSHAG EKQYKNECEKTFSLSFSLTQHMRVQTGEKPYKYNEYGKAFSDCSGH FQRTHTGEKPCCECNDGKPFSSFCALIQHKRIHTRKKP
955	A	2	270	REEKEWPPHTQWPYEGCFKDGQHYEESVIKENCNS*WTAQNYSQF WGMTLEDGFKFRLGTLPPSPMLLSMNEMTVSVPDSRMCMYL
956	A	1	999	MWTGYKFSIFSyltTEIWMKQYLSQREVDLEAYFTRNHTVLQGTRF KRAIFQGGQYCRNFGCCEDRDDGCVTEFYAANALCYCDKFCDRENSDC CPDYKSFCEKEKEWPPHTQWPYEGWTAQIYSQFWGMTLEDGFKFRL GTLPPSPMLLSMNEMTLVSHACYPLFKDQONATNNGCAMASRSDGRGK RDATAKPCPNVVEKSNRIYQCSPPYRVSSNETEIMKEIMQNGPVQAIM QVREDFPHYKTGIYRHVTSTNKESEKRYKLQTHAVKLTGWGTRRGAQ GQKEFWIAANFWGKSWGENGYFRILRGVNESDIEKLIVIAAWGQLTS SDEP
957	A	1	1518	VHCSEFFGRPPRPRTRGRKVEAIPVFORMWTGYKILIFSyltTEIWM EKQYLSQREVDLEAYFTRNHTFLQGTHFK\RAIFQ\GQYCRNFGCCE DRDDGCVTEFYAANALCYCDKFCDRENSDCCPDYKSFCEKEKEWPPH TQWPYEGCFKDGQHYEESVIKENCNSCTCSGQWQKCSQHVLV\R PE\LIEQVNGDYGWTAQNYSQFWGMTLEDGFKFRLGTLPPSPMLLS MNEMTASLPATTDLPEFFVASYKWPGWTHGPLDQKNCAASWAFSTAS VAADRIAISKGRYTANLSPQNLISCCAKNRHGCNSGSDRAWWYLR KRLVSHACYPLFKDQONATNNGCAMASRSDGRGKRHATKPCPNVVEK SNRIYQCSPPYRVSSNETEIMKEIMQNGPVQAIMQVHEDFFHYKTGI YRHVTSTNKESEKRYKLQTHAVKLTGWGTLRGAQGQKEKFWIAANSW GKSWGENGYFRILRGVNESDIEKLIIAAGWQLTSSDEP
958	A	316	411	CSFIPGMEDRFNIRKTINVIHHINRTKNKQNH
959	A	314	391	ECTFFSSVHGTFSTKTDHIIHGKTS
960	A	112	1154	SCGLGHRKTFSFVSLPARNETQPKACREQNMEGDFSVCNRNC*RHVVS ANFTLHEAYCLRFLVLCPECEEPVPKETMEEHCKLEHQV\GCTMCQ QIMHKSSLEFHKANECQERPVECKFKLDMQLSKLEHESYCGSRTE LCQCGQGFIMHRMLAQRRDVCRSEQAQLGKGERISAPERIEIYCHYN QMIPENKYFHHMGKCCPDSEFKKHFPVGNPEILPSSLPSQAAENQTS TMEKDVRPKTRSINRFPLHSESSSKKAPRSKNKTLDPMLMSEPKPRT SSPRGDKAAYDILRRCSQCGILLPLPILNQHQEKCRWLASSKRTSE KFQLDLEKERYKFKRFHF
961	A	103	538	NETQPKACREQNMEGDFSVCNRNCKRHTVSAANFTLHEAYCLRFLVLC PECEEPVPKETMEEHCKLEHQAYGSGIGKRFWFQERLAVLLRSVKRG CEKGRSWKAVRWSVPVSRSLSMSIPPGAPDLSLWRYSSSGSRCQHKTGL MNNS
962	A	1	405	SGFMDHLEEKADLSELVEKEELGFFQYYRERCHQKVYHPITKPGGSA KDAAPGGGHHQAGPGQGGDEGIRMMFCVSPNRAFVVSVPVLSIID VIYGRYLRLKLTKVTDQSLAQATQEERIGNVKNCSFWSPP
963	C	334	471	MRNIFHFTRGSGTTSVGRGYVQAAGGPVPPRRSQEGRLAFLHVP
964	A	1	1137	MGRGAGAALGRWSRAPLEELLPGRGSGRLGGPRGPRTAPGAVGLGPA AAGEEAWRRGRAAPSRDDQRLRPAPGLSEAGKLLGLEYPQRRLAA AVGFLRCPIIDAIYTNPTVDYSDNLTRLCLGLSGVFLCGAAANAI YLMQTSRQRVVRLRLTSLSILGQEVAFDFKAGTGELINRLSSDTA LLGRSVTENLSGDLRAGARASVGIRMMFCVSPNRAFVVSVPVLSI IDVIYGRYLRLKLTKVTDQSLAQATQEERFNTVVGEGKVLVLSGGQKQ IAIARALLKNPKILLDEATSALDAENEYLVQEALDPLMDGRTALVI AHLSTIKNANMVAVLQDGKITIEYKGHEELLSKPNGIYRKL MNKQSF ISA
965	A	1	451	GDRPFRV*DPRAGQAATFWTDPSLS*SLLLGVMFPAAPS PRTPGTGP RRGPLAGLPGSGTPRTASRMGLPLGSAVSSPVLFSPPGGRSSSLISRG

				TPTRMLPHHSITESVNYDAKTIGSSSLPVKMEALTLAEVDDQLTINI NEGGWACLV
966	A	301	1867	ECLCFLAAGVFLTMSRVISMSAPFFLGKIIDVIYTNPTVDYSDNLTR LCLGLSAVFLCGAAANAI RVYLMQTSQQRIVNRLRTSLFSSILRQEV AFFDKTRTGELINRLSSDTALLGRSVTENLSDGLRAGQAASVGISMM FFVSPNLATFVLSVVPVSI IAVIYGRYLRLKLTQVTDQSLAQATQLA EERIGNVRTVRAFGKEMTEIEKYASKVDHVMQLARKEAFARAGFFGA TGLSGNLIVLSVLYKGGLMGSAMTVGELSSFLMYAFWVGISIGGK QECIPSQLGTNDFLVFSLLVFENQDGKVRRGYAVVEGKLGMRNIFH FTRGSGTTSVKRGYVQAAGGPVPPRRSQEGRALFRLHVFKFRAQARL QPDGQIPRCPSCSLESQPPLLRGPRTTIDHRYLKLQIKGNTVY AKFSPVYRVDQVYEVSRETPKLAPHVIGFNNTVKSSPTSISGSYVAS QRLKDLGHAQMVVDELFSHSDLDSDSELDRVAVTQISVDLMDDPAS DPRWG
967	A	57	383	GWLAHTANERPVRCPFVWLEGFLENIRAPTLNF*QIQQSLAIFVEPI KTILLPFCFFRIFSTRVRICTYSSHSFPGPGAGLLHFCSSSLVRFKI SFGDTVAVAPVPDF
968	A	507	904	GKRAGECWRRSLRPRGPRGETRAASPSSARPSLALASAPRPSGPRP RQGPRLWPRGLKGQVCARGPGRGGPGVGRRSASARAPRVPDQ PPPPAPSS*ED/WT*EIGRLSSHAPLAVLHTRSALLNS
969	A	379	858	KWGFCRGLKWLTSKKRAFGLRATRDIAEELFLWVPRKLLMTVESA KNSVLGPLYSDRILQAMGNIALAFHLLCERASPNSIWQPDITLPS EYDTPLYFEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQVSS CLQFKYIFHRVGRKEELSP
970	A	259	483	NKMDLTLDDLLECPVCFEKLDTVAKVLPCHTFCCKPCLQRVFKAHK ELRCPECRTPVFSNIEALPANLLLVRL
971	A	175	588	CTDCCRGCRVSQLELLETALLITRHPSHVIGIEKKAEGPSHQISIPETDT SASILVASSCALRTNLKNQLVCKYLNHIMGLLDRLSVLLGLKKKEVH VLCLGLDNGSKTTIINKLKPSNAQSONILPTIGFSIEKFTSSSL
972	A	1	383	TAKAALYPLVGKGGAGGPVLAMRPNQAPVSGRVYIHRDYSRVTRCQ FQTRFPAQLDNRIAGHPFEKTVLTLNNLYAAEKLGGQAYLEGWCAC LTPYTIFLCMEITNEYKVLKQDFQYIPQLTESIY
973	A	79	445	RRQLGVALIPSHRMDYKSSLIQDGNPMENLEKQLICPICLEMFTKPV VILPCQHNLCRKCANDIFQAANPYWTSRGSSVSMGGQFRCPTCRHE VIMDRHGVYGLQRNLLVENIIDIYKQEC
974	A	1163	1402	TETKINFQNVKAMDLIHLFIYLFYFVFETESCSVARLGCSGMVLARC NLRLPGSGDSPASASRVAGTAGACHHARLIFA
975	A	80	407	LRRRPRRGRKRCEQVQAGSWCGRMAVSHSVKERTISENSLIILLQGL QGRVTTVDLRDESVAHGRIDNVDAFMNIRLAKVTTYTDRWGHQVKLDD LFVTGRNVRYVHIPE
976	C	70	240	MITGTSQADCAVLIVAAGVGEFXAGISKNGQTRDRMRKXLRKSALT RLATTPTQ*
977	B	68	490	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLA*
978	A	261	408	TRRPTARGMLEETNPADSKPGTIRGDFCIQVGRFTFFYSPVFFKNSFF Y
979	A	1	678	MPEPPTHSMGSCAARASPTSTTPCSTAPSPIDHPRAEECERTAQDWQ AASPAAPVRDPLGLAISKLDLVTFLEGKKEPWTVKSEETIAAQPEVG GKLSDLVARGTALGASSTRGLQGPGSGFLVTPSGDQMWAEWLWPVLVA AGHTFGLIRDSKLKKEGILTYPLAQYQQVFFFHKKFCWQGRWRHI VELYANVTLLFALAWTSKGIVTYCWAQQHGDMSLLYGP
980	A	181	340	DVRTSWKLGKGLAISKLDLVTFLEGKKEPWTVKSEETIAAQPVQMYN LIPEHF
981	A	1	375	HCSQGLLPTPLLRVSTLLFKLASFTMGNLPPSISPSSPLACVLKSLK PLHLLPDLKSKHLIFFSNTAWPQYKLDNGSKWPENDTFDFSIPRDL

				TFCRKKGKWSEVPYVQAFFTLCSLLSYMTHT
982	A	1	2583	MVNFTVDQIRAIMDKKANIRNMSVIAHVDHGKSTLTDSLVCAGIIA SARAGETRFTDTRKDEQ\ERCIPIKVNNAIS\LFYEL\SENDLNFIQQ SKDGAGFLINLIDSPG\HVDFFSE\VTAAALRVTMGALVVVDCVSGVC VQTETVLRQAIARERIKPVLMMNKMDRALLELQLEPEELYQTFQRIVE NVNVIISTYGEGESGPMGNIMIDPVLGTVGFGSGLHGWAFTLKQFAE MYVAKFAAKGEGQLGPAERAKKVEDMMKKLWGDYFDPANGKFSKPA TSPEGKKLPRTFCQLILDPIFKVFDAMNFKKEETAKLIEKLDIKLD SEDKDKEGKPLLKAVMRRWLPAGDALLQMITIHLPSPVTAQKYRCEL LYEGPPDDEAAMGIKSCDPKGPLMMYISKMVPTSDKGRFYAFGRVFS GLVSTGLKVRIMGPNYTPGKKEDLYLKPIQRTILMMGRYVEPIEDVP CGNIVGLVGVDQFLVKTGTITTFEHAHNMRVMKFSVSPVVRVAVEAK NPADLPKLVEGLKRLAKSDPMVQCIIEESGEHIAGAGELHLEICLK DLEEDHACIPIKKS DPVVSRET VSEESNVLCLSKSPNKHNRLYMKA RPFPGDLAEDIDKGEVSARQELKQRRARYLAKEYEWDVAEARKIWCFG PDGTGPNILTDITKG VQYLNEIKDSV VAGFQWATKEGALCEENMRGV RFDVHDTV LHADAIHRGGGQI IPTARRCLYASVLT AQPRIMEPIYLV BIQCPEQVVGGIYGV LNRKRGHVFEE SQVAGT PMFVVKAYLPVNESF GFTADLR SNTGGQAF PQCVFDHWQILPGDPFDNSSRPSQVVAETRKR KGLKEGIPALDNFLDKL
983	A	1326	1498	VQLKASTICQISRILSRVLAACLMRESSSEPKEVSGVCVQTETVLRQA IAERIRPSSK
984	A	60	966	RRRNSDGNACQPATHLLL\SARFITGHGQKLKSELKKTLOVIMLNIQ KVRIPTRDGYNEKDILSTGKNVEKLELSNIAGYPSNIEKKEYQE QSV LSCCSEK DANPKSVVCSFFMQEQCTKGEKRF LIPGTLSDVRHLRYF GILPTVSNAAVVKEVPTVSNAAVVTEAPTGSNAAVVTEAPTGSNAAR VMEVPTGSNAAVVTEVPTGSNAAVVTEAPTGSNAAVVKEAPTGSNA RVMEVPTGSNAAVVKEAPTGSNAARVMEVPTGSNAAVVKEVPTGSNA AVVKEVPTGVTLRWSRKRPRE
985	A	1393	1625	EGSNKFANDIQLLSI PYWKKRFLHMKKMPLFSKSHKNPAEIVKILKD NSAILEKQDKKTDKASEEVSKSLQAMKEIC
986	A	358	475	LCEETPSIVKKCKISWEWWHIPVIPATREAEAGELLEPR
987	A	232	329	VGIKMSISSDEVNFLVYRYLQESGFSSHAFTF
988	A	127	461	FREDRLPADLRKAVWKIALNVAGKGD SLASWDGILD LPEQNTIHKDC PASLLDQLSVPEEKAAELLLDIESVITFYWKS RNIKYSTSLSWIHL KPLVHLQLPRSDLYNCF
989	A	562	897	KGLVSNNGPERNTLCPCSTLLEEGSAAVEGSGAWGALRPVLVEPLDHG IREEVVRDWN SKQACTGTHQEACPVSLHKCCGPPQGTCHEC SHCGQS GRIRPEKGPSRSSVRAPP
990	A	282	507	TMGLEK PQSKLEGGMHPQLIPSVIAVVFILLGVCFIASCLVTHHNF SRWKRGTGVHKLKHHAKLKCIKEKSEL
991	A	7	494	IRLDFQLLRTRDRFSRIQAHEDKARGERTLHAAPTGPYPESESIMMA PICLGENHEEQLTVNSKALEILD LISQPAVGVAIVGLYRTGKSYLMN RLAGKRNGFPLGSTVQTETKGIWMWGVPQLFKPNHTLGLLDTEGLGD VEKSNPKND SWIFCLAVLLSS
992	A	206	357	RILGGA KVYGG LQGIIFFLIGGRFKTYLGIFGKDLFFGGGGTYWANFL PEF
993	A	1	101	LRSRYGRAQHSTMLHHA PLQKILPPPVTILMS
994	A	256	407	RILGGA KVYGGWEGNIFFLGGRIKTYLGILGKDPYFGGGTYWANLP TEF
995	A	254	432	RTLGGAKFYGG LQGNSFFLIGSRIKTYLGILEKNLSLGGGTYWANLP PKFKGFRENINF
996	A	249	402	RILGGAQVYPGLQGNSFFLIGGRIKTYLGIFGKNPYFWGGTYWANLP SEI
997	A	37	465	GRARPQONS YDLFLAAAARGAGGHYAPPCTEDCRKSTYPPSGPTNR GAGPWYTINLDLPYKRWHEMLDEAPMLKVI VNSLKNMINTFVPSG

9931

				KVMQVVDEKLPGLLGNFPGPFEEEMKGIAAVTEIPLGKVHLEALKKK SN
998	C	127	216	MRLRKQAEKNVEKKIDKYTEVLKTHGLLV*
999	A	1	1258	LFLPLLEPGERRGLLYRSRPGAVALIILLAAVS\CAV\SQHAPPWT EDCRKSTYPPSRPTYRGAVPWDTIQCLTYHPYKRWHEMLDKAPV/L QKVIVNSLKNMINTF\VP\SGKIMQVVDEKL\PGLLGNFPGPFEE MKGIGRCLLDIPLGEIISFNIF\YE\LFTICTSIVAEDKKGHLIHGR N\MDFGVF\LVWNINNDTWVITEQLKPLTVNLDQFQNNKTVFKASSF AGYVGMT\GFKPGLPSLTNERFSINGGYLGILEWILGKKDAMWIG FLTRTVLENSTSYEEAKNLLTKTKILAPAYFILGNGSQSGEGCVITRD RKESLDVYELDAKQGRWYVQTNQYDRWKHPFLDDRTPAKMCLNRT SQENISFETMYDVLSTKPVNLKLTVYTTLIDVTKGQFETYLRDCPD CIGW
1000	A	2	333	ACPFNKSAEDLLNL/RQGLTAGQLPFLPWWNIVLDSP/SLTSIPATS FSTSLATARARSASEVPIWKTTLFCSLSQVRKTRSSGATKSTVLST SLTTLH*IILRSISSQ
1001	A	292	945	LPPLPACPALHNMQPSGLEPGTFRGWPLLSLLLLLLLLLQPVTCAYT TPGPRALTLGAPRAHTMPGTAPSTLSSPSTQGLQEQARALMRD FPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGTSLDRDLRDLVGA QLHTCTSTITHAYATTYTDTCPPCSCSEEVSTVDVFAPDDRVRFR TCEREQNRVVFQMPLVNTYKVNHSVPTNS
1002	A	46	493	GQEEMAAGETHLYAKVSNKLKSRSSPSLLEPLLAMGFPVHTALKVLA ATGRKTAEEALAWLHDHCNDPSLDDPIPQEYALFLCPTGPLLEKLQE FWRESKRQCAKNRAHEVFPVHTLDCDFTCEDQKVECLYEALKRAGDR LLGSFPTA
1003	A	2	407	QTQREPTMVLAPADKNNVKAGWGKGAHAGEHGAELDRKILYFPTT KNYFPHFYLSHGSAQGGKGGKEDDALTNAVGHGDHMPNLCALSDL HAHKLGVDPDNCKLLIHCLLVTLCAHLPAEFTPAVHATLTK
1004	A	192	548	GLFERKIDIKILNIFSLFLINSKNTNKCVLRYMYRNCCNIIILNNL KQTELPKVGYNERRKGGFLILWNIFQELKRMRIHTHTHTHTHTHTH THSLGIPNPEIQMLQSPKLSDPPT
1005	A	1	528	DNELLDYEDDEVETAAGGSMS/EAPAKKDVKGSIYFSIHSSGFRD KPELLRAIVDCGFEH\PSEV\QHECIPQAILGMDFLCQAKSGMGKTA VFVLATLQQLEPVTGQVSVLVMCHTRELAFQTR*KTRPFWNVTVCPS GEDTRVGVKETLLPPPLTAPTWPWLPSPFASPLLNPHF
1006	A	807	1036	RNSDVRPLVMAENDVDNELLDYEDDEVETAAGGDGAEPAPAKKDVKG SIVSIHSSGFRDFLKPELLRAIVDCGFEH
1007	A	136	1520	LFTPCFHLFCENPSRSPFPSSPAGPVMAENDVDNE\LLDYER*MRWE TAAGGDGAEPAPAKKDVNGLLCLPSHSSGFRDFL\KPELLRAI\VD\ CGFEHPSEVQHECIPQAILGNGMSCARAKSGSGERQAVF\VLATLQQ LEPV\TGQGVACAG*CHTRELAFQISKEYERFSKYMPNVKAVFFGG LSIKKDEEVLKKNCPHIVVGTGPRILALARNKSLNLKHFKHILDEC DKMLEQLDMRRDVQEIFRMTPEKQVMMFSATLSKEIRPVCRKFMQD PMEIFVDDETKLTLLHGLQQYYVKLKDNEKNRKLFDLLDVLEFNQVVI FVKSVQRCIALAQLLVEQNFPAAIAHRGMPQEERLSRYQQFKDFQRR ILVATNLFGRGMDIERVNI AFNYDMPEDSDTYLHRVARAGRFGTKGL AITFVSDENDAKILNDVQDRFEVNI SELPDEIDISSYIEQTR
1008	A	92	191	YHWMGMSNLKLLKYVLFNLFWVRASLLSTG
1009	A	219	424	RKTTSPGAFYLGKGGYPPGRVRGAVKKPPGEFWGGPQLRGDPGGTP PSGIKSGRGKKRFFGASGNNP
1010	A	215	417	RVEVHFKSCDCQKAEEGGCSQKNFTRGPLSDTCIGILKGSHICRYSE CGKIFPDPRYFCVSRNIHTR
1011	A	261	486	GFLGKVLQSPATTVVRTLNDRSSIVMGEPISQSSSNSQ*FFFFKENS RILFCLG*CAVEQHFSIFHCVDYII
1012	A	31	2697	DSPCEPAGGGRERQRRVGLQDGGSVVVTAAAGEQASPGGQRDRGVG CAGEVRNGASGRRGLSGSCHPFSRLNLWSHGEGPLRSRRRRHRHY

				CLYRLLRVRSADDEVSEEAARAVETAATMSDTRRQVEGLYPETKTGN GTTEAPGTSPPLTWRSSRGCRWFGQSPTDHYSWESKINPNTAYQKQ QDTLIVWSEAEYDLALSFOEKAGCDEIWEKICQVQKOPSVETQD LIDSEEEERFEEMPETSHLIDLPTCELNKLLEIADLVTSVLSSPIRR EKLALALENEGIIKLLQLFQACENLENTEGLHHLYEIRGILFLNK ATLFEVMFSDECIMDVVGCLEYPALAQPKRHREFLTAKTAKFEVIP ITDSELRQKIHQTYRVQYIQDIILPTPSVFEENFLSTLTSTFIFFNKV EIVSMLQEDEKPLSEVFAQLTEEATDDDKRRELGMDDLQVRSAAATDI FSYLVEFSPSMVREFVMQEAQQSDDILLINNVIEQMICDTDPGLGG AVQLMGLLRTLIDPENMLATTNNTFTQERYGESLNKLLLPPLYSLQE TRLLKTDIWPDSGMLTALSVPLPHSGPWLQDWLCPTAASHRVVWDG CPPPAEGKGPQAKFLGTSHTGAIQQHDDVRNRSPLPPSGLSRRRRGR GDRENLPNCDPAPRGAERGGSSRAERGGSLAEVLPQSGTPPRESA EHSGLGSACRSGAPARTARASLLEEEKGRESRVTRWRICSSYRGGG RASEPWGAKRRESGCMRGVRSADDEVSEEAARAVETAATMSDTRRRV KVYTLNEDRQWDDRGTHVSSSTYVEELKGMSSLVRAESDGKCLRVS VEGELENTHLVSNMELIDYWWGEILTLGDEGSDSLCCDSVV
1013	A	306	441	VVFVVLIELATMSKCNIKPMGKSEPLFFFESESCSVAQTGVEW
1014	A	149	405	PRQEAQMGKKLDLSKLTDEEAQHVLEVVRQDFDLRRKEERLEALKG KIKKESKRELLSDTAHLNETHCARLLEPLTLVWERQK
1015	A	2	344	LRVSTLLFKLASFTMGNLPPSISPSSPLACVLKSLKPLHLPLDLKSK HLIFFSNTAWPQYKLDNGFKWPENDTFDFSIPRDLDTFCRKKGKWSE VPYVQAFFTLCSLLSYMTH
1016	A	172	341	SRWPGFPQSGEVSAAPMSKLSFRARALDASKPLPVFRCEDLPDLH EYASINRAR
1017	A	73	408	FLQLQERQWFLTQEDSLRNMWNDIELLTNDDTGSGYLSVGSRKHEGT ALYQVDLLVKISSEKASLNPKIQACSLSDGFIIVADQSVILLDSICR SLQLHLVFDTEVDVVLW
1018	A	53	237	FLQLQERQWFLTQEDSLRNMWNDIELLTNDDTGSGYLSVGSRKETS HFLQASNFYPSAKK
1019	A	51	482	ESLRMKLSLTKVNGCRLGKIKNLGKTGDHTMDIPGCLLYTKTGSA HLTHHTLHNIHGVPAQTLTSSLAHHEVLTEYKEGVGKFIGMPES LLYCSLHDPVSPCPAGYVTNKS SVSVSVARRVEMTVSKFMAIQKALQ PD
1020	A	49	399	NTKHPNLAIVLPVEQAALLHNCVKTVDEVFPNEKDLTDRPLRDPDVK YFTGGSSFVLEEFHARYTVVTSDSVVEAQPLPTGTSQAQKALIALT RALLLAKEKKVSIYTNKYASRA
1021	A	564	651	KIGCSAYGVAILLFLYFFNKLAFTLWKK
1022	A	2	368	SLPASDRPPISSPLATSGTIFSAISCFWDLPAFLWLAPSCQPTMSS QIRQNYSTDVEAAVNSLVNLYLQASYTYLS\ LQDIKKPAEDEWGKTP DAMKAAMALEKKLNQALLDLHALGSART
1023	A	18	781	EICPSRPKNSARRGGPAGLSLASTVFGNRSGDWASSLRPPSDFLLR LQPPGPSYRPSPASGTCQHRFLWLAPSCQPTMSSQIR\ QNYSTDVEA AVNSL\ VNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKRE GY*RLMKQNO\ RGGRALFQDIKKPAEDEWGKTPDAMKAAMALEKKL NQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKMGDHLTNLHR LGGPEAGLGEYLFERLTLKGD
1024	A	217	608	DKKLKKSFTATSLCKTSLIITNQGKKSREHRNTAKGNIACFP SFIRQTSCNATTGCICTQFREMPTLLFSYPQFSFLLSFFFSFFETES LLPRLECSGAISAHCNLDLLGSTDPPTLAPQITCTT
1025	A	147	430	GMAAVGNLLGRVQRSTVKVTGPALHRLHTSFWRADSNRASLTVHRQ AYARLYPELLEKQDGTIHIYREPRRLAMPIDDLTSLPEERRARL
1026	A	489	702	TFICSRRLRQSTVKATGPALHRLHTSSWRADSSRASLTVHRQAYARL YPVLLVKQDGTIHIYREPRRM
1027	A	899	1097	QPAGPSLTRCATAQALCTTLPPCCLVKQDGTIHIYREPR/QQCWR MPIDDLTSLPEERRARLRKR

1028	A	59	427	GGALGRAGSPSPVDPASGVAVSEAAARSPLGSGFTSREGVKTENNDHI NLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQ PINETDTPAQLEMEDEDTIDVFQQQTGG
1029	A	1	2148	MVKGSIQQEELTILNRYASNTGAPRFIKQVLSDLQRDLDSHTLIMGD FNTPLSTLDRSTRQKVNKDTQELNSALHQVDLIGIYRTLHPKSTEYT FFSAPHHSYSKIDHILGSKALLSKCKRTEIITNYLSDHSAIKLELRI KKLTQNRSTTWKMNNLLNDYVWHNEMKAEIKMFFETNENKDDTTYQN LWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKELEKQEQTHSK ASRRQEITKIRAELEIETQKTLQKINESRSWFERINKIDRPLARL IKKKKREKNPIDAIKNDKGDITTDPTETIQTIREYYKHYANKLENL EEMDKFLDTYTLPRLNQEEVESLNRPIITGSEIVAIINSLPTKKSPGP DGFTTESYQRYKEELVPFLKLSQSIEKEGILPNSFYEASIIILPKP GRDTTKKENFRPISLMNIDAKILNKILANQIQQHIRKLIHHDQVGF PGMQGWFNICKSINVIQHRNRAKDKNHMIIISIDAFAFDEIQQCFML KTLNKLLEPSNHTALAGVGVHVEDSIAALAYDLNHNHNSQALAAPQD SHIIQSCRKNQLSAPFSAAGSAVHAAPMHSCMASSPYRVTRHFLFCE AAAEETPVFTMANEKPTEEVKTENNNHINLKVAGQDGSVVQFKIKRQ TPLSKLMKAYCEPRGLSMKQIRFRFGGQPISGTDKPAQLEMEDEDTI DVFQQQTGGVY
1030	A	193	564	GDSGGSWPDEKPKEGVKTENNDHINLKVAG\Q\DGSVVQ\FKIKRH TPLSKLMKAYCE\RQGLSMRQIRFRI*PGNPIHETDTPAPVGKWKDE RYQLMVFQQAARPGGVYLLKKGTCFFYSKNSVSF
1031	A	216	372	SGICSDTLTMTTVEEDSDTVTVKTVNSVTLTQDTEGNLILHCPQNG RRTC
1032	A	566	788	EPKSQPDQHGETPSLLKIQKLAGRGGTCLYSQLLRRLRQENHLNPGG RGCSEPRSHHCTLAWATVRLPLKKKKK
1033	A	2	402	QTPDLLPEALEAQVLPKRLRSSEEPTEKEPPGQLQVKAQPQARMTV PKQVRSRDISREEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYH SNSGAQLSHCKSLGHFENLQKYKAAKNPSPTTRPVSRRC
1034	C	379	453	MNIYLYACLIVSVYRARGSTRKFE
1035	A	2465	2796	APRPVSWEVSRGSPDRPTLACFQVRSRDISREEWKGSETYSPNTAY GVDFLVPVMGYICRICHKFYHSNSGAQLSHCKSLGHFENLQKYKAAK NPSPTTRPVSRRCAIN
1036	A	1264	1385	IISRGAYHNQDLPKNSQAWWLVPAPVPAWEAEVGGSLA
1037	A	1249	1457	YWLKSLLLLLLLLLFLRQSLAVTQDRVQWHDLGSLQPLLPFGKQFSC LSLPSRWDRCPHSLIFVLL
1038	A	146	439	PGLIQEPGSMdTAVIVAIRGLATIFLASFANLGLVFRQRYCRPRDL LQRYNSKPIVDLIGAMETQTEPSEIELDDVGITNPHIDAPLENEKRD QIC
1039	A	2	2387	SMHQQLCQELQDNDVLFVQSSLSAKERHLAavasALWRHFFSFLKS QRMSQVVPFSQADAAADFTLLAMDMPTAPSDFPQPVISIIQLFG WDDIICPQVVARYLSHVLQNSTLCEALSHSGYVSFQALTVRWSWIRCV LQMYIKNLGPDLLIDKNLEEAWEKEYMKQLVKLTRLLFNLSEVKS IFSQAQVEYLSISEDPKKALVRFFEAVGVTYGNVQTLSDKSAMVTKS LEYLGEVLKYIKPYLGKKVFSAGLQLTGMMGILVKSQAQIFATSKA QKLLFRIIDCLLLPHAVLQKEKELPAPMLSAIQKSLPLYLQGMCIVC CQSQNPAYLNQLLGNVIEQYIGRFLPASPYVSDLGQHPVLLALRNT ATIPPISSLKKCIVQVIRKSYLEYKGSSPPRLASILAFILQLFKET NTDIYEVELLLPGILKCLVLVSEPQEIQTIGEYKELYTNKLNLE EMDKFLDTYILPRLNQEEVEHLNRPITGIEIEAVINSLPTKKSLGPD RFTTDFYQSYKEELETFLVKLFQSIEKEGILPNSFYEASIIILKPG RDTTTKKNFRSISLMNINAKILNKILANRSQOHKKLIHHDQVGFIP GMQGWFNICKSINIIHHINRTNDKNHMIISIDAFAFNKIQQYFMLT TLNKLIGIDGTCLKIIIRAVYDRPTANIVLNGQKLETFLPKTGIRQGY LSSLLFNIVLEVLTARTVRQEKAIKRIQLGKEEVKLSLFADDMIVYLG NPISVQNLKLLISHFSKVSQYKISVQKSQAFlyTNNRQRDKS

1040	A	1	1329	MNRGSTKDFGGSGNALYDIAMIDAEIWDYVKRPNLRLIGVPDSHGEN GTKLENTLQDIIQENFPNLARSWFFKINKIDRPLARLIKKKREKNQ IDTIKNDKGDITTDPTIEIQTIREYYKHLYTNKLENLEEMDKFLDTY TLPRLNKEEVESLNRPTGSEIEAIINSLPTTKSPGPDRTDEFYQR YKEELVPFLLKLFQSIEKEGILPNSFYEASIIILIQKPGRDTTKKENF RPRSLMNIDAKILNKILANQIQHIIKKLIHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIISIDAEKAFDKIQPFMLKTLNKLGDIG MYLKIIRAIYDKPTANIILNGQKLEAFPLKAGTRQGCPLSPLLFNIV LKVLAIRIRQEKEIKGIQLGKEEVKLSLFADDMIVYPENPNVSTQNL LKLISNFSKVSQYKINVQKS
1041	A	1	283	RQLEQSRHSWVNTTVLITGCTNAAGLLVVGNFQ\LVLGAVFFVHES SQLQHGAALCEWVCVIDILIFYGTFSYEFQAVSSDTLVAALHLAPGP
1042	A	1	1296	MLFPKETSGFGPGQFPCHFLMLCTKWEKGEDGDCSNLKALDDQGV SSQMVESISFPPPPNDVPPAAQDFGGLLRGPQLESAPRGRGACGG GGALRGRRWSGGCLRAADSPPLHWAGTQPLLGVASSVQPFSGPWS LRRRVTPFQMLRSACVSQHAGGIWVDRGGPQCQRVFTFCRGLSNFG RSETQREWRIRSYNESCPPDAEQGGPKCTCTLDVPLISKCSYPP ESCLFSLIGNMGAFMVALICLLRYGQLEQSRHSWVNTTALITGCTN AAGLLVVGNFQVDHARSLHYVGAGVAFPAAGLLFVCLHCALSYQGATA PLDLAVAYLRSVLAVIAFITLVLSGVFFVHESSQLQHGAALCEWVCV IDILIFYGTFSYEFQAVSSDTLVAALQPTPGRACKSSGSSSTSTHNLN CAPESIAMI
1043	A	301	888	WLWQKHLKVAGPPPLSHLPLVLPPTPPPPLAPFLMTAWILLPVLSA FSITGIWTVYAMAVMNHVCPVENWSYNESCPPDAEQGSKTCTCT DDVPLISKCSYPPESCLFSLIGNMGAFMVALICLLRYGQLEQSRH SWVNTTALITGCTNAAGLLVVGNFQVDHARSLHYVGAGVAFPAAGLLF VLLHRLAF
1044	A	3	581	ASAHRLLOHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDLMEGR LLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVWKS NF DIVDHGE VTKVPRPPATLASSMGNLPEVDFPVPVPPGRGRSVESVQSQPQEPVSV QTLTSTLEHIVQQLDVLTVQTVSILEQRLTLTEDKQCLLENQQLIMQ RATP
1045	A	1	741	PLTRAAGIRHEDSQSVGNSSPEIPVLPEPAYQLGPLCQVLPFRAGSS CLPVMTRTVKLWDKSSREC VHSYCEHGGFVTYVDFHPSGTCIAAAGM DNTVKVWDVVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLK ILDLMEGRLLYTLHGQ\GPATTVAFSRTGEYFASGGSDEQVMVWKR NFDIGDHGEVTKVPRPPGTLASSMGNLTVSILEQRLTLTEDKQCL ENQQLIMQRATP
1046	A	526	1272	LSTPIGTCIAAAGMDNTVKVWDVVRTHRLLQHYQWLLELKPTWGFLW RQLEPFVLRWLTLLVHSAAVNGLSFHPSGNYLITASSDSTLKILDL EGRLLYTLHGQHRHIQCAGLVGLFSLGQHIQRGWLLALVCPRGFALP GALVYMSMCTALCQACPSSHLKGLTPGGWLVDQETRVVALVPVYLR LWKVLGPATTVAFSRTGEYFASGGSDEQVMVWKS NF DIVDHGEVTKV PRPPATLASSMGNL
1047	A	57	307	LFISKFKYSIYYFVQMLWENGINGILADEMGLGKTQVOCIATIALMIQ RGVPGPFVLCGPLSTLPNWMAEFKRFTPDVRHASLC
1048	A	1669	1820	IFKICNLKYLFIITGETLEIPDTVMGLTLAAGTSIPDTIASVLVARK GKN
1049	A	212	548	IQGQSSHPSCPMSSQANKPGAHTPDPCVKQTTAETRRIALRSKSA ASSEVTGLKADPTTSCKPGIQETTFFPLPSCVLSSHSPISSSDHS STWVGEEQSHRPEGTTLN
1050	A	670	1296	FHMLFQSNEAHVMEFPSEKKNNFLVSEDHGQKILSVLQNFREQNVFY DFKIIIMKDEIIPCHRCVLAACSDFFRAMFEVNMKERDDGSVTITNLS SKAVKAFLDYAYTGKTKITDDNVEMFFQLSSFLQVSFLSKACSDFLI KSINLVNCLQLLSISDSYGSTSLFDHALHFVQHHSLLFKSSDFLEM NFGVLQKCLESDELNVPEEEK

9935

1051	A	243	335	TCMFISAQFAIAKSWNHPKCPSINEWIKKL
1052	A	1	1170	MEHVYNIFSSNIKKKEVVGRKMYCDKKHHTTKRNCNPKLRQNSGKWSK DYNIQVKADSRKRQLENFTTFLTCLCPSKLAVLKCQKPTFPAPFCPTA DTAFCTLAAVAFCRRGFLPPRLSAPPPPPPLLPAPPPWLFARRGFL PPAVTAFCPAAATFSSPRLFAAAAVAAAFCAARGFLPLPPPFAPAA AAFCPRRRGFLLPRLFAPVAAAFCHRDFLPSPPRI FVPAAAALRAGA AGSAASSTGVLARAAPRGAPGPCGLHRAALPAEAMGEKKDGGGGGDA AATEGGTGAASRALQQCGQLQKLIVIFIGSLCGLCTKCAVSSDLTQ QEIQTLENSVEIKPASPRFSAVLMPNKLSPLHAKIGLKPICYPSYTS SIKVQKCDFEYARV
1053	A	1	1122	MNTRKKEGKKEKERERERERKKGEREEGKEEERMEFIDYSSFTCHGGAY LRLFYVSASVLFRLAGFLPHRRHSFLHPRRRGFLPPRLSAAAFCCP AATAAFCPTAAVAFCPRLFTRHGVLPAAFCCPPLSRLFAPPPQRL FPRRGFLPPPLLPPLFAPAAFCRCCRRLLPPPQRLFVPAAAFCYRD FLPRSPPLFATATFCPRRRGFLSPPAALRAGAAGSAASSTGVLARA APRGAPGPCGLHRAALPAEAMGEKKDGGGGGDAATEGGTGAASRA LQQCGQLQKLIVIFIGSLCGLCTKCAVSSDLTQOEIQTLEGRDDPEK AQVAAGTKSDIVPPVHTPWLCCHAEDRFKGLASLPAKLKEHKLNR
1054	A	1	392	SRRPDPGCRMTMANLERTFIDVKPDGGHRSVLGEI INRFEQKGFRL AMNFLRAFEKHLKHHYIDLNDRPCFPGLVKYMNRSVAAMVWEGLNA LKTGPGMLVETTPSHSMPSIRGDFCIQVGTNI IHG
1055	A	47	296	PEDTGKSIKMPGPPESLDMGPLTFRDVAIEFSLEEWQCLDTAQDDL YRKVMLENYRNLVFLGENNFNTKSLIYPKVFISLFS
1056	A	1	315	RLHCSVSSAPRGASGPVTCRYWESTAKTPGHGPGSLEMDNRYGVYP VKGASGYPGAERNLLEYSYFEKTEFRSCCPGWSAMARSQLTSTSASR VQAILLPQPE
1057	A	1	579	MAILGRAQWMLVIPALWEAEARSLSGEDGFRDVAGFVRFFVFGCRW NSGSRHLHCSVSSAPRGASGPVTCRYWESTAKTPGHGPGSLEMDLRY GVYPVKGASGYPGAERNLLEYSYFEKVWGLVRFTLELFTNEEEREY SKVTEEVTEHVYLPAKEKAAKEGEVHPYPYSAHPYYFEKDPDDLSE PEDTG
1058	A	87	509	PAGIGRSTAKTPGTGPGSLEMLNLSGVYPLKEASGCPGADRNLVYS FYEGKPLTFRDVAIEFSLEEWQCLDTAQDDLRYKVMLENYRNLVFLA GIAGSKPDLITCLEQGKEPWNMKRHAMVAKPPVICSHFPQDLWAEQ
1059	A	866	1002	ARFMLFI FNKAGIAVSKPDLVTCLEQKDPWNMKGHSTVVKPPGR
1060	A	385	573	DPPQKMAPKVKKKEAPGPPKAEAKAKALKAKKVVLKGVHGHKKKKIRM SPTFQRPKTLRLWMP
1061	A	328	530	NPSILVTEARECLYAQAVTKHKPHTILLNLFRAPPRLECNGMISA HCNLHLPGSNDSAPASHIKL
1062	A	6	666	LPGRPTRAPTRPAEHSIVGTRLVSCQLQPSQPNADQGKLTMMRIAVI CFCLLGITCAIPVKQADSGSSEEKQLYNKYPAVATWLNPDPSQKQN LLAPQTLPSKSNESHDMDDMDEDDDDHVDSDSIDSNDSDVDVT D\DDSHQSDSHHSDES\D\ELVTDFTDLPATEVFTPVVPTVDTYDG RGDSVVYGLRSKSKKFRRPDIQYPDATDE DITS
1063	A	2	613	PRVRPRVREEAEHSIVGTRLVSGQLQPSQPNADQGKLTMMRIAVICF CLLGITCAIPVKQADSGSSEEKQLYNKYPAVATW\LNPDPSQKQNL LAPQN\AVSSEETNDFKQETLPSKSNESHDMDDMDEDDDDHVDSD DSIDSNDSDVDVTDDSHQSDSHHSDESDELVTDFTDLPATEVFT PVVPTVDTYDGRGDSVG
1064	A	1	1073	TDCRVDPVRPRVRVEHSIVGTRLVSCQLQPSQPNADQGKLTMMRIA VICFCLLGITCAIPVKQAES\GSSEEKQLYNKYPAVATWLNPDPSQ KQNLAPQ\TLPSKSN\ESH\DHM\DDM\DD\DHVGTARDSI GLGTTLDGCRMDTGWIFHQF*WSLHHFWMESGWNWLDSPRDLAQA TEVFQFQFVP\TVDTYDGRGDSVVYGLRSKSKKFRRPDIQYPDATDE \DITSHME\SEELNGAYKAI PVGPD PDAPSDWDSRGKDSYETSQDD QSAETHSHKQSRLYKRKANDESNEHSDVIDSQELSKVSREFHSHEFH

				SHEMLVVDPKSKEEDKHLKFRISHELDSASSEVN
1065	A	1	1128	LETPIDSPRNRPGNPGATHASGRRQSTASSGPDVSVGQLOPSQPNAD QGKLTMMRIAIVICFCLLGITCAIPVKQADSGSSEEKQLYNKYPDAVA TWLKP*PIFRRQNLLGPTTEWLCPKLTNDFKQGGPFPS*GPTERPWT TWDDMG*WKVDGWTMWDSDSID\NDSDDVDDT\DDSHQSDSHHS \DESDELVTGFSTDLPADEVFTPVVPTVDTYDGRGDSVVYGLRSKSK KFRRPDIQYPDATDEHITSHMESEELNGAYKAIPVAQDLNAPSDWDS RG\KDSYETSQDDQSAETHSHKQSRLYKRKANDESNEHSDVIDSQE LSKVSREFHSHEFHSHEDMLVVDPKSKEEDKHLKFRISHELDSASSE VN
1066	A	514	1000	WYVQPAAQEGSQCWHLLEGPRPCMGAPKSMGRCHCSRQHRPTVCYHSL ALCNKQVNVKIRRLHCCNLNLLSLTKHLFMLKSLHLVVFCEFFFCVICS FIYLYGFCLEENVNFNVLVKCIKFYLHSLWISFFLSSPEIDLPPYMI LKILQFFSSTFIVSFHFVFL
1067	A	1	1098	MGFHHVQGAGLELLISSDPPALASQGAGITGSWKWILAPVILYICER ILRFYRSQQKVITKVKNMHFPLAVIRVIFYRTTELNFYVVTLKEEL GNWAQWVVMHPSKVLELQMNKRGFSMEVGQYIFVNCPSISLLEWHP FTLTSAPPEEDFFSIHIRAAGDWTENLIRAFEQQYSPRIEVDGPFPG TASEDVQYEVAVLVGAGIGVTPFASILKSIWYKFCADHNLKTKKI YFYWICRETGAFSWFNLLTSLEQEMEELGKVGFLNYRLFLTGWDSN IVGHAALNFDKATDIVTGLKQKTSFGRPMWDNEFSTIATSHPKSVVG VFLCGPRTLAKSLRKCHRYSSLDPRKVQFYFNKENF
1068	A	2388	2658	FYKVTFMWKS VKVSLGDNFVLGSVVPFCFLFFFFFLRWSLALLPRLE CSGAISAHCILCLPGSSNS/PASASQVVGITGTCHHAWLIFLYF
1069	A	788	1001	DSFMPLSQLYLIYFFSRPSLALLPRVECSGVISAHCNLRPLPGSSNSP ASASQVAGITGTCHHAWLMFCIFS
1070	A	306	1195	LKSPSRRSWEPQRLTWHATMEKSPKSEVVITTVPLVSEIQMMAATGG TELSCYRCIIPFGVGAFIGIVVTALGICGRFRENLEYKMKKGNEGQ FWGTSVRHRTPSASVLEKSGKKQSQCHGIHAMIKRYPQSIPTYTAW ASSRIWEEMDDTEGVLERLPWQQTDLKPDMSDFLPVRVCQYQSWL LFAHNSKTEGLLGKFGHPSCGIVQRFGEKKETWELYEQECNGETV YWEVKYPFPMNRDVSFPQAAYVCREVELVSQQAQITLSLILAAFA KDIASCMVFGEALRV
1071	A	3	715	FVAHTKGVRGLPSMRSPDCGRMELAAGSFSEEQFWEACAELOQPAL AGADWQLLVETSGISYRLLDKKTGLYEYKVFGVLEDCSPTLLADIY MDSYRKQWDQYVKELY\EQECNGET\VYWEVKYPFPMNRDVSYL RQRRDLMEGRKIHVILARSTSMPLGERSGVIRVKYKQSLAIESD GKKGSKVFMYYFDNPGGQIPSWLINWAAKNGVFNFLKDMARACQNYL KKT
1072	A	1	1128	MHEIWRDSDQETSLGRSIPCPAALCSVRKIHVQPQVLRPTSPRNI PISNLRLLKSDAASSPWKPPGPSRTPSFGLLCVFLSYPTLTTSIGHL YSFPGNRSHAHYHPTKPNHPYPTQRQYPIPPHALKGLKPVITDLLQH RLKLPINSPYNPILPVQKPKDSYRLVQDLRLTNQIVLP IHPVVPNL YTLLSSIPSTTHYSVLHLKDAFFTIPLHPSSQPLFAVTWTDPTDQ SQQLTWAVLPQGFDRSPHYFSQALSHDLSFHPSASHLIQYIDDL CSPSFESSQDQDTLLLLQHLFSKGYQSDDRPAFTSQITQAVSQALGIQ WNLHIPYHPQSSGKVEWTNGLLKL LLLLLLTANIDTSYLQIPHKGLO
1073	A	3	862	RLHPGEINSHVAHTKPVVVFHTDAHEIWCCSDRGTSLGRSIPCPV LCSVRNIYLQPKILRPTSPRNI SLILNQTKETRFICGPKTPAPVTDW DGSLLPLVFNHCRDASLIVHPRFKGVRARRDACLGPSPLAASPAFLGK GQAAPRQAE LGPNASSASAPPPYNLF IASPPHTWSGLQFRSVTSPPP PAQQFTLKKVAGAKGIVKHALKRLKPVITRLQHGLLKPINSPYNP ILPVLKPKDPYKLVQDLRLINQIVLP IHPVMPKHTDGYQNVGPNITQ CVIH
1074	A	1	912	MTDNILELAQNMDKYTKYEMTTTSSILSQPSSSQREQDGGQFQELTVT SEMFRKGKGSFCSHPHEKFLRTFNEIETYLIGNFQDLELESSDDL

				RGCTNEKARKTYDPKKLPLPYT/VRPCWILASKLHI*ESYG*RQ*A* *CHQ*TPWPRPVWWSLHTEAHEIWCRRSDQGTSLGRSIPCPPVLC* ERSTYDLR\PQTDQPSKHLTNLKSASTPPYPNPFITSPPHTRSGLQF RSTSSPPAPAQQFTLKKVAEAKGIVKVNAPFSLSDLSQISVRLGSFI KYEKSSPVHGSFGSNPETLYSPRP
1075	A	611	817	LSQWKHALKRLKPVITCLLQHGFLKPINSPYNSLILPVLKPKDPYKL VQDLRLINQIVLP IHPMVSA
1076	B	1	1500	MRTREVSITGADFTALLVDIIGNSTSYLTEIFKSTSILSVNQSNESD CIFICVMTGKSGRNLSDFEIEEKYPIINYTFTSGLSGVLALLLTQS LFGGLFTRTRMKFGAVTRIGGPPLGNQSPSSCSLLHEKDPPTTSGPQ TDQPKKHLTNFKSGTEEAMNTTSLAPAAEIMATPGSPSQASPTSGA FTHGTQTPSPTKATAPRYPQTGAQSRPRRRFRPPAGAAPKAAAPRH PHPRGTAPPPRRISPESIRPHPPPPLDRGPRPPVTPFLIVLGLCLILA VLTTFKEYETVSGDWLLLLLETFAIFIFGAEFALRIWAAGCCCRYKGW RGRLKFARKPLCMLDIFVLIASVPVAVGNQGNVLATSLRSLRFLQI LRMLRMDRRGGTWWLLGSAICAHSKELITAWYIGFLTILSSFLVYL VEKDVPEVDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWE GRLIAATFSLIGVSFFALPAGILGSGLALK*
1077	A	606	1065	LVARTERLSVSQGFPLPWCTGRIRSHVGLENECKVLLSGSSSQKMGKP EGRWFSFGVGPPLCLAAPALLRPLWKSPPHPTGGWPASVPVPVGVLF CQRAPLDDQLLVCWPARVLEKRYWQPPLS*LCPSCAHMNGYGGSGAY VWVLTELTVDFAFWA
1078	A	1	822	MWNAVTLWQQRESCIEESEIGTLETKEHFIRGPKTLAPVTDWEGS LPLVFNQCRDASLIHPRFKGFRPRRDACLGPSPLAASPAFLGKGQA APRQAEGLPNSSSASAPPYPNPFITSPHTWSGLQFHSMTSPPPPAQ QFPLKKVAGAKGIVKRLKTDARLPWKPPDHRRRASGNHSHGRVQP P/CPAAFVGC*VSQAFPGARCKLSVDLPFWDLED\RVFMCVRVKRP PNRLCVSNMAVYFTWVQLLQAIWAYTCKSQGMRWLGLGSEA
1079	A	38	639	MTLIKSPIVIWTIRSRLKWSQMEMRNLGTGAKRQRRHVLSVDPKLR RWSRTGKAAPFWCLIIAGR PALVLHP*QVLLSWGRGKI*LTSPSRC TII EKSCNSWPPL*DKPQPHLQHTRTSKRLNRSGQAFQLNLLPQELA TSTRN/PDHQACECLQPRIPPKPCPICAGPHWKLD CSTHLAATPRAP GTLAQGS LTDSFSA
1080	A	1	1611	MGLVHLQRQSYWTVQRSSINHFLGCNPHTGDKDTLYMRWTKSFRKVE DPPTTSGPQTDQPKKHLTKFKSETKETRFIHGPKTPAPVMDWEGSLP LVFNHCRDASLIHSHFKGVRPRRDACLGPSPLAASPAFLGKRQHAL KRLKPVITHLLQHGLLKPNNSPYNSPILPVLKPKDPYKFVQDLCLIN QIVLP IHPMLYSLFVESPTITIVSGPDFNPASHIIPDTTPDPHDCIS LIHMLSPFPFHISFFPISHPDHTWFDGSSSTRPNRHSKAGAYAIIS STSIVEATTLPSTTSQAKLVALTQALTAKGLRVNILLILNMPFI FGTTMQSYGLKEGLFRSPFPPTHQARGFAPAQDWQIDFTHMPVRKRL KYL LVWVDAFTGWVEAFPTGSEKATAVISSLLSDIIPRFGLPASTQS DNGPAFTSQITQAVSQALGIQWNLHIIYRPQSSGKVERTNGLLKTHL TKLSLQLKKDWTVLLTLALLRIRACPRDATGYSPFELLYGHTFLLGP NLIPDTSP LGNYLPVLQAR
1081	A	17	1173	MADSRIKRTWMRMKFGAVTRIGGTSLGRSIPCPALCSVKKIHLRPR VLRPTSPRNISPILN/TARFKRIKACYSPATAWPFKAYKLPLQFPH FT/WS*NQTRLTA*FS*KHTCSP*LSSPANLPNPNPFYKTTTPFLPR HG**GQ\ILTQELGPRPIAFLSKQLDLTVLTQPSCLHAAAAAAILL KALKITKYAQLTLYSSHNQNLFSSSYLMHILSAPWLLQLYSLFVES PTITIVPGTDFNPASHIILDTPDPHDCISLIHLTFTPFPRISFFPV PHPNHIWFIDGSSSTRPKCHSPAKAGYAIVSSTSIIEATALPPSTTSQ QAEVALTQALTAKGLCVNIYTD SKYAFHIVHHHARSFLTQKGSSI INPSLIKTLNAA
1082	A	324	548	SFYHLPSSHVLLTVSFRD*PSPTCPAIYS*KGWSQRHSQGACYKC QKSGHWAKECPQPRIPPKLRPICVGP

1083	A	760	1260	HTDGVLVWMSFLFVSFSPNSQDPQLQLCWSLLEVHSRSCPLPGYQQWR LSWKCRNHSSSASLTLRAVDWSCSYSAILEPRWYCLLYFIQSIILKK HRGRRWIFLMEQRTGGQRIDLPRGGPPI*VTAPNLMHVRVKRPPNRL CVSNKAVYFTSKSGPLSQDVVTVVIH
1084	A	908	1192	LFSGNFIPKSFFSLISPTVGSHAAPNPTRSSPEKHRPLSLHTTPQKF RCPNTSPLFCFVFLCPSAGMLTFHVKRGCDFTSCASLNPEGTPPVEM
1085	A	1	420	WVLGLADFKNEAADPRETKETHFIRGPKTPAPVTDWEGSLPLVFNHC RDASDYSPTFQRCQTMQGRLPWSFTLSGKSFRSGGARACYKCQKSD HQAKECLQPRIPPKPCPSVRDPTGNRTVQLTWQALPEPLEFWPKAL
1086	A	287	515	LFTHVSKELATSARNLTTRPRTAGSPGFLLSHVPSVWDPTANRTVQL TWQPLPEPLE\SGPRLSD*LLPRSSRLSG
1087	A	1	5127	MLFWAFDKIQPFMLKTLNKLIGDGYLKIIRAVYDKPTANIILNGQ KLEAFPLKTGTROGCPLSPLLFNIVLEVLARAIROEKEIKGIQLGKE EVKLSLFADDMIVYLENPIISTQNLHKLISNFSKVSQYKNNVQKLQA FLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKP LLKEIKEDTNKWKNI PCSWIRRNIVKMAILPKRTPLLSLPSTLYEE LWRLRSYFPLCPQLYNMEQNTTDWVIYKEQCIWLTALETGESKSTAP AFGKGYPMAEYIIWGRLTPHMAGYSSETKLPEERSGSNICCSPISAV LQPLLLIPRQTGSGVDLQQTPTDLQLRVLTVRRKTNKQKGHPHQNPI CTSPSSKTKGSNSHITILTLNVNGLNAPIKRHRLANWIKSQDPSVCC IQETHLTCRDTHRIKIGWREIYQANGKQKAGVAILVSDKTDKFKPT KIKRDKEGHYMMVKGSIQOEELTTLNIIYAPNTGAPRFIKQVLRDLQR DLDSHTLIMGDFNTPLSTLDRSTRQKVNKDIQDLNSALHQVDLIDY RTLHPKSTEYTFFSALHIIYSKIDHIVGSKALLSKYKTEIITNCLS DHSAIKLELRKIKLTQNRSTTWKLNLLNDYVWHNMKAEINTLFE TNENKDTTYQNLWDTFKAVCRGKFIALNAHKRQERSKIDTLTSQK ELEKQEQTHSKASRRQEITKIRAKLKEIETQKILQKINESRSWFFEK INKIDRPLARPIKKKREKNQIDAINKDKGDIITDPTETIQTIREYYK HLYANKLENLEEMDKFLNTYTLPRLNQEEVESLNKPITGSEIEAIIN SLPIKKSPPGPDGFIKAFHORYKEELEASIIILIPKPRDPTTKENFRP IPLMNIDAKILNKLILANRIQQHIKKLIHHDQVGFIPGMQGSFCKS INVIQDINRTNDKNHMIISIDAEKAFDKIQQPFILKTLNKLIGDGY LKIIRAIYDKPTANIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLE VLARAIROEKEIKGIQLGQEEVKLSLFADDMIVYRENPIVSTQNLHK LISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELPFTIASKRIK YLGILQTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFFTELEKTTLKFIFWNQKRARIASIL SQRNKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGNDSLFNKWCWENWLAICRRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTLEENLGNTIQDIGMGKDFMSTTPKA MATKAKIDKWDLIKLSFCTAKETTITVNRQPTWEKIFTIYPSDKG LISRIYKELKQIYKRTNNPINKWVKDMNRHFSKEDIYTAKRHMKKC SSSLAIREMQIKTTTRYHLIPVRMAI IKKSGNNRPSSNVFVKLSEI QSLALIETRCLMNADEQGVPLIQEMLESWASICKVPKYPNAAEVRPE EQTPHLHPGEINSHVAHTKLVWWSLHTDTHIEWCRDSDRGTSGLRSI PCPPALCSVRKIHLRPQVLRPTSPRNISPISNPHTRTSKRLNRSGQA FLQNLPLQELATSARNLTTRPRNACSPGFLLSRVPSVRDPTGNWTVQ LTWQPLSEPLELWPKAL
1088	A	3	721	TRMKFDAMTQLGDLPEINPLSSCSLLREKDPPTTSGPQTDQPKHEL TNFKSTTNHAPLTIPLKPNHSYPAECQYPVPQHALKGLKSIITRLLQ HGLLPINCPYNPILPVLKPKDKAYRLLQDLRLINQIVLSIHPVLPK PNTLLSSIPPSTTHYSVLDLKHAFFTIPLHLSSQPLFAFTWTDPDTH QAQQITWAVLPQGFDTSPHYFNQAQISSSSVTYLGIILMKTHVLSLL IVSG
1089	A	144	410	GYEIWCRRSDRGPSLGRSIPRPPALCSVRKIHLRPQVLRRTTRPRNIS PISNLVSGFLSSPTSILTIPQLSSFNLDLTLQSLPSLNF

1090	A	265	769	RQKRHVLSVDPKLRWSRTGKAAPWCLIIAGRPALVLHP*QVLLS WGRGKI*LTSPSRCTII EKSCNSWPPL*DKPQPHLQHTRTSKRLNRS GQAFLLQNLPLQELATSTRN/PDHQAKECLQPRIPPKPCPICAGPHWK LDCSTHLAATPRAPGTLAQGS LTDSFSA
1091	A	69	634	KQKRSTYNLRSSDPPAQETSHQFQIRDKGDTFYLTQNSGAHGLGR QPSLDV*SLQGHLSDYSPMFPRCQTMQGRLP*SFTLSGKSRFSGEGA STPQPLLHP*WQVPLFWGRGKYPSTPSSPLVASPAFLGKGQKPPRPS RMPSTFG
1092	A	1	655	MGATHPFELLTKMTSQGSDISGDLPEINPLSSCSLLHEKDPPTTSG PQTDQPKKHLTNFKSEKETHFIRGPKTPVLVTDWEGRLPLVFNHSR DASLI IHPRFRGVRPRRDACLGPSPLAASPAFLEEGQVPQPLLSMSL TPSLLFWRRGKKPSTPSSPLAASPAFLEEGQVPQPHIS/GA/LDPLF LHPNLL*LCTPTPFPLFWKTVRKYSNNQKGE
1093	A	756	880	LSQWRSDNGPAFISQITQAVSQAPGIQ*NLIIPIYHPQSSGK
1094	A	781	1194	FPGGGPPI*VIAPNFMVRVRKPPNRLCVSNKAVYFTWVQVGCRL GA/PAPCIPAAPVP/VHGSEGPYNSRCLAEKPA*ALAASMWYLSL KALGIESGRVSITAILINISSARKA/SCVPLGSRILESLMLSTVRAL R
1095	A	400	687	RQVLLFWGRGKYPSTPSPSPLAASPTFLGQGGELVTSARNLTTRPRN ACGPGFLLSHVPSVRDPTGNRTVQLTWQPLPEPLE\SGPRLSD*LLL RL
1096	A	1	883	MASSAQLLGSSQETYNHRSKRQGGEMSHMAGARRKREREMLHTFKQ PDLMRWSSVCRKNKEKVGNSRKRRNVRYCFSRKFNGTSKVFESWQV VVGELNSHYAHTKPVWLSLHTDAHEIWCRRSDRRTSLGRSIPCPPVL CSMRKIHQAQVLRPTSPRNISPIILNRRKRHVLSVDPKLRHRSWTR EGSLPLVFNLCRDASLI IHGFRGVRPRRDTCGLGPSPLAASPTFLGE GARACYKCQKSGHQAKECLQPRIPPKLCPI\WRDPAGNRTVQLTWQPL LPKPLELWPKVL
1097	A	2	551	CGKVVNFLETFSMALTKMLIMIWTMKFRLRSSQMEMRNLGTGISLE TWCPAS*PL*P*LKGDKIQLRPWLQVQGSIGSFQEVLPVWLRNQ ELRFGNLCYFAGCMKPVCPGRSLLQGQGF/PWYVPAVVGAKVHD VNLHMLSFPSKWLHTCMKFGAVTWIRGPPLGDQSPVLLLFAP
1098	A	1436	1699	RQVPLFWGRGKYPNPFSPCLYFPFAPGTGSLQVPEIYLTTRPRNA CSPGFLLSRVPSLRDPTGNRTVQLTWQTLPEPLELWPKAF
1099	A	1099	1250	LVYLKVTGRMEPSWKTLCRILSRRTSPI*QGRPTFRFRKYREHHKDT PRD
1100	A	303	1413	VRRQRSDRERSDARMVRFNLYM*RKNPFILH*LFR*TLRQTKPDSS A/V*MCQNLMTSHSKSTEWKITK/QIFDGDGKTYQNVQQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLVFEANTGTENGYSQSAHLHPGEINSHV AHTKPVWWSLHMDAHEIWCRRSDRGTSLGRSIPRPPALCSVRKIHQ PQVLRPTSPRNISPIISNPGFCFRNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQYANRLSPRVGRFINAAGTTGFPT GKRAVSATQLMDFADFGTTTKQDFRLLGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQ
1101	A	846	1825	APCDPYSCPPENNPFSFTYPNPIKQPHYPPLSLTFFSDSAHLHPGE INSFIAHTKPVWWSLHTDTHIWCRRSDRGTTLGRSIPCPPVLCSKR KIHLPWSSDRPAQETSHQFQIHLCLVLLYSPTTLTKYISTPSLAT DHAPLTISLKNHPYPAQCQYPIQHALKGLKPAITRLLQHGLLKPI NSPYNSPILPVLEPEKIYRLVQDLRLINQIVLP IHPVVPNPYTLSS IPPSTIHYSVLDLKRAFFTIPLYPSSQPLFAFTWTDPTLQAQQTW AVLPQSFTDSPHYFSQAQISSLSVTYLSIILIKHTLSLLIMSD
1102	A	2141	2384	AEQWPSVKILRQELATSARNLATRPRNARSPGFLLSVPSVWDPTGN QTVQLTWQPLPEPLE\SGPRLSD*PLPRCSRLSS
1103	A	305	1148	TVLLLTQSLFGGLFIWTRMKFGAVTRIGGPPLGDQSPVLLLFALERQ RRHVLSMDPKLRCSRTGKAAPWCLIIAEMPDYSPTFQRCQTTQGR LPWSFTLSSKSRFSGEGATQRYPIPOQALKGLMPAITRLLQHGLLK

				PINSYPHSPILPVLKPKPYKLVDLRLINQIVLP IHPMVPNPYTLL SSIPASTHYSVLDLQQAFFTIPLHPSSQPLFAFTWTDPDTHQAQOI TWAVLPQAFTDSPHYFSQAQISSSSVTYLGIIILIKTHVLSLLFVFD
1104	A	2779	3182	DKTQPHLLHTGTSKCLNCSGQAFLOLQELATSARNLATRPGNSC SPGFLLSHVPSVPDPTGNRTVQLTWQPLPEPLELWPKVLSRVMYI* MVY*STIPQNSAIVLTDLLLGVIIPSESKHARPKVVLWAH
1105	A	2286	4921	PQVLRPTSPRNISPISNPGETKETRFIRGPKTPAPVTDWEGSLPLVF NHCARDASLI IHPRFKGVRRDACLGPSPLAASPDFLRKQVPLNPF SPCLYPFSAFLGQGEPLNPFSTLSGKSRFPAGAGAKGDVSGSQDNC GERVSRQTRQORSLHHRQDSAHLPGEINSHVAHTKPVWWSLHTDVH EIWCRDSDWGGDLPEINPLSSCVLCSVRKIHLRPQVLRPTSPRNIS PILNWWLKTDAARLPRKPPRPSLMPASRNHFHSGGLQPHLIVALLPNP KPPSCLPLVSPHLNPQVWDISNPSLATDHMPITIPKPNHPYPAQCQ YRIPQHTLKGLKPVITPLLQHCCLKPINSYPNSPILPVQKPKDSYRL VQDLRLINQIVLP IHPVVPKPYTLLSSIPSSITHYSVLDLKAFFTI PLHPSSQPLFAFTWTDPDTHQSQQLTWAVLPQGFDRDSPLYFSQALSH DLSFHPASASHLIQYIHDLLLCSPSFESSQDPTLLQLHLSKGYQV SPSKAQISSPSVTYLGIIILHKNTSRSLPADRVQLISQTPPTSTKQQLL SFLGMVGYFRLWIPGFAFLTPLYKLTGKNLADPIDPKSFPHSSFHS LKTALETAPTLALPDSSQPFSLHTAEVQGCAGVILTOGPGWHPVAF SKQLDLTVLGWPSCLRAAAAAALILLEALKITNYAQRITLYIAHNQON LFSASFLRHILSAPQLQLYSLFVESPTITNVPGPDPFNPASHIIPDT TPDPHDCISLIHLTFTFPFHISFFPVSHPDHTWFDIGSSSTRPNRHTP AKAGYAIVQANSPLRTSHILSIVEMYPQGNFVSFVHLLFPYSSGII QAPSLPYTSSSGICHLRLGLANQRYSTCPESGN
1106	A	1	761	HPLPSASLGLPSVSLGVSLCVRSALEAVVPMPLPKRRRARVGS AASSTPPSTRFPGVAIYLVEPRMGRSRRRAFLTGLARSKGFRVLACS SEATHVMEETSAAEEAVSWQERRMAAAPPGCTPPALLDISWLTESLG AGQPVPECRHRLEVAGPRKGPLSPAWMPAYACQRPPTLTHNTVLF GPSLQEALEILAEAGFEGSEGRLLTFCRAASVLKALPSVTTLSQL QGLPHFGEHSSRVVQELL
1107	A	1	969	MVNPDTGYINQDQLEENARLFHPKLI IAGTSCYSRNLEYARLRKIAD ENGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTHKTTLRGCRAGM IFYRKGVKSVDPKTGKEILYNLESILNSAVFPGLQGGPHNHAIGVA VALKQAMTLEFKVYQHQQVANCRALEALTELGYKIVTGGSDNHLIL VDLRSKGTDDGGRAEKVLEACSIACNKNTCPGDRSALRPSGLRLGTPA LTSRGLLEKDFQKVAHF IHRGIELTLQIQSDTGVRATLKEFKERLAG DKYQAAVQALREERGNHVSHTLPPHYLV I QWHAKGELN
1108	B	1	2175	MVNPDTGYINQDQLEENARLFHPKLI IAGTSCYSRNLEYARLRKIAD ENGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTHKTTLRGCRAGM IFYRKGMAPLGTATLLQALFSLFLSKSRDVPGTGADPGVMYVKRR PRGTDSGCVLEPRRFLPSGMAFTKEEEYEEEPYNEPALPEEYSVPL FPFASQGANPWSKLSGAKFSRDFILISEFSEQVGPOPLLTIPNDTKV FGTFDLNYFSLRIMSVDYQASFVGHPPGSAYPKLNFVEDSKVVLGDS KEGAFAYVHHLTLTYDLEARGFVRPFMAYISADQHKIMQQFQELSAE FSRASECLKTGNRKAFAGELEKCLKDLDTYTRTVLHTETEIQKKANDK GFYSSQAIEKANELASVEKSIIEHQDLLKQIRSYPHRKLKGHDLC EMEHIQDQASQASTTSNPDESADTDLYTCRPAYTPKLIKAKSTKCFD KKLKTLEELCDTEYFTQTLAQLSHIEHMFGRDLCYLLTSQIDRALLK QQHITNLFEDFVEVDDRMVEKQESIPSKPSQDRPPSSSLEECPIPK VLISVGSYKSSVESVLKIMEQELGDEEYKEVEVTELSSFPDENLDY LDMDMKGSISSGESIEGLGTEKSTSVLSKSDSQASLTVPSPQVRS KAALLQPHPNPTHRLRSSMEYKPDPPHFRFSEPWPNEPEANLSSPA VKDSVTKELOQTARPSREQT*
1109	A	2	964	DIIPLMVNPDTGYINQDQLEENARLFHPKLI IAGTSCYSRNLE\ EYA RLRK\ IADENGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTHKT

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				LRGCRAGMIFY\RKGVK\SVGSPRLGKEILYNLESINSVFPGLQG GPHNHA\IAGVAVAL\KQAMTLEFKVYQHVVANCRLSEALTELG KIVTGGSDNHLILVDLRSKGTGGRAEKVLEACSIACNKNTCPGDRS ALRPSGLRLGTPALTSRGLLEKDFQKVAHFIHRGIELTLQIQSDTGV RATLKEFKERLAGDKYQAAVQALREEVESFASLFPLPGLPDF
1110	A	172	375	IWHHSFYNELRVAPEEHPTLLTEAPLNPKANREKMTQVSMPLQHTTL WGLGKLLLEGGYAAQQREGRS
1111	B	827	1276	MATAAWSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAG IHETTYNSIMKCDIDIRKDYANNVLSGGTTMYPGIADRMQKEITAL APSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDEAGP SIVHRKCF*
1112	A	144	261	FPKINNIFYFTFLQDPTGIFSLDKTIGLGTYGRIYLV
1113	C	122	253	MGWVGATATSPHPVAWRTRRPSSSLRSLPSVRALVVRTERRVPCG*
1114	A	50	368	RQAILTAAPRRAAARAASRHRGGARALSPGMEQRRRR\RTTWSLLQ PRPRRRWAARRPRGRRAQVARRTARRICPCGRPPPVRAPAADPWARR AWSTSRSPAGTE
1115	A	336	689	PLRPPAAPRSRGIRAPGASALPPTPSLWLRASASSHHRVGTRCGPYP AHTCTTWSLLQPRPRRRWAARRPRGRRAQVARRTARRICPCGRPPV RAPAADPWARRAWSTSRSPAGTE
1116	A	164	370	SPQDPQRQNPRESSQPTLRDGTALGPASRSAGSWCSRVLSLRSR IKSVGNRIGPWKLNRNVDTS GP
1117	A	974	1112	NPEIPVCTTWSLLQPRPRRRWAARRPRGRRAQVERRTARRICPCGR
1118	A	179	406	FSSSIGSLRRQRGMKTPFGKAAAGQSRSTGAGHGSVSVTMIKRKA HKHRSRPP\SQPRGNIVGCIIQHGWKDG
1119	A	1	1698	MVNGPIQQDELITILNIYAPNTGAPRFIKQILSDLRDLDSTIKIGE FNTPLSTLDRSMRQKVNKDIEVNSALHQADLIDIYRTLHPKSTEYT FFSGLHHTYSKIDHIVGSKALFSKCKRTEITRNCLSDHSAIKLELRI KKLTQNHSTTWKLNLLNDYWVHKEMKAEIKMFFETNENKGTYYQN LQDTFKAKKKEETAQQRLVGVRGCGRAAATATAAATRAEDAGAKS KGRRHGSLRRQRRGVRFVHLRPAIRDGGESAPPGRVLEAGRGWGN ASYFTEPQILARLSWGGRLLOALSQGMKTPFGKAAAGQSRSTGAGHG SVSVTMIKRKAHKKHRSRPTSQPRGNIVGCRIQHGWKDGDEPLTQW KGTVLDQVPVNPISLYLIKYDGFDCVYGLELHRDERVSSLEVLPNRVA SSRISDTHLAEIMVGKAVEHIFETEESKNEWRGMVLAQAPVMNTWF YITYEKDPVLYMYQLDDYKDGDLRILQDSNDSPLAEREPEVIDSL VGKQVEYAKDDGSKRTGMVHQVEAKPSVYFIKDDDFHIYVYDLVK TS
1120	A	264	799	WESDVGEGLRPPPPPPPPGRRRTQEPRARDAATVIFACPAALLET LIAYGSSSPSFCKHRAARPLIFLLHRLTAEATARCPICALERNPGRWG ICASWPGMKTTPFGKAAAGQSRSTGAGHGSVSVTMIKRKAHKKHRSR PTSQPRGNIVGCIIQHGWKDGDEPLTQWKGTVLDQLL
1121	A	231	353	RMERKGRWNKKRKEEERRKTKGRQLFRIEGVKS VFFGPDF
1122	A	1	3654	MDKFLDITYTLPRLNQEEVESLNRPIGTAEIVAIINSLPTKKSPPGPDG FTAKFYQSKILANQIQHIKKLTHQDQVDFIPGMQGWFNIRKSINVI QHINRSKDKNHMIIISIDAEKAFDKIQHFMLKTLNKLRIDGTYLKII RAIYDKPTANIILNGQKLEAFPLKTGTRQGCSLSPLLNFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPVISAQNLLKLISN FSKVSGYKINVQKSQAFLYTNNRQTESQIMSELPFTTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAIL PKIIYRFNAIPIKLPMTFFTELEKTTLKFIWNQKRARIAKAILSQKN KAGGITLPDFKLYYKATVTKTAWYQNRDIDQWNRTEPSEITLHIY NFLIFDKPEKNEQWKGDSL FNKWCWENWLAICRKLKLDPLFTPYTKI NSRWIKDLNVRPKTIKTEENLGITIQDIGMGKDFMSKTPKAMATKA KIDKWDLIKLNKFNCTAKETTIRVNRQPTKWEKIFTTYS SDKGLISRI YNELQQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMKKCSPLA IREMQIKTTMRYHVT PVRMATIKKSGNNSWRSLQPWAAHSTTYRHP

				GTMEKKTSSGDTPTVFPSTLGRKKSTSAQLTELTALELSKGKVRN APSKLDLSPFEMLYGWPFLTNDPLLDQETSELGKHVNSLARFQQELT QVAEAQPQEVGPPLFNPGLVLPKQGGPYTILLSMPSAVKVTGIDSW IHHAQVKAWKTERAIPGSPAECGLGYQCEEIRDLKLKIKRDKKMSKGY SSYSVPVIHSVIQSSSLCTTGTQKSRIEVWEPLPRFPKMYGYAWIPR QKFAAGAGPSWRTSVKAVQKGNVGSKP HHRDPTGALPSGAVRRGPPS SRPQNGRSTGSLHRVPGKARPQHQPVKAAAREAVPYKATGVELPKTM GTHLLHQCDLDPATFSLSLHIKYLKHRHSYSPHLHLLFTVMGPHAR QMIRISGIDVDTRNLYKLNKLVKWLEVLDDQEEPEYSRTTSRKKQGF NSDEEDVLWMEKQLSCFCDKYQKWIPTRQLKGQLSYVKEADLIPDVM PPQALFHDDDEMEGNGAIDAGMEYVYNIDTLLRWSDGEEEGEGGEG RGGGRGGEGGGKREEGEGKKEEQGGWGGGQVEVEEGGGGGGN
1123	A	1376	3462	TKPKTKTTLLSQ*MQKKPLTKFNPNPSC*KLSIN/IVLEVLARAIRQK KEIKGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTKNRQTESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWNIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLKFIWNQKRARIAKSILSQKNKVGGI TLPDFKLYYKATVTKTAWYWYQNRVIDQWNRKEPSEITPHTYNYLIF DKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPTTWEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPIKKWVKDMNRHFSKEDIYAAKHKMKCCSSSLAIREMQ IKTTMRYLTPVRMAIIKKSGNNRQTGSGVDLKTPTDLKLRDLTVR RKMNKQKEIASTSTKRTSTPNPTCRSVGPKDCSSLGAMEQSWTENDF DKLTEKKALEENQEEMDKFLDTYTLPRLNQEEVESLNRPI TGSEIEA IIDS IPTKKYPGPDGFTAKFYERIKVFCTESLAKWIKWTHTKTFIME FHTIGNAKILQASSFTEVKTKTKTLEHKRLESIMALTSQ
1124	A	485	2347	TEPKTKTT*LSQ*MQKRPLTKFNNTSC*KLSIN/IVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDMIVYLENPTVSAQNLLKLIGNFSKVS GYKINVQKSQAFLYTNNRQTERQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENNKPLLKEVKEDTNEWKNIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLKFIWNQKRACIAKSIFSQKNKAGGI TLPDFKLYYKATVTKTAWYWYQNRDIAQWNRTEPSEIMLHIYNYLIF DKPEKNKQWGKDSL FNKWCWENWLAICRKVKLDPLTPYTKMNSRWI KDLNVRPKTIKTLEENLGITIQDIGVGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPTTWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDVNRHFSKEDIYAAKHKMKCCSSSLAIREMQ IKTTMRYHLTPVRMAIIKKSGNNRKIQ/GGIWCDRIL*RTTCRVAK EIQSL*RRI/WKRLQRTLSIPVLDAV*PPMF*ASVIDTMTI*CFEAR DTCFTLTLESFWDHMRCLAASKGIGLLLC*PLIWHMSLMGVKSPPFV FSCLWTSAVRPTT
1125	A	1	2784	MQTTIREYYKQLYANKLENLEEMDKFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKS PAPDGFTTKFYQRTEDKNHMIISIDAECTF DKIQQLMLKTLNKLIDGMYLKIIRAIYDKPTANII LNGQILEAFSL KTGTRQGCPLSPLLFNIVLEVLARAIRQEKEIKGVQLGKEEVKLSLF ADDMITYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNR ETENQIMSELPFTIASKRIQYLGIQLTRDVKDLFKENYKPLLNEIKE DTNKWNNIPCSWIGRINIMKMAILPKVIYRFNDIPIKLP LTFTELE KTILKFIWKQKRARIAKSILSKKNKAGGIMVPDFKLYYKTTVTKTAW YWYQNRDINQWNRTEPSEIMPHICNYLIFDKPKDKNKKWGKDSL FNKW CWENWLATCRKLKLDPLFPYTKINSRWIKDLNVTSTIKTLEENLG NTIEDIGMGKDFMFKTPKAMATKAKIDKWDLIKLSFCTAKETTIRV NRQPTWEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAAKGHVKKCCSSMAIREMQIKPTMRYHLTPVRMAIIK KSGNHRWCWRCGEMGTFLHCWWDCKLVQPLWKS VWRFLKDLELEIPF DPAIPLLSIYPKDYKSCCYKDTCTRSRPGQYLLLELQAQWYCFVNSP

				AECIFLLSLETWKHLDSRIFATLRSRDPLMSPHQQGLEPETELCGIS AEQLLRHAETQELYIPWPRYPQQGGSHSSLQALESPPSPDEEGSPKL STAALPECVQIASLNETPSIPPHWVNNEIKAQIKKFFETNESKDTMC QNLQDAAKAVLRGKFIPLNAHIKKLERSEVNNLTQQKELENQEQTN SKASRRQEITKIRAELEKMGTHKPLQKSMNVGAVF
1126	A	1	3000	MGKKQSRKTGNSKKQSASPPPKECSSSPATEQSWTENDFDELREEDF RRSNYSELQEEIQTGKGEVENFEKNSDECITGITNTEKCLKELTELK AKARELHEERRSLKSRCDQLEERSVSMEDKMNEMKREGKFREKRIKR NKQSLQEIWDYVKKRPNLRLISVPESDRENGTKLENTLQDI IQENFPN LARQANIQIQEIQRTPQRYSSRRATPRHIIVRFSKVEMKEKMLRAAR EKEIQTNIREYYKHRYANKLENLEEMDKFLNIYTLRRLNQEEVESLN RPIRGSEIVAIINSLPTKKSPGPDGFTAEEYQRYKEELVPFLKLQFQ SIEKEGILPNSFYEASIIILIPKGRD'TTKKENFRTISLMNIDAKILN KILANRIQQHIKKLIHHDQVGFIPGMQGWFNIRKSINVIQHINRTKD KNHVIISIDAFAFDKIQQFLKLTNLKLGIDGYLKI KRAIYDKPT ANIILNGQKLEAFPLKTGTRQGCPLSPLLFNIVLEVLARAIQKEKEI KGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTETQIMSELPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTKKWKNIPCSWVGRINIMKMAILHKVIYRFN AIPIKLPMTFFTELEKTTLKFTWNQKRARIAKSILSQKNKAGGIMLP DFKLYYKATVTKTAWYWYQNRDIDQWNRTEPSEITPHIYNYLIFDKP EKNKQWKGKDSL FNKWCWENWLAIWRKLKLDPFPTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAIATKAKIDKLDLI KLKSFCTAKETTIRVNRQPTWEKIFATYSSDKGLISRIYNELKQID KKKTNNPIKKWAKDMNRHFSKEDIYAAKKHMKKCSPLAIREMQIKN TMRYHLTPLRMAIIKSGNNRWELNNENTRTQEGEHHTLGTVVGWGE GGGIAVGDI PNAK
1127	A	1	3045	MEYYAAIKKDEFLSFAETWMKLETIILSKLSQGQKTKHRMFSILVLE VLARAIQKEKEIKGIQLGKQEVKLSLFADDMIVYRENPIVSAQNLLK LISNFSKLSGYKINVQKSQAFLYTNNRQTESQIMSELPFTIASKI IK YLGIIQLTREVKDLFRENYKPLLNEIKEDTNKWKNIPCSWVGRINIMK MAILPKVIYRFSAPIKLPMTFFTELEKTTLKFIWNQKRARIAKSIL SQKNKAGGIMLPDFKLYYKATVTKTAWYWYQNRNIDQWNITEPSEII PHIYNYLIFDKPEKNKQWKGKDSL FNKWCWENWLAI RRKLKLDPFLLP YTKINSRWIKDLNGRPKTIKTVEENLGITIQDIGTKDFMYKTPKAM ATKAKIDKWDLIKLSFYTAKETTIRANRQPTWEKIFATYSSDKGL ISRIYNQLKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKKHMKKCS LSLAIREMQIKTTMRYHLTPVRMAIIKSGNNRCWRGCGEIVTLLHC WWDCKLVQPLWKS VWRFLRDLELEIPFDPAPFLGIYPKDYKSCCYK DTCTLLEVLARAIQKEKEIKGIQLGKQEVKLSLFADDMIVYRENPIV SAQNLLKLISNFSKLSGYKINVQKSQAFLYTNNRQTESQIMSELPFT IASKIIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWV GRINIMKMAILPKVICRFSAIRIKLPMTFFKLEETTLKFIWNQKRA HIAKSILSQKNKAGGIMLPDFKLYYKATVTKTAWYWYQNRNIDQWNI TEPSEIMPHIYNYLIFDKPDKNKQWKGKDSL FNKWCWENWLAI CRKLK LHPFLTPYTKINSRWIKELNVRPKTIKSLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSFYTAKETTIRVNRQPTKWEKLFET YSSDKGLISRIYNQLKQIYKKKNKQPHQKVGEHETLLKRRHLCSQ KTHEKMLIITGHQRNANQNHN EIPSHAS
1128	A	1	2736	MIISIDAFAFGKVQPPFMLQTLNKLIGDGSYLKII RAVYDKPTANI TLNGQKLEAFPLKTGTRRGCPSPLLFNIVLEVLARAIQKEKEIKGI QLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSQYKIN QKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIHLTRDMKDLFK ENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILP\RFNAIPIKL PMTFFTELEKTTLNFIWN/QKRARIAKSILSQKNKAGGITLPAFKLY YKATVTKTAWYWYQNRDIDQGNRTEPSEITLRIYNYLIFDKPEKNKQ

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				WGKDSL FNKWCWENWLAICRKLKLD PFLTPYTTINSRWIKDLNVRPK TIKTLEELGITI QDIVMGKDFMSKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTKWEKIFETYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKAMNRHFSKEDIYTAKRHMKKCSPSLAIGEMQIKTTMRYH LTPVRMAI IKKSGNNRSAMI QMFVFPQDSYVEILTINVVVVGVLP SQ LQRTLKDSKEALETPSPSPSPSPFCFPRKLHTDFSFGPKAKAFMH KRLNQEEVESLNR PITGSEIVVI INSLPTKKSPGPDGFTAIFYQRYK EELRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNI PCSWVG RINIVKMAILPKNWKKTTLKFIRNQKRARTTKSILSQKNKAGGITLP DFKLYYKATVTKTAWYLYQYRDIDQWDRTEPSEITPHIYNYLIFDKP EKNKQWGKDSL FNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITI QDIGTGKDFMSKTPKAMATKAKIDKWDLI KLKS FCTAKETTIRVNGQPTK
1129	A	1	2955	MGKKQNRKTGNSKTQSASPPPKERSSSPATEQSWMENDFDELREEGF RRSNYSELREDIQTGKEVENFEKNLEECITRIINTEKCLKELMELK TKARELREECRSLRSRCDQLEERVSADEMNEMKPNLRLIGVPESD AENGTKLENTLQDIIQENFPNLARQANVQIQEIQRTPQRYSSRRATP RHIIIVRFTKVEMKEKMLRAAREKDFKPTKIKRDKEGHYIMVKGSIQQ EELTIILNIYAPNTGAPRFIKQVLSDLQRDLDSHTLIMGDFNTPLSTL DRSTRQKVNKDTQELNSALHQADLIDYRTLHPKSTETFFSAPHHT YSKIEHIVGSKALLSKCKRKEIITNYLSHSAIKLELR IKNLTQSHS TTWKLNNLLNDYVWHNEMKAEIKMFFETNENKDTTYQNLWDFAKAV CRGKFIALNAYKRKQERSKIDTLTSQLEKEQEQTHSKAGRRQEIT KIRAELEIETQKTLQKINESRSWFFERINKIDRPLARLIKKKREKN QIDTIKNDKGDITTDPTETIQTIREYYKHLIYANKLQNL EEMDTPLDT YTLPRLNQEEVESVNKPITGSEIVAI INSLPTKKSPGPDGFTAIFYQ RYKEELVPFLLKLFQSIGKEGILPNSFYEASIIILPKPGRDITTKEN FRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGFIPGMQGWFI RKSINVIQHINRAKDKNHMIISIDA EKA FDKIQQPFMLKTLNKL GID GTYFRIIRAIYDKPTANIIILNGQKLEAFPLKTGTRQGCPLSPLLFNI VLEVLARAVRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIVSAQN LLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRIN IVKMAILPKHGWGCLVAPHVPTVLTIQLRSPRYPCTVVNVLAGV
1130	B	1	3105	MGKKQNRKTGNSKEQSTSPPPKECSSSPAREQSWTENDFDELREEGF RRSNYSELWEDIQTGKEVENFEKNLEECITRIINTKKCLKELMELK TKARELREECRNLRSRCDQLEERQINETESQQGYPIELSSAPSGPN THLQNSPPQINRIYIFSA PHHTYSKTDHILGSKALLSKCKRTEIITN YLSHSAIKLELR IKNLTQSRSTTWKLNNLLNDYVWHNEMKAEIKM FFETNENKDTTYQNLWDFAKAVCRGKFIALNAHKKRQERSKIDTLTS QLKELEKQEQTHSKASRRQEITKIRAELEKAMETQKTLQKINESRSWF FERINKIDRLLARLIKKKREKNQIDTIKNDKGDITTDPTETIQTIRE YYKHLIYANKLENLEEMDKFLDTYTLPRLNQEEVESLNR PITGSEIVA I INSLPTKKSPGPDGFTAIFYQRYKEELVPFLLKLFQSIGKEGILPN SFYEASIIILPKPGRDITTKESFRPISLMNIDAKILNKILAKRIQQH IKKLIHHDQVGFIPGMQGWFIICKSINVIQHINRAKDKNHMIISIDA EKA FDKIQQPFMLKTLNKL GIDGTYLKIIRAIYDKPTANIIILNGQKL EAFPLKTGTRQGCPLSPLLFNIVLEVLARAIRQENEIKGIQLGKQEV KLSLFADDMIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKSL KEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRFNAIPIKLPMPF FTELEKTILKFIWNQKRARIASILSQKNKAGGITLPDFKLYYKATV TKTAWYQYQNRDIDQWNRTEPSEITPHIYNYLIFEKPDKNKKWGKDS YLINGPQSTMSAQPMHGYSAQPRHRFSRRQCTALAQADGOMQQLLL ISTDSITAGYGRAPPNACEVWIKVWIPHLTSADIHGEDTPHYLCPPG DSLASKIKKSYLWGN EEPDPMENGGSQIHRI PATGKGIQAPLEGA

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1131	A	1	2827	MEYYAAIKNDEFMSFAGTWMKLGTTIILSKLPQGGQKTKHHMFSLTAPH HTYSKIDHIIGSKALLSKCKRTEIITNYLSDHSAIKLELRICKLTQON RSTTWKLTNLLNDYWVHNEMKAEIKMFFETYENKDTTYQNLWDAPK AVCRGKFIALNAHKRKQKRSKIDILTSQLEKEKQEQTSHKANRRQE ITKIRAELEIETQKTLQKINESRSWFFERINKIDRPLARLIKRRB KNQIDAIKNDKGDITTDPTDIKTIREYKYRLYTNKLENLEEMHKFL DTHTLPRLNQEEVESLNRPIITGAEIVAIINSLPTKKSPGLDGFATAK YQRYKEELHHPDTKAGQRHNQKENFRPIPLMNIDAKILNKILANRIQ QHIEKLIHHDQVGFIPGMQGWFNIRKSINVIQHNRTKDKNHMIIISI DAEKAFDKIQQPFMLKTLNKLGDGTLYLKIIRAIYDKPTANIILNQ KLEAFPLKTGTROGCPLSPLLFNIVLEVLAIRKEKEIKGIQLGKE EVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSQYKINVQKSQA FLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKP LLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKF IWNQKRARIASILSQKNKAGGITLPDFKLYYKA TVTKTAWYQYQNRDIDQWNRTEPSEIMPHIYNYLIFDKPDKNQWGK DSLWNKWCWENWLAICRKLKLDPFLLPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMGKDFMSKTPKAMATKDKIGKWDLIKLSFCTA KETTIRVNRQPTWEKIFATYSSDKGLISRIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEGIYAAKHKMKK\CSPSLAIREMQIKTMMRYHFT PV
1132	A	1709	2974	TEPKTKTT*LSQ*MQRPLIKFSNASC*KLSIN/IVLDVLARAIRQE KEIKGIELGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFKVS GYKINVQKSQAFLHTNNRQTESQITSELPFTIASKRRKYLGIQLTRD MKDLFKDNYKPLLNEIKEDTNKWKNI PCSWVGRINIMKMAILPKATV TETAWYQYQNRDIDQWNRTEPSEIMPRIYHYLIFEKPDKNQWGKDS LFNKWCWENWLAICRKLKLDPFLLPYTKINSRWIKDLNVRPKTIKTL EENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKLSFCTAKE TTIRVNRQPIEWKIFANYSSDKGLISRIYNELKQVYKKKTNNPIK WAKDMNRHFSKEDIYA\ANRHMKKCSRLAIREMQIQTMMRYHLTPV
1133	A	1	2856	MVKGSIQEEELTILNIYAPAGAPRFIKQVLSDLQRDLDFTLIMGDF NTPLSTLDRSTROKVNKDTQELNSALHQADLIDIYRTLHSHKSTEYTF FSAPHHTYSKIDHLLGSKAFLSKCKRTEIITNYLSDHSAIKLELRICK NLTQNRSTTWKPNLLNDYWVHNEMKAEIKMFFETNENKDTTYQNL WDAFKA VCRGKFIALNAHKRKQERSKIDTLTSQVKELEKQEQTSHKA SRRLNQEEVESLNRPIITGSEIVAIINSLPTKRVQDQMDSQPNSTREK EGILPNSFYEASIIILIPKPGRDTTKKNFRPISLMNIDAKILNKILA NQIQQHIIKLIHHDQVGFIPGMQGWFNHKS VNVIQHINRAKDKNHM IISIDAEKAFDKIQQPYMLKTLNKLGDGTLYFKIIRAIYDKPTANI I LNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAIRKEKEIKGIQ LGKEEVKLSLFADYMIYYLENPIVSAQNLLKLISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSELPFTIASKRIKHLGIQLTSDMKDFFKE NCKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKLPMTFFTELE KTTLKF IWNQKRACITKSNLSQKNKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYNYLIFDKPEKNQWGKDSL FNKR FWENWLAIFRKLKLDPFLLPYTKINSRWIKDLHVRPKTIK TLEENLG ITIQDTGMGKDFTSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRV NRQPRKWEKIFATYSSDKWLISRIYNELKQIYKKKTNNPIK KWKADM NRHFSKEDIYAAKHKMKKCSPLAIRETQIKTMMRYHLTPGHPILNL KHSELHHAPQSSSWKREGLDLEERVEFGQIKKNAGTLQKRRGCEPRH GDTNIGDIFVRQ
1134	B	1	3786	MVKGSIQEEELTILNIYAPNTGAPRFIKQVLSDLQRDLDSTLIMGD FNNPLSTLDRSMRQKVNKDTQELNSALHQVDLIDIYRTLHSHKSTEYR FSAAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSGHSIAIKLELKI KNLTQNRSTTWKLNLLNDYWIHNEMKAEIKMFFETNENKDTTYQON

				LWDAFAVCRGKFIALNAHKRKQERSKIDTLTSQLKELEKQEQT HSK AGRKKEITKIRAQLKEIETQKTLKKLMNPGAEIQT TIREYYKHL YAK KLENLEEMDKFLD TYTL PRLNQE EVESLNR PITGAEIVAI INSLPTK KSRT RWIHSRILPEEAS I ILIPKPGRD TT KKENFRPISLMNIDAKIL NKILAKRIQQHIKKLIHHDQVGFI PGMQGW FNHKSINVIQHINRAK DKNHIIISIDA EKAFDKIQPFMLKTLNKL GIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGT RQGCP LSP LFNIVLEV LARAI RQEKE IKGIQLGKEEVQLSLFADEMIVYLENPIVSAQNLLKLISNFSKVS GY KINVQKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDV K DLFKENCKPLLNEIKEDTNKWKNI PCSWVGRINIMKMAILPKVIYRF NAIPTKPPMTFFTELEKTTLKFIWNQKRARI AKSILSQKNKAGGITL PDFKLYYKATVTKTAWYWYQNRDL DQWNRTEPSEITPHIYSYLIFDK PEKNKQWGKDSL FNKWCWENWLPICRKLKLD PFLTPYTKINSRWIKD LNVRPKTIKTLKENLGITIQDIGMGKDFMSKTPKAMATKD KIDKDWL IKLKSFCTAKETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQI YKKKTNNPINKWVKDMNRHFSKEDIYAAKHKMKCSSSLAIREMQIK TTMRYHLTPLRMAIIKKS GNN SASPTARNKTARNQRTKMI AVTAPRN RAPLELELILYRQNRQSKTHILETNNTS AELLVPFEEDYLI EIRTVS DGGDGS SSEEIRIPKMSMIDHILPKSIPEELQNGEGFGYIIMFRPVG STTWSKEKVSSVES SRFVYRNESIPLSPFEVKVGVYNNEGESLST VTIVYSGEDDGYVFLWMVEPQLAPRGTS LQSFSASEMEVSWNAIAWN RNTGRVLGYEVLYWTD DS KESMIGKIRVSGNVTTKNITGLKANTIYF ASVRAYNTAGTGPSSPPVNVTTKSRYLIT TAYLEVPEI*
1135	A	1	3276	MGDFNTPLSTLDRSTRQKVNKHTQELNSALHQADLIDIYRTLHPKST EYTFCSAPHHTYSKIDHIVGSKALLSKCKRSEIITNCLSDHSAIKLE LRIKKLTQNRSTTWKLNLLNDYWVHNEMKAEIKMFFETNQNKD TT YQNLWDTFKA VCRWKFIALNAHKRKQERSKIDTLTSQLKELEKQEQT HSKASRRQEI TKIRAE LKEIETQKTLQKINESRSWFFERINKTDRPL ARLIKKKRQNNQIYAIKNDKRDITTDPT EIQTTIREYYRYLYTNKLE NLEEMDKFLD TYTL PRLNQE EGD SLNR PITGSEIVAITNSLPTKKSP GPDGFTA EFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEAS I ILIP KPGRHTTEKENFRPISLMNIDAKIILNKILANRIQQHIKKLIHHDQVG FIPGMQGW FNIRKSRNVIQHINRTKDKNHMIISIDA EKAFDKIQQR F MLKSLNKLGV DGTYLKIIRAIYDKPTANIILNGQKLEAFPLKTGTRE GCPLSP LFNIVLEV LARAI RQEKEIKGIQLGKEEVKLSLFA DDMIV YLENPIVSAQNLLKLISNFSKVS GYKIHVQKSQAFLYTNNRQTESQI MSEL PFTIASKRIKYLGIQPTKDV KDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTQLEKTTLKF IWNQKRARI AKSILSQMNKAGGIMLPDFKLYYKATVTKTAWYWYQNR DIDQWNRIEPSEIMPHIYNLIFDKPEKNKQWGKDSL FNKWCWENWLP AIWRKLKLD PFLTPYTKTNSRWIKDLNV RPKTIKTL EENLGITIQDI GMGKDFMSKTPKAIATKAKIDKWDLIKLR SFCTAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYKELKQIYKKKTNSPIKKWAKDMNRHFSK EDIYAAKHKMKCSPSLAIREMQIKTTMRYHLTPVRMAITKKS GNNR CWRGCGEIGTLLHCWNPTYKGCEGPLOGERQTTAQGNKRGYQMEEH SMLMGRKNQYRENGHTAQERVQQLMVLNQANS CFECLEICLGVERKG PCGTSIYVREG
1136	A	1	3042	MGKKQSRKTGNSKNQSASPPP KERSSSPAMEQSWMENDFDDLREEGF RQSNYSELKEEV RTHGKEVK NLEKKLDEWLTRITNAEKS LKDLME LK TTARELHDECTSLKRVSVTEDQM NEMKREEKFREKRIKRNEQSLQEI WDYV KRPNLHLIGVPESDRENGTKLENTLQDIIQENFPNLVRQANIQ IQEIQRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKGRVTHK GKPIRLTADLLAETLQARREWGP I FNILKEKNFQPRISYPAKLSFID RSTRQKVNKDTQELNSALHQADLIDIYRTLHPKST EYTF SAPHHTY SKIDHIVGSKALLSKCKRTEIITNCLSDHSAIKLELRIKKL TRNHST TWKLNLLNDYWVHNEMKAEIKMFFETNENKD KTYQNLWDTFKTV C

				RGKFIALNAHKRKQERSKIDTLTSQLKGLEKQEQTHSKASRRQEITK IRAELEKEIETQKTLQKINESRSWFFKINKIDRPLARLIKKNREENQ IDAIKNDKGDITTDPTETIQTATSEYYKHLIYANKLENLEEMDKFLDTY TLPRLNQEEVESLNRPTITGSEIEAIINSLPTKKSPGPDGFMFAEFYQR DKEELVPFLLKLFQSEIEKEGILPNSFYEASIMLIPKPGRDITTKENF RPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGFIPGMQGWPNLR KSLNVIQIHNRNDKNHMIISIDAEKAFDKIQPPFMLKTLNKLGDG MYLKIIIRAIYDRPTANIILNGQKLEAFPLKTGTROGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMTVYLENAIVSAPNL LKLIGNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSELPFRIASKR IKYLGQQLTRDVKDLFKQNYKPLLNEIKEDTNKWKNIPCSWVGRINI VKMAILPKGTQRPYAKVRVQLNSGEELHFLGLLDTSTQVTVIPTNPC IKMRRKQIVFSDFGLLLTSVVMAPTTE
1137	A	1	3663	EHSSSPATEQRWTENDFDELREEDFRRSNYSELWEDIQTKGKEVENF EKNLEECITRITNTEKCLKELMELKTKARELRKECRSLRSRCNQLEE RVSAMEDGMNEMKQEGKFREKRIKRNKQSLQEIWYVVRPNLRIGV PESDGENGTLENTLQDIQENFPNLRQANIQIQEIQRTRQRYSSR RATPRHIIVRFTKVEMKEKMLRAAREKGRVTHKGKPIRLTADLSAET LQARREQKPSFFETNENKDTTYQNLWDAFKAVCRGKFIALNAHKRKQ ERSKIDTLTSQLKELEKQEQTHSKASRRQEITKIRAELEKEIETQKTI QKINESRSWFFERINKIDRPLARLTAKKREKIQIDAIKNDKGDITTD PTEIQTITREYYKHLIYANKLENLEEMDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKSPGPDGFTAIFYQRYKEELVPFLLKLFQ STEKEGILPNSFYEASIIILIPKPGRDITTEKENFRPISLMNIDAKILN KILPNRIQQHIKNLLHHDQVGFIPGMQGWPNICKLINVIQHINRTKD KNHMIISIDAEKAFDKIQPPFMLKTLNKLGDGTYLKIIRAIYDKPT ANIIWNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLARAIRQEKEI KGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSAYK INVQKSQAFLYTNNRQTESQIRSELPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILPKIYIRFN AIPKLPMTFFTELEKTTFKFIWNQKRARIKSIKSKNKGAGITLP DFKLYYKATVTKTAWYWYQNRDIDQWNRTEPSEITPHIYNYLIFDNP EKNKQWKGKDSLFNKWCWENWLAICRKLKLDPLTPYTKINSRWIKDL KVRPKTIKTLEESLGITIQDIGMCKDFMSKTPKAMATKAKIDKWDLI KLKSFCETAKETTIRLGVELHKGHPCGHHHYDTTGSDLPKPAQHWVSPKA YYNHSQAIANVHSRCDFTISMWQSQSGLCPSLQDGKVSALGRLAP LWPREGPEMPSKYQVLESSTPSILLMLYPSVAMLVPKVQDKVTFTFP STFLKQMEFLHAASTAGEGRGGVASEIQDCFFYLFSASLSMDMLKPG TVDAHWTFGSYEAIIAKNSGKSMVSLPLASTSLIISRNASDPVTS
1138	A	1	3144	MGDFNTPLSTLDRSSRQKVNKDTQELNSTLHHLADLIDYRTLHPKST EYTFFSAPHHTYSKIDHVVGSKALLSKCKRTEIITNCLSDHSAIKPE LRIKKLTQNRSTTWKLNLLNDYWVHNKMAEKIMKFETNENKDTT YQNLWDTFKAVSRGKFIALNAHKRKQKRCIDTLASQLKEVEKQEQT HSKASRRQEITKIRAELEKEIETQKTLQKINESRSWFLERINKIDRPL ARLIKKKREKNQIDVIKNDKGDITTDPTETIQTITREYYKHLIYANKLE NLEELDKFLDTHTLQRLNQEEVESLNRPTITGSEIVAIINSLPTKKSP GPDGSTAIFYQRYKEELLPLLLKLFQSEIEKEGILPNSFYEASIIILIP KPGRDITAKENFRPISLMNIDAKILNKILANQIQQHIKKLIYTMIKW ASSLGCKAVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSE IPFTIVSKRIKYLGIQLTRDMKDLFKENYKPLLNEIKEDTNKWKNI CSWLGRINMVKMAILPKVIYRFNAILIKLAMTFFTESEKTTLKFIWN QKRACIAKSILSQKNKVIGITLPDFKLYYKAIWNKTAWYWYQNRDID QWNRTEPSEITPHIYNYLIFDKPEKNKQWKGKDSLFNKWCWENWLAIC RKLKLDPLTPYTKINSRWIKDFHVRPKTIKTLEENLGITIQDIGMD KDFMSKTPKAMATKAKIDKWDLIKLSFCRAKETTIRVNRPPTEWEK

				IFVITYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEYI YAAKRDMMKKCSSSLAIREMQIKTTMRYHLTPVRMVIKKSGNNRCWR GCGEIGTLLHCWWDCKLVHPLWKSVMRFLRDLELEIPFDPAILLLGI YPKDYKSCCYKDTCTHEKAEIQKSKGIRDYGEIGTRTEDMDSQFRPL SVVRAQIIPFEFPWEGIPLGPFPRHSCSYVGLALLYHSSSAAGPV RGHLSLQWNSRMTS
1139	B	1	3380	MVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQRLDLSHTLIMGD FNNPLSTLDRSMRQKVNKDTQELNSALHQVDLIDIYRTLHHKSTEYR FFSAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSGHSAIKLELKI KNLTQNRSTTWKLNLLNDYWIHNEMKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKEKQEQTTHSK ASRRINKIDRPLARLIKKKREKNQIDAIDKNDKGDITNDPTEIQTITIR EYKHLIYANKLENLEEMDKFLDITYTLPRLNQEEVESLNRPIGTSEIV AIINSLPTKRVDQMDSQPNSTRVLEVLARAIQEKEIKGIQLGKQE VQLSLFADEMIVYLENPIVSAQNLLKLISNFGKSVGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENCKPL LNEIKEDTNKWKINIPCSWVGRINIMKMAILPKVIYRFNAIPTKPPMT FFTELEKTTLKFIWNQKRARIAKSILSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDLQDQNRTEPSEITPHIYSYLIFDKPEKNKQWQGD SLFNKWCWENWLPICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIKT LKENLGITIQDIGMGKDFMSKTPKAMATKDKIDKWDLIKLSFCTAK ETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIN KWVKDMNRHFSKEDIYAAKHKMKCSSSLAIREMQIKTTMRYHLTPL RMAIKKSGNNSASPTARNKTARNQRTKMIAVTAPRNRAPLELELIL YRQNRQSKTHILETNNTSAELLVPFEEDYLIBIRTVDGGDGSSEE IRIPKMSTGGEEGMAAVFKNKCRCSSWSRVVIAYHSSSGNQMGTNPEQ DPGQHAIPLEX*
1140	A	1	3345	MGDFNIPLSTLDRSTRQKVNKDTQELNSALHQADLIDSYRTLHPKST EYFFSAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSDHSAIKLE LRIKNLTQNCSTTWKLNLLNDYWVHNEMKAEIKMFFETNENKDTT YHNLWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKEKQEQT HSKASRRQEITKIRAELEIETQKTLQKINESRSWVFERINKIDRPL ARLTKKKSEKNQIDAIDKNDKGDITTDPTIEIQTIREYYKHLIYANKLE NLEETDKFLDITYTLPRRNQEEVESLNRPIGTAEIVAIINNLPKTKSP GSDGFTAIFYQRYKEELVPFLKLQFSIEKEGILPNSFYEASIIILIP KPGRDTTKKNFRPISLMNIDAKILNKILANQIQHKKLIHHDQVG FIPGMQGWFNICKSINVQIHINRTKDKNHMIIISIDAFAFDKIQQPF MLKTLNKLKIDGTYLKIIRAIYDEPTANIILNGQKLEFLKGTGRQ GCPLSPLLFNIVLEVLARAIQEREIKGIQLGKEEVKLSLFADDMIV YLENPIVSAQNLLKLISNFGKSVGYKINVQKSQAFNTNNRQTESQI MSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLEIKEDTNKWK NIPCSWVGRINIMKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKF IWNQNRACIAKSILSQKNKAGGITLPDLKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITLHIYNYLIFDKPEKNKQWQKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDLNIRPKTIKTEENLGITIQDI GMGKDFMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTK WGKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKFAKDMNRHFSK KDIYAAKHKMKCSPSLAIREMQIKTTMRYHLTPVRMAIKKSGNNR TGRGLHPGRDWSVT CARSPGDPEPSGKGGCGSGTPSPSPSKQTVRR PWTQIPEMKPLLLAVSLGLIAALQAHLLASDEEIQDVSGTWYLLKAM TVDREFPEMNLESVTPMTLTTLLEGNLEAKVTML
1141	A	1	3429	MGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLIDIYRTLHPKST EYFFSAPHHTYSKIDHILGSKALLSKCKRTEI IANYLSDHSAIKLE LRIKNLTQNRSTTWKLNLLNDYWVHNEMKAEIKMFFETNENKDTT YQNLWDAFKAVCRGKFIALSAHKRKQERSKIDTLTSQLEKEKQEQT HSKASRRQEITKIRAELEIETQKTLQKINESRSWFFERINKIDRPL

				ARLIKKKREKNQIDAIKNDKGDITIDPTEIQTTIREYYKHLIYANKLE NLEEMDKFLDITYLPRLNQEEVKSILNRPITGAEIVAIINSLAIKKSP GPDGFTAIFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEASIIILIP KPGRDITTKENFRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVG FIPGMQGWFIHKSINVIOHINRARDKNHMIISIDAFAFDKIQQPF MLKTLNKLIGIDGTYLKIIRAIYDKPTANIILNGQKLEAFPLKTGTRO GCPLSPLLFNIVLEVLAIRQEKEIKGIQLGKKEEVKLSLFADDMIV YLENPIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQI MSELPTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWK NMPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMAFFTELEKTTLKF IWNQKRARIAKSILSQKNKAGGITLPNFELYKATVTKTAWYQNR YIDQWNRTEPSEITPHIYNYLIFDKPGKNQWGKDSLFWKWCWENWL AICRKLQDPLTPYTKINSRWIKDLNVRPKTIKTLEEDLGITIQDI GMGKDFMSKTPKAMATKDKIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSFDKGLISRIYNELQQIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKHKMKYSSSLAIREMQIKTTMRYHLTPVRMATIKNSGNRR SLCFYKENLSLCLAILLSVPVQEGGARSFLAPAGGVAGRATSHYGGH MATAERLSVELSGQALKEFQKGPLSPKQFKGHHSQQLRWTHRLNPSY GQSKTPKNTLLMRGPTTWALGGTDVAASDNNNGNAHFETLQVMDMP RPWCCLLDGALLVSV
1142	A	1	3030	MGKKQSRKTGNSKKQSASPPPKCESSSPATEQSWTENDFDELREEDF RRSNYSELQEEIQTGKGEVENFEKNSDECITGITNTEKCLKELTELK AKARELHEERRSLKSRCDQLEERVSVMEDKMNEMKREGKFKREKRIKR NKQSLQEIWDYVVRPNLRLISVPESDRENGTKLENTLQDIIQENFPN LARQANIQIQEIQRTQORYSSRRATPRHIIVRFSKVENKEKMLRAAR EKEIQTNIREYYKHRYANKLENLEEMDKFLNIYTLRRLNQEESVSLN RPIRGSEIVAIINSLPTKKSPPGPDGFTAIFYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIIILIPKPGRDITTKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGFIIPGMQGWFIHKSINVIOHINRTKD KNHVIISIDAFAFDKIQQFLKTLNKLIGIDGTYLKIIRAIYDKPT ANIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAIRQEKEIK KGIQLGKKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTEQIMSELPTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTKKWKNIPCSWVGRINIMKMAILHKVIYRFN AIPKLPMTFFTELEKTTLKFTWNQKRARIAKSILSQKNKAGGIMLP DFKLYYKATVTKTAWYQNRDIDQWNRTEPSEITPHIYNYLIFDKP EKNKQWGKDSLFWKWCWENWLAIWRKCLKDPFPTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAIATKAKIDKLDLI KLSFCTAKETTIRVNRQPTWEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMKKCSPLAIREMQIKN TMRHYHLTPLRMAIIKKSGNNRASRSARGESLGPSQSFPEHVHCPGPL HTALHRPMTFQIPRDMLEVSSAH
1143	A	1	4171	MNSLEQNPRSKWELLHRGTMELWPTMWADDEEQGLKAVLALSAAKFV PGARSKTGLTDCMGVGGGLLLPAFPHIPGKRDSHNPLWNITPENQSP TPTVAMERSSSPATEQSWMENDFDELREEGFRRSNYSELQEEIKTKG KEVKNFEKNLDECITRINTTEKCLKEVMQLKAKARELREECRSLRSR WNQLEERVSVMEDEMNMKREGKFKREKRIKRNEQSLQEIWDYVVRPN LRLIGVPESDGENATRLNENTLQDIIQENFPNLARQANIQIQEIQRMP QRYSSRRASPRHIIVRFTKVEMKEKMLRAAREKGRVTHKGKPIRLIA DLSAETLQARREWGPFIENILKEKNFQLRISYPAKLSFISEGEIKSST DKQMLRDFVTTRPALKELLKEALNMERNNRDTHRLKTKGWRKIYQAN GKQKKAGVAILVSDKTFDKPTKIRRDKEGHIYIMVKGSIQEEELTILN IYAPNTGAPRFIKQVLSDLQRLDLSHTIIMGDFNTPLSTLDRSTRQK VNKDTQELNSALHQADLIDIYRTLHPKSTEYFFSAPHHTYSKTDHI VGSKALLSKCKRTDIKTNCLSDHSAIKLELRIKKLTQNHSTTWKVVN LLLNDYVWHNEMTAEIKMFFETNENKDTTYQNLWDTFKAVCTGKFIA

				LNAHKRKQERSKIDTLTSQLKELEKQEQTHSKASRRQEISKIRAEK BIETQKTLQKINESRSWFFERINNINRLLERLIKREKNQIDTTKN DKGDITTDPTIEIQTIREYYKHLIYANKLENLEEMDKFLDYTLPRLN QEEVESLNRPIITGSEIVAIINSLPTKSPGPDGFTGEFYQRYKEELV PFLKLQFSMEKEGIPPNISFYEASIIILISKPRDITTKENFRPISLM NIDAKILNKILTKRIQQHIKKLIHHDQVGFIPGMQGWFNIRKSINVI QHINRTKDKNHMIIISIDAFAFDKIQQHFMLKTLKLGIDGMYLKII RATYDKPTANIIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIISAQNLLKLISN FSKLSGYKINVQKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIKEDTNKWKNSPCSWVGRINIMKMAIL PKLPMTFFTELEKTTLKF IWNQKRACIAKSILSQKNKAGGITLPDFK LHYKATVTKTAWYWYQNRDIDQWNRTEPSEITPHIYNYLIFDKPEKN KQWGDLSLFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVR PKTIKTLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKWDLIK\S FCTAKETTIRVNRQPTKWEKIFATYSS
1144	A	1	3921	MGKKQNRKTGNSKTQSASPPPKERSSSPATEQSWMENDFDELREEGF RRSNYSELWEDIQTKGKEVENFEKNLEECITRITNTEKCLKELMELK TKARELHEECRSLRSRCDQLEERVSADEMNEMKREGKFRKRIKR NEQSLQEIWDYVVRPNRLRIGVPESDVENGTKLENTLQDIIQENFPN LARQANVQIQEIQRMPQRYSSRRATPRHIIIVRFTKVEMKEKMLRAAR QKAPHHTYSKIDHIVGSKALLSKCKRTEIITNYLSDHSAIKLELRIR NLTQSRSTTWKLNLLNDYVWHNEMKAEIKMFFETNENKDTTYQN WDTFKAVCRGKFIALNAYKRQETSKIDTITSQLKELEKQEQTHSKA SRRQEITKIRAEKBIETQKTLQKINESRSWFFERINKIDRPLARLI KKKREKNQIDTIKNDKGDITTDPTIEIQTIREYYKHLIYANKLENLE MDTFLDYTLPRLNQEEVESLNRPIITGSEIVAIINSLPTKSPGPDG FTAEFYQRYKEELVPFLQLQFSIEKEGILPNSFYEASIIILIPKGR DTTKKENFRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGFIPG TQGWFNIRKSINVIQHINRAKDKNHMIIISIDAFAFDKIQQPFMLKT LNKLGIDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTROGCPL SPLLFNIVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKF IWNQ KRACISILSQKNKAGGITLPDFKLYKATVTKTAWYWYQNRDIDQ WNRTEPSEIMPHIYNYLIFDKPEKNKQWGDLSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDLNVRPKTIKTLEENLGITIQDIGVGK DFMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTTWEKI FTTYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEDIY AAKKHKCCSSSLAIREMQIKTMYHLPVRMAIIKSGNNSKMWVE ADGPGNLTGVLHLETNEKSLKAVFGKYGPILEDNFLDGKAMKVEQV NKPSFQSGGNVEITIFLEKQEPFRKSETGKKFFKLFLTLANFFKFS DHDDYSGGLGRDHSEHPNGSSYRDAYQSYGTGYGAPPA
1145	A	1	2884	MVKGSIQQEELTILNIHAPNTGAPRFIKQVLSDLQORDLDSHTLIMGD FNTPLSTLDRSMRQKVNKDTQELNSALHQADLIDIYRTLHPKSTEYT FFSLPHTYSKIDHIVGSKALLSKCKRTQIITNYLSDHSAIKLELRIR KTLTQSRSTTWKLNLLNDYVWHNEMKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLKELEKQEQTHSK ASRRQEITKIRAEKBIETQKTLQKINESRSWFFERINKIDRPLARLI IKKKREKNQIDTIKNDKGDITTDPTIEIQTIREYYKHLIYANKLENLE EMDTFLDYTLPRLNQEEVESLNRPIITGAEIVAIINSLPTKSPGPD GFTAEFYQRYKEELHINRAKDKNHMIIISIDAFAFDKIQQPFMLKTL NKLIGIDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTROGCPLS PLLFNIVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELP

				FTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKAIYRFNAIPIKLPMTFFTELEKTTLKFIWNQK RARITKSILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRK LKLDPFLTPYTKINSRWIKDLNVRPKTIKTLEENLEITI QDIGVGKD FMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKKKTNNPIKKWARDMNRHFSKEDIYA AKHMKKCSSSLAIREMQIKTTMRYHLTPVRMAI IKKSGNNRNI \RL CSYSGSHSRAWFLPPAGRHIQ
1146	A	1454	3917	SIAYQQRKRVQDQMQDSQPNSTREKEGILSNSFYEASIIILPKPGRDIT KKENFRPISLMNIDAKILSKILAKRIQQHIKKLIHHDQVGFIPGMQG WVNIHKSINVIQHINRAKDKNHMIISTDAEKAFDIIQQPFMLKTLNK LGIDGMFKIIRAIYDKPTANIILNGQKLEAFPLKTGTRQGCPLSPL LFNIVLEVLAIRAEKEIKGIQLGKEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINVQKSQGFLYTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTKKWKNIPCSWV GRINIVKMAILPKVIYSFNAIPIKLPMPFFTELEKTTLKFIWNQKRA RITKSILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNR TEPSEITPHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRPKTIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTTWEKIPAT YSSDKGLISRIYNELKQIYKKKTNNPIKKVVKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYHLTPVRVAI IKKSGNNRCWRGCGE IGTLLHCWWDCKLVQPLWKS VWRFLRDLELEIPFDPALPLGIYPKD YKSCCYKDTCTRMFIAALFTIAKTWSQPKCPTTIDWIKKMWHIYTME YYAAIKNDEFMSFVGTWMKLEIIILSKPLQEQT KHRMFS LIVSSKV IRRLSQKLPKIVAMCIPVKRN
1147	A	11537	15574	AKSPANIIMTGSNSHITILTLNINGLNSAIKRHRILASWIKSQDPSVC CIQETHLTCRDTHRLKIKGWRKIYQANGKQKKAGVAIILVSDKTDFKP TKIKRDKEGHIIMVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTPLSTLDRSMRQKVNDTQELNSALHQADLIDI YRTLHPKSTEYTFPSAPHHTYSKIDHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRKLNLTQSRSTTWKLNLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVCRGKFIALNAYKRKQERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIRAELEIETQKTLQKINESRSWFFE RINKIDRPLARLIKKKREKNQIDTIKNDKGDITTDPTETIQTIREYY KHLIYANKLENLEEMDTFLDTYTLPRLNQEEVESLNRPIITGSEIVAI NSLPTKKSPPGPDGFTAIFYQRYKEELVPFLLKLFQSIEKEGILPNSF YEASIIILPKPGRDITTKENFRPISLMNIDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGFNIRKSINVIQHINRAKDKNHMIISIDA AFDKIQQPFMLKTLNKLIGIDGTYFKIIRAIYDKPTANIILNGQKLEA FPLKTGTRQGCPLSPLLFNIVLEVLAIRAEKEIKGIQLGKEEVKLS SLFADDMIVYLENPIVSAQNLLKLISNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQKNKAGGITLPDFKLYYKATVTK TAWYWYQNRDIDQWNRTEPSEIMPHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIKTLEE NLGITIQDIGVGKDFMSKTPKAMATKAKIDKWDLIKLSFCTAKETT IRVNRQPTTWEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKHMKKCSSSLAIREMQIKTTMRYHLTPVRMA IIKKSGNNRVGDYHSYENDDDNLGATAAQSC TLLFSLIAHLLQDPY TIPAYMTQVQNSAAGNYWKNTDAAKKLETIILGKLTQEQT KHRMFS LISGS
1148	A	115	450	VWQPEAWTPFLDSLGGCLRPSSWFAAFQWEGVPLPGVQSVKLSPL SRDPAPPAGTLPCVALEADWFLDMPGGRGPRSQQLSRSALPSLQTL

				VGGGWGKGTGLRNRKGRA
1149	A	278	886	NWLTTINLGLQLQVALEADWFLDMPGRRGPSRQQLSRSALPSLQTL VGGGCGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLVPDG SLLFEFLFFIYLLAALFIQYINIKYKTAWGYPYNHPASCTSLNFHLTD YDLAAFITKMLAKRLVWALISQATKAGAASMIHYMDLTSARLGLLTL CGWVLCWTLVNLFR
1150	A	2	379	CGLPLEAPRCPTFRTPALSRHRRRLTEAVSTEEKESDRMSAIQN LHSFDPFADAREGDDLPAAGPEDYLHIQHRIGGKTLTTGQGIADD HDKKKLVVASKKRSGCDGTVTGPPDYGEVIE
1151	A	172	464	ASHRVGLLQPFNLWPSGCSTVLAKMKSVLVATEGAEVLFYWTDQEF EESLRLKFGQSENEEEVGLLML*AR*PHPTPPVLSGLNEGKKKS FIT
1152	A	164	529	ASHRVGLLQPFNLWPSGCSTVLAKMKCVLVATEGAEVLFYWTDQEF EESLRLKFGQSENEEEELPALEDQLSTLLAPVIFFSMTMLEKLSDTY TCFSTENGFLYVLHLFGCECLFIAING
1153	A	1	1122	MVLLTLDGDYTHADRNLEWGLKVLSATPQADKKKLASADNPETVS LLAKNALFPCRSVGVSTTELVSQIHAGPGPEVSLVEPVGAMWMTV LRAVLKQSQVEAPSRALKLPSLECAASLGQLHTPADLTYCQEKVLF VDFLLQGGIGFKTTGSWLISNKEHKTFFKAQQAEEEGISAFQFLH YKVQSPVNNKNNKEGIIKKGKEHSSSPATEQSWTENDFDELREEGFR SVITNFSELKEDVRAHCKEAKNFERRLDEWLTRINSKEKTLDLMEL KTMARELCDACTSFSSQFDQVEERVSVIEDQMIEMKQEEKFREKRVK TNEQSLQEIRDYVKRPNLRLIGVPSSTIVEDSVAIPQSGSTRNTI
1154	A	1	558	MPGNSEAKSYNAKTVLESCTLLWEQFKKVTKPYSQGLLREALE DDTCLWLCSILPDEEQEEKHSFAEVSVPISGLSTQPPLLYLLKLPW HNYHLLTQITAKHNRNTAPPATEQSGTENDFDELREEGFRRLVITNF SKLKGEVRTHLKEAKNLEERLDEWLTRINSVQKTLNDQMEKLTMA
1155	A	1	495	MKPPKGPPLSQVPSAPPKKLRTDGRITTPSTHSLHWQLIGWCPFTLR VGLPLLGHQLNCQSSLATPSQTHPETVLHQPSRHPSIQSSGHLITI TSPGTMASAAVVMRQTGSDHFPSSLHLSLRECSSSPAMEQSWTENDF DELREEGFRRSVITNFSELKKLP
1156	A	51	581	LRSSSPATEQSWTENDFDKLREEGFR*SNYSELQEEIQTKGKEVENF EKNLEECITRITNTEKCLKDLMELKAKARELHEECRLSRCDQLEE RVSVMEDEMNMKREGKFRKRIKRNEQSLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENFPNLARQANIQIQ
1157	A	286	456	FCHLSSTSWGGADGTCREGGPLGGFMGPSHQ*ESSPVPEAASSFRTF KSSAVSQSPL
1158	A	1	1760	MDDIPQEARQYRHNQAYAYSIIQGDGAEDDDERIVRFHTRVTVSDTL ASDAARLTCRHGLGNQDRSSSPAMEQSWTENDFDELTEVGFRRSVIT NFSELKEDVRTHRKEDHSAIKLELRICKLIQNLTTTWKLNLLNDY RVNNEMKAEIKMFFETNENKDTTYQNLCDTFKAVCRGKFIALNAHCR KQERSKIDTLTSQLEKEKQEQTHSKACRRQEIITKIQAELEIETQK TLQKINESRSWFFKINKIDRPLARLIKKKREKNQIDAINKDKGYIT TNPTEIQTIREYYKHLIYANKLENLEEMDKFLDITYTLPRLNQEEVES LNRPIITGFEIEAIINSLPTEKRPVPGFTAKFYHSSADCTRSMAPAP ASGEALRLLPLMGEGEGETCDRDIAREEAQECSSSPATEQSWMEND FEELGEEGFRRSVITNFSELKEDVQTHFKEAKNLEKRLDEWLTRINS VEKTLNDLM*LKTVA*ELRDTYTSFNSRFDQVEERVSVIEDQMNEME REEKFRKRV*RNEQS/LQEIWNYVKRPNLHLIGVSEIDRENGTKLE NTLQDIFQENFTYLARQANIQIQ
1159	A	138	326	GLYYTGCYGISRMPDL\$RAPWKDSFYLLPVPMPVEGPPI\$ISGRGPK GQMGEPLLPYTGKK
1160	A	1	525	MKTILSNQTVDIPENVNVTLKGRTVIIKGPRTLRKDFNHINVELRL LGKKKKRLRVDKWWGNRKELATVRTICSHNGSLVEIRNFLGEKYIRR VQMRPGVACSVPAQKDELILEGNDTELVSNSAALIQQPTTVKNKDI RKFLDGIYVSEKGTVQQVDESRLRVIQLQKEDAR

1161	A	319	1035	EWSSVRRSLVEKRALRRPHQPCLCFRMTIL\SNQTCRPFPE\NVDI TLKGRTVIVKGP/REGTLRRDFNHI\NVELSLLWKEKKRGFRVVK\W WGNRKEL\ATGRD*FVSHVQNMKGCTGASGYKMKVLWYAHFPIQR LLFQGEGLGPSLLKSRNFLGGWKNTSRRVSG*GPGCLLVSVSQGPRKD EINPLKG\NDIELVSKFQRALIQQ\ATTVKNKG\IRKFFGWVSMLE KGTVPQGLIE
1162	A	232	338	VGIKMSISSDEVNFLVYRYLQESGFSHSAFTFGIE
1163	A	474	647	EPSLSQLPQNGDLLAARRREHPACSTGCTSGARVRSRVWRAGQALVP GCAGCAYILH
1164	A	1	413	QLSHKSDSVVLVSQSRQRTCRRKYPNYGRNRNSWRELSSGNESSSV RHETSCDQSESGSSEDEWRSRDKSESYSSESSSDSSSRYSWTADA GINLQPLRTSCRRRITRFCSSSEDEISTENLSPPKRRRKRKK
1165	A	2	2545	LSMSEEIILHPVVLSSALGGPLQCISSRAALALVFGPYAVGEGLWEK IVVLSNKHVAPDHLQICQRIGPMLDKEIPPSISRVTSLLGAGRQSL LRTAKDCRHTVWKGSAFAALHRGRPPPEMPVNYGSPPNLVEIHRGKQL TGCSTFSTAFPGTMYQHIKMHRRLGHLSAVYCVAFDRTGHRIFTGS DDCLVKIWNTHNGRLLSTLRGHSAEISDMAVNYENTMIAAGSCDKI I RVWCLRTCAPVAVLQHTGTSITSLQFSPMAKGSQRYMVSTGADGTVC FWQWDLKFRFLSGSRDGTARIWRFEQLEWRSILLDMATRISGRI QWFWYHSLDKGHVGVNIQIMVEEIVAGETSCDQSESGSSEDEWRS DRKSESYSSESSSDSSSRYSWTADAGINLQPLRTSCRRRITRFCSS SEDEISTENLSPPKRRRKRKKENKPKKEIWQDRRQLGIATVWVDVAM VLSTHLEMGAVELLGCPAVKLGAGIGLMGIVAALLGAHVTVIDRKNL RRMTPAELANMEHLYEFHPPVWITDITLRSPPFVPMGDEVIFYRQ HEAYIEAVRRNNIYELNPNKEPWRKMDLRLKKEFHILASGKDVGLLT VIQIAGGDQELVKIVGIRYEVGPPTLCCLKLAFIDPATGKMDKSFS IRYHMPDVIDFLVLRQFYDEARQNRWQSCDRFRSIIDDAWWFGTVL SQEPYQPQYPDSHFQCYIVRWDNTEIEKLSPWDMEPIPDNDPPEEL GASISVTTDELEKLLYKPQAGEWGQSRDEECDRIISGIDQLNLDI AAAFAGPVDLCTYPKYCTVAYPTDLYTIRMRLVNRFYRLVETCFQN V
1166	A	1364	1618	SQHSGRPRQADHLRSGVRDQPGQHGEILSLLKIQKLAGRAGSRL*SQ LLERLRLYHRTPA*VTE*DMASKNKKKPHRIQARKYF
1167	A	3	342	LTQELPGAHAHACNPSTLGGQGGQIMRSGARDQPGHSGTPSLLKIQ K\LAGRGGTHL*SQLLRRLRQENRLNLGSGGCSELRLRHCTPAWVTD SVSKNELEKESYLIFSSLT
1168	A	2	232	WAGRGGSR*SQHFGRPRRADHERWKNWELRQLNLGQAPCSRNGMR RYGERRHHPDEPGQPSVEGFLRVLSMCIC
1169	A	1294	1624	GQLYEKLGRGPGGAVAHACNPSTLGGRGGWITRSGDRDHPG*HGETP SLLKIQK\LAGRGGHL*SQLLRLRQENGVPNGA/RGCSELRSY CTPAWGTERDSVSKKKK
1170	A	427	730	SQHFGRPRRADHLRSGVRDWPQGHGEALSLLKIQKLAECGGVCLWSQ LLRRLRQGNRLNLGDRGCSEPRSYRCTPAWVTEQDSVSGRKEKGMK RKKKKKK
1171	A	6497	6788	SQRFGRPGQANCLSSGV*DQPGQYGETLSLLKIQKLGCGGTCL*S* LLGWLRLQENHLNLGDGGCEPRMCHCTPPWTTEGSA*KLKKKKKKR KYL
1172	A	173	396	VNSHPKGATSEHLEPRGPTSKPLGRTGWTLSLRLGYSPSLQKAVTHS LGCLLVRALEKARSSAQLQTNYPSSDN
1173	A	239	405	HSPTPPTSPrASTMEDVKLEFPPLPQCKEDAEWTPMRREMQLPVL QKHGITHI
1174	A	126	915	SACVSCNPAALLLALRSAGPPSFLPPHPARGSAGCVTLSSHPTHQAG QHHGWTVKLE\FPSLPQCK\EDAE\EWTPMRREMQ\EILPG\FLG PYSSAM\KKQDPSLLAVSSHGQENEFLLTRVQSCHGGFYPHDLNL KLIIIFQRLHHHILGLPVLQKHGITHIICIRQNIENFIKPNFQQLFS AAFVIAIYIMETFGMKYRDAFAYVQERRFCINPNAGFVHQLQEYIAIY

				LAKLTIQMMSPL/RDRKVIICSFWYHRQFEENT
1175	A	1	924	MLRARPRPGSPWRPAREEPTGTGRALVVAGVAAPHQSRAPRLGRRRV RVLLSCTRCLGSARRGPPPGFEDGGVATGSDPAMASDGNACALHL PGASTCPVARATGSSATPTLRTTPGRETSYPKNNPNAHGDFLKINRA YEVLKDEDLRKKYDKYGEKLEDNQQGGQYESWNYRYDFGKDGLVNV GWMDCATQDNLCCKSLDITTTSTAYFPPGATLNNKEKNSILFLNSLDA KEIYLEVIHNLPDFELLSANTLEVGRFDCSSAPDICSNLVVFQPSLA VFKQGQGTKEYEIHHEYLANSKLPFKT
1176	A	441	709	IRTCIRKRMGVWLNKDDYIRDLMKIILCCLIVYMAILVGTDHDIYSL LGVSNTASSRDIRQAFKRLASKLHPDKYPNNPYAHGDFLKIK
1177	A	109	437	NQRRKWRRSRTQLQTLQEALKAETQGHQKLAQMKQDPQNADL*KQL YELQAKITALSEKQKRVVEQLRKNLIVKQEQPDKFQIQPLPQSDNKL RTAQQQPLQQLQQQQ
1178	A	343	670	RMEQLTLQEALKVEIQVHQKLVAQMKQDPQNADLKKQLHELQAKITA LSEKQKRVVEQLRKNLIVKQEQPDKFQIQPLPQSENKLQTAQQQPLQ QLQQQQQYHHHAQQ
1179	C	130	390	MAEQSLISGGPKPKSVNSLRWINLXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSWVDK*
1180	A	238	435	KKYLSWVMEGGACSEPSLHHCTPAWVTERDSVSKKIKNKMGLTNYL IKSDNTISQGGRGYSHAR
1181	A	615	947	QQQQQGVVGTEQKDPYASCLCWEAPLPQGPTQVSQERHWFPLSLTLC FSALRRGAWSPPRRTHPQEQCGLWGRPPLEPPHPLSERTRRPPVT PAEAEPCLPTPKHSVY
1182	A	232	564	GLQIIQSLCLVAFWKKRVFGGQAGWLAESWMLGWLVPFLILASQMY VPGKLHDVEHVLIDVGTGYVEKVSSEMLDAPLNREGKFRGSSIAQH GQRESPFSPLFTSDLVE
1183	A	3	487	LPNMAQSINITELNLPQLE\MLKNQLDQEVFLSTSIAQLKVQTKY VEAKDCLNVLNKSNEGKELLVPTDGVLCMSPGKLH\DEHVLID\VG TGYVVKTA\EDAKDFKRI\DF\LTQMEKIQPALQEKHAMQAV M\EMMS\QKIQQLTA\LGQAQATAKA
1184	A	187	423	NLRQRKQGSSSYSLRRAHQFSRKFVGQFLLLLFRHSLAVAQPTSF SGTISAHCSLHFLGSSDSPASASQAAGTTAPA
1185	A	539	871	SPWYLWRTYLCREAVDSEVTCRKNVSFPLHMLLIFFPIKFVSFLEKIE RTVQIEASTVEIERGVKLRLTVVDTPGYGDAINCRDWYAPPCPGIC ICLLNILHKFIDSUNE
1186	A	158	1330	SVDLVIHPLWPPEVLGLQQQPTQFINPETPGYVGFANLPNQVHRKSV KKGFEFTLMVVGESGLGKS/TLS*NSLFLTDLYPERVIPGAAV*FFS RKN*KELVQIEAST\VEILRARGSSRLASG*DTPG\YG*PLFN\CR DCF*GQFISYYLMRQF*GGYL\HDESG\LNRRHIIDNRVHCCFHFI PF\GHGLQPLDVAFMKAHNKVNIVPVIKADTLTKERERLKKRIL DEIEHNIKIYHLPDAESDEDEDKEQTRLLKASIPFSVGSNQLIE AKGKKVRGRLYPWGVVEVENPEHNDFLKLRTMLITHMQDLQEVTDL HYENFRSERLKRGRKVENEDMNKDQILLEKEAELRRMQEMIARMQA QMOMMQGGDGDGGALGHHV
1187	A	405	632	PSKRDFADGINVFWFFGVFFETESHVSTQARVQRCKHSSLHPRVPSP RPSSHVSCPVAGTIGTRHYVQLILKNFL
1188	A	111	377	PINMSCERKGLSELSELYFLIARFLEDGPCQQAQVLI REVAEKEL LPRRTDWTGKEHPRTYQNLVKYYRHLAPDHLLQICHRLRPL
1189	A	428	575	CLKEKAQGSFPALPFCHVRMQQKGIIFEADGKPSPDTESAGTLILDF PA
1190	C	216	458	MNRDRTSRNRCVCDVFRNAVKGQTVLGRQLFGRVVRVPVRPGEGFLP WGFLPVSPWPCPSWGLSTHALWWAEAVPGRALVH*
1191	A	1	594	RTRGRTRGLLPSGAFEPEAAGSATAPRGCKNPGAKGLLAAMAGRQD IFHAIVKADERFHGEGYREGYEKGSILGVKEGRQHGTLHGAKIGTEI GRYQRFAPAWKCLLH\IAPLRRTA*T*RS*HAWIGRIQIFPYDDPTY

				DKLHEDLDKIRGKFKQVRALCVSSC*EHLIAPFPGGAHSRGRGNG LGLRAPRNC
1192	A	482	789	VGGPGQFLAISLTHLIGEAPSPACLAHSTQQGLPGEALHFHVTFELO LQSPCPHGGLRQVPQGPLQGPPGLLSLPGPPHCLGPHAPGWVVG PALGSACA
1193	A	572	677	SLWILPFLFVFFSFETRSRSVVQAGVQWCNHSLLR
1194	A	1	396	KGGSMMHYAKNFYGGNGIVGAQQQIFEAYNMAALWKLPCIFICENNR YMGMTSVERAAPST\DYKRGDFIPGLRVDGMDILCVREATRFAAAY CRSGKGPILMEL\QTYRYHGHSMSPDGVSYRTREEIQE
1195	A	641	723	LLPGPDISKLYNMAALWKLPCIFICEN
1196	A	354	1145	KQISCINRKLFFVSVTCVMVRKLAVWAWRPASTPQTISSQPTGLTAL LSPGAFPSSEKFSQSLQDEKEVVLKKGEDRCTCMPRTSTGAMASWERR CPWAAGIALACKYNGKDEVCLTYGDGAANQQQIFEAYNMAALWKLPC IFICENNRGMGTSTVERAAASTDYKRGDFIPG\LRVDGMDILCVR EATY\IGRAYCRSGKGPILMELQTYRYHGHSMSPDGVSYRTREEIQE VR\SKSDPIMLLKDRMVNSNLASVEELKGI
1197	A	2	506	ELSTPLCWDKSLIGYGSAAQHLPYLTSLPLMKLLQYCLADAWVAEIG LAFNILEMVFVAFATITPLMFTGYGLLFLSLVITPVIRAKLSKLVRE TEQGALFSAEACVNSLTMLTASGIFNSLYPATLNFMKGVPFLLGAGL MLIPAVLIEMLEQADPHLEFQQVPQSP
1198	A	1	1455	MEGSASPPEKPRARPAAAVLCRGPVEPLVFLANFALVLQGPLTTQYL WHRFSADLGYNTRQRGGCSNRSADPTMQEVETLTSHWTLYMNVGGF LVGLFSSTLLGAWSDSVGRRPLLVLASLGLLLQALVSFVVLQQLHV GYFVLGRILCALLGDFGGLLAASFASVADVSSSRSTFRMALLEASI GVAGMLASLLGGHWLRAQGYANPFWLALALLIAMTYAAFCGETLK EPKSTRLFTFRHRSIVQLYVAPAPEKSRKHLALYSLAIFVIVITVHF GAQDILTLYELSTPLCWDKSLIGYGSAAQHLPYLTSLALKLLQYCL ADAWVAEIGLAFNILEMVFVAFATITPLMFTGSIYRFQGYESDAIGH HYSASYASEPSCDEGLIIFLIQGVRIREGYGLLFLSLVITPVIRAKL SKLVRETEQGALFSAVACVNSLAMLASGIFNSLYPATLNFMKGVPF LLGAGLLIPAVLIG
1199	A	509	840	QVAKPRQGSFPFLDYCLPTLTIKEVLPGSNLSPTWGMDRSSAAFPL DAPLPSPIFLMSVCFSTGYGLLFLSLVITPVIRAKLSKLVRETEQGE CQNPFPVCGSSCPGIRR
1200	B	109	267	MEETPCRELEEEEEEWGSGSEDASKKDGAVESISVPDMVDKNLTCPEE EDTVKV*
1201	A	856	1030	VPNLQVGDEKQDSPNGEHWGQE\DTAEPAEVKAMMSVAVV*KNLT TPPPLGRSSV
1202	A	67	264	PTWPGVTWHESAPTQMPLPSLSSECCVPPGMACSWTGLNRSTRRKQE RQVPPLWRWPSARRCLRWP
1203	A	3	1253	SFNIRGPHSLCFPNHHLPHATYRDKAKMKLPLLLALLFGAVSALHLR SETSTFETPLGAKTLPEDEETPEQEMEETPCRELEEEEEEWGSGSEDA SKKDGAVESISVPDMVDKNLTCPEEEDTVKVVGIPGCQTCRYLLVRS LQTFQAWFTCRRCYRGNLVSINHFNINYRIQCSVSALNQGQVWIGG RITGSGRCRRFQWVDGSRWNFAYWAAHQPSRGHCVALCTRENDAP HLESLETQADLGQDLDSKEQERDLALTEEVIQAEGEVVKASACQDN FEDEEAMESDPAALDKDFQCPREEDIVEVQGSPRCKTCRYLLVTRPK TFAEAQNVCSRCYGGNLVSIHDFNFNYRIQCTSTVNQAQVWIGGNL RGWFLWKRFCWTDGSHWNFAYWSPGQPGNGQGSCVALCTK
1204	A	1403	3362	PGVGLSVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFG VLCAPWNGLLMDRLKQKYQKEARKTVPPLPRRQRRRGHRAVRLKLR GGRVLHAEKTPAPARLRAGPTGLRTRRESVALPEASAAAGCSFAGDR RLGASMAPTLQQAIRRRWMACTAVLENLFFSAVLLGWGSLLIILKN EGFYSSTCPGKSEKEDRDGKREGLIHVVPLWLKAVGRRQYSPPTFNR APLPAWVFLHEKAYQVRDTAIESSVVTKVKGSGLYANRVMVDSDYV TPPQGSTVFVIIITKMIVTENHMQGFCPESEEKYRCVSDSQCGPERLP

				GGGSETSTFETPLGAKTLPEDEETPEQEMEETPCRELEEEEEWGS EDASKKDGAVERISVPMVDKNLTCPEEEDTVKVVGIPGCQTCRYLL VRSLSQTFQAWFTCRRRCYRGNLVSIIHNFNINYRIQCSVSALNQGVW IGGRITGSGRCRRFQWVDGSRWNFAYWAAHQPSRGGHCVALCTRGS STLAVALCSTVPSLALTSLLCLGFALCASVPILPLQYLTFILQVISR SFLYGSNAAFLLTAFPSHFGLFGLVMALSASVSLQFPFIITLIK SLQNDPFFVNVFMFLAILLTFHFPFLVYRECRTWKESPSAIA
1205	A	388	1711	ACALGMAPQRKRKQLSMKTGSYSQRSSFORRKRPPQGGRSRNSAPS GATLSLGALAWHLEWLSVIQLWHYLFITLNSLLTNMAGGDMARVST YTNAFAFTQFGVLSAPWNGLLMDRLKQKYQKEARKTGSFNIRGPHSL YFPNHHLPHATYRDKAKMKLPLLLALLFGAVSAL\HLRSETSTFETP LG\AKTLPEDEETPEQEM\EETPCR\ELGGRGREWGLWEVEDASQER WGLFESILQCPDMGGTKTFTCS*GKEGHQLKVGWIGPGGCPRPARYL PG*ESLSRRFSSKLWFYFARSC\YRGQTWVFHSTTFQY*LSESKCSV \SALN\QGQVWIG\GRI\TGSGR\CRRFQWVDGSRW\NF\AYWG\AH QPW\SRGGHCVALC\TRG\GYWA\RAH\CLQKNFPFICFPLSWSQPA VQVVPSPGQLPPLLCPLSLPPPCNNNGFY
1206	A	97	441	MAPEQDPKPKVQEGERVLCFHGPLYEAKSVKVAIKDKQVKYFIHYR GWNKNWDEWLPESRVLYLDTNLQKQRELQKANQKTNNKQKTPGNG DGGSTRETPQPPRKKRARVDP
1207	A	19	432	MAPKQDPKPKFQEGERVLCFHGPLYEAKCVKVAIKDKQVKYFIHYS GWNKKSARVPRRSEKSLKTHEDIVALFPVPEGAPSVHHPLLTSSWDE WVPESRVLYVDNLQKQRELQKANQEYAEQKMRGAAPGKRHL
1208	A	165	257	TVRIGAMLAYTPLDEKSLALLLNLYLHDFLK
1209	A	80	1239	GAVVGGGRRRRRRITYKCLPKLDPKPKFQEGERVLCFHGPLYEAK CVKVAIKDKQVKYFIHYRGWNKNWDEWVPESRVLY\VDNLQKQRE LQKANQEYAEQKMR\GAAPGKKTSGLQKNVEVTKKKNQKTP\GN \GDGG\STSETP\QPPRKKRARVD\PTV\ENEETFM\NRVEVKVKIP EELKPWLVD\WD\LITR\QKQLFYLPKKNVDSILEDYANYKKS/R VGNTDNKEYA\VLNEVVAGD*KNTFNV\MLG\TQLLYKFERPQYAEI LADHPDAPMSPGVWSAQHLEIIWYRIGAMLAYTPLDE\K\SLALL NYLHDFLKLYLAKNSATLFSASDYE\VAPPEYHRKAVWKSTLTHLCLD LRKHIFVLSLSPWYKPMCFEDVSV
1210	A	31	1029	WWNSEVPHGPFMRKAAVLT/AVPLFSDG*ARRRHFWQGG*SPPRAA WDRV\K\DLATRVPTVLKEQRTETYVSQFEGLRLGENS*TLKLL\DN NW\DSVDLPPFS\KLREHSFGPC*PRDFLGINLGKRETRGALRQGR RQRIFGRRLLKGPRLQ*LGDDFPRKKLARKBIGALTRQKGSRLRAR TSKKGARPELHELARSLSPLEAVSRPRARPMWDALRTHLAPYSD EM\SQLGAR\LGALRENGGARMGQYHA\QATE\HLSTLSEKAKPAL ED\LRQGLLPVLESFKVSFLSALEEYTKKLNTQLRRPPPPYPVLRI NVSKVGKKKKKK
1211	A	3	450	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALER\MFLSFPT TKTYFPHFDLSHGSAQVKGHGKKVADALNAVAHVDDMPNALSALSD LHAHKL RVD PVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASV STVLTSKYR
1212	A	9	675	NSARATDSETHHGARLLPDKTNVKA\AWGKVGGAHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHG\SAQG*RAHGK\KVA\DALT\NAVA\ HVD\DMPTALSALSGPATAHL\RVDPVQLSSS*SHLPCWWTLGRP TSPSEFNWRLHAFPGTKFPGLLVEAPLLEPSKLPLKGLSLRVGHAF FAPLGLPPRALLPFPGTRNPVGLLNKILNWGGKKKKKKKIF
1213	A	1	645	KIFLSDCLACDSCTAEKGVQLSQQNAKDFFRVLN/LNKKCDTSKHK VLVSVCPQSLPYFAAKFNLSVTDASRRLCGLKSLGVHYVFDTTIA ADFS/H/RWRMLKWQRPSPDSSRTCG*GPAAADGRHLR*HPCAASGV QCKRAGAVPGVAGDQLPQGPRAAYHVPEPGAWHTQPGHQVVKSGQ GLPAALGARAKSLSVEGGAALSGVLKTLKKT
1214	A	193	564	CPQEVWFHSFCHCTSAFMKDLYFLCLVRFGDLKEDKVTRHDGASSDG

				HLAIFRHAAKELFNEDVEEVTYRALRNKDFQEVTLKNGEVVLRFA AAYGFRNIQNMILKLLKGGSSIHVRSRCLE
1215	A	211	1795	TPLGRRRRRKTHDKRKPGQGPFGAECSSKTK\ADDQENVASADAPS PAQENGEGKEFHKLADAKIFLSDCLACDSCMTAEEGVLSQQNAKDF FRVLNLNKKCDTSKHKVLVVSVCPSLPYFCWLNFNLSVTD\ASRRL CGFLKSLG\VHYVFDTTIAADFSIL\ESQKEFVRRY\QOHSEGGNAP CPMLTSACPGL/WVRYAGAGCWGRPITG/HTFLAPPKSPQQVMGSLV KDYF\ARQONL\SPEKIFPRSLVAP\C\YDKKL\EALQGKPFPLALH G\SRGRLTCV\LTSGEICFKLM\EQGDLSVRDAAVDTLFGDLKKDKV TRHDGASSNGHLAIFRHAH\KELFN/ERDVEEVTYRTLNRQRFQK VTLEEEPKRWV*TFVLEPYAFRNIPET*SLKPLKKGKVPFF\HFVEG SSPCA\GGCL\NGKRPKPKIQDGHGDKAPAAGRMGIY/SLDIPVRR PES\SAHVQE\LYQ\EWLEGI\NSPKARKVL\HTTYQSQ\ERGTHSL GHSSWLKFRPGPSSCSWGQSQEPLSRGRGLP
1216	A	1	201	TLQQAAYEFLSFVRQQTTPGLCPLAGNSVHEDKKFLDKYMPQFMKHL HYRIIDVSTVKELCRRWYP
1217	A	15	304	CWSGRLRDWGRGCWSRVMLGGSLSRLLRGVGGSHGRFGARGVREGG AAMAAGESMAQRMVWVDLEMTGLDIEKDQIIEMACLITDSDLNILAE GT
1218	A	51	283	TWVKEAQNDGLCVCIYIFIFNCQMTGLDIEKD\QIIEMACLITDSDLN ILAEVRDAHVIQSYFLKGTGNITIIFFSFFI
1219	A	2	520	QRRRLDWGRGCWSRVMLGGSLSRLLRGVGGSHGRFGARGVREGGAA MAAGESMAQRMVWVDLEMTGLDIEKDQIIEMACLITDSDLNILAE/G NSVHEDKKFLDKYMPQFMKHLHYRIIDVSTVKELCRRWYPPEYEFAP KKAASHRALDDISESIKELQFYRNNIFKKKISC
1220	A	2	206	EFGTRRHVPPCLINFFKQDQSP*LARLVSNWPQVIHPPWPPTVLGL RGVGHCPWPRLGNSSWVWGGH
1221	A	1	1405	MRSQKTSLYFSLEAKFYCSLRNERIASCDIINDAGIQTKTLMKRSHV AYALKKPVEQGDSELESKGFMAITIAVCIEQNLRHSSSLFICMSST QSGTTNASSLIPSYVFTPPHFNLLDKQGRTAGKSHCGEDRKEHNN ACHQEEEAPDVNPLHGLQASGSPGKTQRIKSQALEGTRLYSHSEETR SGLIRLLRLRQRRRLDWGRGCWSRMLGGSLSGR\LLRGVGGSHGRF GARGVRKRGAA\AA\GESMAQRMVWVDLEITGLDI*KVQIIEMACL ITDSDLIIAEGPNLII\KQPD\ELL\DSMS\DWCK\EHKGK\GLT K\AVKESTNYHCQAE\YEFALWYDQPDSPGLCPTCQEIKFHE\D KKFP*QNTCPQFMKHLHYRII\DVSHC*KELCQTAGYPEEYEF\PK KAASFISGLDD\ISENL\KKVPFFPENNLPRKKIRMKRKEGKL*KM GENEKTVS
1222	A	1	456	RPRRPQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERMFL/ SFPTTKTYFPHFDLSHGSSQVKGHGKKVADALTNAVGHVDDMPNALS ALSDLHAHKL RVD PVNFKLLSHCLLVTLAAHLPAEFTPAVHAFLDKF LASVSTVLTSKYR
1223	A	2	435	QTQREPTMVLSPADKTNVKAAGKVGGAH/AGEYGAEALERMFLSFPT TKTYFPHFDLSHGSAQVKGHGKKVADALTNAV/EHVDDMPNALSALS DLHAHKL RVD PVNFQAPKATGLLVDPGPAHFPGRVSPRLRQGLGFK FLGFC
1224	A	9	390	NSARATDSERTHHGARLLPDKTNVKA\AWGKVGGAHAGEYGAEALERM FLSFPTTK\TYFPHFDL\SHG\SAQ\VKGP TAKKVAERADQTPWRNV DDMPKRRCPP*SDLH\AHKL\RVD PVQLSSS*SHLPCW
1225	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNAVHVDDMPNALSALSDL HAHKL RVD PVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
1226	A	26	636	NSTDERTHHGARLLPDKTNVKA\AWGKVGGAHAGEYGAEALERMFLS FPT\TKTYFPHFDL\SHG\SAQV\KGHGQ\KVADALTNAVHV\DDM P\NALSALSDLHAHKL\RVGPGSTFKLLKPLALLG*TLGRPPSPAEF

				QPLGGCKASLGTKFLGFLVEAPLLEPSKLPKLKGLSLRLAMLSLPLWA FPPAPPPLSCTRTPVVFEIKS
1227	A	17	233	AFGTRELQCCVFLASMLGVPIPTVQGFQWTLRGTDVETSPFGAPRA TSHGVGQMKSCQIPQPLKIRMVKQNNIIPGETQILLRFTGWESKVNA KKQPPVGIKCEPMDQGNEQTGGHETDGHRISSVVSAATQECLI*NT TRNVWTQ*TKSNLTRCGPNEELPDPTALEDKDGQTK
1228	A	1	433	STLIGSSSHVEWEDAVHIIIPQNESDDEEEEEKGPVSPRNLQESEEEE VPQESWDEGHRWDQVKKEDQEATGPRLSRELLDEKEPEVLQDSLDR YSTPSVYLGLTDSQPYRSAFYVLEQQRIGLAVDMDEIEKQCEVEED QDP
1229	C	312	443	MHKRNFHRAGRSQAVQDNWKELENNIYPVSPARLQALLPPAAPC*
1230	A	1	94	LMEVEEPEVLQDSLDCYSTPSMYFELPDNC
1231	A	2	122	DLTCPQMG*GWKLTALSQCQLDGIERSRAKASQCCLSI
1232	A	3	53	VTSLHLVFMQGVIFPQ
1233	A	1	2680	SAVGSDHIFHNIPDSTSSATNVSMVVSAGPWSSEKAEMNILEINEKL RPQLAENKQQRNLKERCFLTQLAGFLANRQKKYKYECKDLIKFML RNERQFKEEKLAELQKQAEELRQYKVLVHSQERELTQLREKLREGD ASRSLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQQLVQKLSPE NDEDEDEDVQVEEDEKVLLESSAPREVQKAEESKVPEDSLEECITCS NSHGPCDSNQPHKNIKITFEEDKVNSTVVDRKSSHDECQDALNILP VPGPTSSATNVSMVVSAGPLSSEKAEMNILEINEKLRLPQLAEKKQF RSLKEKCFVTQLAGFLAKQNKYKYECKDLIKSMLRNELQFKEEKL AEQLKQAEELRQYKVLVHSQERELTQLREKLREGDASRSLNEHLQA LLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPENDEDEDEDVQV EEDEKVLLESSSPREMKAEEESKVPEDSLEECITCSNSHGPCDSNQ HKNIKITFEEDKVNSSLVVDRESSHDECQDALNILPVPGPTSSATNV SMVVSAGPLSSEKAEMNILEINEKLRLPQLAEKKQFRSLKEKCFVTQ VACFLAKQNKYKYECKDLIKSMLRNELQFKEEKLAEQLKQAEELR QYKVLVHSQERELTQLREKLREGDASRSLNEHLQALLTPDEPKSQ GQDLQEQLAEGCRLAQHLVQKLSPENDNDDDEDVQVEVAEKVQSSS PREMKAEEKEVPEDSLEECITCSNSHGPDYDSNQPHRKTITFEED KVDSTLIGSSSHVEWEDAVHIIIPENESDDEEEEEKGPVSPRNLQESE EEVVPQESWDEGYSTLSIPPER\HRWDQVKKEDQEATGPRLSRELLA
1234	B	33	2996	MLRNERQFKEEKLAELQKQAEELRQYKVLVHAQERELTQLREKLREG RDASRSLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLS PENDNDDDEDVQVEVAEKVQSSAPREMKAEEKEVPEDSLEECIT CSNSHGPDYDSNQPHRKTITFEEDKVDSTLIGSSSHVEWEDAVHIIIP ENESDDEEEEEKGPVSPRNLQESEEEEVVPQESWDEGYSTLSIPPEML ASYKSYSSTFHSLEEQQVCMAVDIGSEYSIVKVIKLQFMAQSQAMPV PTWTDCHDIELKAGHRWDQVKKEDHEATGPRLSRELLDEKGPVQLD SLDRCYSTPSGCLELTDSCQPYRSAFYVLEQQRVGLAVNMDEIEKYQ EVEEDQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLG QPYSSAVYSLQYLGALDLDRIKQDQEEEDQGPCPRLSRELL VVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSL DVGEIEKKGKGGKRRGRRSKERRRGRKEGEDQNPPCPRLSRELLD EKGPEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYSTPS GCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEEDQDPSC PRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSL EEQYLGALDLDRIKQDQEEEDQGPCPRLSRELLVVEPEVLQDS LDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGENRSQEP LAGDSMSRPTLPVQNMNSAMFLQKTLNLSFIGVFEPKHIPTVFCDYH LAPTLVLVFGAVPGSWCLCLGHQEPGTARHQLEGRTHETSSVPCILR ARPAGRLSKALEDRRDWSVAFGAAELPLPSSDPVFRTGAPPEQGSW *
1235	B	16	1041	MVKQNNIIPGETQILVRFTGWESKVNAKKQPPVGIKCEPMDQEYEEC

				KDLIKSMLRNERQFKEEKLAEQLKQAEELSMVVSAGPWSSEKAEMNI LEINEKLRPQLAENKQQFGNLKERCFTVQLAGFLANQQKKNYEECK DLIKFMLRNERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLRE KLREGDASRSLNEHLQALLTLDEPDKSQGDQLQEQLAEGCRLAQHL VQKLSPENDEDEDVQVEEAQKQSSAPREVQKTEESKVPEDSLE ECAITCSNSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESSHDECQ DALNILPACMTE*
1236	A	1	2219	MSQSVQDNLKELNNIYPDHSSSPAMEQSRMENDFDELTEVGFRKLVI TNFSELKEDVRTHRKEAKNLEKRLDEWPTRMNSVEKTLNDLMELKTM ARELRDACTSFSSQFDQVQETPLKIRMVVKQNNISAESQILVRFTSW ESNVNAKKQLPVGIKCEPMDQECIPGSRACITLLVRFPSNGGPPMDPGS ERKDLLQLGGELARTSRAVQEAGLGLSTGLWLAESRAKAALEKQALL QAQLEEQLRDKDLAQQQMQSDLDKADLSARVTELGLAVKRLQKQNP EKDQVNTDLTEKLEALVQMLPLESQLPIPTSGTLTPPGYSLVWSPLC VGPGLGSRSGSPPIDCVTWGKTDSTMQAHAEDAQREVQRLRSKELLR RLSGMLMEVEEPEVLQDSLDRCYSTPSMYFELPDSFQHYRSVFYSFE EQHISFALDVD/E*VSYFDGNKSPPGLPDGSHIPTRTAGQARLLH ARRRIPQERTTTPKVSQLASWVSLG/RQYLHPAGSLRWL*TTLPPTS SSMFPLCPQ/YPSEDSREAGIKKDQEEEDQGPPCRRLSRELLEAVE PEVLQDSLDRCYSTPSSCLEQPDSCLPYGSSFYALEEKHVGFSLDVG GYLELTDSCQPYRSAFYILEQQRVGWALDMDIEKYQEVEEDQDPSC PRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYRSAVYSL EEQYLGALDLDVD/E*VPYYEDEETEAQRSED TGAGSHSW
1237	A	3	1270	RTRVSFNLHVPIGPPCGNDISQLSNGHLEQEYDLYMEDSVDPYHLHR KKLSTKKWKKTKTHHAPGNFEQLWMLNSVLTGPDAREVQKAESKV PEDSLEECALTCNSHGPCDSNQPHKNIKITFEEDVNSTLVVDRES SHDEWQDALNILPEIEKYQEVEEDQDPSCPREVQKAESKVPEDSLE ECAITCSNSHGPCDSNQPHKNIKITFEGYRARIRIMGALGGPRITDG IAQCMEMAQQDEGPACGNDVSRVSKGHLEQEYHPYLEDQVEAYHLHS KVLTVHVKSQAKVPSMGPDPSFSEAPKLSRELLDEKGPEVLQDSLDR CYSTPSGCLELTDSCQPYRSAFYVLEQQHVGLAVDMDPRQYLGAL DLDSEYLLTVKVISLHVVFQIGVIFLQVPLTDRPDVIAAGRTYGR
1238	C	160	267	MGPLTLSSSSLHTETFLCPILTQGHQSCQCNRR *
1239	A	1	1233	MLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQADGTV AEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDNIDSWKAGRVFK DSDKFDANDPILKDQTQEWSSATFTSDGKIRLFYTDYSGKHGKQS LTTAQIHFPILISILSYATWGLSLLCIPGSPVCTLLVRFPSNVGTRWS LEVGRDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLES GHCLEQPDSC QPYGSSFYALEEKHVGFSLDVGGKTFNLITPAEVGVLVKGDWSSFVM NGLTLGGQKYTVVLDSSLQDGELTTDLCKMSIGGAPT FNVIVTMTAK TLGLLMGKEGICFQSIFTSHHSEFTVRERDVALP
1240	A	401	2582	SAVGSDHIFDNI PDSTSSATNVSMVVSAGPLSSEKAEMNILEINEKL HPQLAEKKQQFRNLKEKCFVTQLACFLANQONKYKNEECKDLIKSML RNERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGD ASCSLNQHLQALLTPDEPDKSQGDQLQEQLAEGCRLAQHLVQKLSPE NDNDDDEDVQVEVAEKVQKSSAPREMPKAEKEVPEDSLEECALTC NSHGYPDSNQPHRKT KITFEEDKVDSTLIGSSSHVEWEDAVHIIPEN ESDDEEEEEKGPVSPRNLQESEEEVPQESWDEGYSTLSIPPEMLAS YKSYSGTFHSLQVCMVAVDIGGEYSIVKVIKQFMAQSQAMPVPT WTDCHDIELKAGHRWDQVKKEDQATGPRLSRELLDEKGPEVLQDSL DRCYSTPSGYLELTDSCQPYRSAFYILEQQRVGWALDMDGYRRTCP SCSVPPPPGMPQNTQRVSSPAPTRVGLRAAAAGEESSAGNSGPGGA RPPTAPTRPRARATKLATAAPRPSCAPAGPGFTARPAWRGALTSETL GGLRVTSHSQSGSRQPRRRASAQLLAPQIARPAFPKAPRSLRSSGSLA TLTYASQYRRCLNRHPAPRLRLRLQPTGSSGSRWACQDNPRRRRGA

				LKGPGLFCTTGSSRLGAAQAEERSNPGEGPSAAGTGKSLSPRLLSF KAPALDPPNRWFPRPLEQPLPG
1241	A	946	2563	FPLAYSLLFPP/CSRLSRELLEVPEVLQDSLDRCYSTPSSCLEQP DSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKRRRGRSTKKRRR RGRKEGEDQNPPCPRLSRELLDEKGPEVLQDSLDRCYSTPSGYLEL TDSCQPYRSAFYILEQQRVGWALDMEIEKYQEVEEDQDPSCPR*L* AITDA*FCVDTWRCQVQKQECVQFHVFNEG*ITPTDIAVGFHCSRC LGFHFFLPLSFTHLL*VDHTSKAVWQLHGILSKFMENY*AHSFHDHC SLCVPRALTQSVL*PLHQCVRPIR*AHFLLSLSLPLPVFLFHSFLP GPGLSQHKGNNSLPH*WICPFSF*TVPYVSHEI*LGLCGF*FPLAYS LLFPT/CSRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPY SSAVYSLEEQLGLALDVDRIKKDQEEEEEDQPPCPRLSRELLEVVE PEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVG EIEKKGKRRRGRSSKKKKGRP
1242	A	442	5178	HQELPDPTGPCGGRLLSLTIHGVTRIYHALLWARGPIMSKSQVLGEW EPVQGGKSSSENDKWTMSDPAEAPTCSRAASGVDEKQQRWQGLWNS HIKPLKIRMVQNNIIPGETQILLRFTGWESKVNKKQLPVGIKCEP MDQENQGTGGHETDGHRIVSVLIHFPLISILSYATWGLSLEECIPGS PVCTLLVRFSNVGTRWSLEVRGSPCGFGSNKVCVMTPEIKMVCVCE GKAGKAVGSGGVEGTKEVSTGNAEGPVRHEAVDGGVHLAFALLQGLL WSLLLGPPGLAGWGGGELDAVPDSTSSATNVSMVVSAGPWSSEKAEM NILEINEKLRPQLAENKQOFRNLKERCFLTQLAGFLANRQKKYKYE CKDLIKFMLRNERQFKEEKLAELQKQAEELRQYKVLVHSQERELTQL REKLREGRDASRSLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQ HLVQKLSPENDDEDEDVQVEDEKVLLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNIKITFEEDKVNSSLVVDRESSHDG CQDALNILPVPGBTSSATNVSMVVSAGPLSSEKAEMNILEINEKLCP QLAEKKQQFRSLKEKCFVTQVACFLAKQONKYKYECKDLIKSMLRN ERQFKEEKLAELQKQAEELRQYKVLVHSQERELTQLREKLREGRDAS RSLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPEND NDDDEDVQVEVAEKVQKSSAPREMOKAEKEVPEDSLEECAITYSNS HGSYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEWEDAVHIIIPENES DDEEEEEKGPVSPRNQSEEEEEVPQESWDEGYSTLSIPPEMLASYQ SYSSTFHSLEEQQVCMAVDIGSEYSIVKVIKLQFMAQASVTLVYLSV KDVTQVSLNLPFVSVSSKFACFSSSVRHVPGHRWDQVKKEDQEATGP SRELLDEKGPEVLQDSLDRCYSTPSGCLELTDSQPYRSAFYILEQQ RVGLAIDMEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQSLDR CYSTPSGYLELPDLGQPYSSAVYSLEEQLGLALDVDRIKKDQEEEE DEDQDP\PCPRLSRELLEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQ PYGSSFYALEEKHVGFSLDVGEIEKKGKRRRGRSMKKRRRRGRK EGEEDQNPPCPRLSRELLDEK\GPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGFADFMDIEKYQEVEEDQDPSCPRLSRELL \GEKEPEVLQDSLDRCYSPSGYLELPDLGQPYSSAVYSLEEQLGL ALDVDRIKKDEEEEEEDQPPCPRLSRELLEVVEPEVLQDSLDRCYST PSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKRRRGR RRSKKERRGGRKEGEEENPPCPRLSRELLDEKGPEVLQDSLDR*YS TPSGWLELTDSCQPYRSAFYVLEQQHVGLALDVDSEYLTVKVISLHL VLQIGVIFLFQVPLTDPDPRDVIAAGRTYGR
1243	A	1	3242	MDKPRPGKTTFVIMVSPLPAPYTSPTFTHMVTCPAHPRAFALTHSWD PQVRPAVLNPLPRHGSSFVVKQPVAKQQPLRCLIIYIEVALSVMSPTA PSSSRSPWKRPGLRPGFEQPGGSREAERLVGSRDGSRSLSLHHPVR EPVPSLLSRIRGAAELPLPSSDPAFTGAPPGQGSWQYKVLVHAQER ELTQLREKLREGRDASRSLNEHLQALLTPDEPKSQGQDLQEQLAEG CRLAQHLVQKLSPENDNDDDEDVS/QVEVAEKV\QKSSAPREMOKAE EKEVPEDSLEECAITCSNSHGPDYDSNQPHKKTITFEEDKVDSTLIG SSSHVEWEDAVHIIIPENESDDEEEEEKGPVSPRNQSEEEEEVPQES

				WDEGYSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQV KKEDQEATGHRLSRELLDEKGPVQLQDSLDRWYSTPSGCP*LTDYCO PYRSAFLHYWSQQRIGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLD EKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQLGLAL DVDRTKKDQEEEEEDQPPCPRLSRELLEVVEPEVLQDSLDRCYSTPS SCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGGKRRGRRS KKKRRRGRKEGEEDQNPPCPRLSRELLAEKEPEVLQDSLDRWYSTPS VYLGLTDPQCPYRSAFYVLEQQRVGLAVDMDEIEKYQEVEEDQDPSC PRLSRELLAEKEPEVLQDSLDRWYSTPSVYLGLTDPQCPYRSAFYVL EQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPE\VLQD SLGRCYSTPSGYLELPDLGQPYSSAVYSLEEQLGLALDVIDRIKKDQ EEE/EQDQGPCCPR\LSRELLEVVEPEVLQ\DSLDRCYSTPSSCLEQ PDSCQPYGSSFYALE\EKHVG\FSLDVG\IEKKGKGGKRRGRSTK KRRRRGRKEGEEDQNPPCPRLSGVLMEVEEPEILQDSL\DRYYSTPS MYFELPDSFQH*RSVFYSFEEQHISFALDMDNRFFTLTVTSLHLVFQ MGVIFPQ
1244	A	148	197	DPLGFL*QKRNNQEDD
1245	A	1333	2383	RMKKEHVLHCQFSAWYPFFRGVTIKSVILPLPQNVKDYLLDDGTLVV SGRDDPPTHSQPDSDEAEIQQWSDDENT\ATLT\APEFP*SLPLKV QGSYQIPLGGQVSFPKV*FGS\APRD\AYWIAMNSSLKCKTSLDIFL LFKSSDFITRDTQPFHCTDDSPDP\CIEYELVLEKWCCEMIPGG\B FRCFVKENKLIGISQRDYTYQYDHISKQK\BEIRRCIQDFFK\KHIP VQIL*MKDLVFDIYR\DSRG\KWLIDF\NPFGEVTDLSLFTWEELI \SENNFKRRFLVKVDAQEQDSPSFVAQTSEVTVQOPLICSYRL\P KDFVDLS\TGEDAHKLIDFLKLKRNQPEGR
1246	A	1	322	SSCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTANDSENWKE VHKMVVESAYEVIKLGYTNAIGLTSVINQKLKDDDEVAQLKKSADT LWDIGCRNLKTTM
1247	A	68	1224	LCLLRTTVTEVSRAFSLLCKMATLKEKLIAPVAEEEEATVPNNKIT\V VGVGQVQMA\CAISIPGKVSWPDEL\ALVDVLEDKLGEMMDLQHGS LFLQTP*NCGQDKDY/SLWTANS*DL*WVTAGS/RRQPRKGESGNSP VAEKWLMSFKFI\IPQDRPSTVPD\CIIIGGFNPQLDIPTYVT\WET KVGLPKH\RVIGSGCNLDS\ARFRYLMAEKTWHFIPASC\HGW/IFW GEHGDSSVGLV\WNGVNVAGVSLQELNP\EMG\TDNDSEKW\KEVHK DGGLKSPYEVI\KLKGYP\NWGYLDLSVA\DLIE\SMLKNPIPGFHP VSTNG*RGMYGH/VEVEVFPAGAPCIL\NA\RGLTSVIN\QKLK\DD EVAQL\KKSADTLW\DIQKDLKRPVTSEL
1248	A	66	703	RRRLPSVAIMIILPGPSSSHDEM\SDIYK\IRGDRGRGLCLEGGR GRWVSRT\GTID\DSLIGG\NA\SAESPRGAKGTERHK*STGV\DI VMNHHLPGNKFSQKEASKKVHQRITMKSI\KGKP*KNRRPRKSKTFL *QGAAEQIKHILANFKKLQF/YFIGENMNPRAWVLLLDY*RDGVP P\YMIFFK\DG\LEMEKMLTNVAIILDLSPCHP
1249	A	1	521	MKNRSRNKGNVEWQAEGIRSKRSVKGQRPSKAKIPSGDKNGVSLTHN EVINNDNPLESNDKEGEQATCSRPOIVP/EFQQ**LFRPE*WRRAS GNLQILPKKRVSA*GTRGSPSKKGERVRRDAQQTATW*TRSPASGCF QICEGNKQDEACDVRGLQHCHERHSLAGPREYMP
1250	A	3	170	SCEQIAVQVNNGDAGREMPCLPCDEEIISSSESTVDVDEPLEVF ISAPRSEP
1251	A	3	251	YYSIDLVLPSYIESKKGHLLLSAVIGQDHDFFSESSEEEAPAEASSGAL RSKHGEKGFSSSDFSDLSNGEELQETCSSSLRRGS
1252	A	23	2669	GGKMAGGGGDLSTRRLNECISPVANEMNHLPAHSHDLQRMFTEDQGV DDRLLYDIVFKHFKRNKVEISNAIKTFFPFLGLRDRDLITNKMFE SQDSCRNLVPVQVVYNVLSELEKTFFNLPLVLEALFSDVNMQEYPLI HIYKGFENVIHDKLPLQESSEEEEREERSGLQLSLEQGTGENSFRSLT WPPSGSPSHAGTTPPENGLSEHPCETEQINAKRKDTTSDKDDSLGSQ QTNEQCAQKAEPTESECEQIAVQVNNGDAGREMPCLPCDEESPEAEL

				HNHGIQINSCSVRLVDIKKEKPFSSNSKVECAQARTHNOASDIIVI SSEDESGSTDVDEPLEVFISAPRSEPVINNDNPLESNDKEGQEATC SRPQIVPEPMDFRKLSTFRESFKRVIGQDHFSESSEEEAPAEASS GALRSKHGEKAPMTSRSTSTWRIPSRKRRFSSSDFSDLSNGEELQET CSSSLRRGSGSQPEPENKKCSCVMCFPKGVPQRSQEARTESSQASDM MDTMDVENNSTLEKHSKRRKKRRHRSKVNGLQRGRKKDRPRKHLTL NNKVQKKRWQQRGRKANTRPLKRRRKRGPRIPKDEINFKQSELPTV CGEVKGTLYKERFKQGTSSKCIQSEDKKWFTPREFEIEGDRGASKNW KLSIRCGGYTLKVLNENKFLPEPPSTRKKRILESHNNTLVDPCEEHK KKNPDASVKFSEFLKKCSETWKTIFAKEKGKFEDMAKADKAHYEREM KTYIPPKGEKKKKFKDPNAPKRPPLAFFLFCSEYRPKIKGEHPGLSI DDVVKKLAGMWNNTAAADKQFYEKKAALKKEYKKDIAAYRAKGKPN SAKKRVVKAESKSKKKEEEDEEDEQEEENEEDDDK
1253	A	97	1609	GGKMAGGGDLSTRRLNECISPVANEMNHLPAHSHDLQRMFTEDQGV DDRLLYDIVFKHFQR\NKVEISNAIKCTFPFLEGLRDRDLITNMFE DSQDSCRNLVPVQVRVYN\VLSELEKTFNLPVLEALFSDVNMQEYPD FKFHIYKGFE\NVI\HDKLPSPRKVEEEEKGRRLGLPTKSLNKG TG ENSFRKPDFGPPSGFPHPCLGTTTPE/NMGLSEHPCETEQINAKRK DTTSDKDDSLGSQQTNEQCAQKAEPTECEQIA\QOVN\MGDAGREM PCP\LPCDE\ESPRGKSLHNHNPKFNSLVLCVLDIKKEKPFSSNSK VE\CAQARTHNOASDIIVISSEDESGSTDVDEPLEVFISAPRSE VINNDNPL\ESNDEKEG\QEATCSRQIVPE\PLIFRKLFT\FRESF RKRKRVIG\QKTHDFSESQ*GGGAPQEASSGGTEEARHGEKAPIDF*EV HLTWEEYPSR\KETFPVSDFSDE*MGRAFQETC\SSS\LRRGLG
1254	A	3	274	FFASLLESPVSPRLAMPNCSCAAGVSCCTCAGSCKCKECKCTSCCKS ECEAISMVWGCG*GCCSCCP/AAASKCAQGCVCCKGASEKSCCD
1255	A	788	1174	PSCTRLRRRRQNRSLKTNISPRKRATVLKLPQMLGLVPGVDGRSP RGGRGGLGWRSCFLSDGEWILRTGVSGLVGSRGSGAGGRLEMDPN CSCTTGGSCCTCAGSCKCKECKCTSCCKSCCSCCP
1256	A	80	231	IRPLPPRFKTESRSLPGPCLQPGTFLWSRNRRLVGFPSMNGEDMGLL FLCSEWERSSEGWLCTEKGEVD\TQLNPTAVPSCISLTAHCVFLLVG GSCTCAGSCKCKE\CKCTSCCKSECG/CH/PPGIWGCG*GAWFSQHE WRGHGASLPLL
1257	C	81	476	MGPRWYKKKSRFVTCLSVYIWEKGPCWHQFAAAALSLTPLCKHNPW GTLANNPRGGREGAALSCRRVHLHSFALAGNQRVQGGHPAGAGSSW GVHLQARGRDWDFSQGEAAKHVGQVEGVDPNSRPLL
1258	A	3	452	QTQREPTMVLSPADKTNVKAAGWKVGAHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKVADAL\TNAVAHVDDMPNALSALSDL HAHKLVRDPVNFKLLSHCLLVTLAAHLP AEFTPAVHASLDKFLASVS TVLTSKYR
1259	A	9	486	NSARATDSERTHHGACLLPDKTNVKA\AWGKVGGAHAGEYGAEALERM FLSFPTTK\TYFPHFDL\SHG\SAQG*RAHGK\KVA\DALTKRRGAT WDDM/PQTALSALSDLH\AHKL\RVGPGSTFKLL\SQLPCLGEPWAA HLP\EFQPLAVARLPWNKVSFGFC
1260	A	3	497	PTLLVPTDSERTHPWLLSPADK\TNVKA\AWG\KVGGAHAGEYGAEAL ERMFLSFPTTKTYFPHF\DLHG\SAQV*GPRARKVADAL\TNAVAQ RGTDIAQRACPPSLDLH\AHKL\RVGPGSTFKLLKATC/HCLGEPWA AHLPAEFQPLAVARLPWQSFGLGFLKQRC
1261	A	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRNQAEESFVSALSIDLSGGGMMA LLSMVCLKFPGG\SCMAALTVTLMVLSSPLALAG\DTR\PPVRLRKT EDEPLGCVLSGLRVGPDVFPGRFCNRIVLVPPARFLEQVKHECHF FNGTERVRFDRYFYHQEYVRFDSVGEYRAVTELGRPDAEYWNSQ KDLLEQKRAAVDTCRHNHYGVGESFTVQRRVYPEVTVYPAKTQPLQH HNLLVCSVNGFYPGSIEVRWFRNGQEEKTGTVSTGLIQNGDWTFTL VMLETVPRSGEVYTCQVEHPSLTSPLTVEWRARSESAQS KMLSGVGG FVLGLLFLGAGLFIYFRNQKGHSGQLQPTGFLS

1262	A	3	825	LFSSMVCLKLPGGSSLAALTVTLMVLSSRLAFAGDTRPRFLELRKSE CHFFNGTERVRYLDYFHNQEEFLRFDSDVGEYRAVTELGRPVAESW NSQKDLLEQKR\AAVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTQ PLQHHNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVST\GLIHNGDW TF\HTLVMLETVPR\SEEVYTC\QVEAPRA*QAPLTVE\WRARSESA QSKMLSGVGGFVLGLLFLGAGLFIFYFRNQKGHSGLQPTGFLS
1263	A	11	885	DLPASLAPGPVLFSSMVCLKLPGGSCMTALTVTLMV\LSSPLALAGD TRPRFLWQPKRECHFFNGTERVRFLDRYFYNQEESSVRFDSDVGEYRA VTELGRPDAEYWNQKDFLEDRR\AAVDTYCRHNYGVGESFTVQRRV QPKVTVYPSKTQPLQHHNLL/VFCSVSGFYPGSIEVRWFLNGQEEK GMVSTG\LI\QNEGDPF\QTLVMLETSFFGVERVNT\SQVEHPKCAR P\LTVE*RARSESAQSKMLSEVGG\FVLG\LLLPLPGPLF\IFYFRNQ KGHSGLQPTGFPELKCR
1264	A	25	628	EFHRLRENPPWCLSPADKTNVK/APAWGKVGAHAGEYG\SEALER\M VLFPPTPKPYFPHF\DLSHG\SAQV*GPRARKVADAL\TNAVAQRG TDIAQRAVPPLSDLH\AHKL\RVGPGSTFKLLKATC/HCLGEPWAAH LP\AEFQPLAVATSSLGTKFPFGFLVEAPLLTFQITFKGWKLWLAIVF LPPGLPPSPSSPFLHPYPRGL
1265	A	1	625	CKFIRVMAHTRRLRLPLRRKKAHLMEIQVNEGTVAEKLDWARERLEQ QVPVNVQVFGQDEMIDVIGVTGKGKGYKGVTSRWHTKKLPRKTHRGLRK VAC\KDGLIKNNASTDYDLSDKSINPLGGFVHYGEVTNDFVMLKGC VVGTKKRVLTLRKSLLVQTKRRALEKIDLKFDITTSKFGHGRFQTM EKKAFMGPLKKDRIAKEEGA
1266	A	1	1251	MASKLRLSDMTGEKGLNLAPIKIILNSLFEDGSSIGLQGAQGAVDKP CGLEQPVVPTKCDCTASPKCSSGHCGKVKSLPKDDPSKPVCLTGF LGKAGMTHIVQEVDPRPGSKVNKKEVVEAVTIVETLPMVMVGIVGYV ETPQGLRTFKTVFAEHISDECKRRFYKNWHKSKKKAFTKYRKKWQDE NGKKQLEKDFSSMKKYCQKKAHLMEIQVNGDTMAKKLDWARERFEQQ LPVNHVFGQDEMIDIIRMTKGKGYKGVTSWHAKKLPRKTHQGPRKV SCIGAWHLVHVAFSVARTWQKGYCHHTEINKKIHKIGQGYLIKDDKL IKNNASTDYDLSDKSINPLGVFGHYGEVTNDFVMLKGCVTQKRALQK TDLKFTDITTSKFGHGRQLQTMEEKKASMGRLKKDQIAKEERA
1267	A	1	903	KCSSGHCGKVKSLPKDDPSKPVCLTGFLGYKAGMTHIVQEVDPRGSK VNKKEVVEAVTIVETLPMVMVGIVGYVETPQGLRTFKTVFAEHISDE CKRRFYKNWHKSKKKAFTKYRKKWQDENGKKQLEKDFSSMKKYCQKK AHLMEIQVNGDTMAKKLDWARERFEQQLPVNHVFGQDEMIDIIRMTK GKGYKGVTSWHAKKLPRKTHQGPRKVCSCIGAWHLVHVAFSVARTWQ KGYCHHTEINKKIHKIGQGYLIKDDKLKNNASTDYDLSDKSINPLG VFGHYGEVTNDFVMLKGC
1268	A	1	1131	MSHRKFSTPRHGSGLGFLPWKRSSRHCGKVKSFPPKDDPSKPVHLTAFL GYKAGMTHIVREVDPRPGSKVNKKEVVEAVTIVERPPVGIVGCVETPQ GFRTCKTVFAEHISDECKRRFYKNWHKSKKKAFTKYCKKWQDEDEGKK QLEKDFSSMKKYCQVICVIAHTQMQLLPLCQKKAHLMEIQVNGGTVA EKLDWAGERLKHQVPVNVQVFGQDEMIDVIRVTGKGKGYKRVTSRWHTK KLPRKTHQGLCKVACIGAWHPARVGFVGYLIKDGKLIKNNASTDYD LSDKSINPLGGFVHYGEVTNDFVMLKGCVVGTKKWVLTLRKSLLVQT KQRALEKIDLKFDITPSKFGHGHFQTMEEKKAFMGPLKKDRIAKEEG A
1269	A	1	1345	WALPAGFDGVMSHRKFSAPRHGSLGFLPRKRSSRHGKVKSFPPKDDP SKPVHLTAFLGYKAGMTHIVREVDPRPGSKVNKKEVVEAVTIVETPPM VFVGIVGYVETPRGLRTFKTVFAEHMSDECKRRFYKNWHKSKKKAFT KYCKKWQDEDEGKKQLEKDFSSMKKYCQVIRVIAHTQMRLLPLRQKK\ AHLM\EIQV\N\GGTCARESWDWGPREGKQQVPVKPSVLGRDE\MI ELHRG*PKGQKAYKGHPVWHTQESCPKRD/HHPRACAKVACIGA\ FHPARV\AFSVARAGQ\KGYHPRT\EINKKI\YKIGQG\YLIKGG\K LIKNNASTDYDLSDKSI\NPLGGFVHYGE\VTNDFVMLKG\CVVGTG

				K\RVLT\LRK\SLVQTKAAGLWRRITLKF\IDTTSKFGHGRFQTM EKKAFMGPLKDKDRIAKEERSLMPGTDFAVGGVSIKIVIFH
1270	A	3	451	QTQREPTMVLSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDL HAHKL RVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
1271	A	9	487	NSARATDSERTHHGARLLPDKTNVKA\AWGKVGAGHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGFCPRLKGPQRORWPDALTK\AVA\HV DGHAQTALSGPEATLHGAQSGFVDPVQLSSSLSH\CLLG*PWAHL RPSSTPGGWNAPGTFKFPWVSC
1272	A	197	821	RLFHSNQTVDHSQKNVDITLKG\RPSNRVRAPKGTLR\RDFNPHQM* NSALLGKEQQRGFRVD\KWWGYQKGNWPTRSGLFSGHVQD\MIKGWL PLGLPVTKMR\SVYAHFPHPTLLSRENGVSLLKSRNFLG\EKYIPQG FRMKTRVLLCQYLKAQKR*N*SLEGND\IGLVS\NFSRLLIPASPTR LKTGKIRK\FLDGIFCLLEKGLFRQA
1273	C	22	282	MSEGPSVRSEEAIPLYEELGGGARQTHVRRPLSECS PGDWSHSGVA EGPXCIQFLHITSHGAKEALSTWLGLLTSGPATTAAVLP*
1274	A	60	1576	GYLGAVALG\LW\ALCWSLAIATPLPPTSAHGNVAEGETKPDPDVT ERCSDGWSFDATTL\DDNGTMLFFKGEFVW\KSHKWGPV*SSERWE GFSPSPCGMLAFPFKVHNSVLS*SKGGDKVLGY*PSLKKKGRKGLPK VCSKIDFGIPHSP\LD\AAVECHRG\ECQAE\GV\LFFQGDRE\WF W DFA\TGNHGRERSW\PAVWGTCSS\ALRWAGPLTYWLSRGNQF\LR FRPCQGEVPPR\YPRDVRE\YFMPCPGKGH\GTQEWGLGHGNSNH GP* IYAACSP\HLSLCLALTS DNH\GANFCLSVGTHYWR\LDTS\RD GWHSLAPLLIKWPQGPSAVDAAPSW\EKLYLVQGHGPGYVFLTKGG Y\TLS*GGYPKRLGEREV\GDPSWGFIL\DSVDAFI\CPGVFLRLH YSWAGRRLWVGW\VP*KSGSPKPTW\TELSFGPHE\KVDGALCMEKS PFGPKFMFPNGPGL\Y\LIHGPNFTL\YSVVEK\LNA\AKALPQPQ NVTQSPGACTH
1275	A	1	3431	MLPHERGLETTPRGECPVRIDTKLFEMLVPOCHKEIALEHKFIYSF LVTLNTKPPGYSHSHPEALLDPEVGDPNGTNAQLIKCFLPLCPSPF LCPEECMHCSGENYDGIKISKTMSGLEQCQAWDSQSPHAHGYIPSKFPN KNLKNYCRNPDREL RPWCFTTDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTNRTPENFPCKNLD ENYCRNPDGKRAPWCHTTNSQVRWEYCKIPSCDSSPVSTEQLAPTAP PELTPVVQDCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPE NYPNAGLTMYCRNPDADKGPWCFTTDP SVRWEYCNLKKCSGTEASV VAPPPVLLPDVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQ EPHRHSIFTPETNPRAGLEKNATECGGASTELCSTSLCAFTMLMDYE GQGEPLDDYVNTQGASLFSVTKKQLGAGSIEBCAAKCEDEEFTCRA FQYHSKEQQCVIMAENRKSSIIIRMRDVVLFKKVYLSECKTGNGKN YRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN DPQGPWCYTTD\PEQRYDYCDIPECEBECMHCSGENYDGIKISKTMSG LEQCQAWDSQSPHAHGYIPSKFPNKNLKNYCRNPDREL RPWCFTTDP NKRWELCDIPRCTTPPPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQ HWSAQTPHTNRTPENFPCKNLDENYCRNPDGKRAPWCHTTNSQVRW BYCKIPSCDSSPVSTEQLAPTAPPELTPVVQDCYHGDGQSYRGTSST TTTGKKCQSWSSMTPHRHQKTPEYYPNAGLTMYCRNPDADKGPWCFT TTPSVRWEYCNLKKCSGTEASVVAPPPVLLPDVETPSEEDCMFGN GKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCR NPDGDVGGPWYTTNPRKLYDYCDVPQCAAPSFDCGKPQVEPKKCPG RVVGGCVAPHSPWPQVSLRTRSPRPSSYKVILGAHQEVNLEPHVQE IEVSRLFLEPTRKDIALLLSSPAVITDKVIPACLPSPNYVVAADRTE CFITGWGETQEHFYFN
1276	A	111	2785	VNNVLGLGHTFWALLASPKMEHKEVVLLLLLFLKSGQGEPLDDYVNT QGASLFSVTKKQLGAGSIEBCAAKCEEG\EEFTCRAF\QYHSKEQQC

				VIMAE\NRKSS\IIIRMRDVLFLLKKKVYSLSQAKT\GNGKNYRGTM SKTKNGIT\CQKW\SSTSP\RRPRFSPATHPSEGL\EENYCRNPDND PQGPW\CYTIDPEKRYDYCDILECEEECMHCSG\ENY\DGKISK\TM SWDWECQGLGTFQEPHTVHG\YFPSQIFPNKNLKEGIVTRNPDRGL\ RPWVFSPPDPNKRWGTF/CDIPR\CTTE\PPSSGPTYQCL/RRGTGE NFRGNVAV*PCSGKTVQHWECTGPLHTHNR\TP\ENFPWQNLGWKTT CRNP\DGKKGPLGCHYNQQAALRVGSYC*GYRSC\DSSPVSTEQLAP TAPPELTPVVQGLATHG*WDRAYRGNIPPTHPTGKESVKSWSIL*H PHRHPEDPQKTTTPNAGL\TMELLSGIPDGRLLKAPWCFYHRTPAFRWE YCNLKKC\SGTEASVV\APPPVLLPDV*TPSEEDCMFGNGKGYRG KRATT\VTGTPCQDWAQEPHRHSIFTPETN\PRAGLEKNYCRNPDG \DVCGPWCYTTPNPKLYDYCDVPQCAAPSFDCGKQPVEPKKCPG\RV VGGCVAHP\HSW\PWQVQSLEQGFGLHFCGGLTISP EWV\LTAACHL EKSPRPSSYKVLG\AHQEVNL\EPHVQIESV/SRLFL\EPTRK\D ICLAKAKAVLPFIHLTKLIPA\CLAIPQIFVVRTGTGTECFITGL/WG ETQGTFGSWAF\LREAQLPC*FENKVCKSAL*SFENGKKSQSHPKL LCLGHFGPEGHLNKLPPRVNSGRAPLVCPKRDQNTIL\QGSPPPWG VLACARPPITPGVLCVFPFVYLGLKGS
1277	A	29	455	EFQFSVVYAKCDSSPDSEAEDVRKVCQDCPLLAPLNDTRVVHAAKAAL AAFNAQNGSNFQLEEISRAQLVPVTSQPPQEGANEAVPTPVVDPDA PPSPPLGAPGLPPAGSPDSDHVLAAAPPGHQLHRAHYDLRHTFMGVV S
1278	A	1	1368	MKSLVLLLCLAQLWGCHSAPHGPGLIYRQPNCDPTEEEAALVAIDY INQNLPGWKYKHTLNQIDEVKVWPQAVEGDCDFQLLKLDGKFSVVYAK CDSSPDSEAEDVRKVCQDCPLLAPLNDTRVVHAAKAALAAFNAQNGSN NFQLEEISRAQLVVKTEILLTGEPHVDGEPGDLRFRIKVVKHPIFER RGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW KKGEGLPNFDNNNIKGLIITFDVDFPKEQLTEAREGIKQLLKQGS VQKITFYEDKNFQGRRYDCDCDCADFHLYSRCNSIKVEGGTAVAYE RPNFAGYMYILPQGEYPEYQRMGLNDRLLSSCRAVHLPSGGQYKIQT FEKGDPSGQMYETTEDCPSIMEQFHMREIHSCKVLEGVWIFYELPNY RGRQYLLDKKEYRKPIDWGAASPAVQSFRRIE
1279	A	1	1269	PPTRPPTRPAPGLVPKPSTTCTPACQGLSGAAMKSLVLLLCLAQLWG CHSAPHGPGLIYRQPNCDPTEEEAALVAIDYINQNLPGWKYKHTLNQ ID\EVKVPWPQPSGRAVLRFEIRTPWGTTLPCCWDPTLVGQDASLEG SLKEHAVEGDCDFQLLKLDGKF\SVVYAKCD\SSQDSAEDV\RKVCQ H\CPLLAPL\NDTRVVHAAKSCPGPPFNAQNGGFQFFSLEEISR\AQ LVPLPPS\TYV\EFTVSG\TDLLFA*KKATEAAKCNLSGQKSNMGFC K\ATLSEKLGSGQRLQLTCTVF\QTQPV\SQPNPEGANEAVPTFV\ VDP\DAAPPSPPLGAPGLLPSWLTPTKTTMVL\AAPPGHQLHR\AHYD LCHTFMGVVS\LGSPFRRKCSHPRKNT/RTVVEA*WLGAAAGATGFL PLFRGGIRHFKV
1280	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGFEFAGISKNGQTRHALLAY TLVAFVPISGWNGDNMLEPSANMPWFKGWKVTBKDGNASGTTLLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLPKGMVVT FAPVNVTEVKSVEMHHEALSEALPGDNVGFNVKNSVKDVRGNVA GDSKNDPPMEAAGFTAQVIIILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQAQAK
1281	A	1	921	KFETSKYYVSIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGFEA GISKNGQTHEHALLAYTLGVKQLIVGVNKMDSIEQPYQSQKTYEEIVK EVNTYIMKIGCNLDTAAFVLISVNVTEVKSVIHHHEALSEALPGDN VGFNVKNSVKDVRHGNNAGDSKNDPPMEAAGFTAQVIIILNHPGQIS AGYALVLDCHTAHTACKFAELKEKIDRCSGKKLEDGPKFLKSGDAAI

				IYMPGKPMCVESFSDYPPLGHFAVGHMRQTVAMGIIKAEDRKAAGV GKVTKSAQKAPKPSEYYPLYLPPQS
1282	B	70	572	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMIILNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRS GKKLEDGPKFLKSGDAAIVDMVPGKPI*
1283	A	1	1410	MTSPNELNKAPWTNCGETGWIKDLNGKPKTIKILEDNLVNTILDIGT GKDFMTKTPKAIATKAKIDKWNLIKFSFCTAKETINSINRQPTWE KIFTNYAFDKGFDLLTPVMTTTSIKNVITGTSQVDCAVLIVAAGVGE FEAGISKNGQTSEHALLAYTLQVQLIVGVNKMDSSTEPSCQKRYEE IVKEVSTYIKKIGYNPNTVAFVPISGWDDNMLEATANVPSFKGWKV TCKDGNASGTTLLEALDYILPPSGPTDKPLRLPLQDVHKIGGIGTVL GGQVKTGVLKPGMVVSFAAVDVTTEINFIPGNNEGFIKNVSVKDVR CGNIAGDSKNGPPMKAAGITAQVILNHPGQISAGYTPVLDCHMAHT ACKFAVLKEKIDHRSGKKLEDGSKFLKSGDAAIDMVPGNLMCIESF SDYPLGHFGVCDMRQTVAVGVIIKAVDQKAAGAGKVTKSAQKAQKAK
1284	A	1	1386	MDIKKGITDISASLRVESGWEARTREKTHINTVIGHVDSGKSTTT GHLIYKCGGVDKRTIEKFEKEAAEMGKCSFKYAWVLDKLKAERHGI TIDISLWKFETSKYYVTIIDAPGHRDLIKNMITGTSQADCAVLIVAA GFGEFEAGISKNGQTRHALLAYTLGVKQLIVGVNKMDSSTEPYSHK RYEEIVKEVSTYIKKIGHNTDTVAFVPVSGWNGDNTLEPSANMPWFK GWKVTRKDGNASGTTLLEALDCILPPTPTDKPLCLPLQDVYKIGGI VNVATEVKSVMHHEALSEVLPGDNVGFNVKNVSVKDVRGNVAGDS KKDPPMEAAGFTAQVILNHPGQISAGYAPVLDCHTAHIACKFAELK EKTDHRHSGKKLEDGPKFLKSGDAAIVDMVPGKPVYVESFSDYPLGR FAVHDIRQTVAVGVIIKAVDKKAAGAGKVTKSAQKAQKAK
1285	A	70	1538	KPKWERKRLIFNIVVIGHVDSGKSTTT\GHLIYKCGGIDKRTIEKFE KEAAEMGKDSFK\FAWVLDKLKAERERGITIDISLWKFETSKYYVTI IDAPG\HRDF\IKNM\ITGDISRLDCAVLDLFA\SGVGEF*SLVSPK NGQ\TREHALLAYTLG\VEQLIVGVNKM\DSSTEPYSQKRYEEMWLR EVSTF\IKKIWLQPTQ*HFVPISWFGIGDNM\LEPSA\NMPWFKGW \KVTRKDGNASGTTLLEALDCILPPTPTDKPLR\LPQGVH\KLGG IGTVSSAPMET\GFSNPGMVVTFAPSPR*QRKVKSCRKCTHEALK*S SFLGTNVGLQLSGIVSCQGMFRPWQTVAG*PAKNDPTQWESSWASLV RGDYP*PIPGQNKAPGYAPCIGIGAHGLTFACK\FAELKEK\IDRR\ SGKKLEDGPK\FLKS\GDAA\IVDIVPG\RPMCVESFSDYPLGRFA VRDMRQTVAVGVIIKAVDKVCWSWARSPPKFAQKG
1286	A	41	601	APSPRRPWGHFTEEDQGLLSTSLWGK\VKCGKNAGRKKPLGKAPLVV L/HPWDPKRSFEQALGNPVPLPSA\IMGNPPKSRAGK\KVLT\SLG EMPIKHPG*SSKGTFAQA*SELH\CDK\LHVDPENFK\LLG\NVLVT \VL\AIPFSAKEFTPGGCRASWAERWTVSWPVPCSSRIPLSSLAHD CRAFQG
1287	A	2	287	KNMSFVNDLTVTDQGRKIYFTDSSSKWQRRDYLLLVMEGTDDGRLL YDVTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRSSLVKR R
1288	A	36	427	GKQWDFAFCFGSHVWVSVDLLAFFECELLSNLHHLHAYLKCFKSKQ KTCVFQSGCAGCDLLFSQETVMKFVPRNSLVLELSDSGAFRRSLHDP DGLVATYISEVHEHDGHLYLGSFRSPFLCRLSLQAV
1289	A	247	1183	CCWESPVDQPLRQISGIALFCSFKEPPLLGLVHLHPNTKLRQGRKGC LKINLLGPES\MAHIGGCDVYWGQMQMRVVKLENG*NRRPLPGFGSG PLAKPEDDEPCVWGDPLGIRGRGPKWGLLFVGRHLHTRGLF*R*NPWE TVKVLLLSSETPI*GGRNMSF\VNDLTVTPGWKEDLISPNPKQONG QRRKLPAFWVMGGHKMTGRLLLEV*YCDPGK*KFYWTQLRFPNGVQPV S*QKTLSLVAETS\MARIRRVYVSGPDERR\ADLFVENMPGFDPNIR PSSSGGYWGMSTIRP*P\GSSMLDFLSERPWD
1290	A	2	217	LGVRIPTVALHVMELFDTTVEQLYSIFTVKELTNKKIIMKWRCGNWP

				EGMLLITALHIKGPCTLRLGFSYG
1291	A	1	2283	MAASIALEALEALYGIVKESGVKHKGLIEIPNLSEENEVDDTESSFC YRHAFQIVLIRLCGSCVVRVPCGGPVCREGLPYCGGSVLCGAGVV QERESTLSKKKG DG VILKDL MKTAGTAKVREALGDY LKAL KTEFTTG MILPTKAMATQELTVKRKLSGNTLQVQASSPVALGVRIPTVALHME LFDTTVEQLYSIFTVKELVQKFSKSTAVLETEKGGKFQMF DGNITGE YLGLLTNNKIIIMKWR CGNWPEGLNCTDPLVSGFSPNSGTPKAARPTP HLPPPLLLPDQCEDHEDEDLYDDPFPLEEQTERDATSLSKGKFQELL VGIVVENDAGRGEINELKQVEGEASCSSRKGLIFFYEWNIKLGWKE RTVPFCPSIAFVTASPLQGTPLSCFAQAKSTLGQEEBYGCTCPTLLS GRRTADSSCPLLGHGLPDLSSVAAQGALEWWNPVRAAELFSIVKESG VKHKGLIEIPNLSEENEVDDTESSFCYRHAFQIVLIRLCGSCVVR VPCGGPVCREGLPYCGGSVLCGAGVVQERESTLSKKKG DG VILKDL KTAGTAKVREALGDY LKAL KTEFTTG MILPTKAMATQELTVKRKLSG NTLQVQASSPVALGVRIPTVALHMMELFDTTVEQLYSIFTVKELVQK FSKSTAVLETEKGGKFQMF DGNITGEYLGLLTNNKIIIMKWR CGNWPE EHYAMVALNFVPTLGQTELQLKEFLSICKEENMKFCWQKQHFEI KG SLQLTPLNG
1292	A	249	433	KWRCGNWPRTLMPWLH*NFVPTLGQTELQLKEFLSICKEENMKFCW QKQHFEENKKVPAS
1293	A	778	1578	PRQVDPSWGFHSRLSGPW/H/WTERDATSLSKGKVP GAGPGHPLWKN DAGRGEINE\LKQVEGEASCSSRKGLIFFYEWNIKLGWKIVKESG VKHKGLIEIPNLSEENEVDDT/EEFTTG MILPTKAMATQELTVKRKL SGNTLQVQASSPVALGVRIPTVALHMMELFDPT/S*SSLSIFTVKE EERVCVLFSLTNKKIIMKWR\WGTWPEEHYAMVALNFVPTLGQTELQ LKEFLSIYL*RKVP*NFCWQKQHFEI KGSLQLTPLNG
1294	B	46	386	XIRHESGSRSHSHCSTLSSIGDVA KKL GEMWNNTAADDKQPYEKAA KLKEYEKDIAAYRAKGPDAAKKG VVKA EKSKKKKEE EDEEDED EEEEEDXEDDDEEEDDDDE*
1295	A	263	484	CFFLPYCFILPLLWKDIAAYRAKGPDAAKKG VVKA EKSKKKKEE E DEEDED EEEEEDEEDED EDEEEDDDDE
1296	A	157	886	TWKGDLKKPRANMSSYAFFVQTCRGG\HKKKHPDASVNFS/ESFSK KCSERWKTMSA*R/EKGKFEDMAKA\DKARYER\EMKTYIPPQRGRQ KRKFKDSQLHPRGPPSGLSSSCSEYRPKIK\GEHP\GL\SIGDVA K KLGRDVGINTAAD\DKQPY\ERRAAKLKEYEKDIAAYRAKGPDA A KKG\VVKA EKSKKKKEE EGE EDEEDED EDEEBIEE\DEEDED EEDD GLMNKLGSGAVFFF SCL
1297	A	1	450	CKSRGSNLRVHFKNTRETAQAIKGMHIRTATKYLKDVTLQKQCV PFR RYNGGVGRCAQAKQGWGTQGRWP KKS AEF\LVIEHIQVNKAPKMRRR TYRAHGRINPYMSSPCHIEMILTEKEQIVPKPEEEVAQKKKISQKKL KKQKLMARE
1298	A	1	1725	MAHKEGDMPAEQFGAGYGFKRFYVPMKEGLKGSWSFLKYQRRRKYS LSAVFHSATMLQDVGEAIQFEV SIGNYGNKFDTTCKPLASTTQYSRA VFDGNYYYL PWAHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLYP QEKNNGP KVPVELRVNIWLGLSAVEKKFNSFAEGTFTVFAEMYENQA LMFGKWGTSGLVGRHKFSDVTGKIKLKREFFLPPKGWEWEGEWIDP ERSLLTEADAGHTEFTDEVYQNESRYPGGDWKP AEDTYTDANGDKAA SPSELTCPGWEWEDDAWSYDINRAVDEKGWEYGITIPDHKPKSWV AAEKMYHTRRRRLVRKRKDLTQTASSTARAMEELQDQEGWEYASL IGWKPHWKQRSSDTFRRRRWRRKMAPSETHGAAAI FKLEGALNTCET AQAIKGMHIRKATKYLKDVTLQKQCV PFRYNAGVGRCAQAKQRGWT QGRWPRKSTEFLLHMLKNAESNAELKGLD VDSL VIEHIQVNKAPKMR RWTYRAHGRINPYMSSPCRIEMILTEKEQIVPKPEEEVAQKKKISQK KLQKQKLMAWE
1299	A	278	879	SVKMVRYSLDPGGT PRKSCK/SQRGSNLRVPFKDHS*KLPQAHQGVC HIRKSPTKY\KLDVHLTRNQCVPIPDY\NGGICKVCRRPKQWG\WT

				QG\RWPQKGVNLNLLHMLKNAE\SNAELKG\LDVDFLV\IEHIQVVK AP\KM\RRRTYRAHGRINPYMSSPCH\IEM\ILTEKEQIVPKPEEEV AQKKIS\QKKLKETPTLWHGE
1300	A	85	266	LSHCLPLQTTTEVGFGNLLGYWIACSIGCVLSTGMLSHQLKQHVIDG EKTIIQNPTDQOK
1301	A	1	1776	MSATGDRHPTQGDQEPVSQEGAQAEAAAGAGNQEGGDSGPDSSDMVP AAEVVGVAGPVEGLGEEEGEQAAAGLAAPVQGGSAEEDSDIGPATEEE EEEEEGNEANFDLAVATRRYPAAAGIGFVFLYLVSLLRRLYHNDHI QIANRHLSRLMVGPAAVPLWDPNPLLLLSQRLGAGAAPEGEGIG LIQEAAASVQEAASVPEPAVPADLAEMAREPAEEAADEKPPPEAAEBK LTEEATEEPAAEBPTSEEAVAPEGKGASGSSGEAGIHVSKGSGQCG AGTAGAGELEIISRFGWEIYWKKGKYSVPVEMIKQQQQVTKSQPEK WDEEAQDAAGEEKEQEKEKDVENKVFKRKTSSMALLPHTKYQCAPB SHQLEASSSGVLVLSLCEKDDAMIMEEIGKIFKKKIEMRKGIAPPTS ISVNNCICHFSPKSNQDYILKEGDLVKIDLGHVHVDGFIANVAHTFV VDVAQGTQVTGRKADVIKAIHLCDLRLVVKPGNQNTQVTEALNKA AHSNLCTPIEGMLSHQLKQHVIDGEKTIIONLTDQKKKDHEKAELAV HEVYAVDVLVSSGEGKSKDAGQRTTIYK
1302	A	207	1645	LSQRALLSPRARSFSLSPACPLPCLLALLSLSSRIEGTLTTACGW GRETEAAAAQKGRGCSGGSRKMSGEDQEQEQITVD/DSLVTYKIMG GDIANRVLRLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKKE\KEM KKGIAF\PTIS\VNNWCM/CHFSPFERSDPGLYSSKEGDLVK\IDL GVPCWMGFIANVASH/SFVVDVAQGTQVTGRK\ADVIAAHLCAEAA \LRLVKPGNQNTQVT\EAWNKAHSFNCTPI\EGMLSHSLKQHVIDG EKP*FQNPTDKQK\RAHEKADFEV\HEVYAVDVLVVKPQERARPKDAG QRTTIYKRDPSKQYGLKMKTSRAFFSEVERRFDAMPFTLRAFEDKK ARMGV\VECAQT*TCWQPFNVLY*EGRVILFAQFKFTVLAHGPNP RI\TS\GPFEF\DFYK\SEMEV\QDAELKALLQ\SSAKSEKPKKKK K\KASKTA\ENATGGILCSLGNIRK
1303	B	29	200	MSRTRLVCPSLIPFCIYVVDVGFSPGPQSCTSHEPKDIHAKCELAFL HHQRFYKNEGK*
1304	A	138	1908	ASRTAVARWECVLQNVREPSPSRAWPSQLRPIASTATKCRE\CGPG YSTPLEAMKGPREEI\VYL\PCILPETQGTGEPRLSWATVDVDPKSP QYCVIH\RLMPN\LKDELHHSW\NTC\GSCFG*LAPSRGK\LV LPSFHLFGIYVGGTWGSEPRAPKLAQGSLSPRDIHAKC\NWAFLHT SHCLASGEVMISLGDVKNGKGGFVLLDGÉTFEVKGWTWERPGGAAP LGYDFWYQPRHNMISTEWAAPNVLRDGFNPADVEAGLYGSHLYVWD WQRIE\IVQTLSLKDLIPLIIRFLHNPDRCPKAFVG\CALQAPNIQ RFLQRTRGGLFSGRR*FQV\PPRKLKGW\LLPKMPGL\ITLILASP WNDGF\LYFS\NWLAWGP*GKYDISDPQRPALTQGLFLGGSIVKEGP \VQVLEDEEL/TSPSPEPLVVKGKRVGEGP\QMI\QLSLDGKRLNNH HGRCTSAHQSSFP*SQSGERLLVNAGRVIEW*DNSKKGGA*KLNPK LSWVDFGEGAPLPKPLPH*ARYP\GG\DCSS\DIWILNSPPSHPSL FWALHFPFGGGLSFCISLGRTRLGKHVPTTAKLRLWQCVES
1305	A	1	1000	STRAPSPGFPSSKLAGAYKSWCRRDPRTHSAGAQAARSVPIRCP APTASATMSHHWGYGKHNGPEHWHKDFPIAKGERQSPVDIDHTAKY DPSLKPLSVSYDQATSLRILNN\GHAF\NVEFDDS\QDKAVLKGKGPL \DG\TYRLISVFTFWGSF*WDKVSEAYCGIKKKYAAE\LTLGHWNT KYGDFGKAVQEPDGLAVLGIFLKVGSAPGLQKVVVDVLDISIKTKGKS ADFTNFDPRGLLPESL\DYWTYPGSLTTPPLLECWTW\IVLNF\PFSS VSS\EQVFEIP*TLTFNGGGVNPEELMVDNWRPA\QPLKNR\QIKAS FQIRWSHSLYSK
1306	C	127	435	MAASKNPEVLDTTEETHLSRFLEGVRNVASVCLQIGYPTXASVPHSI INGYKRVLALSVETDYTFPLAEKVKAFLADPSAFVAAAXLGCCHHSC SXCCSPS*
1307	A	1	689	KCFI/VGADNVASKQMQQIRMSFRGKAVC*WGKNTMMRKPIRGHLEN

				NPALKLLPHIRGNVGFVFTKEDLTEIRDMLLANKVPAARAGAIAP CEVTVPAQNTGLGPEKTSFFQALGITTISRGTIEILGVRNVASVCL QIGYPTVASVPHSI INGYKRVLALSVETDYTFPLAEKVKAFLADPSA F/VAAAP/VAAATTAAPRAAAAPAKVEAKEESESEDEDMGFLFD
1308	A	68	1111	RTAVMPREDRATWKSNYFLKIIQLDDYPKCFIVG\ADNVGSKQMQQ IRIVPWGEACVLMGQKTM\MGQAHPKGTL*NNPSLWRKLLP\HIRG\ NLGFCFTQGGPSLEIKGHVCLANKGLPSWLPVVGANCPHGESHWWPA PEHWSSGPEKTSFFPGL*AITTK\ISQGAPIENPEVNVPAESRTGDQ SGEPSEANAA*TCSNISPF\SFGAGSSQPGVSTNGSHLPPLKGLDIH RRNLCIFWLSWEGVRKCCPVSVQIG\YPTVA\SVP\HSI INGYKRV LA\LSV\EPDYTFPLAEKVKAFL\ADPSAFVVAATCGLLPPQLLLVV VAAPAKVEAKEESESEDEDMGFLFD
1309	A	60	569	STDLEELPTLGWF*KQELIILSCPFVSLTYRERLPANFFKFQFRNVE YSSGRNKTFLCYVVEAQGGQVQASRGYLEDEHAAAHAEAFFNTI LPAFDPALRYNVTWYVSSSPCAACADRI IKTLSTKTNLRLILVG\R LFMWEEPEIQAALKKLKEAGCKLRIMNLV
1310	A	62	858	QLRWDSGARAWPRPACLSPLPQRLLSHSPSMAQKEEA AVATEAASQN GEDLENL\DDPQKLKELIELPPFEIVTGERLPANFFKFQFRNVEYSS \GRTKTL\LCYVV*STGARGGKVQASWG\YLEDE\HAACPLQKESFS FNTILPAFRPKPLAVTNVT/WGYVSSSPC\AACADR\IVKTLSTKN LRLILVGRLFMWEEPEIQAALKKLKEA\GCKL\RIMKPDFRILSW E\NFVEQ\BEGESKAFQPWEDIQENFLYYEEKLADILK
1311	A	1	729	NTEDQRNEEKAQREANKKIEKQLQKDKQVYRATHRLLLLGAGESGKS TIVKQMRILHVNGFNGDEKATKVQDIKNNLKEAIETIVAAMS NLVPP VELANPENQFRVDHILSVMNVPDFDFPPEFYEHA KALWEDEGVRACY ERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLLR\CRVLT\SGIF \ETKFQV\DK\VNFIHIV*RGVGQDERRKWIQCFNDVTAIIFV VASS SYNMVIREDN
1312	A	2	1271	PVRSSAPRRGHSVASAPRSGLRQVAGRRGAALPCSLAPGCGAAAGAS PCPGAGRRRAAGGRCLACECTSLTCAGESGKSTIVKQMRILHVNGFN GEGGEEDPQAARSNSDGEKATKVQDIKNNLKEAIETIVAAMS NLVPP VELANPENQFRVDYILSVMNVPDFDFPPEFYEHA KALWEDEGVRACY ERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLLR\CRVLT\SGIF KFQVDKVNFMFVGGQDERRKWIQCFNDVTAIIFV VASSYNMVI REDNQTNRLQEALNLFKSIWNNRWLR\TISVILFLNKQ\DLAEKVL AGKSKIE\DYFPE\FAR\YTPE\DATPEP\GEDP\R*TRAK\YFIR \DEFLRISTASGDGGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHL RQYELL
1313	A	235	1571	GRPRPPPPQGRAPPPPPPRMGCLGNSKTEDQRNEEKAQREANKKIE KQLQKDKQVYRATHRLLLLGAGESGKSTIVKQMRILHVNGFN GEGGE EDPQAARSNSDGSEKATKVQDIKNNLKEAIETIVAAMS NLVPPVELA NPENQFRVDYILSVMNVPDFDFPPEFYEHA KALWEDEGVRACY\ERS N\EYQLIDCAQYFL\DK\IDVIKQAD\YVPSDQDLLR\CARVLT\G IF\ETKFQVDKVN\HMF\DVGGQ\RDERRKWIQCF\NDVT\AIIFV VGSSSYN\MVIREDTGHNGLAGRL*TSPKGIWDRWAAAPSLVILFL TKQ/EILLA*ESPLAGNSK\IKDYFPE\FAR\YTPEGCYSRRPGE PHGVYRGQVTPFEDEFLLRSSNCPVEDGRHYCYPHF\TCAVDTENI\R RVFNGLAVDIHFSGMHLSFSYGAGFKEGEPKFNKA
1314	A	3	786	PLFVVFPSPDIAGRPGGVVGPGGPAWAAAPAMNGLSLSELCLF CCPPCPGRIAAKLAFLPPEATYSLVPEPEPGPGGAGAAPLGTLRASS GAPGRWKLHLTERADFQYSQRELDTIEVFPTKSARGNRVSCMYVRCV PGARQGHQAQGGHPQLAWVGRGDSNNPAPGGCLLGKSWGTAALAC GYIHLARYTVLFSHGNAVDLGQMSSFYIGLGSRLHCNI FSYDYS GASSGRPSERNLYADIDA AWQALRT
1315	A	3	2231	PAMNGLSLSELCLFCCPPCPGRIAAKLAFLPPEATYSLVPEPEPGP GGAGAAPLGTLRASSGAPGRWKLHLTERADFQYSQRE\RTIEVFPT

				KSARGNRVSCMYVRCVPGARYT\VLFSHGNAVDLGQMSSFYIGLGSRLHCNIFTYDSSGYGASSGRPSERNLYADIDATWQALRTR*GRPLVGRVRARWRPRLTLRRRQVRHQPGQHPSCGTGRSIGHGAPPWDWASRYEC AAVILHSPLNLGHARRIPRHRKTYCFDAFPLHSRKVSKINVSRCSS SHGHEGRGDRLSRTGWALYEALPPRRVEPLWVEGAPGTTDIEPLQPV PGAAGVAFILPGAAQPARLAAAPNRPDLNKAAPGLHPAPAPTQGLA CGPPGRPRWRPGLGARHEWAVDDVQATRTHSFPFGSKKKIRENGQ LKI
1316	A	1	1347	MTSTVLLQRGSRMKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQNRFTQFRLSETKEITNPYAMRLYE SLCQYRRTSLSKFFMVKGVERTPIFGGLDPSSVIEGDLGNESLGN LVWFVDILQGNSPARSPGKVHRQYSTLRASSLFFSPYSSIQQTIGLP ELRESLAIDRSQSEHQKPIWTCAEAFVVI FGQKSQVAIAAENWRE EEPQAGPSGGVPEGIAVRDDSSMRVVVPEDLLVGEDVEVKDDRVQTN PKAPISRSFKASESKNFQKHTEAEGREYKGYARISCFQKFGNLV PSRGHIALARAPEEPQAGPFGGVPEGIAVRDDSSLRVVVPEDLLVGE DVEAEQKKVAII SAEGYSKAAELIANSLATARI RLMELCKLEAAED IAYLSRSRNITYPPAGQSVLLQLPQ
1317	A	53	1027	NFRVEAGVRGVQKQKTCFAFKVLESIGKLG\LALSVAGGAENSALYNV DAGHRAVIFDPIPGQK*QDIVVGEGTHF\LIP\WVQKPQLSNDCSR PRNCCQSITGSK\DLQNV\NITLRHPSSGPVRQPSFPRIFTSIGED\ YDERVLAVPSQLENLK\SVWARFDAG\ELITQR\ELVSRQV\SDDL\ TERA\ATFGLILDDVSLTHLTFGK\DFT*AV\EAKQVAQGGKQRRAR FV/VLEKAEQKK\AAII SAEGDSKAAELIANSL\ATAGDGLIELRK LGKLQRTFAYQLSTLSGTSPYLPAGQS\VLLQ\LPQLRAHPCLAPPA GLTWGHSPD
1318	A	424	598	MTKGRSASAKEGQGGIGIGGGHPRSWRLCGQMCRDIKGLWLREIKPC PLTNRAGAGPS
1319	A	3	371	SIKPSVKEFTTETSAVFEDGTMFEAIDSVIFATGYDYSYPFLDETIMK SRNNEVTLFKGIFFPLMEKPTLAVIGLVQSLGAAIPTADLQAWWAAK VFASRWAILSFIFINEHLLNTCYKLKW
1320	A	1	1596	MSKRVGIIAGAGVSGLAIIWCCLEEGLEPTCFERSDDVGGLWKFS DHT EEGRASIIQSVFTNSSKEMMCFDPDFPYDDYPNYIHHSKLQEIYIKTY AQKKELLRYIQFETLVSGIKKCPFLVTGQWVVVTEKDQKQESTIFD AVMICSGHHVYPNLPTDSFPGLDQFRGNLYHSRDYKNPEAFKGRVL VIGLGNSGSDIAVELSRLATQVIISTRASWVMSRVWDDGYPWDDMY VTRFASFLRNVLPSFISDWLYVQKMTWFKHENYGLMPLNGSLRKEP VFNDLPSRILCGTSLIKPSVKEFTTETSAVFEDGTMFEAIDSVIFAT GYDYSYPFLDETIMKSRNNEVTLFKGIFFPLMEKPTLAVIGLVQSLG AAIPTADLQAWWAAKVFANSCTLPTTNEMMDDTDEKMGKKLKWFGQS QTLQTDYITYVDELGSFIGAKPNIPWLFLTDPRLALEVYFGPCSPYQ FRLMGPGKWDGARNAILTQWNRTVKPTRTRVSEVQRPHFPFYNLLKM LSFPLLLAVTLTFY
1321	A	2	557	WDDMYVTRFASFLRNVLPSFISDWLYVQKMTWFKHENYGLMPLNGY LKMEIFFIQKRGALI**IYLSIKPSVKEFTTETSAVFEDGTMFEAIDS VIFATGYDYSYPFLDETIMKSRNNEVTLFKGIFFPLMEKPTLAVIGL VQSLGAAIPTADLQAWWAAKVFASRWAILSFIFINEHLLNTCY
1322	A	955	1187	IFFFFFFFKMESCFFAQAGVQWCDLGS LQALPPGFTPFSCLSLLSSWD YRRPPPHLANFLYF**TWVFTVLARMVIS
1323	A	6345	9041	ERNCHERRESVALMLMFKCLMLFQCYGLLQVFLGNELPTARVFASHC CSSLRKEPVFNDELPSRILCGTSLIKPSVKEFTTETSAVFEDGTMFEA IDSVIFATGYDYSYPFLDETIMKSRNNEVTLFKGIFFPLMEKPTLAV IGLVQSLGAAIPTADLQAWWAAKVFASRWAILSFIFINEHLLNTCY MQSTVLGIQ
1324	C	182	433	MHLDFLNLKTLQPQIRGVESEQSSRLHPLPDPRGRHRMADNLPMEIH GSSATSSGKPSDFNQAQAVDGAGERGGKEVLGGTLDVL

1325	C	72	254	MVSTQLRQASDPRTTIGRERFELLRRVDKLMSPRLPTGTLPNPHFW TLSIPQVGRGNAP*
1326	A	225	735	GELRVNSLHVSTHFQIPEETDIGWLVSPGQGPAPPFEDIQLWPPGSL MAAEPTDQSLEESH*DRWITTFTFAR\QEGRK\D*PQRSNEFKE\L VTQQLPHL\LKDVGSLDRKN*GAWDVNQDFGGSRFN\EY\WRLIGGA WPKEIRKEEKTLLKIERSKAAWLEDGVGQGR
1327	A	55	391	PAGRDAQPLHHWFLRAQRHHPATGDPHGFLWPPTRAAGWQCLLHCV LHPHGGPLPGRSSVSVDIPGAVPELWWHLPNVHFTHTGTLLPNPS DHATARSKSSPMPSVPSP
1328	A	996	1334	WASVGLSGPRSPSSRPQ*ARPRPGAPASLRQADLGRGWRDRLGAPR PRPRTGGWRSCCRGRGSRPRGARAGLGPGAPGGWRRSRRSWTRA RAATRPRAAARGSRTPRG
1329	A	1	993	MDWRIKDCVDAPTQGTVLGDARPIFFCAPLHPTQDDLFADLANLSH LFLHGNRLRLLTEHVFRGLGSLDRLLHGNRLQGVHRAAFRGLSRLT ILYLFNNSLASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQ RARVSSSDVTCATPPERQGRDLRALREGRFQACPPAGPTRPGSRARG NSFSNHLYGPSRGFTVYISTHVSFPIFIGLQNRFTQFRLSETKEITN PYAMRLYESLCQYRKPDGSGIVSLRVDWIIERYQLPQSYQRMDFRR RFLQDKAKMKPLLLLALLFGAVSALHLKTWFQVSPFRPELSPLMPQA QV
1330	A	72	496	PPWARGSARRPPAWRTVRMPSPCHPRMFGAPQKTFLRVSVWSRCRPWG IVMRMM*PMRGQVRRHNSCMAPKTEE*NPTVSATFCCCSFVSCSWPP VTRYSSILFTAAM
1331	C	202	378	MTPYLTLFLSPLPPKGEIWGLLLFLTPLGFLPLSPLLLLPCPAPAGV RRQWDGPTEGA*
1332	A	1	1541	MDPLRAQQALAAELEVEMMADMYNRMTSACHRKCVPPHYKEAELSKGE SVCLDRCVSKYLDIHERMGKLTLSMQDEELMKRIHF IQAQLRRPL APGGFPVPPLLPRRQRRRGHRAVRLKLRGGRVLHAEKTPAPARLRAG PTGLRTRRESVALPEASAAAGCSFAGDRRLGASMAPTLQQAYRRRW MACTAVLENLFFSAVLLGWGSLIILKNEGFYSSTCPAESSTNTTQD EQRRWPGCDQQDEMLNLGFTIGSFVLSATTPLGILMDRFGPRPVRL VGSACFTASCTLMALASRDVEALSPLIFLALSINGFGGICLTFTSLT LPNMFGNLRSTLMALMIGSYASSAITFPGIKLIYDAGVAFVIMFTW SGLACLIIFLNCTLNWPIEAFPAPEEVNYTKKIKLSGLALDHKVSGDL FYTHVTMGQRLSQKAPSLLEDGSDAFMSPQDVRGTSENLPERSVPLR KSLCSPTFLWSLLTMGMTQLADHLLHGCCEQDAGVPCDWWPGA
1333	A	9	345	YLSEVGVSIGVIRPRQWIRRPEDPFHGGRLKMDPLRAQQALAAELE VEMMA\DMYNRMTSACHRKCVPPPF\KEAELSKGESVCLD\RCVSKY L\DIHGA*WGKKFDRVLLQG
1334	A	170	842	EHVYKLPKSAKITRPLMLSSARGGAESERAEPPLRWAFLLGLGTV VGVDDESTAFSWPVCDCMCGNRLRQRPEDRGAFSCGDCSRVVTSPVLK RHLQVS\LDCRSRPQCRVKVLLQRSISSLLRFAAGEDGLYSQWLIR SLLRIWKEADRRWVPEGPG*RC*LRDTQYGFQFSGATK*RSVFGKE VGLLNCFVQSVTAHTSCIGLEEIELLSAGGASAEH
1335	A	2	2925	FVLRRCQAALPEMPRGSRARGSKRKRSWNTECP\FPGERPLQGR RAGLRTAGAAASLSEAWLRCGEGFQNTSGNP\SLTAEKT\ITEKHL ELCPRPKQETTTSTKSTSGLTDITWSSSGSDLSDKTLSQLQDELQ FIDWEIDSDRAEASDCDEFEDDEGAVEISDCASCASNQSLTSDEKLS ELPKPSSIEILEYSSDEKEDDLENVLLIDSESPHKYHVQFASDARQ IMERLIDSRKSPETILHTPQNPTVKFPRTAENSAKKLLRGGLAER LNLQNRERSAISLWRHQCSYQKTLSGRKSGVLTKILKLHEECAM QVAMCEQLLGSPATSSSQSVAPRPGAGLKVLFTKETAGYLRGPPQDT VRIFPPWQKLIIPSG\SCPVILNTYFCEKVVAKEDSEK\TCEVYCPD IPLRRSISLAQMFVIKGLTNNSPEIQVVCSGVATTGTAWTHGHEA KQRIPTSTPLRDSLL\DVVESQG\AASWPG\AGVRVVQRVYSLPSR DSTRGQQGASSGHTDPAGTRACLL\VDQAC\GMF\GEVH\LEFNM\S

				KARQ\LEGKSCSL/VWGMKVLQKVTRGRTAGIFRL\IDTL\WPPAIP L\KTPG\RDQPC\EEIKT\HLATPAFGYNLTAHPNLGQIDIIDEDPI YKLYQPPVTRCLRDILQMNLDLT\RCSFYATVIYQKPT/QLKSLLL/ LWEQREIWLVDVT\LOTKEE\RDPRLPKTLVYVAPLCLVGLSEVL \EALAGAAP\HSLFFK\DALRDQGR\IVCA*TNWSSLLQKPLLSVVS GASSCELPGP\VMLDSLDSATPVNSICSVQGTVVGVDESTAFSWPVC DMCGNGRLEQRPEDRGAFSCGDCPRVGPPFV\LKRHCRRFL\DCRSK PQ/CARVRVK\LLQRSISSLVKVCPPGEDGSYEVKEVSLGKSGGGLL NCFVQSVTAHP\TSCIGWEEI\ELLSA\GGASARTLAVAPRIWGTLP MWPAGWVVVVVIGG
1336	A	1	480	NFALEAKNSARAISVVQTPMGHFTTEDQ/ALTITSLWGK\VNVE\D AGGETPGKGSLLVYP\WT\QRFDSFGNLVLLPSCPSMGNPQKSKAT WPRKVL\SLGDA\TKHL\DDLKGHLKPKEVNLHLTLTLHVGS*GT FKLPGEILLVTRFWAIPFSAKEFHP
1337	A	52	454	SQTQREPTMVLSPADKTNVAAA/WGMFLSFPTTKTYFPFHDLSHGSA QVKGHGKVVADALTNAVAVDDMPNALSALSDDLHAKLRVDPVNFKL LSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
1338	A	3	616	PTLLVPTDSETHPWLLSPADKQDQGPAGW*G*GSHPPSNVAKTLE R\MVLFPPPTPKPYFP\HFDL\SHG\SAQV\KGHGK\KVADALTNAV AHV\DDMPNALS\LSDLHAKL\RV\DPFNFKLL\SHCLLG*PWAA HLPRPSFTPCGCKASL\DKFPGLFVEAPLLEPSKLPLKLGSLRLAML LCFPGFPQPLLPFAPVPPWSLK
1339	A	2	390	GWDWNCVWEPHHWLQCSL/NSVTQAGVQLCNLSSLQPLPLGFKQFSC LSLPSSWDYRNPSSLKQQLFSYAILGFALSEAMGLFCLMVAFLI\SLP CEGAVSTSHSSPASGWRVFLFLYLPRQPGERGWLVR
1340	A	13159	14007	VSLSPRLKCSGTISAHCNLCPLGSNDSPASASQVAGITGAHHARLI FYFFILFYFIFLR/HESDSVTQAGVQLCNLSSLQPLPLGFK\HSLAS ASQVAGITGTHRYPLIFVFFFLF/SFLRQSL/DSVAQAGVQW\RG LGSLLPLPPGFTPFSCSLSSWDYKRLPTRLANFLYF**RQGVTVL ARMVSI*PRDLPTSASQSAGITDMSHCAQ/LIFVFLVETGFHQVGQ AGLE/PPDLKQSTHLGLPKCWDYRREPPRLA\NFCIFSRDGVSPCWP GWSPTSQFK
1341	A	1	532	DSGTRDTVLKLLREWYMIISREMFPMYALFRTSPGDRVITYTINPSS HCNPNHLSYFKFVGRIVAKAVYDN\RLLECIFYTRSFYKHILGKSV\R YTDMESEDYHFYQGLVYLLENDVSTL\GYDLTFSTEVQE\FGVCEVR DL\KPNGG\NILVTEE\NKKEYVHLVCQMRMTGAIRKQFG
1342	A	1	532	AEADAI IQMVBREGQARRRQQAATSESSQSEASVRREESPMVDQPS PSAQDTQSIASDGTPOG\EKEKEERPELPLLSEQL\ALDELWDMLG ECLKELEESHDQHAVLETHRTVLNQILRQSTTHLADGPFVLDYIR VLDFDVKRKYFRQELERLDEGLRKEDMAVHVRRDHVF
1343	A	262	589	PVSKESSRVAPLCDFCLPFIQSESSQSEASVRREESPMVDQPSPSAQ DTQSIASDGTPOGEKEERPELP/LLSEQLSLDELWDMLGECLEKE LEESHDQHAVLVLQPA
1344	A	1	2502	MTPPHLPRRASDDEFENLRIKGPNAVQLVKTTPPKPSPLPVPIDTI KEVIYDMLNALAAYHAPEEVGFTSPMLFDERKYPYHMLQKFLCSGG HNALFETFNWALSMGGKVPVSEGLEHSDLPDGTGEFLDAWMLVEKM VNPTTVLESPLSLPAKLPGGVQNFQFSALRFLVVTQKAFTCIKNL WNRKPLKVYGGMAESMLAILCHILRGEPIRERLSKEKEGSRGEED TGQEEGSSRREPQVQQQLQQLMDMGFTREHAMEALLNTSTMEQATE YLLTHPPPIIMGGVVRDLMSSEEDQMMRAIAMS LGQDIPMDQRAESPE EVACRKEEEERKAREKQEEEEAKCLEKFQDADPLEQDELHTFTDTML PGCFHLLDELDPDVYRVCDLIMTAIKRNGADYRDMILKQVVNQVWEA ADVLIKAALPLTTSCTKTSEWISQMATLPQASNLATRI LLLTLLFE IEVRSWSYPPFQDKHCKKEKENFEAIAAALAAERESKPPVRDTRES QLAHSKDEPPPLSPAPLTPATPSSLDPPFSREPSSMHISSSLPPDTQ KFLRFAETHRTVLNQILRQSTTHLADGPFVLDYIRVLDFDVKRKY

				FHQELERLDEGLRKEDMAVHVRRDHVFEDSYHTASQSLTHTNDWMPY GFSAQFLSASAFLCRYIVFEGEEGQDAGGLLREWYMIISREMFNPMY ALFRTSPGDRVTYTINPSS\HCNPNHLS\YKFVGR\IVA\KAVYDN RLLECYFTRS FYKHILGKSVRYTDMESDYHIFYQGLVYLLENDVSTL GYDLTFSTEVGQEILITAHPSQSGRSNSQVHLRTSTA
1345	A	1	2219	MPQLPGISLPEGVDPSFLAALPDDIRREVLQNLGIRPPTRTAPSTN SSAPAVVGNPGVTEVSPEFLAALPPAIQEEVLAQQTAEQQRPELAQN ASSDTLMDPVTLIQTLPSDLRRSVLEDMEDSVLAVMPPDIAAEAQAL RREQEARQRQLMHERLFGHSSTSALSAILRSPAFTSRLSGNRGVQYT RLAVQRRGGTFQMGSSSHNRPSGSNVDTLRLRGRLLLDHEALSCLL VLLFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSESE LCIETPKLTTSEEKGKSSKSCGSSSHENRPLDLLHKMESKSSNQLS WLSVSM DAALGCR TNIFQIQRS GGRKHTEK HASGGSTVHIHPQAAPV VCRHVLDTLIQLAKVFP SHFTQ QRTKETNCESDRERGNKACSPCSSQ SSSSGICTDFWDL LVKLDNMNVS RKGN SVKSPVSAGENKVSEAQA NSGSGASSTTTATSTTTSTTTTAASTTPTPTAPTPTVSAPALVAAT AISTIVVAASTTVTTPTTATTTVSISP TTGSKSPAKVSDGSSST FKMVSSGLTENQLQLSVEVLTSHSCSEEGLEDAANVLLQLSRGDSGT RDTVLKLLNGARHLGYTLCKQIGTLLAELREYNLEQQRRACETLS PDGLPEEQPQTTKLKGKMQSRF\SGLGSASSIQAAVRQLEAEADAI I QMSSESSQSEASVRREESPMDDVDQPSPSAQDTQSI A
1346	A	59	6349	KISQYYMHTPISPHRLLISPSIAPRKVEWTGLKVKSQDRFLFAQQLQ VELVALPLVLCLAASALGRSTTSFVSLGQPHAAIQTYSQKWPTAVSA SPFLPLRGSGTGNGSSRI PRESAPEMATAESLVEELSEDAAGGASPG VELPALGCSELPAAEVSPTASSKNLETICEYAYCMAMLPETGLDPYP KRGFLDLTQERIWTDIPSPGNIPTTHPLMVRHADHSSLTLGSGSST TRLTQGIGRSQRTLRLQTLANTGHTIHHVHPGNRPNPPLILQRLGP SAAADILQLSSSLPLQSRGRARLL\VGND DVHI IARSDELDDFFH DQ\STATSQAGTLSSIPTALTRWTEECKVLDAESMHDCVSVVKVSI V NHLEFLRDEELEERREKRRKQLAEETKITDKGKEDKENRDQSAQCT ASKSNDSTEQNLSDGTPMPDSYPTTPSSSTAATESKETLGLTLQSSQ QQPTLPTPPALGEVPQELQSPAGEGGSSTQLLMPVEPEELGPTRPSG EAETTMELSPAPTITSLSPERAEDSDALTAVSSQLEGS PMDTSSLA SCTLEEAVGDTSAAGSSEQPRAGSSTPGDAPPAVVALEGGSGES AQPPEDSSPPASSESSSTRDSAVAISGADSRGILEEPLPSTSSSEED PLAGISLPEGVDPSFLAALPDDIRREVLQNLGIRPPTRTAPSTNSS APAVVGNPGVTEVSPEFLAALPPAIQEEVLAQQRAEQQRRELAQNAS SDTPMDPVTFIQTLPSDLRRSVLEDMEDSVLAVMPPDIAAEAQALRR EQEARQRQLMHERLFGHSSTSALSAILRSPAFTSRLSGNRGVQYTRL AVQRRGGTFQMGSSSHNRPSGSNVDTLRLRGRLLLDHEALSCLLVL LFVDEPKLNTSRLHRVLRNLCYHAQTRHWVIRSLLSILQRSSESELC IETPKLTTSEEKGKSSKSCGSSSHENRPLDLLHKMESKSSNQLSW/ LSSVSM DAALGCR TNIFQIQRS GGRKHTEK HASGGSTVHIHPQAAPV VCRHVLDTLIQLAKVFP SHFTQ QRTKETNCESDRERGNKACSPCSSQ SSSSGICTDFWDL LVKLDNMNVS RKGN SVKSPVSAGGEGETSPYS LEASPLGQLMNM LSHPVIRRSSLLTEKLLRLLSLISIALPENKVSEA QANS GSGASSTTTATSTTTSTTTTAASTTPTPPVHPPRVTSAPA\ L VAATAISTIVVAASTTVTTPTTATTTVSISP TTGSKSPAKVSDGGS SSTDFKM\VSSGLTENQLQLSVEVLTSHSCSEEGLEDAANVLLQLSR GDSGTRD'TVLKLLNGARHLGYTLCKQIGTLLAELREYNLEQQRRAC CETLSPDGLPEEQPQTTKLKGKMQSRFDMAENVAIVASQKRPLGGRE LQLPSMSMLTSKTSTQKFFLRVLQV I IQLRDDTRANKKAKQTGR LG SSGLGSASSIQAAVRQLEAEADAI IQMVREGQARRQQQAATSESSQ SEASVRREESPMDDVDQPSPSAQDTQSIASDGT PQGEKEKEERPPPELP LLSEQLSLDELWMLGECLKELEESH DQHAVLVLQPAVEAFFLVHAT ERESKPPVRDTR ESQLAHIKDEPPPLSPAPLTPATP\SSFDQFFSGE

				PSSMHISSSLPPDTQKFLRFAETHRTVLNQILRQSTTHLADGPPFAVL VDYIRVLDFDVKRKYFRQELERLDEGLRKEDMAVHVRRDHVFEDSYR ELHRKSPEEMKNRLYIVFEGEEGQDA\GGLLREWYMIISREMFNP\M YALFRTSPG*SESPNTINPS\SH\CNPNHLS\YFKFVGRIV\AKAVY DNRL\ECYFTRSFYKH\ILGKSVRYTDMESDYHFYQGLVYLLEND VSTLGYDLTFST\EVQEFQ\VEVSWTSNPMGANIL\VTTEEIKEGVL LHLV\COMR\MTGAF\RKQLPAFL\EGFYEIIP\KRLISIF\TEHEL ELLISGLPTIDIDDLNPNTEYHKEYSINSI\QIQWF\WKKHCRSFRIK TDPCKFPFSLFTGYLPRVTPGKGFACPSKGMWGFQEVFRFPSEVD RS\TDR\LPSAHTCFNQDLDPAYESFEKLRHMLLLAIQECSEGFGLA
1347	A	1	746	MAAAGAFRLRRAASALLRSRPLPARSCRPRPDSITRSPDPVRLPLE KQLKNAINQRGTGKPYIRYYPEVVDHYENPRNVGSLDKTSKNVGT\G LVGAPACGDVMKLQI\QVG*KRGRFVGC*GFKTFSAVGSAI\ASSSL SHLNGVKGKT\VEEALTIKNTD\IA\KELCLSF PWKLALAPMLGLKV AFKAALADYKIEIETRTQKKGEAEKKWSPPLGEASSRPTPAVPQPAVPV TLDVSGSRLPSPTGAL
1348	A	2	832	SARGSTVAIIICSPRLTPPRTRDAKAACERLRRVGVEPQLSRGLALF WSPRPNPPEEMSGGLAPSKSTVYVSNLPFSLTNNDLYPDIFQSIGKS L*KVTNQ*KSKRY\HRKEVKGVAFILFLDKDSAQK\CARA\INNQL FGRVIKASIA\IDNGRAAEFIRRRNYFDKSK\CYECG\ESGHL\SYA CPKNMLGEQ*/RLPKKKEKKKKKKAPEEEEEIEVEESEDGEDPAL DSLSQAI AFQQAIEEEQKKWETQFQGVPSNIRMI PRRTRIKKSTYF Q
1349	B	165	520	XNLKLLDNWDSVTSTFSKLEQLGPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLL PVLESFKVSFLSALEEYTKKLNTQ*
1350	A	3	560	RSPTALQDESCGADLGRALPDGLKLLDNWDSVTSTFSKLEQLGPVT QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELY RQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTH LAPYSDEL RQRLAARLEALKENGARLA EYHAKATEHLSTLSEK
1351	A	3	118	KAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ
1352	B	28	384	MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLEQLGPVTQEFWDNLEKETEGLRQEMSKDLEEV KAKVQPYLDDFQKKWQEEMELYRQK*
1353	A	2	1093	GGASCLPRSLWLPSSRFRPCPRPGLWVPEVFSRVPFSSPGCNEWG STGLLHAEGLPLSQALLLLQVPHGPFMRKAAVLTAVLFSQG*ARRR HFWQGG*SPPRAAWDRV\K\DLATRVPTVLKEQRTETYVSQFEG\S ALGK\QLNLKAPLTGDSVDLPPFS\KLEQF\GPC*PRDFLGINLG KRETEGP*GKGR*GKDLWKEVKAKVAALTDDFQERSWQEEIGAFTR QKV\EPLARKNFQEG\ARPESLHELARRSLSPLEEMRDRARA\HVD ALRT\HLAPYSDEL RQRLGAR\LGALRENGGARMGQYHA\QATEHLS TLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ
1354	A	119	301	INDKRRKKRPARPGAGGLHLQLCLSQPPQPRGHAPAPIPTQGAGPRDS GPGASP*/GRDPPSD*WTPADLGSDPWAGPLPTPQEP*GSRWPSSAT VSLASASTATGTPCTYSHGTGWTQRLWTRGLPLSRDPPSD
1355	A	1451	2495	RGLAGNFEDRKS AHYVFQTFRGGERRSLELEAHLEGSWGLGLRFLG LKGPPA\QGHFHPSLP ISSWRGAGVPHSR/SPFPTLGIPG*IFPPKP GRRPRGP RKEDLGPGMVG/RPSGPLPQLPSAVLSADPAGPRPHVFP CEP/SPSHGVRASPGSKWVEEIEGGEGRQ/PKCRQAFQEAWLMOG/ GARGQGLPGS/GCWRINKPSKPSKRGKGLTCQTFSTNIC*SPPLMP RSLP/GPSFILHLISSQQP*SGLLFIDPIPEKGRGGLSERWGRAFG DSVACSFQKPTPGPWEVFEQDAWPNPWP/QGPPPENFPKGNPSSRN IHKGDEQSPVTRKTEPTPWGGKHSQFASR
1356	A	2024	2160	KCLCPPR/RCPQPLTPYPC*GVKCPPSEIKYKP*MCPIGCPKPSIQ
1357	A	15717	16041	KNYNYLSHISNSTGFFPIFLSYFRKTRIQLNRIFPLSEDYSGSGF GSGSGSGSGSGSGFLTEMEQDYQLVDES DAFHDNLRSLDRNLPSDSQ

				DLGQHGLEEDFML
1358	A	41	544	TKLVMQKLLKCSRLVLALALILVLESSVQGYF\TRKPRHQWVRCNP DSSSAHCLEEKGHMFELLPGESNKIPRL\RTDLFPKTRIQ\DLN\RI FPLSEYSGSGFGSGSGSG\SGS\GSWFLTGNNGNRNYQL\UDE\SDA FQ*PQLGSLDRNLP\SDSQDLGQHGLEEDSMV
1359	A	60	403	FLLGLVLSISGSRIQEDGRGRGCPQSLHLEETPEGRQPEGRSHPRLL PAPRPAHAHAHRESAGCAGGHGKWGGAHTAGGKEVSGGERRKRDDQ RRGGTRSEVLLVSEDGKILA
1360	A	59	420	QQHGRDLWGCRGLIGTDKCVERINEMVNRKRKAGVDPLVPLR/MLG GVVLISGTGSNCRLINPDGSESGCGGWGHMMGDEGSAYWIAHQAVKI VFDSIDNLEAAPHDIGYVKQAMFHYFQV
1361	A	80	384	KEHNFVTSVFARGTMGSLTHLLGNSLTEKCKLPSPWLPITAEGNSLK GFL/LALTQCKEIQANFFSSFILMKLRHSSALGGASLLPMDYSANA IAFYSYTF
1362	A	3	124	FPVRRFRLEGRRCQAVRDANGGTISDGSSSMAAIYGGVEG
1363	A	189	242	LCYATACPQSSWELWPR
1364	A	420	557	ICGKQQLYADRSAAWHSNGNSGLAGCGGTARARLLGPLLPRDAG
1365	A	284	362	RGFQQTGGGTARARLLGPLLPRDAG
1366	A	2087	2226	DQEPNTSGHTYTLGTGRSGFACRCLEPGSAAPCPSHCRSAGPEGTL
1367	A	1	2956	MNTSQLLEIANQVFNRAAVSLEENRKENGHQARRNTDLVVSCSNQR GQESLEKLLGRYFYISHLSALAKTMRQRFVTCRHHNARQGPVPPGI QAYAAPIEDLQAIRNNITAGVYTPCDIGGNIILCPLAYYQRYQTGV VYTPCDIGSIIILSTSGCPSHTEPRNLGTGVSEFLLGLSDELPQPV LPGLSLSMYLLTVLRNLLIILAVSSDSHLHTPMYFFLSNPSWADIAF TSATVPKMIVDMQSGVVVSVMYTVVTPMLNPFYICLRNRDIQSALWR LRSRTVESHDLFHPFSCVGIHCQVSELDVMSLDTASGAFRWMAFGV EVAAPAYQPSQSCPGSQSSGEGARKGWSSRSLSETVSAVYSGLTQER RCQPQSPTSTVGSIIIMGNSNMANTSPSVKSKEDQGLSGHDEKENPFA EYMWMEEDFNQVEEELQEQDFLDRCFQEMLDEEDQDWFIPSRDL PQAMQQLQQQLNGLSVSEGHDSIEDILVHGRRSLSPQLRGLAEHASQ PTRPRAVTRNLTRDCQQLPGVYRQAGSRRTGGAAADRSRSTWRRHQ KEDSLRDAAIPGSYRRPAPRMRTRTGSQLAAREVTGSGAVPRQLEGR RCQAGRDANGGTSSDGSSSMAAIYGGVEG\GTRSEVLLVSEDGKIL AEADGLSTIHWLIGTDKCVERINEMVNRKRKAGVDPLVPLRSLGLS LSGGDQEDAGRILIEELRDRFPYLSSEYLITDDAAGSIATATPDGGV VLISGTGSNCGLINPDGSESGCGGWGHMMGDEGSAYWIAHQAVKIVF DSIDNLEAAPH\DIGYVKQAMF\HYFQVDPRLGLTHLYKOL**NAR FAGF/CARKIAEGAQQG\DPLSRYIFQGRLGRCWGRHIV\AVLPEID PGLIPQK\IGLPILS\VGSVW\KSWELLKEGFLAL\QGREI\QA QNF\FSKLSPLMKA*GNSSALGGA/SALGARHIGHLPMMDYSANA\I AFYSYTF
1368	A	149	1323	PRNEPNSPERRPPLAMDAGVTESGLNVTLTIRLLMHGKEVGSIIIGKK GESVKRIREE\SGARINISEGNCPERIITLTGPTNAIFKAFAMIDK LEER/DINSSMTNSTAASRPPVTLRLVVPATQCGSLIGKGGCKIKEI RESTGAQVQWGRGICLPNSTE\RAITIA\GVPKS\VTECVQADFAWV MLETL/SPSFPQGRSSWTI\P\YQMPASFPSSSCAGGQD\RCSDVG G\YPHGHP*PGKGPLLDGLDFDKGQHTISPLDLGQA*TRIGKPTSLN VHMMHGGT\GF\AGIDSASPE\VKGYWAKFECIYKTPHELT\PNN LI\GCIIGRQADSDLMRSAQMSGAQDQKLA\NPVE\GSSGR\QVTI\ TGLCCPVISLAQYLINA\RLSSEKGMGCS
1369	A	2	125	VILKELCGNLCFLCGFNERNLMSRVDVYTTTHSPCSFSPK
1370	A	18	1374	LAEQIVPRGVGIRPPDKADQAPCRSPIRTPAPESWHCDNRQRFRQDS SRMKMRVLGLVVCLVLVTLHSEGGKLTAVDPETNMNVSEIISYW FPSEEYLVETEDGYILCLNRIIPHGRKNHS\DKGPKPVVF\LQHGLLA DSSNWVT\NLGNSRLGFILADAAIDVWGMNTRGNTWSPKHKTLSVSQ DEFWAFSYDEMAKYDLPASINFL\LNKTG\QEQQVYVGHSSQTTIGF

				IA\FSQMLELAKGLKMFFAWGPVASVAFCTSPMAKLGRLPDHLIKDL F\GDEEFLPQSAFWKVAGVPHLATHVIL\KELCGNLCFLLCGFNERN LNMSRVDVYTTHTSPAGTFVQNM*HWSQAVKFQKFAFDWGSSAKNYF HYNQSYPPTYNVKMDLVPTAV*\TGGHDWLEDVYGVNI*LTQIT\NL VFHESIPEWEHLDFIWGLDAPWRLYNKIINLMRKYQ
1371	B	77	471	ANREKMTQIMFETFNVPAMRACPSTPPEDHRHRAGLRRRVTHNVPIY EGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIK EKLCYVALDFENEMATAPPPPPWKRATSCQTGX*
1372	B	101	391	MCDEDETTALVCDNGSGLVKAGFAGDDAPRAVVPSIVGRPRHQGMV GMGQKDSYVGDEAQSQRGILTLYLIEHGIITNWDMEKNGPHLLHE LRV*
1373	A	92	1323	LPAQKLDTCDEDETTALVCDNGSGLVKAGFAGDDAPRAVFPSPVGR PRHQGMVGMGQKDSYVGDEAQSQRGILT\LYKYP\IEHGIITN\WDD MEKI\WHHTF/YTNELRVGFPKEDP/TTLA*PKAPLKFPKANREE/M NEPQIMFETFNVPA\MYVAIQAV/LCSLYASGR\TGIVLDSGDGVT HNVPIYEGYA\LPHAIHAPWTMAGRDLTDY\LMKILT\ERGYSFVT TAER\EIVRD\IKEKLCY\VALDFENEMATAAIHPSS\LEKSYELPD G\QVITIGNE\RFRCPET\LFQPSF/LSGMEVGGAFHETT\YNSIMK CYIRHPGRTFYANNV\LSGGT\TIVPLGFAD\RMQERDSPALAPQHP *GSRHSPPPERK\YSVW\IGGFHPWRLSTSQQKW/VSPKQY\DE AGP\SIVHR\KCF
1374	B	53	302	MTSALTQGLERIPDQLGYLVLSEAGLASSGDLENDEHAASAMSELV STACGLRLHRGMNVHFKRLSVVFGHEHTLLETRVLTEX*
1375	B	277	573	TSALTQGLERIPDQLGYLSSGDLENDEQAASAISELVSTACGFRHR GMNVFPKRLSVVFGHEHTLLVTVSGQRFV*
1376	A	209	413	EAGRREAEPKLGSSPPLPVPPPRAGAGAHQTGA*RAHSMPCRSRKPO AVLTSSSEMALAACSSFSRSPDDASTAPSLSTR*PSTTTKGRGRGSPD RRLKGTFFNAAVQPETAGCADQLRDGTGCLLIILQVPR
1377	A	116	1253	NPGPVQVGVEGGQEEGPSSKKQAKTRQWSPASITEAPGPKIRFSEPL RPPAGCRHQLASRPRVLP/PSPQTPFCPG/PPSPSSVCSPKDHWRD TPDRRLKGTFFMPCRSRKTAGCAEQQRWHWLPAAHSPGPQMTPALHL HSVPGSRAGLGFAPAGSAQKSSG*RCKS*EAC*RDGRPDTLHLQTQ VSGLT\WPQVFSFPSQVPSRPPPPYMLNTDLPEPPSAPTAPRLPW PSTSHLCYPKGPVLPWPLPSDP\SSPPFVSARPA/ALPAAPEHPPT DPSPAFSSPSLPFPSPPLPRADRR*GWSAGPPGG/EPHRLGSRDAEP PAGPLAHASSLTIAVFGAGGAPYQIGSFRLQAPVTCLOPLRSSFCLR HWPLAPPLA
1378	A	24	364	PTEY/ENL/FPCIKEAF/VVEEWVKETLAVL/WPAKQYPFVTPIEER ILMEEGKAFFPSRSTAKQKLDGNPVSPTPV\IGLSPTPNKEEKHLNL CPFEPTGHLDGARDTAGPSWLHHRF
1379	A	24	2858	VAGNKRGFPGLDLRRMTPLRLDIKRLTARS DRVKSVDLHPTWPMLA SLYNGSVCVWNHETQTLVKTFEVCDLPVRAAKFVARKNWVVTGADD QIRVFNNTLERVHMFEAHSDYIRCIHVHPTQPFILTSSDDMLIKLW DWDKKWSCSQVFEGHVMQIVINPKDNNQFASASLDRTIKVVQLG SSSPNFTLEGHEKGVNCIDYSSGGDKPYLISGADRLVKIWDYQNK CVQTLEGHAQNVSCASFHELPIIITGSEDGTVRIWHSSTYRLESTL NYGMERVWCVASLRGSNNVALGYDEGSIIVKLGREEPAMSMDANGKI IWAKHSEVQQANLKAMGDAEIKDGERLPLAVKDMGSCIEYPQTIQHN PNGRFVVVCGDGEYIIYTAMALRNKSFSGAQEFWAHDSSEYAIRES NSIVKIFKNFKEKKSFKPDFGAESIYGGFLLGVRVSNGLAFYDWDNT ELIRRIEIQPKHIFWSDSGELVCIATEESFFILKYLSKVLAAQETH EGVTEDGIEDAFEVLGEIQEIVKTGLWVGDCFIYTSVNLNYYVGG EIVTIAHLDRMTMYLLGYIPKDNRLYLGDKELNIIISYLLVSVLEYQT AVMRRDFSMADKVLPTIPKEQRTVAHFLEKQGFQKQALTVSTDPEH RFELALQLGELKIAYQLAVEAESEQKWKQLAELAISKQFGLAQECL HHAQDYGG\LLFGHCPLKMPIMVNQPSQVRVRDRDQK*LAF\MASF

				LPG\RVVACLRL*IR\TGRL\PEAAFLARTYLP\SOVSR\VVKLWRE NLSKVNQKAAESLAAPNRVSKHLFPICIKRRPFLKNVVKETHVD\LG PAKTIPTLSRPNE\ERNAHGSGQKTFSPSRSTASTGTLMGNPAFSLP PVIVALPTTANQEKRVYPE\LEVOLD\NLE\LEDIATT\DIINDED YFGGLTGMAPHLP
1380	C	110	508	MLLICSFAPATLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XX XXVSA
1381	A	93	180	KKTCSLNCFAMLLICSFAPATLPQPL
1382	C	128	382	MYLGISRRLSSMLTFLAYLHPRERPPHRAPXXXXXXXXXXXXXXXXXX XX
1383	A	3	140	KSGRLAHPGIVPSLELNYDIDYFAHMFDDFLIITLLSYYISFC
1384	A	1	609	MASWDEKDLTVPQPDTRKGSVLSYLHPLIDLVTQGLDTSIHTEDSQ MGIFSSSELSPHFRFAYPAVFSASPLGVYLLGGVEGEAPVGTGANGSS GWAWSQWARTQRLAVPQAPGSRAPDLQAMPEPPHAPSSPIWAPAQG SLPDKCRPLLHGAQSHHHLRAEERLRLALDWQAAPPVALVRYPLGEA SWAPESDGDLENLYV
1385	B	1	690	MASWDEKDLTVPQPDTRKGSVLRCLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAMVPGRSESWERGEPRPALYFCGSIRGGREDRTLY ERIVSRLRRFGTVLTEHVAAAELGARGEAAAGDRQLIHEQDLEWLQ ADVVAEVTQPSLGVGYELGRAVAFNKRILCFRPSGRVLSAMIRG AADGSRFQVWDYEEGEVEALLDRYFEADPPGQVAASPDPTT*
1386	B	1	975	MSPPGREQGLLLNLLRPSGLDNAGKTTILKKFNGEDIDTISPTLGFN IKTLEHRGFKLNIWDVGGQKSLRSYWRNYFESTDGLIWWVDSADRQR MQDCQRELQSLLEVVEVGSSYPLCTWRFFSYLRIEQMYNLVLYRDIQF PDFCFNSNTDWSKGLKTHARFGNTSLHVAHTDSTNTTNFVDVWRGRT KSLACLLQLSSLTCIYTAGKMLQDRIATFFFPKGMMLTTAALMLFF LHLGIFIRDVHNFHCITYHYDHMSFHYTVVLMFSQVISICWAAMGSLY AEMTENKYVCFSAITILMLNGAMFFNRLSLEFLAIEYREEHH*
1387	A	25	353	EVCYYSSEAFFSELIKVILRHLCSVAGKGLCSIPQLNTRREGSVLRR ISKRGSPLAIVEIEGHCL\CLPLGTECLGIKP\IVHLLNSEIGEKKP FSPLSPCSSAAFLLLR
1388	A	79	467	RPESQRANGVDSGPNLKTVPQPDTRKGSVLKWISKRGKPLAVEIEES HCL\CLPLRTECLGIKP\IVHLFSCTRPVIVPSLELHYDIDSIAHMF VADLLLIITLLSYYIPFYLGFQNGITGINHRAWFY
1389	A	368	611	LCPSHFAPTTLTQSGSSLKTCVVLNSRFKACRAVPGPCLVNQMFASS ILG\KSHHSLVPINQGHNALWKAAG\PLPLKAGY
1390	A	441	1178	FVALPQPLCPSHFDPTTLIQSGAHKNMCCIKSRFKRDLGLCRTCLVN KMFTSSILGKSHCHSLVSINQGHNAWKAAG\PLPFRAGYC\QGFS CDSLKYG\SWDEKDLTVPQPDTRKGSVLRWISQRGKPLAVEMEEGHC L\CLPLGTECLGIK/PIVHLFNSEIGE\NRP\MVGG\RHLVQ*CCL G*FL*PLRCLG\GEKHKSG/LHVHPIVIVLS\LELNYDIDSFAHMF F/SVDLLLIITLLSYYIPFC
1391	A	3	1079	TRAAGLRAGVRVPRSPGPSRRMPARSGAQFCRRMGQKKQPARAGQP HSSSDAAQ\APAEQPHSSS\NPAQAPCPRECL\GPPTTPGPYR\SI YFSSPKGHLTRLGV\EFFDQPAVPLARAFLGQVLVRRLPN\GTELRG PHRWETE/YTLPED\EAAPLQGGWPGKTPR\NRGMFH*KPGD/LW VVYIIYGMYFCMNISSQGDGA\CVFL\RALEAPGKSWRPMQLRS\T LR\KGTRQARVLKGPPLKCSGP\SKL\CQA\LPINKSF*PEGTLAQD EAVWLERGPLEPSEPAVVG/APRVGVGHAGEWARK\PLRFYV\RGS PWASVVDRAEQDTQACAKGLPRQDFLHCLKTRINVLFLEKKKKK
1392	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAELERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKQVADALTNAVAHVDDMPNALSALSDL HAHKLVRDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
1393	A	26	493	NSTDSETHPWLLSPARQRPSTRPAWGKVGAAVRSMAEALERMFL

				SFPT\TKTYFPFHDL\SHGFCPG*RATGKKVDDSDAQTPWPTWDDMP KRRCP*SDLHAKLS/RLDPV\NFKAPKATCLAG*PLAAHLP\AEF QPLAVARLPWGQISWGFC
1394	A	1	409	PGNPVYLKTLHLPQAPPYTDAPPAYSELYRPSFVHPGAATVPTMSAA FPGASLYLPMAQSVAVGPLGSTIPMAYYPVGPIYPPGSTVLVEGGYD AGARFGAGATAGNIPVKEDQDHDREQQEEDNGDNNLERRGKM
1395	A	9	817	HGSSSEQEEDKNNQSATPIHSGPATTMNSIG*YPTQP\TYPVQSPG NPVYPQT\NLN\QAPPYT\DAAPPAYSELYRPSFVHPGAATVPTMSA AFPG\ASLYLPMAQ\SVAVGPL\GSTIP\MAYYPVGPI\YPTLAPQV LGGKGGYDAG\ARF\GAGA\NGGNI\PSPP\PG\CPP\NAAQLAVMQ GANVLVTQ\RKGNFFMGSGDGGYTHLVRNQGHLCAREKTSHTLQHFS QCNCFSHINLKLQFRHMLLGCLSGAQTFRHFSNLIRNHVMVAVPP
1396	A	1	367	GTRSYVDNLMCDGCCQEAGIGGYCDAKYVWAATAGGVFQSITPIEID MIVGKDREGFFTNGLTLGAKKCSVIRDSLYVDGDCTMDIRTKSQALV IVMGKEGVHGGTTLNKKAYELALYLRRSD
1397	A	625	2919	NAKGSKMAGWQSYVDNLMCDGCCQEAAIVGYCDAKYVWAATAGGVFQ SITPIEIDMIVGKDREGFFTNGLTLGAKKCSVIRDSLYVDGDCTMDI RTKSQGGEPTYNVAVGRAGRGDACHHPMEDLMDMDMSPLRPQNYLFS CQQKADKDYHFKVNNDENEHQSLRTVISGTGAKDKLHIVTEAMNY EGSPIKVTLATLKMSVQPMVSGGLEITPLVILRLKCASEPVHISGQH LVAVEEDAEEDEEBEYVKLFIWKAICPRRWQKSSTEEKKEEEKSKS LENIFALIIDENFLGFVRDLDIQIQEAQRTPGKFITKRTPSRHIIIR LLKVTKTERILRVVRQKHQLNAVRQEVKSLCGLEASHVPABEALSGA GEPYDIIDSSDEMDAQEENIHERTVSRKKSKRHKELDGAGGEEYP MDIWLLLASYPEDIVNFSLICKNAWTVTCTAAFWTRLRYRRHYTLD ASLPLRLRPESMEKHLCLRACVIRSLYHMYEPFAARISKNPAPIEST PSTLKNKSKCLLFWCRKIVGNRQEPMWEFNFKFQKQSPRLKSKCTGGL QPPVQYEDVHTNPDQDCCLLQVTTLNFIPIPIVMGMIFTLFTINVST DMRHHVRVLFQDSPVHGGRKLRLSEQGVQVILDPVHVSRLFDQAPC MKSNNALIVILGTVTLDVAVGIGLVMPVLPGLLRDVIHSDSIASHYGV LLALYALMQFLCAPVLGALSDFRGRPVLLASLLGATIDYAIMATTP VLWIYPLVNSPSC
1398	A	2	76	HHYAKLGTRAVRRARRCAGWQSYVDNLMCDGCCQEAAIAGYCDAKYV WAATAGGV\FQSITPIEIDMIVGKD\RKGFF\TSGLTGAG\KKCSVI RDSLYV\DGDCCTMDIRDKQS/QGGEPT\YNVA\VGRSG\RALVI\VM GKGKVFHRRHTLTRKAYETPLYT*RQAWHEGSAKGSKMCRLAELRG
1399	A	149	421	SLALSFPFLEEEAEGDLEIKVEVRRLLFPSTFLVSLLLHGAVERNGLV FCYSLGDALDSSNSMQTIQKTTTRRIVDGKVSETNDTKVLRH
1400	A	1	1107	MGHRRQSLSPVLSLSPDSMSFTTRSTFSTNYQSLGVSQAPSYGAR PVSSAASVYAGAGGSGSRISVSRSTSFRGGMGPGLAAGMAGGLAGM GGIQNKKTMQSLNDRLASYLDRVRSLETENRRLESKIREHLENKGPQ VKDWSHYCKTIEDLRAQIFANTVDNACIVLHIDNARLAADDFRVKYE TQLAMRQSVENDIHGLRKLETEIEALREELLFMKNHEEEVKGLQAQI ASFRLTVEVDAPKSQDLAKIMADIRAKYDELAGKNREELDKYWPQQF EENTTVVTTQSAEVGAEMTLTELRRTVQSLEIDLDSMRNLKASLEN NPREVEARYSLQMVLIGILLHLESELAQTRAERQQAQAE
1401	A	25	1486	GPQQPHSRSTHASGRPQSLSPVLSLSPDSMSFTTRSTFSTNYRSLGS VQAPSYGARPVSSAASVYAGAGGSGSRISASRSTSFRGGMGSGGLAT GV\AGG\LAGMGGIQNEKETMQSLNDRLASYLDRVRSLETENRRLE SKIRE\HLEKKGPP\VRDWSHYFKI\IEDL\RAQIF\ANTCGTMPRI RSARIDNA\RLA\ADD\RVKYEDRSWPMCPVLWRDIIHGLPKVH/I DDTNYHTDLQLETEI\EALK\EELLFQ*RRNHEEGS*KALRRQI\SS SGMNAWRLD\APKSQDLAK\IMADIR\AQ\YDELGSKKNPRGSLDKY \WSQOI\EESTTGGSPQKSAEVG\AVETHAHRSLKRTVPVLGRSTLD SM\RNKGLWRTSLREG*RPAYALTRLEPAPTGSLL\HLESEL\AQ TRARGTAARPREYEALLN\IK\VKLEABIAT\YRRL\LEDGEDFNLG

				DALDSSNSMQTIQKTTTRRIVDGKVVSETNDTKVLRH
1402	A	36	389	PALQEFGTSRNEPDVYETSDLPEDDQAEFDAEELTSTSVEHIIIVNPN AAYDKFKDKRVGKTGLDFSDRIGKTKRTGYESGEYEMLGEGLVKET PQQKYQRLLEHVQELTVILYNCF
1403	A	204	433	QHKCGTIIIVTIKQLHEQAMQFGQLLTHLDTTQQMANSCLKDNTLLT QVQTTMRENLATVEGNFASIDERMKKLGK
1404	A	3	392	GNFARNEPDVYETSDLPEDDQAEFDAEELTSTSVEHIIIVNPNAAAYDK FKDKRVGKTGLDFSDRIGKTKRTGYESGEYEMLGEGLVKETPQQKY QRLLEHVQELTTHVQYCFAWCGEGLGLVPQHSFCG
1405	A	1	1314	MADPKYADLPGIPILRPRAPAARSPIGLSTPRTLTLRLGRAAGRHOA PFPVAVARPRNRLRARNNEPDVYETSDLPEDDQAEFDAEELTSTSVE HIIIVNPNAAAYDKFKDKRVGKTGLDFSDRIGKTKRTGYESGEYEMLGE GLGVKETPQQKYQRLLEHVQELTTEVEKIKTTVKESATEEKLTPVLL AKQLAALKQQLVASHLEKLLGPDAAINLTDPDGALAKRLLQLLEATK NSKGGSGGKTTGTPDSSSLVTYELHSRPEQDKFSQAAKVAELEKRLT ELETAVRCDQDAQETVELLQAKVSALDLAVLDQVEARLQSVLGKVN IAKHKASVEDADTQSKVHQLYETIQRWSPIASLTPELVQRLVTIKQL HEQAMQFGQLLTHLDTTQQMANSCLKDNTLLTQVQTTMRENLATVE GNFASIDERMKKLGK
1406	A	2	279	FVFPLPEHRPRLFRCPGPPARLAAAMADPKYADLPGIARNEPGVYET SDLPEDDQAEFDAFAQVRPFNASSLHVFFICHLACNALPLCYCCS
1407	A	3	1462	TSCSSAAPFAAALARDPNPASPLPEHRPRLHRGPGPPARLAAAMADP KYADLTGIARNPDVYETSDLPEDDHAEFDAFAQLEELTSTSV\EH I\IVNPNAAAY\DKFKDKRVGDKGI*FSQIVLGKTKRTGYESGEYEML GEGLVKETPQQKYQRLLEHVQELTTEVEKIKTTVKE\SAAEKLT VLLAKQ\LAALKQ\VVASHL\EGKLLGPDAAINL\TDPDGRPGLR RLLQ\LEATKNSLGGSRGKTPGTPPD\SSSLVTYELHSR\PEQDKFS SSLPKSQLLEKRL\TEL\ETAVTLTIQDAQNPLSAGLQACLMETVE LLQAKVSALDLAVL\QV\EARL\QSVLGK\VNEI\AKH*SLC*EGA GYTKARLHQLIIETITALGAPLPSTLPGAGCRRLVTHQSSSHEASPC QFGQLLDT/HLDTTQPM\IANPLGRTNTNPL*PQVADKPLRENLAHQ LKGNFAQQ*RNK*KKLGKSEAHLGKLEEPGG
1408	A	1	4629	MAPPLAAGPSPPLHPSAAGLEAGRLCKRVLGPCGDGEATPRPLNRIP PRVTDVQLCCVQETDIHSFSQSVNQCFLTPEHMADSSPLVGSTPTGY GTLTIGTSIDPLSSSVSSVRLSGYCGSPWRVIGYHVVMAGIPLL LFRWKPLWGVRLRLRPCNLAAHAETLVIEIRDKEDSSQLFTVQVQTB AIGEGSLESPQSQAEDGRSQAAGVAVPEGAWKDTAQLHKSEAKRV LRYLFFQGRYIWIETQQAQFYQVSLDHGRSCDDVHRSRHGLSLQDQ MVRKAIYGNVISIPVKSYPQLLVDEALNPYYGFQAFSIALWLADHY YWYALCIFLISSISICLSLYKTRKQSQTLRDMVKLSMRVCVCPRGGE EEWVDSSELVPGDCLVLPQEGGLMPCDAALVAGECMVNESLGTESI PVLKTALPEGLGPYCAETHRRHTLFCGTLILQARAYVGPVHLAVVTR TGFC TAKGLVSSILHPRPINFKFYKHSKMFVAALSVLALLGTIYSI FILYRNRVPLNEIVIRALDLVTVVVPPALPAAMTVCTLYAQSLRRQ GIFCIHPLRINLGGKLQLVCFDKTGTLTEDGLDVMGVVPLKGQAFPL LVPEPRRLPVGPLLRLALATCHALSRLQDTPVGDPMDLKMVESTGWVL EEPAADS AFGTQVLAVMRPPLWEPQLQAMEEPPVPVSVLHRRFPSS ALQMSVVVAWPGATQPEAYVKGSPELVAGLCNPETVPTDFAQMLQS YTAAGYRVVALASKPLPTVPSLEAAQQLTRDTVEGDLSSLGLLVMRN LLKPQTTPVIQALRRTRIRAVMVTGDNLQTAVTVARGCGMVAPQEH IIVHATHPERGQPASLEFLPMESPTAVNGVKDPDQAASYTEPDPRS RHLALSGPTFGIIVKHFPKLLPKVLVQGTVFARMAPEQKTELVCLO KLQYCVGMCGDGANDCGALKAADVGISLSQAEASVVSPTSSMASIE CVPVIREGRCSLDTSFSVFKYMALYSLTQFISVLILYTINTNLGDL QFLAIDLVIITTVAVLMSRTGPALVLRVPPGALLSVPLVSSLLQ MVLVTGVQLGGYFLTLAQPFVPLNRTVAAPDNLNPNYENTTVFSLSS

				FQYLILAAVSKGAPFRRPLYTNVPFLVALALLSSVLVGLVLPGLL QGFLALRNITDTGFKLLLLGLVTLNFGAFMLESVLDQCLPACLRRL RPKRASKRKFQLERELAEQWPPLPAGPLRKKGKEPLVVEASHGPE LSSVGEAGLREAAGLAGEAEGKPRQESVLEAGRRQREIEAYFLAE GPRDAGESGVGEAAVEEARAVLSDTTPACLFVAMRAAYLFLFLPA GLLAQQQYDLDPLPPFDHVQYTHYSQIDNPDYDYQEVTPRPSEE QFQFSQQVQQEVIPAPTPEPGNAELEPTTEPGPLDCREEQYPCTRL YSIHRPCKQCLNEVCFYSLRRVYVINKEICVRTVCAHEELLRVAPP PYPPAPALPCPERCVMTVYARMRVVGIAREMEGFRDTAF
1409	A	96	721	PGQLSSLTPPRPASLLPWRAAYLFL\LFPLAGLLAQGYDLDPLPPF PDHGQYTHYMDQIDNPDYDYQEGTPR\PSEGQFQ\F\QSQQEVQQG VIPSPNPRAQGNAEL\EPTEPGPLDCREEQYPC\TRL\YSIHRPCK\ QCLNEVCFYSLRRVYVINKEICV\RTVC\AHE\ELLRA\DLCSGTSP SKCGR*WASSGL\CQSV\AASCA\RSCGSF
1410	A	118	256	MFCFFLKPIAEAPFKFDMELDDLPEK\LKELIFEETARFQPGYRS
1411	A	457	839	AVGGFWGCPRVELHMLVHITPLSHFKCGCFSNHVPCLRI*QRGTLR *MRKYTILFPSTACQHLKFIFQPTV*QFVIKPPGAHDVKHCSVLKYS NISDTAESDCQKKLSTNSCLELYPYFTDLFKYL
1412	A	310	1784	RRRPRQPTMAAAVVGGRGPEVWSAGTLFDVGPRTNLSYIRGRIT CVCSAYDNVNVKRV\AIKKISPFH\QTYCQRTLREIK\ILLRFRHE NI\IGINDII\RAPT\IEQMKGCI**YRDLMETDLYKLLKTQHL\SN D\HIWYFLYQILRGLKYIHS\NVLHR\DLKP\SNLLNT\TCDLKI CDFGL\ARVADPDHDTGFLTEYVATRW\YRAPEIML\NSKGYSKI \DIWSVGCIL\AEMLS*QGPFQGXHYL\DLQ\NHI FGVFLGSPSQB \DLNCIIKF*KLGNLYLLSSHTSKIMVPLEHACPNADSKSSGTLGQ NCLTFNP\HKRIEVEQALA/HTPYLEQY\DPSD\EPFAEAPIQVRP WKLDDLPEKELKGTNFKRLARF\QPGVQILNFVQTKGSEGLDVLHR RCSSSQFLTTPGPVFQPCGLSTLTPLNPFGRGRFLGSCGFYGFYSKIS FSPGGFLLGQPCCVHPLVTLRAVCTSVHLTAYCCFSH
1413	A	2	294	GNKMAAPKGS LWVRTQLGLPPLLLLTMALAGGSG\TASAEAFDSVLG DTASCHRACQLTYPLHTYPKVGPVRSGLRPFPCSPFLGSPHVCRLWQ PGC
1414	A	366	1412	QRGTRWRRERGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVL GDTASCHRACQLTYPLHTYPKKEELYACQRCRLFSICQFVDD\GI DLTRTKLECESACTE\AYSQSDQYALPFLGCNQSACHFAE\LRQEQ LYVPRWPKMAPTFFL*LLGEGSFWEFT*WDSAQ\SFITSSWTFYLA \DDGKIVIFPV*SQKSQYAPHFGAREPTNFEENHLLSKMSSDLQMGK FHQAHQGIFLKNEERDGLFKKPSILNSGWILTT\TLVLS\VMVLLW\ ICCATVATAVEQYVPSGEAGVTMGDLEFMNEQKLN\RYPASFSCGLV RSKTE\DHAEAGPSYLPKVNLAFFLEI
1415	B	76	384	MSGWGLSGRLNPAAREKDVERFFKGYGRIRDIDLKRGFGFVEFEDP RDADDAVYELDGKELCSERVTEIHARARSRGGRGRGRYSDRFSRRP RNDRRNAPP*
1416	A	3	229	SRSRSRSRSRSRKSYSRSTRSRSRSRSRKSRSVSRSPVPEKSQKRG SSRSKSPASVDRQSRSRSRSRSDSGN
1417	A	152	536	PDIMSGCRVFIGRLNPAAREKDVERFFKGYGRIRDIDLKRGFGFVEF EDPK\DAADAVYELDGKEL\CSERVTEIHARARSRGGRGRGRYSDRF SSRRPRNDRRNAPPVVTENRLIVENLSSRVSWQVC
1418	A	771	1383	ILIEYKCGKCHVCTLSNIFSSSLVFFISCDCLCVFPPLLCLTQLSC VKDLKDFMRPAGE\VTFA\DAHRPK\LNEGVEFASYGDLKNAIEKL \SEKEINGRKIKLIEGSKRHSRSTRSRSTRSSSRSRSRSRSS\ KSYSRSRSR\RSRSDVPVLLSRSPRA*EEPRNRGSSSRKSPAS VDRQSRSRSRSDSGN
1419	A	236	1377	PDIMSGCRVFIGRLNPAAREKDVERFFKGYGRIRDIDLKRGFGFVEF EDPRDADDAVYELDGKELCSERVTEIHARARSRGGRGRGRY\SDRFS SRRPRNDR/RVCEGWMAALNNYWG*PFKIQESLAVMILGPAV*SVL

				LFPR*PIVLDESI*VIEHKSIDGSH*NGL*YLMA*TCPQLNTSAVIA FLPL*IRIFFLRNAPPVRTENRLIVENLSSRVSWQDLKDFMRQAGEV TFADAHRPKLNIEGVVEFASYGDLKNAIEKLSGKEINGRKIKLIEGSK RHRSRSRSRSRTRSSSRSRSRSRSRSRSRSRSRSRSRSRSRSRSR VSRSSPCPEKS\QKRGSS\SR\SKSPSHLWNRPEVPGPRSRSQIQLD QWPIKPVK
1420	A	568	770	PDIMSGCRVFIGRLNPAAREKDVERFFKGYGRIRDIDLKRGFGFVEF EDPRDADDAVYELDGKELCS\ERVITIEHARARFTRLGRGRGRYSDF NNSAELRNDRRNAPPVRP\ENRLIVENLSSRVSWQDLKDF\MRQAGE \VTLPDTRRLNL\NEGVVEFASMGDLRNAIEKLSGRELNGRKIKLIE RPAKRQ*VQSRSSDPGTQKSPGLGPRSRSPVAVANLSRSKK\RR GSREPGSPEPSRSC*VGSSPVP*ERFFKGYGRIRDIDLKRGFGFVE FEDPRDADDAVYELDGKELCS
1421	A	1	1317	MTQRFLIVLGLCLILAVLTTFKEYETVSGDWLLETTFAIFIFGAEFA LRIWAAGCCCRYKGWGRGLKFARKPLCMLDIFVLIASVPVAVGNQG NVLATSLRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWY IGFLTILSSFLVYLVEKDVPEVDAQGEEMKEEFETYADALWWGLIT LATIGYDKTPKTWEGRLIAATFSLIGVSFFALPAGILGSGLALKVQ EQHRQKHFEKRRKPAAEILQAARYYATNPNRIDLVAWRFYESVVS FPFFRQVGTHLNAQGVTSLSCEESNFDPEGNEKLDEPENDISRSTF QEDDSKECGGWIYGLKSKQEDQLANIAGFRVRGNEGLDQGNRQHQ PDFSAYICEMKELKQMPKACQGYHGFRLSANNPELAPRLSFMWSH QLYEFNMNAEKEPNGN
1422	A	1	816	MTDEDLVFRKHRVTWQKECSFPFQPPQHDLHTAPSFKDKVTEAQK GHRFAEQPDGKGLGLKSSQKLGLLDRVRLSNPRGSNTKGKLFPTL NVDAIEESPSKEPKPVGLNNKESLRTAFRMKAYAFWQSSDAGTGDP MAEDRGYGNDFPIEDMIPTLKAARAVRILQFRLYKKFKETLRPYD VKDVIEQYSAGHLDMLSRIKYLQTSICGWRVNIWTSDCISPAMLTLR GKRERKCRQWRSSWVSKEETEGAMTVSGCIIILMVLDL
1423	A	19	2867	PPDPLPGLPCPPGGPPLPAFGGGWGGARGSWHWSSRACSRRLVHA PRAPLLPRAAAEKAKRPAGARQMGKARRAAGAAGGGDGGGGGGGA ANPAGGDAAAAGDEERKVGGLAPGDVEQVTLALGAGADKDGTLLLEGG GRDEGQRRTPQGIGLLAKTPLSRPVKRNNAKYRRIQTLYDALERPR GWALLYH\ALVFLIVL\CLILAVL\TTFKEYETVSGDWLLETTFA IFIFGAEFALRIWAAGCCCRYKGWGRGLKFARKPLCMLDIFVLIASV PVVAVGNQGNVLATSLRSLRFLQILRMLRDGPGEAGTWKLLG\SAIC AHSKELITAWYIGFLTILSSFLVYLVEKDVPEVDAQGEEMKEEFET YADALWWGLITLATIGYDKTPKTWEGRLIAATFSLIGVSFFALPAG ILGSGLALKVQEQHRQKHFEKRRKPAAEILQAARYYATNPNRIDL ATWRFYESVVSFPFRKEQLEAASSQKLGLLDRVRLSNPRGSNTKGK LFTPLNVDAIEESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSDA GTGDPMAEDRGYGNDFPIEDMIPTLKAARAVRILQFRLYKKFKET LRPYDVKDIEQYSAGHLDMLSRIKYLQTRIDMIFTPG\PPSTPKHK EVFRKGQHTFPSSQSSRGLNHM*ARPST\SEI\EDQRH*WGKFVKS LKGQV\QGLGRKLDLFLVDMHMQHMERLQVQVTEYYPTKTSSPAEAE KKEDNRYSDLKTIIICNYSETGPPEPPYSFHQVTIDKVSPYGFFAHDP VNLPRGGPSSGKVQATPPSSATTYVERPTVLPILITLLDSRVSCHSQA DLQGPYSDRISPRQRSITRSDTPLSLMSVNHEELERSPSGFSISQ DRDDYVFGPNGGSSWMREKRYLAEGETDTDTPFTPSGSMPLSSTGD GISDSVWTPSNKPI
1424	A	2	508	PDSSGPHRLRENPPMVAVSCPTKTNVKGPPGGKVGAGAHAG\EYG\SEA LE\RMFLSFPT\TKTYFP\HFDL\SHGLCPRLKGHG\KKVADALT\N AVAHVD\DMP\NGVVRP*SDLH\AHKL\RVDPVNFKLLSH\CLLVTL A\AHL\AEF\TPAVPRPPWDKFPWLSVKHRCLTFKYR
1425	C	257	358	MILLVFLPXHQVFLERXQSEILHHLNTLADVL*
1426	A	64	468	PAAWLPILVAARQLTVQMMQNPQILAALQERLDGLVETPTGYIESLP

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				RVVKRRVNALKNLQVKCAQIEAKFY\EEVHDLQRKYAVLYQPLFDRK FEIINAIYEPTTEEECEWKPDDEDEISEELKEKAKIEDEKKD
1427	A	1	795	MDVTVSELLEFLQSPVLTWVKTFGPFGSGSQDNLTMYMDLVDGIFL NQIMLQIDPRPTNQRINKHVNDVNLRIQNLTLVRNIKTTYQDMGY GQTQAWGAGILESFLGGNVCLRLVGLTGREGVSSGEERHLQSFQDIK QPEGWGVSCGYRFRKGELEPLEVAVFVGTGSGVGAAMVMAMGAATLEA PEALESINQESSCGCIKPCGNSLEWRQLARALLVRWGDDYDEEGEEA DEEGEEGGDEENDPDYDPKKDQNPTECKQQ
1428	A	1	836	MDVTVSELLEFLQSPVLTWVKTFGPFGSGSQDNLTMYMDLVDGIFL NQIMLQIDPRPTNQRINKHVNDVNLRIQNLTLVRNIKTTYQDMGY GQTQAWGAGILESFLGGNVCLRLVGLTGREGVSSGQERHLQSFQDIK QPPEAQGRMVGSFERTPQICGLGYRFRKGELEPLEVAVFVGTGSGVGA AVMVAMGAATLEAPEALESINQESSCGCIKPCGNSLEWRQLARALLV RWGDDYDEEGEEADEEGEEGGDEENDPDYDPKKDQNPTECKQQ
1429	A	1	410	ARAKTYMRSEPDDSDPFPDGPFGPEIMGCTGCQIDWKKGKNVTLTKIK \KKQKHMGRGTVRTVT\KTVSNDSSFNF\APPEVPESGDL\DDDAE AILAADFEIGHFLRERIIPRSVLYFTGEAIEDDDDDYDEEGEKSG
1430	A	502	765	LQKQKQANKQKIT*K*ACQMV/SNSSFPGKQKVDPTTKRCLVNGGL NLKIQL/I IQANF*KSRFIHLTVVPVTLISQVTLQLTMSPKTQ
1431	A	58	1335	VTACAAPAAWLPILVADIWSSYNMADIDNKEQSELDQDLDDVEEVEE EETGEETKLKAR\Q\LTVMQNPQILAA\LQERLDGLV\ETPTGYI ESLP\RVVKRR\VNALKNLQVKCAQKETQ\FYEEVHDLERKYAVIYQ PLFDKRFEIINAIYEPTTEEECEWKPDDEDEISEELKEKAKIEDEKKD EEKEDPKGIP*IW\LTVPK\NVDLLSDMVQEHDEPILKHLKDIKVKF SDAGQPMFVLEFHFEPNE\YFTN\EVLTKTLR\MSSIPD\DSDPFF F*MEPEH*GCTGCQIDWKKGKNVTLKTIRK\RPKPQGTWGQFRTVN* NQFPNDSFSNFFCPLLKFLSEDRND\DAEAILAADFEIG\HFL\RE RIIPRS\VLYFTGEAIEDDDDDYDEEGEEADEEGEEEGDEENDPDY\ DPKK\QNPTECKQQ
1432	A	1	645	PLKRS DGCNDGRPTRPPTTPDTTVFTSNLQTLVHLTPVE\KSAVT ALWGVNVD\VGKALGRLLVLPWDPKRSFQSPLGESVPTP*MAK EKVLGCPVGLASPGTTLKGHLCPHWSELALLTSLPRGIPEELQGS WGKRAGSCVAAQSTFGQKNFNPKNLQGLPNQENWLAWCWLNALGPT SNHLSLAFLAGPISN
1433	A	240	463	GLVFSRLSPEYYDLARAHLRDEEKSCPCLAQEGPQGDLLTKTQELGR DYRTCLTIVQKLKMMVDKPTQRSVSNA
1434	A	2	206	TMSTVLLLRQSVSNAATRVCRTGRSRWRDVLSCGRSTGSCPQIPGT SATSAGSSSLPRSRIHSPVSLP
1435	A	2940	3296	PVCTVSGPMAPGASSHPVLPLLGLLEPAGLAELGRTHPITMSTVVL LLQRSVSNAATRVCRTGRSRWRDVCRNFMRRYQSRVIQGLVAGETAQ QICEDLRICIPSTGECRGDSRDT
1436	A	189	736	ENKISSVFKADFLPPAPCSLPGLEVSVSPKGKNTSGRESGFGWAIWM EGLVFSRLSPEYYELA\RPHLRDEEKS\CPC\LAQE\GPQG\DLLTK TPELGP*ITRTC\LTIVQKT*RMVDKP\TQRSVSNAATRVCRTGR SRWRDVCRNFMRRYQSRVTQGLV\AG\ELAQONLVSTSLCIPSTGP L
1437	A	3	452	QTQOREPTMVLSPADKTNVKAAGKVGAGAHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALS HAHKLVRDVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
1438	A	3	485	PTLLVPTDSERTHPWLLSPADK\TNVKGPPGGKVGAGHAVRSMCAEAL ERMFLSFPTTKTYFPHF\DLSHG\SAQV*GPRARKVADAL\TNAVA\ HVGRTLPNALVPPSLDLHAHKL\RVGPGSTFKLLKATCLAGLTL\AA HLPARVQPLAVASLPWDKVSWASC
1439	A	217	474	RTCASLKS LHRPHGSHHGQGGFL*VFSSSFSSDGWVQVCSPPGGQ IPPTCPHHCDDPESPDSSSGPPVPWHLPCA VQGPSPGGL

1440	A	569	737	REHPVAGLQEHLOGGGSGQDLRG*WAYFS/HR*SRKVPTSW*RRWK MVAPWAARRV
1441	A	520	1319	SWPQVPKTNKIEPRYSYII\TSCGI\RRLGPAINTLIFSK*NASGPA GHSAKSIEGAPRGKGRGVARLAADRPPAPKIQLPSFV/LRSTL*Y PLLELE\LPRLATHLPSNGS\SLK\DLKWT\HSNYRASKEP\CIVI F\VTTPSG\REWVICAPAAFLG\CGSRFSGSPLPE\SNP*FPV\TRG HHGRHGDYHRKLIQOTFEWVVRRHGG\RAIGPRLSRVTKAAGARPP AGAGEG/LDRVGFDLINA\PSPPAKGVSARRHVLALQLSK
1442	A	2	239	RKTQTTRRGPGWLWAGPGG*RGGWWSRRLLLAAGFLGTHPGSTHPGLQ QPRFKWDHTRSSQGAFFITFFPRGGQEHSTFS
1443	A	234	493	LKQSWVWEGPAGMPGLGAAGPGHPGAGPVCPLDGSSYPYFYFVTRE VMQRDISAGDFIEHAEFSGNLYGTRWAMRGCGWAPRVAV
1444	A	126	890	PRSIGEGLGPSLLCGSGRARFSSGGMSGPRLVVLSGPSGA\GKSTLL KRLLEHSG\IFGFSVSRESRALVEG\TTRNPRPGEGRRQKITYFVT REVMQRDIAAGDF\IEHAEF\SGNLYG\TSKV\AVQAVQAL*PHRVC LDV\DLQG\VRNIRPTDLRPNLHLLFSPFFTATCWKQPGFRQPQQL TEGRAWLKAGLLAQA\DMEEPAKEAPALF\DVVHPLNDQPGTQA\Y AELKEALSEEIKKAQRTGALRLAVCSR
1445	A	978	1440	AGVGVRGTTGRLVVRKFLTLIFGNPLFLVAPPKPHSEWSQRLTY\RR RPSPYNTA\SNKT\RLSPNPDGNRICLPFIPKKVGKAPQSLHVVCAP GRLRG\VRVVRPKV/LL*RLSKTKKHVSRAYGWFHCVLKCGRD\RIK ACFSLIGGSRKIRCGKSV
1446	B	43	674	MDWTWSILFLVAATTGVHSQVHLVQSGAEVKKPGASVKVSCKASFNS FDTYGFNWVRQAPGQGLEWMGWVSFNGDNTYIRKLQGRVTMTTSS TSTAYLELRSLKSDSAIYYCAATNSDKYFWGQGTTLVTVAASPTSP KVFPLSLCSTQPDGNVVIACLVOGFFPQEPPLSVTWSESGQGVARNF PPSQDAFGDLYTTSSQLTLPATH*
1447	A	3	1637	SPGIFRGFSQVIRTEQRELTMESGLNWLVLVAVLKGVQCEVQILESG GGQVQPGGSRTLSCAASGFI FSNYVMTWVRQAPGKLEWVSSTAASG ANTFYAESVKGRFTVSRESENMMYLQMSLRDEDGTIYYCAKGDV PNLGVAVIVAGPGNVRPRKWFDAGWQGTTVTVSSASPTSPKVFLSL CSTQPDGNVVIASCLVQGFPPQEPPLSVTWSESGQGVARNFPPSQ\ MASGDLYTTSSQLTLPATQCLA\PKSVTCHVKHYTNPHDPVDG\PCP VPSTPPTP/CSLNSTYPI SLMLPPPTVTAPTGPSKDLFLGSEANLTC TLTGLE\NASGCHFQSEGLQVGKSAVQGP\PEA*PSVAAYSVVQLSC RGWREAMEPLVRPFTCTAALPRSPRTRANRPPSSKSGKHISGEGPP CCRPPSEELALNELVTLTCLAR\AFSPQGPCWVRWLQGS PKLPPRKS T*LG/PPAGAARAPTTFVAVTSILGR/VQPEDWKKGDTF\SCMAGH \EALALAFQTIDRLAGKPTHVNVSVVMAEVDGTCY
1448	B	113	249	XAAMTTASTSQVRQNYHQDSEAAINRQINLGA LRLLRLPVHVL*LL
1449	A	846	1193	VMGPKPLPGIVPEFLKNWPRPSGLLIEFCPHWDTTDMTSN/CLV*EE NYSEQCLELLNPVGMDLILRGDCESYHGHKPNRKLGSQHLSDQAALT GRLSSPCLMKRRRSASFRTQAG
1450	A	2	1087	AIEHCQSGDNPESSRGFLQQLWGRNPALVPHPGRTGHSQPPVTFHR HPSDCQSRPAGRFKGGPSHRGQPPPFHKSPPMTTARPTSQ\VRQN\Y HQ\DEAAINR\QINLE\LYASYVY\LSMSYFFDRD\DVALKNF\AK YFLHQSHEER\BHC*ENLMKACRTNEGWPNL SFQDIKETKTCD\WE SGAECQWKALH\LEKNVESHYWNLHKL\ATDKN*PPICVDFI*DT FTLNEQ/V*KAIKRIWGDH/V*PKLWRKMGSA PNLFGEYLF*QSTP W\ETVIMKAKPRANFPNSRGVTFVLTKAVHACWGFLYLFYKLYQNIH LSSLIC TIPS NK EI WXP GVVFEVLDESEIYPGYLPDLS SAVVQF
1451	A	24	452	APSPDAMG/HSLWKGVNVEDAGGETLGRLLVVYPWTQRFDSFGNLS SASAIMGNPKVKAHGKVLTS LGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
1452	A	41	542	APSPRRPWGHFTEED\KATI\TSLWKG\VNVE\ DAGGRKPLGKAPWL

				STPWTQRFDFSFGNLSSASAIHGQTPKVKAHG\KKVLT\SLGDA\TK HLDDLKG\TFAQA*SELH\CDK\LHVDPENFK\LLG\NVLVT\VL\A IPFSAKEFTPEGCRASWAERWVTWSWPVPCSSRYH
1453	A	1	1233	MGEAFAQENMAENPYISVVNSHILNNWEFPKWSLDDSTKVQLNSMKL GGTEMAPRRWQLVCEGTLAPRGCSPPFSWTERPAGFPFPLSPALRQRT ASTHSAGARIAPHHTRLRLLEPVTETRSNEILPPGEEARGGCSAVG AAPPSPSRPGPPPHAAPMHPFYTRAATMIGEIAAAVSFISKFLRTKG LTSERQLQTFSSQLQELLAGEQEGVGGRTRAPHWVRVRPSGLREPR QRPAGRAWAPPRDRWQNGEKTTRTTKKLKPTTEAGAAVRGPSADLG TKEPWGWEHYKHHWFPEKPCCKGSGYRCIRINHMKDPLIGQAAQRIGL SSQELFRLLPSELTLWVDPYEVSYRIGEDGSI\CVLYEASPAGGSTQN STNVQMVDSTRISCKEELLGRTSPSKNYNMMTVSG
1454	A	233	884	ESPGVGCSARRGPRRSPGPPPAAPGTTPRHGIPLYTRAGHQ**GEI RRRPCTFISKFLRPQGGASERQLPDLQARAWQELLGRPFKNH\HWF PR*SPCKGIGVTRCI\RINP*KWIPLIGPQOHAIGLSSQELFRLLP \SEL\TLWG*PPIEVSYRIGEDGSHLCACMKPSPA\GGST\QNQT\N VQMV\DS\RISCKEELLGRTTEFPKTNMMTVSG
1455	A	363	487	GRFLSLSHFCPPAPTSQVRPWALELRDSPHSPPTPAPSLML
1456	A	742	990	GTPRGDMRGRLYCSLPGQCLCGFIKCGAPLRPLFPSSVPAAGNAFC QAAQLHLQLQSKHDAATCFVDAGNAFKKADPQGEGL
1457	A	1	198	LFPAFSDSRECKLMKKLLEAHEEQNVDSYTESVKEYDSISRDL\QWL TTMLLRIKKTIQGDDEDLR
1458	A	281	584	GRFLSLSPILLSQAYKAHVAAETCCFCLGAGSSSPSPGSLPQLPAA PTSQVRPWALELRGFSPPQPHTCSPFNALRFFWLEAAAGPRKKIKNH PFEKKKK
1459	A	120	1069	KPFEAAMYNNGKEAEAMALLAEAEPKVKN\SQSFFSGLFGGSSKIEE ACE\IYARAANMFMAKNW\SAAGN\AFCQA\AQLHLQLQSK\HDAA T\CFVDGWQLHSRKADPQGGPFNCFDCVAFEIY\TDMGR\FTIAAKH HISIC*DLLRQKLVDIEKAIHLRGQSADY\YKGRGSSNSPTNKCLL EGGLVTPALLGAVIQKAIGHFTEQVGGPNAHWTSPPPSKY\SAKDYF F\KAALCHFCMDMLQA\KLAF\QKYEELFPVFSDSRECKLMKK\LLK A\HGEQNVGQLTPSSVKGITTPISRL\DQWL\TTHCLRI\KKTIRGD
1460	A	255	2154	LAPEVATDSGQOQADLPAEGGDPRAEASCSVLHSPHAMADSRDAAS DQMQRHWEQRAAQ\KYLGVDDLGHKKADVLTTGAGNPVGDKNVITV GPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDI TKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPGRGFAVKFYT EDGNWDLVGNNTPIFFIRDPIILVSFLFSDRGIPDGRHMMNGYGSHTF KLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFN AIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVG KLVLNRNPVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDT HRHRLGPNYLHIPVNCYPYRVRVANYQRDGPMDQNDQGGAPNYPNS FGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQTSLYLTYRFMENI EKVRAFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKAVKNFTEVHP DYGSHIQALLDKYNAEKPKRSLAFIRVTRSSLEDESPVLDVQMQASG FKIENPTFYSLCENNFAISPGENEALTIEQMGSTEANCLLRNSVQL VAFVIEITSRKSDIVERHKCAWT
1461	B	129	321	XYWMLCSKAEGCCSGAPKAVGVVIWSTTLIVLHAHRAVTLVVGHSS GRDSSQVYEDNWVPGRWR*
1462	A	70	2954	RMLITGSPALGSAIPGTPGRRGEALQLLGQSGTLFPRTLIGISGLQA SFGEPCSEPIGLPILACLAPSSQSEGSPPEGAGRGGGADWLSLKSPR TRGNRQICLLRVETHEPRPPAVFCTANRTLWLTAGIPPAATRCSTGRS SGPRRIEMRACTTSIQGNNVQDKWKSNEVPDVECACTFLESKPGW LGQSKQGAKRSGGDECLQSSHLWEFVRDLLLLSPEENCIGILEWEDREQ GIFRVVKSEALAKMWGQRKKNDRMITYEKLRLALRYYYKTGILERVDR REKLFNSAIRDTSNAPIPKVQKFSNCGSSPKVRAFYVNVLNEEQRK RLCENIAGHLKDAQIFIQKAVKNFTEVHPDYGSHIQALLDKYNAEK

				PKVWPHKDYPLIPVGKLVNLRNPVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQKADVLTTGAGNPVGDKLNVITVGPRGPF\LVQDVVFTDEMA HFDREIRIPEEKLCMLKG\AGAFWYF*RSHIDITKYSKGKRYFE\HIW KRRLPIAV\RFFHCLLGESGFSLTQFR\DRPGF\AVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQK\RNPQTHLKDPDMVWDFWSLRPE SLHQVSFLFSDRGIPDGHHRMNGYGSHTFKLVNANGEAVYCKPHYKT DQG\IKNLSVEDAARLSQ\EDP\DYG\LRDLF*TPLATGK\YPSWTF YIQVMTFNQAETFPFNPFDLT KVWPHKDYPLIPVGKLV\NTRNPVN YFA*GWN R*PFDP\SNMPPGM*GPVP\DKMAFRGRFLCFLDTHRHS PGGPNYSFILPVELVPYRGSEWGQLTRDGPVALQDNQGWVVPKFI NPNSFG\AREQQPSALE\HSIQYSGE\VRRFNTAN\EMDNVNSGGGH FYVERAELREQE/RKRLC*GTFAGHLEGMAQIFIPEGKRVKNPH*GS HP*PTGAHIPRLFWTKYKA\ENPKNAI\HTFVQSGISP
1463	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAELERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKVVADALTNAAHVDDMPNALSALS HAHKL RVD PVNF KLLSHCLLVTLAAHLPAEFTPAVHASL D KFLASVS TVLTSKYR
1464	A	2	521	PDSSGPHRLRENPPWCLSPADKTNV\KAAGKVGGAHAVRSMCAEAL RMFLSFPTTKTYFPHFDLSHG\AQV*GPRARKVADALD/TNAVANV GRTL PNALVRPL\SDLHAHKL SGGTRFNFKAPKGHL PCLGEPWAAHL PRPSFNPWRLQRLPWGQSFLGLLKHRCNLNPNYR
1465	A	154	678	PPLHLRDCFSPPGRALSPVGLYPYR\RSVP\TWLKL\SDDVKE\QI YKL\AKKG\LTPS\QIG\VILRDSHG\VAQVRLG\TGHDTFKI\LKS KGLDPELDPEDLYHLIKK\AVAVRKHLERN\RKDKDAKF\RLILIE\S RIHPFWLRYK\TKR\VLPP\NWEI*NHLTASALGRINLVWCTPSK
1466	A	23	636	FSYLPPGPGSHGTWGLWELQFKMRFGVCRHLMEDSMDMDVSPLR/PQN YLFSCELKADKDDHFKVDNDENEHQLSLRTPVSLGVFEITPPVLLW LKCGSGPVHISGQHLVAVEEDAEESEDEEEDVKLLRISGKTKTFMAT NGKEYKHYKISSEKSLDNKYKTRTPGFQAFGFEDLHPWPLGSQAFYL SLRVTPPVFLVLRLLDFD
1467	A	3	618	AKD/ELHIVEQGHDIRGSIKIT/LATLKMS/VQPTFS/LGGFEIQP TVV*GLKCVSGPCHISGQHLVA/VEEDAEESEDEEEENVKLLSISERR SAPGVVSMVPQKKVK\LAADDDDDDEEDDDDDDDDDDFDDEEAEE KAPVKKSIRDTPAKNAQKSNQNGKDSKPSSTPRSKGQESFKKQEKTP KTPKGPSSVEDIKAKMQASIEKAH
1468	A	1	1689	MEDSMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNYEGSPIKVTLATLKMSVQPTVSLGGFEI TPPVVLR LKCGSGPVHISGQHLVAVEEDAEESEDEEEDVN RVLFMKP KGRGLKHMFGDLVCSWKLA AIETQSSSSEEIVSPSPSPPLPRIYKP CFVCQDKSSGYHYGVSA CEGCKGFFRRSIQKNM VYTCHRDKNCI INK VTRNRCQYCR LQKCFEVGMSKESVRNDRNKKKKEVPKPECSES YTLT PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDF SELSTKCI IKTVEFAKQLPGFTTLTIADQITLKAACLDILILRICT RYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLPLEMD DAETGLLSAICLICGDRQDLEQPD RVDMLQEPLLEALKVYVRKR RPS RPHMF PKMLMKITDLRSISAKGAERVITL KMEIPGSMPLIQEMLEN SEGLDTLSGQPGGGGRDGGGLAPPGSCSPSLSPSSNRSSPATHSP
1469	A	3	535	DSVLRGCSLEQRSFISVRLLSYLSACRHPMEDSMDMDMSPLRPQNYL FGCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAM NYEGSPIKVTLATLKMSVQPTVSLGGFEITPPVLR LKCGSGPVHIS GQHLVVYRRKHQELQAMQM\DCRALSTS*ASSAPRPS
1470	A	1	1025	SVLRGCSLEQRSFIYGRLLSYLSACRHPMEDSMDMDMSPLRPQNYLF GCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMN Y\EGKSN*T*HLATLKMS\VQPTVSL/GGA FEITPPVLR LKCGSGP VHIKWTSTYVAVEGKMQKSRRLKKEGRIVKLLKVYL GK\RSAPWKVG SKVSTEEKVKTLA*WKDDDRMNDEE\DDD\EDDDDDDFDDEEAEEK

				AP\VKKSI\RDTPAQKCSSESONQNGKRLQKPSFTPKNQKGQESFQET RKLLKTPKG\P\SSVEDIKAKMQASIEKGGSLPKVEAKFINYVKN\ CSRMTDQEAIQDLWQWRKSL
1471	A	3	490	SSGPTRLRENPPMVAVSCPTKTNVKA\AWGKVGAAHVRSMCAEALER MFLSFPT\TKTYFPHFDLEPRFLPRFKGHGKKVADALNAVAHV\DD MPKRAVPPPLSDLHAHKF\RVGPGSTFKLLKPLALLG*TLGRPTSPSE FQPLAVARLPWGQSFGLGFLKQPC
1472	A	35	1288	KSSHCIKMGPIFHKTSELFLPATSCPCPDQNEEDVSQTQYKECCG GGWCSHSIFAVWHFAALGAGFSDKTPAHTVTMACISANQAMTTGVGL IASGQCDVIVAGGVELMSDVP IRHSRKMRLMLDLNKAQSMGQRLSL ISKFRFNFLAPELPAVSEFSTSETMGHSADRLAAAFVSRLEQDEYA LRSHSLAKKAQDEGLLSDVVPFKVPGKDTVTKDNGIRPSSLEQMAKL KPAFIKPYGTVTAANSSFLTDGASAMLIMAEKALAMGYKPKAYLRD FMYVSQDPKDQLLLGPTYATPKVLEKAGLTMDIDAFEFHEAFSGQI LANFKAMDSDWFAENYMGRTKVGLPPLEKFNWGGSLSLGHPFGAT GCRVMAAANRLRKEGGQYGLVAACAAGGQGHAMIVEAYPK
1473	A	1	1641	MLPRSPTPNPQDPQDLRRNARQPARSHAAQDTRDRAARPLSRLGEAG SRERGIRPAVCTYQSQPAAPGSPSHDDPKTERPLGSDSRLQGCDDT QAPHRLGKDGDWAAREALFVASFASVKIGELRGLLHRTSVPKEVVD YIIFGTVIQEVKTSNVAREALGAGFSDKTPAHTVTMACISANQAMT TGVGLIASGQCDVIVAGGVELMSDVP IRHSRKMRLMLDLNKAQSMG QRLSLISKFRFNFLAPELPAVSEFSTSETMGHSADRLAAAFVSRLE QDEYALRSHSLAKKAQDEGLLSDVVPFKVPGKDTVTKDNGIRPSSLE QMAKLKPAFIKPYGTVTAANSSFLARGVESGVVPTGWNTTLLSPGGE ELVRLVICKTELDDRAMWHGLHLPDLNPFDFYQGMKLVQVYLTGAS AMLIMAEKALAMGYKPKAYLRPTYATPKVLEKAGLTMDIDAFEFH EAFSGQILANFKAMDSDWFAENYMGRTKKFNWGGSLSLGHPFGAT GCRVMAAANRLRKEGGQYGLVAACAAGGQ
1474	A	212	371	HPVTYVLLLYLLFQLPCGSEFSTSETHGHSADRLG\AAFAVSRLEQ DEYAPG
1475	A	63	255	VLMFSSSHG*GYQSS\RLQCKLQIVQLIQDILLFFSF*IFE*LLS*L TPLKIFPLHQNGPSDFVS
1476	A	169	391	FLKHISVEKIYKACGSIELKKFIFLIGKDTVTKDNGIRPSSLEQMAK LKPAFIKPYGTVTAANSSFLELAMLV
1477	A	85	1534	KSSHCIKMGPIFHKTSELVLPATSCPCPDQNEEDVSQTQYKECCG \GGWCSHSIFAVW\HFI*RPDAT*FGLEQRLTGLLASGPVSLREV* LYSSLGTVISGK*KTSNVG*RLGALGSWAFSDKYSWFTWACISG PTKAL\TTGV\GLIAF\GQCDVIVAGGVELMSDVP IRHSRKMRLML DLNKAQSMGQRLSLISKFRFNFLAPELPAVSEFSTSETMGHSADRLA AAFAVSFL\QDEYALRSHSLSKKAQDEGLLSDVVPFKVPGKDTVTK DNGIRPSSLEQMAKLKPAFIKPYGTVTAANSSFLTDGASAMLIMA EEKALAMGYKPKAYL\RRDFMYVSQDPKDQLLLGPTYATPKVLEKAG L\TMNDIDAFEFHEAFSG\QILANF\KPMDSDFAE\NYMG*KKPRF GLPPLWRRFNWNG\GSLSLGHPFGT\TGCR\LV\MTAANRLRKKGG QYGL\VAACAPG\GQGSATDYVEAYPK
1478	A	2	359	LDQQCKQTSEYLRVEDTLLEDQPTGENEMVIMRPGNKYEYKGFEL PQGPLGTSFKGKYGCVDYWVKAFLDRPSQPTQETKKNFEVVDLVDVN TPDLMAPVSAKKEKVCILNNVQ
1479	A	1	585	PRGVIGHGPLGTSFIGYGCDDYWVKAFLDRPSQPN\QGPKNFE\V WDLVDVNT\DLMA\PVSAKKERKVS CMFIPDGRVSVSARIDRKGFC EGDEISIHADFENTCSRIVVPKAAIVARHTYLANGQTKVLTQKLSSV RGNHIIISGTCASWRGKSLRVQKIRPSILGCNLRVEYSLLIYVSVPG SKQVFIKAL
1480	A	218	1677	SEIIFCKGVSSIWSFFFLPPSFLTLKINSVPSWVMFK\KIKSFEV\V FNDPGKGVTA VGEKVA\GRVNSGRCEVTRV\KAVRIP\ACRSGLK LWMPGIPSRCKQTS\EYPRYEDTVFL\EDQPTGEN\EMVIMRPGNQY

				EYKFGFELP\QGPLEHSFKGKYCVDY\WVK\AFLDRPSQPTQETKK NFEVVDLVDVNT\DLMAPVS/ALKKEKKVSCMVIDG/RVSVSARI DRKGFCEGDEISIHADFENTCSRIIVPKAAIVARHTYLANGQTKVLT QKLSSVRGNHIIISGTCASWRGKSLRVQKIRPSILG/CNILRVEYSL IYVSVPG\SKKVILDLPL/V*LGSRSGLSSRTS\SMGSRTS/SLRMS WVDLNIP\DTPEVPS\CILGCSFPEGSTVWESPTTP\LLDDMDGSQN SP\IFMYAPEFKFMP\PRTYTEVDP\CIFNHQCAVSMWKKRSSFTLL VSFWPSLPWTVHFFQRLNSLNGSVGPTLSPLTS
1481	B	21	410	MPSKVRCSVQVFDAMKTATAVAHCKRGNGLIKLEPVLGKERFA GVDTRVRVKGGGHVAQIYAIRQSISKALVAYYQYVDEASKKEIKDI LIQYDRTLLVADPRRCESKKFGGPGARARYQKSYR*
1482	A	1	456	MPS/KGPLQSVQVFGRRKKTATAVAH/CKRGNGLIKVNRPLEM/IEP RTLQYKVLGSGTGVSGWRTLGDREDVVALESWGAGISNGMFRSCVGC QWAAGASSASRQERFAGVDIRVRVKGGGPWPRFMSKKFGGPGARARY QKSTDKPIVTQNSLV
1483	A	172	661	LLEPVLGKERFAGVDIRVRVKGGGHVAQIYGESQELGAWRRWLWE GGLHSAPVPFNCVSFSQSVSPIS\KALVAYYQK\WSEHGSFP*GRW VCGDQVKDSV*LSKSSSLLFLPDVDEASKKEIKDILI\QYDRTLLVA DPRRCESKKFGGPGARARYQKSYR
1484	A	1	556	GAARVRLSSPRSDAMPSK/GVPLQSVQ\VF\RKKDSGQLLAH\CKR A\NGLIQG*TTGGPLEMIEARARLQYK\LLEP\VLLGK\ERFAG\VD IPCPV*KGGWSTWPIYAIRQS\ISQKPLVAYYPEM*VSMGPSHE/Y VDEAFQRREIKDILHPSY\DRNPAGLAGPFVRC\SKKF\GGPGA\R ARYQKSYR
1485	C	127	435	MAASXNPEVLDITEETLHSRFLEGVRNVASVCLQIGYPTXASVPHSI INGYKRVLALSVETDYTFPLAEKVKAFLADPSAFVAAAXLGCCHHSC SXCCSPS*
1486	A	1	689	KCFI/VGADNVASKQMQQIRMSFRGKAVC*WGKNTMMRKPIRGHLEN NPALKLLPHIRGNVGFVFTKEDLTEIRDMLLANKVPAAARAGAIAP CEVTVPAQNTGLGPEKTSFFQALGITTKISRGTEILGVRNVASVCL QIGYPTVASVPHSIINGYKRVLALSVETDYTFPLAEKVKAFLADPSA F/VAAAP/VAAATTAAPRAAAAPAKVEAKEESESEDEDMGFGLED
1487	A	66	1104	RTAVMPREDRATWKSNYFLKIIQLLDDYPKCFIVGADNVGSKQMQQI RIVPWGEACVLMGQKTMNGPSEGHLENNPASEELLPH*\RGHLGF CFT\RED\LTEI\RDMLLAQ*GCQAAARCWCQLPPCEVTVPA\QNTG LG\PEKTSFFPGL*VSPTKNLPGGTH*KS*SYVQL\IKT\GDKMGSQ TKAKAAEKMLKNLPPSPFGAGQPKQGV\RKNGKHPTNPESA*ISTRG KLCHSRF\LGGCPANVAKCLSCKIGYP\TVASSTPIPII\NGYKRV GPCLWTPDYTFP\LAEKVKAFL\ADPSCLCVLLPPVG\AATTACFAL LLQPPAKVEAKEESESEDEDMGFG\LFD
1488	B	98	264	XQVVCCKYRGFTIPEAFRGVHRYLSNAYAREEFASCTPDDREIELAY EQVAKALK*
1489	A	155	1217	DPPSPVPAPPSSPRDGHFLVDPATMAEEQPV\ELFVKAGSDGAKIG NCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPPGQLPFLLY GTEVHP\DTTKIEEFLEAVL\CPPR\YPK\LAALNPEVQHSWGWDIF AKFFLPNIQEFQTPALN*QSGRRGFLESP*KVLDNYLT\SPSPPEEV DETSC*KIEGVSQ\RKF\LDGQRRPHPWLDLQCCPKVTH*VQVV\C KRK*PGNSPHPPKAFPGKCHRV*SKMPYAPGKNSPSHPVPDDEEIE LRPMSKVAKALQISPSLGLPSTPSIFSTKAPGGFHIATPMGHTPKLA SGQGILGDI EFAKGVVEEGMRERNGGPGSD
1490	A	2	746	AVIMANLGCWMLVLFVATWSDLGKCKRKPCKGGWNTGGSRYPGQGS GGNRYPPQGGGGWGQPHGGGGWGQPHGGGGWGQPHGGGGWGQGGTHSQW NKPSKPKTNMKHMAGAAAAGAVVGGGLGGYMLGSAMSRPIIHFGSDYE DRYYRENMHRYPNQVYRPMDEYSNQNNFVHDCVNITIKQHTVTTTT KGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSSMVLFSPPV ILLISFLIPLIVG

1491	A	217	1007	LNHNRLAVIMANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRY PGQSPGGNRYPPQGGGGWGQPHGGGGWGQPHGGGGWGQPHGGGGWGQPH GGGWGQGGGTHSQWNKPSKPKTNMKHMAGAATAGAV*GGLCSYS\LG SAMSRIIHFGSDYEDRYRE\NMHRYPNQVYYRPMDEYSNQNNFVH DCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQA YYQRGSSMGLFSSPPVILLISFLIFLIVG
1492	A	32	487	SRRHGSSLWGKVNVEDAGGETLGRLLVVYPWTPQRFDSFGNLSSASA IMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVPD ENFKLLGNVLVTVLAIHFGKEFTPEVQASW/QEDGDWSGQCPVLQIP LSSLPMMQSFQG
1493	A	41	597	APSPRRPWVISQRRTKATI\TSLWGK\VNVE\DAGGET\LGRL\LVV YP\WT\QRFDD\SFG\NLSSASAIHGQPPKVQGTWSKKVLTFLGEMP *KHL\DDLKGHLLPKPEVNLHC\DKPAMWDP\ENFKAPGEMLLVTRF WAIPFSAKEFHPWRLAGLPGQKDG*LGVGQCPCSFQIPLKPLGP*IQ \SFQG
1494	A	1	478	DTRFLERLRLSISLVPDA\MGHFTEED\KATI\TSLWGK\VNVE\D AGGET\LGRL\LVVYPMDPGRGFFDSFGNLSSASA\IHGQTPKVKATR AKKVLTSLGKMPIKHLGLIFKGTFCPSLS*TCTC*QACMWDP*GTFK LPGEMLLVTRFWAIPFSAKEFHP
1495	A	3	370	SVCVRAHESVVKSEDFSLPAYMDRRDHPLPEVAHVHLSASQKALKE KEKASWSSLSMDEKVELYRIKPKESFAEMNRGSNEWKTVVGGAMFFI GFTALVIMWQKHVGL\ASKWDYEKNEWKK
1496	A	24	305	RAVAAGSGGRMLTTSVFSLVGKRAISTSVCVRAHESVVKSEDFSLPA YMDRRDHPLPEVAHVHLSASQKALKEKEKASWSSLSMDEKVECGY
1497	A	197	745	LASEQFSTSVCVCTSSMKVFKSEDFSLPT\YMEAVTHPLAGRWPVH KAPCSAQPRRPLKEKEKALLGAAPSMG*GKFELLFALKFKKEEALLED *TRGLRTELGKTGLFGPVPLFPSIGFSPRLVIHVQKHVLTAPFP\ QSF*TKSWVGPSRTKRMLGQ*R*TPIQG\LASK\WDYEKNE\WKK
1498	C	78	281	MELSNNHQLSMSLVELSMSLVWDANLLGWGKSCELTKPSWSLVRSTS RHSRKKGSSWHLPAKLCSTC*
1499	A	302	688	TIAIFSCVVRRLRFSGPKTSIICSPMTSLKTSMDMVPSLFSSPGDRVA IESGAPRENDEFCKMGRYNLSPSIFFCATPPDDGNLCRFPEIVKLSL EEAKCLPFCVAPHQPSRGALGCRSAAPLTPQPRC
1500	A	1	1622	MSKPKCLVILVGIQKSSQMPQFPFPFAGSERRRGIRQWEMGVVGGEMG VWWPPGVQGSPPQAHRRLGSRQLFAPPLKEKSHIPWGYSENYP PEPGNRPVTEVWGSPPGPTVQWGWGLHEALSPALINQAQKDPEVR LGAMVRVSVDTHTPPPLTPRQSGPLSALEELGVSPFTLSYLTPEPQLL GEHQIKGSFPGRSTALLLKEVLLRMHVSIGSDVH\YWEYLS/RFG NFIVKKPMVLGHEASGTVRKSGIIGKSTLKPG\DRVAIEPGCSPEEN *WNSCQDG/RRYNLSPSIFFCATPPDDGNLCRFYKHNAAFICYKLPDN VTFEEGALIEPLSVGIHACRRGGVTLG\NKVLVCGSWANRGVWVTLV AKAMGAAQVVVTDLSATRLSKAKEIGADLVQLISKESQPQEIARKVEG LLGCKPEVTIECTGAEASIQAGIYATRSGGTLVLVGLGSEMTPVLL \HAAIREVDIKGVFRYCNW\PVAISMLASKSV/DMSKPLVTHRVSS WRKVLEAFETFKKGLGLKIMLKCDPSDQNL
1501	A	1	804	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGMA ADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQEQEYS CVVKMPSGEFARICRDLSHIGDAVVISCAKDGKVSASGELGNGNIK LSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLS MSADVPLVVEYKIADMHLKYILAPKIEDEEGS
1502	A	178	1093	TFLLPACLLAALLPLRHHVRGRAWVQGSILNEGVG*ALKD\LINE\A CWGY*APAGVNLQSMGHRPTVSL\VLTLRV*GASTPYRC\DRNLGH GR*NLTS\MSKILKMAAGNED/ISLTLRAEDNAGYLGR*YFEGTKPG RKFSYEMKMLMDLDVEQLGIPEQE\YSCVVKMPSGEYA\RICRESQP ILGDAVV\ISCA\KDGSENFASGELGNET\IKLSQTSNVDKEEEA\

				VPIKMNEP\VQPNFCH*GYLNFFTK\ATPLSSTVDTPVCSADGTPLV GRSIKIAGYGDHLKYLLGLPKDPRIEEGSLGHS
1503	A	32	487	SRRHGSSSLWGKVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLSSASA IMGNPVKVAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDP ENFKLLGNVLVTVLAIHFGKEFTPEVQASW/QEDGDWSGQCPVLQIP LSSLPMMQSFQG
1504	A	1	591	NFALEAKNSARAISLVPDAHGVISQRRTKATI\TSLWGK\VNVE\D AGGET\LGRLLVVYPWTQRFDDQLLANLSSASAHGQPPKVQGHMAK KVLTFLGEMPIKHLDDLKGHLLPKPEVNCTVDKPAWDPENFKAPGE MLLVT/LFWAIPFSGKEFTP*RLQASWAERWVTWS\GQCPCSFQIPL KPLGP*IQ\SFQG
1505	A	49	273	IRMTEKAPEPHVEEDDDDELDSKLNYPKPPQKSLKELQEMDKDDES LKYKTLGDPVVTGMCVQRTGWVEDR
1506	A	81	720	LFAKAPEPHVEEDD\DELDSKLNYPKPPQKSLKELQEMDKDDES YKKT\LLGDGPVVTDP\KAPNV\VVTRLTL\VCESAPG\PITMDLTW KIWKALKKGNHVLKGRFWNIRSSKFHFPKLNRG*LLFRA*NYVQHT YRTG\VKVDKATF\MV\GSYGPRPEEYEF/LSLPVEASQRAWLARR HVTTKSPFFTTDDDKQDHLW\EWNL\SIKKEWTE
1507	A	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLDRSLPALTNIIKILRHDIGA TVHELSDKKKDTVPWFPRTIQELDRFANQILSYGAELDADHPVSPW PVG
1508	A	68	312	PLQSPGVLSILNPFSLVPCLPSSLLGSYSTLNPHYLLVSCLYPQLL PSILTQQPEGVLGNTSEIMTIYLPKIVTSIELL
1509	A	317	917	TSSPPSSLCFLSFDICHELLGHVPLFSDRSFAQFSQEIGLASLGAP DEYIEKLATIIYWFTVEFGLCKQGDSIKAYGAGLLSSFGEQYCLSEK PKLLPLELEKTGIQNYTVTEFQPLYVAESINDAKEKVGNSAATIPR PFSVRYDPYTQRIEGLDNTQQAHDLG*FHLTVEIGILCSALQKNKV AMDRMVVCQAVE
1510	A	389	1881	NLQPHVLFANLPVPEALKSQRPHSRGASMSTAVLENPGLGRKLSDFG Q\ETSYI\EDNCNQKWVPISLDPPHLKERKLGALGPYCALF\EEND VNLT\HIES\RPSRLK\KDEYGFPPPPGFIKRSPL\ALTNIKILRHD IGATVHELSDKKKDTVPW\FPRTIQ\ELDRFANQILSYGSGNWDAL DHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYMEEEKKTWGTVF KTLKSLYKTHACYEYNHIFP\LLEKYCASHEDNIPQL\EDVSQFL/Q TCTGFRLRPVAGLLSSRDFLGDLAFRVFHCTQYIRHGSKPMYTPED ICHELLGHVPLFSDRSFAQFSQEIGLASLGAPDESIEKLAPIYWFTV EFGLCKQGDSIKAYGAGLLSSFGEFQYCLSEKPKLLPL/ESLEKTAI QNYTVTEFQP\LYYLAELSFNDAQGEI*GTFAATI\PRPFSV\RHDP HTPQRIGGSWDNTQQL\KILA\DSI*Q*IGIPFAVALQNIK
1511	A	1	191	MQK*ITAWAPAPMKIKIIASPERKYSVWIGGSINPQLST/FQQMWIS KQEYDESGPSIVHRKCF
1512	A	1	360	SGACPAFLVDRNLRHETTFNLIMKCDVDIRKDLYANTVLSGG\TTM YPGIADRMQKEITAL/APPSTLRFRIAPP/ERRKYSVWIGG\SILA SLSTFQQ\MCLGKQEYDESGPSI\VQRKCF
1513	A	13	1277	INPPPLSRRCQLSHSVLPPLRRRVSLPVAMEEEIAALVIDNGSGMCK AGFAGDDAPRAVFPISVGRPRHQVMVGHGPRTDSYVGDEA/QRSKR GILTTLKYPIDHGIWNTWDDME\KIWHHTFYNELRV\APEKHPVL\LT EAPLNPKANREKMTQ/ILCFETFNTPGHVPWPPIQAVLSL*SLWAQPI GIVMDSG\DGVTHTV\PILRGATTLHAI\LRLGPGLARDLTDYLMK ILT\ERGYSFTTHGSPGKTFRNIKGEACATSPLDSEQ\EMGT\AASS SSLEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFN SIMKCDVDIRKDLYANT\ALSGGTTMDPG\IADKIAEGRSTALAAPA P*KIR\IIAPP\ERK\YSVWIGGSILASLSTFPARFWI\SKQE\YDE SGPSI\VHRKCF
1514	B	93	366	XTSVVRPFAKLVRPPVQVYVYEGRYATALYSVLNPNVVKRSIKVKS DITAKERFSPLTTNINLLAENGRSNTQGVVSAPSTMMSVHRGE*

1515	A	1	785	FRRQRARAPLRVFLFPLGFDLQPPGRRWAAPAV\SGLS\RKVRCFST SVV\RHFAKLVGPS\VOVYGIEGRYAT\ALYSAASKQNKLE\QLEKE LLRVAQNPEGNPKVAAS\VLNP\YVKR\SIKSEKALN\DITSKRRF SPPSTTQPWIKFALPE\NGSD*SKYPQGSFPFALFPTHDEVSHPR\G GYPCTVDLWHLLEGSQTPPGI*KLSLKSLP*VKGQVLKLEAKTDP I\LGGMIVRIGE\KYVDMSVKTKIQKLG\RAMREIV
1516	A	1	2199	MAQFSIVGMCLGLFNQSPDTGSGVQLFVIMNQVMAANLAETHAALCP TLSSGTSARFRGKNQFSGGLPQITLSPLAQPCGRLAAMYSNVIGT SGKSLPSTSPPLVPLLSGFAPLFLKGLQNWQTQTQEGKSPSAAPASS QPQACPTDHSVRESALGACLSLPGEDGKIQKVYLLSLLIGFWDCVTC HGSPVDICTAKPRDIPMNPNCIYRSPEKKATEDEGSEQKIPEATNRR VWELSKANSRFATTFYQHLADSKNDNDNIFLSPLSISTAFAMTKLGA CNDTLQQLMEVFKFDTISEKTSQDIHFFFAKLNCRLYRKANKSSKL SANRLFQDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRRAINK WVSNKTEGRITDVI PSEAINELTVLVVNTIYFKVLRMALERPQGLP LALQLTPFFFFKWRDRSPERANGLPKATQGLWKSKEFSPENTRKELFYK ADGESCSASMMYQEGKFRYRRVAEGTQVLELFPKGDDITMVLILPKP EKSLAKVEKELTPEVLQEWLDELEEMMLVHMPRFRIEDGFSLEQ QDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLVNEEGSEA AASTAVVIAGRSLNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANP CVNLSEALAVLVNLTTLMKRTHGESLDFMERKRRPAESILLVSPPK CQRTKTGQGLTVRMNIDRFEELAGYGGD
1517	A	9	1618	PALCPTLSSGTSARFRGKNQFSGGLPQITLSPLAQPCGRLAAMYSNV IGTVTSGKRKVYLLSLLDSFGDCVTCHG\SPVDICTAKPRDIPMNP M\CIYRSPEKKATEDEGS\EQKIPEATNRR\RVW\ELSKAN\SRFCL PLSYSAPGQNSKD*H*LTFFCSPLSIFQGFLLWTKV\GACNDTLQQL MEVFKF\DTIS\EKTF*SRSHFFFA\KLN\CRL\YRKANKSSKL NRLFQDKSLTFNETYQ\DISELVYGAKLRPL\DFK\ENAEQ\SR\AA INKW\VSNKTEGRIHRCSFPSGRPFNELTVLGGGFNTIYFQGACWK\ SKFSPENTRKELFYKADG\ESC\SASMDVTREGKFRYSGAWLEGT/Q VLVCPFKGDDIT\MVLILPKP*EGAWAKVEK\ELTPEVLAKSGWD* FWREMMLVHMPRF\RI\EDGLQV*REQL\QRHGPLSDLFSP*KSPK L/LPGIVAEGRDDLYVSDAF\HKAFLVNEEGSEAAASTA\VIAGR SLNPNRVTFQGGQLFPGFLLREVPL\NTIYLHGAELANPCV
1518	A	2	363	ELDTLCDLYEP*PSPSIIIFINTRRK/VDWLTEKMHARDFTVSAMHGD MDQKERDVMREFRSGSSRVLITTDL\RIGRGRFRGRKGVAINMVTE EDKRTLRLDIETFYNTSIEEMPLNVADLI
1519	A	201	648	GPCGHGRVFPPLPSLAAHMDA*GLLLRDRVSSVHMLKRLSFLT*ARGI DVQQVSLVINYDLPTNRENYIHR*A*IWNTPLPLHTWPSLGLKLLIF LIPFLVFQ\IGRGRFRGRKGVAINMVTEEDKRTLRLDIETFYNTSIEE MPLNVADLI
1520	A	49	1720	GSTISSASQDSRSRDNGLDGIEPEGVIESNWNEIVDSFDDMNLSESL LRGIYAYGFEPKPSAIIQRAILPCIKGETSQSQKTLWTVPLGRVASG W*CPSHISQGSNLLVHPSLAFDPCPCLVHALDT*VSFKEVV*PAY ICIYSHVSSPAWCAILDELITGPCF*SGSHCVTVLIGKVCEP*NAW FIGCLLTSLT*DLNIPKGMLFTTFNS*FICLGYDVIAQAQSGTGKTA TFAISILQQIQ\KVVMALG\DYMG\AS\CHACIRGAPTCVAEVQKL\ QMEAPHIHRGVPPGRVF*YALPEDTLSPKYI\KMFVLDEA\DEM\LS RGFKGQIYGHQKAQAAPRVVLLSATMPFD\VLEVTKKFMRGPPFR ILVQKGELT\LEGIRQ\FYI\NVEPEE\FNLDTLCDLYENLDHHPRP VIFHQPPGGKVDWPHPRRMHAADF/TLYSAMHWRFWTQKERRT*L*R EF\RSWLLARIFDTQLDLLQORALMCQOV\SLVIQTYDPFPPTRGKL LIHR\IGSRVDRFGRKGVPINMLTE/EKTKRNLEDIETF\YNTSIE\ EMPLNVA
1521	A	3	607	FCPRGQEFEGGNKLLSPRRPWVISQRRTKATI\TSLWGK\VKCGKNA GKEETPGKGSVLVL/HPWTPRGSFEQLWQTCPSALCPSMGNPQSQGT

				MAKKVLTSLGRCP*STLD\DLKGHLLPKPEVNLHLLTSLHVG*RTF KLPGEMLLV/LFWAIPFSAKEFHPLKVAGFPQGKG*LGVGQCPCS FQIPLKPLGP*IQ\SFQG
1522	A	23	437	KTPGKGSLLVVL/HPWT\QRFDSFG\NLS\SASAHHGQPPKSKAHGK KVLTSLGDA\IKH\LDDLKGTFQAQLSELHCDKLHVDPENFKLLGNVL VTVLAIHFGKEFTPEVQASWQKMTCSGQCPVLQIPLSLLPMIQSFQ G
1523	A	23	249	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLLVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHL\DDLKGTF QLE*TCPLPLPSWATPKSRHMARRC
1524	A	46	379	SQTPMGHFTEED\KATI\TSLWGKGEMWKKCWKEKTPGKGSLLVVL/H PWTGRSGF\DSFGKPVPLPSAHPWATPKVKAPWPRRCLTSLGEMPIK \HLGLIFKGTFCPSLK*TCTC
1525	A	21	457	NPRVRGALTMELSESQKGFQMLADPRSFDSNAFTLLLRAAFQSLLD AQADEAVL\DNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHR MYRPAYLVTLVQNTDPSYPEISSSCSMEQLQDLGGKLDASKSLG KSTQL
1526	A	1	455	RKGSKMLADPASFDSNAFTFSSGAQFQSLNLNASPDEPRVSTYLEDN FDRERIELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKT NQLHRMYRPAYLVTLVQNTDPPSYPEISFSCSMEQLQDLVGKLDKDA SKSLERATQL
1527	A	3	470	VSRGVRVEGHGALTMELSESQKGFQMLADPRSFDSNAFTLLLRAAF QSLLDQAQADEAVLGKPLGSARSWIRRGGGALGEEPAEREGESPGKR KSPGFALRSGRSGDVALPGLGADSEHCFGPTWHLHRANSTFLARFP SQSLCSFVKPVFKS
1528	A	50	895	THASDGALTMELSESQKGFQMLADPRSFDSNAFTLLLRAAFQSLLD AQAD\EAULDHP\DLKHIDP\VVLKHC\HAAA\ATYLEAGKHRA\D KSTL\STYL\EDCKILTEKRIELFFAREYQ\NNK\NSLEI\LLGKY* GRSLPSYNRVFSWALWIIQVKDQSTFHRM\YRP\AYLGDLKVQNTG IPPS\YPRELVFSCQPNQL\QDL\VGETLKDASKKPWKRTATSVVTL GKVNRSPPSSRRKTQKPLPFSWNHRLCRAGCPFSVEKNFSLNLYP FIHFGHFKNV
1529	A	1404	1586	ENESRFSRDNQASAGLYLSDSL*QWIVGNGHATDLWQNCSTSSSGN VHHCFFFFSPNGSG
1530	A	187	701	AELAARMLLLLLSIIVLHVAALVLLFVSTIVSQWIVGNGHATDLWQ CSTSSSGN\VHHCFFFFSPNEW\LQSCSRGTMDPVDSSFSILSLFLFF CQLFTLTGKG\RFYITGIFQILAGLCV\MSAAAIYTVRHPW\NLNS GY\S*RFA*I\LAWVAFL\ALLSGVIYVILRKRE
1531	A	1	485	PPKLYNKVEPLRKKARAPEAQFEMPYVVRHNSQLSAPKSCFTFSH PNRDP MIDNNRYCTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPE THSPGMFSWFPILFPPIKQPIAHIPLASSPACQVSRALAAAGSAP VVQKGSSHQSMKTSQGQVRN
1532	A	2	460	SARRKMAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLC MPVFHPRFKREFIQEPAKNRPGPQTRSDLLLSGRAFLPLNQEDNTN LARVLTNHIHTGHSSMFWMRVPLVAPEDLRDDIENAPTTHTTEYS GEEKTMMWWHN
1533	B	1	2784	MAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCMPVFH PRFKREFIQEPAKNRPGPQTRSDLLLSGRALEIGADLP SNHVIDRWL GEP IKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLKLEVQFIIITGT NHHSEKEFCSYLQYLEYLSQNRPPNAYELFAKGYEDYLQSPQLPLM DNLESQTYEVFEKDPKYSQYQQAIIYKCLLDREVPEEKDTNVQVLMV LGAGRGPLVNASLRAAQADRRRIKLYAVEKNPNAVVTLENWQFEW SQVTVSSDMREWVAPEKADIIVSELLGSFADNELSPECLDGAQHFL KDDGVSIPEGYTSFLAPISSSKLYNEVRACREKDRDPEAQFEMPYV RLHNFHQLSAPQPCFTFSHPNRDP MIDNNRYCTLEFPVEVNTVLHGF AGYFETVLYQDITLSNRNYPSSSTPHNLIKGTERTGTGPGDPELDEQQ

9992

				RKEVKKDYPSTTSSTNSGNETSGSSTIGETSNRSRDRDRYRRNS RSRSPGRQCRHRSRSDRRHSGSESRSRDHREDRVHYRSPPLATGEP VDNLSPEERDARTVFCMQLAARIRPRDLEDFSAVGKVRDVRIISDR NSRRSKGIAAYVEFCEIQSVPLAIGLTGQRLLGVPIIVQASQAEKNRL AAMANNLQKNGGPMRLYVGS LHFNITEDMLRGIFEPFGKIDNIVLM KDSDTGRSKGYGFIITFSDSECARRALEQLNGFELAGRPMRVGHVTER LDGGTDITFPDGDQELDLGSAGGRFQLMAKLAEGAGIQLPSTAAAA AAAAQAAALQLNGAVPLGALNPAALTGKSVAQYTASLCLWLPLHIY SSMAPFLHFVDQAILRAWTLRLKLGPPRLRYQEKLLPMVPLEMDSAE QSHQLKRTSTPALNTCFSMCIVSEITFLPFPTP*
1534	A	2	608	FGPRDFLCMPVFHPRFKREFIQEPAKNRPGPQTRSDLLSGRDWNTL IVGKLSPWIRPDSKVEKIRRNSEALEVQFIITGTNHSEKEFCSYLQ YLEYLSQNRPPPNAYELFAKGYEDYLQSPLOPLMDNLESQTYEVFEK DPIKYSQYQQAIYKCLLDREVPEEEKDNTVQVLMVLGAGRGPLVNASL RAAKQADRR IKLYA
1535	A	1	207	PETHSPGMFWSFPILSAIKQPIITVREGQITCVRFWRCSNSKKVWYEW AVTAPVCSAIHNPTGRSYTIGL
1536	A	232	755	LSCCADDGVSIPGEYTSFLAP\IFSPKLYNKVRACRKKARDLKAQFE MPIVVRLHNSNQLSAPQPCSTFHPNRDPMIDNN\RYCTLEFPVEVN T\VLQCFAGYFETVLYQDITLSIRPETHSPGMFWSFPILFPIKQPIIT VREGQITCVRFWRCSNSKKGSSHQSMKTSQGQVRN
1537	A	35	2271	LCDWLLVSRNPGVDSARRKMAAMAVGGAGGSRVSSGRDLNCVPEIAD TLGAVAKQGFDFLCMPVFHPRFKREFIQEPAKNRPGPQTRSDLLSG RDW\NTLIVGK\LSPWDFVPD\SKV\EKIRRNSEGGPCLQELNFG\A YLG LPAFLPLNQEDNTNLARVLTN\QIHTGHDFYMFWR\RIHLKKP EDL\RDDI IENAPTHTTEEYSGEETWMMWNFRTLCDYSKRIAV EIGADLPSNHVID\RWLGEP\KAAILPTSIFLTNNKGFVLSKMHQ RLIFRLKLEVQFIITGTNHSEKEFCSYLQYLEYLSQN\RPPPNAY ELFAKGYEDYLQSPLOPLMDNLESQTYEVFEKDPIKYSQYQQAIYK LLDRVPEEEKDNTVQVLMVLGAGRGPLVNASLRAAKQADRGIKLYAV EKNPNNAVVTLENWQFEWG\SQV\TVVSSDMREWWAPEKADIIVS\B LLGLIC*PIELSP*VPWIGAQHFP*KMIGVKHPPGSYTSFLAPIS KLYNEVRACREKDRDPEAQFEMPVYVRLHNRQLSAPQPCFTFS\HR NRD\PM\IDNNRY\CTLG\FPVEVNTVLHGFAGYFETVLYQDITLSI RPETHSPGMFSW\FPIPLPY*GSPLTVRERAKPFCV\REFW\RCRQFP RKVWVWSSGGC*QAPVCSCLIQKPPKGPQYTHWPLLSPCRAPSVPEA LGKPAFRFLPPCSNSKVPVTSYGAVIPWPPIQRREHFQSCFPCPYIQ GGPRDYN
1538	A	137	303	LSGGLELSGFDRAGPETLPPLPSVSVREAGSCHSHSGSEWLELLVCV QVQDTTNW
1539	A	122	385	YPALEHILKAQAIQSRCGCDSCLPSPAPWDHPGPTTP\SPGRRAAAD PWHLSPIDGREHLR*VPVLPVTPPSPTLGHWVTDPSPGVGG
1540	B	277	480	GTGHFYGRTPSDTNCQEQYTHRKLCKIKSKADLVLMKNSKSLTRVIR NILAPQDQNHQQNPLNSQFLQ*
1541	A	32	1386	VLLGPKAERTNSRRNYQRRDYFSAPRSITSNQSAKSSSSSRGVYSAYQ APDIHECCHFRSASF LDKMATPAVPVSAPPATPTVPAAVPASAPA SVPAPTAPAAAAPVAAAAPASSSDPAAASATTAAPGQTP\ASAQAPA QTPAPALPGPALPGFPFGGRVV\RLHP\VILASIVD\SYERRNEGAC PS*SGTLFGKLVK\HSVE\VTN\CFSVPHNESEDEV\AVDMEFAK\ NMYETGIKKVS\PNKLILG\WYATGHDITEHSVL\IHEYYSREAPNP IHLTV\DTSLPGTGRMSIKA\YVST\LMGIPLGRT/LWGVMFTPLTV \KY\AYYDTERIRRLTLIMK\TCF*PPTRVIWTSQVDLQOEGGGIQL RNPGMPLSTSVANMEGCTCLGKVSADNTIRKVGHFLMSL\VN\QVP ENRKPMTFETMLNSNINDLF\MVTYLANLTQSR\IALNEELVNL
1542	A	1	3399	MLVGQAGPLGPAVVTAAVVLLLSGVGPAHGSEDIIVGCGGFVKSDV EINYSLEIKLYTKHGTLKYQTDCAPNNGYFMIPLYDKDHLMSRDV

				FVVTSVAVRYSHPGDFILKIEPPLGWSFEPTTVELHVDGVSDICTKG GDINFVFTGFSVNGKVLSSKGQPLGPAGVQVSLRNTGTGTEAKIQSTVTQ PGGNSCLSPLSNPVECSVTGPCCATRIGFMPPEILEIKGDVSTPLSDQ HMEHPSWHTASTTVRVNTSNANAASPLIVAGYNVSGSVRSDEGPMKG VKFLLFSSLVTKEPQDESLVYLCYTVSREDGSFSFYSLPSGGYTVIP FYRGERITFDVAPSRLDFTVEHDSLKIEPVFHVGMGFSVTGRVLNGPE GDGVPEAVVTLLNNQIKVKTAKDGSFRLENITTGTYYTHAQKEHLYFE TVTIKIAPNTPQLADIVATGFSVCGQISIIIRFPDPTVKQMNKYKVVL SQDKDKSLVTVETDAHGSFCFKANPGTYKVQVMVPEAETRAGLTLPK QTFPLTVTDRPVMDFVQFLASVSGKVSCLDTCGDLVTLQSLSRQ GEKRSLLQSGKVNAMTFTFDNVLPKGYKISIMHEDWCWKNKSLEVEV LEDDVSAVEFRQTGYMLRCSLSHAITLEFYQDGNNGRENVGIYNLSKG VNRFCLSKPGVYKVTTPRSCHRFEQAFYTYDTSSPSILTTLTAIRHVL GTITTDKMDVTVTIKSSIDSEPALVLGPKSVQELRREQQLAEIEA RRQEREKNGKEEGEERMTKPPVQEMVDELQGPFSYDFS YWARVLCFV GTGPAKLKYINFRSGEKITVTPSSKELLFYPPSMEAVVSGDESCPGK LIEIHGKAGLFLEGQIHPELEGVEIVISEKGASSPLATVTFDDKGYA SVGPLHSDLEYTVTSQKEGYVLTAVEGTIGDFKAYALAGSPGQYFK PMMKEFRFEPSSQMIIEVQEGQNLKITITGYRTAYSCYGTVSSLNGB EQGVAMEAVGQNDCSIYGEDTVTDEEGKFLRLGLLVGNNDIDDVNI VFRQINQFDLSGNVITSSEYLPVLWVLYKSENLDNPIQTVSLGQSL FFHFPLLRLDGENYVVLDDSTLPRSQYDYILPQVSFTAVGYHKHFTL IFNPT
1543	A	1	3126	MASTTVRVNTSNANAASPLIVAGYNVSGSVRSDEGPMKGKVKFLLFSS LVTKPEQDESLVYLCYTVSREDGSFSFYSLPSGGYTVPVFHVGMGFSV TGRVLNGPEGDGVPEAVVTLLNNQIKVKTAKDGSFRLENITTGTYYTH AQKEHLYFETVTIKIAPNTPQLADIVATGFSVCGRISIIIRFPDPTVKQ MNKYKVVLSSQDKDKSLVTVETDAHGSFCFKAKPGTYKVQVMVPEAE TRAGLTLPKQTFPLTVTDRPVMDFVQFLASVSGKVSCLDTCGDLV VTLQSLSRQGEKRSLLQSGKVNAMTFTFDNVLPKGYKISIMHEDWCW KNKSLEVEVLEDDVSAVEFRQTGYMLRCSLSHAITLLRCLCSPYLL SLSSSLTYSGLLIVSLIRGYCLLVLIYRCFDDSFNADRALVGLFGG GGPWGLVACPSLSWQDSECQAPQVCNRAQGDVGRDVSNNLRALDV GLLANLSALAELDISENNKISTLEEGIFANLNLSEINLSGNPFECDC GLAWLPRWAEQQVRVQPEAATCAGPGSLAGQPLLGIPLLDSCGGE EYVACLDPDNSSGTVAAVSFSAHEGLLQPEACSAFCSTGQGLAALS EQGWCLCGSAQPSSASFACLSLCSGPPPPAPTCTRGPTLLQHVFPAS PGATLVGPHGPLASGQLAAFHIAAPLPVTATRWDFGDGSPVEDAAGP AASHRYVLPGRYHVTAVLALGTGSALLGTDVQVEAAPAALELVCPSS VQSDSESLDLSIQNRGGSGLEAAYSIVALGEEPARAVHPLCPSDTEIF SGNGHCYRLVVEKAAWLQAQEQCRAWAGATLAMVDSPAVQRFLVSRV TRSLDMWIGFSTVQGVVGPAPQGEAFSLESCQNWLPGEHPATAEH CVRLGPTGWCNTDLCSAPHSYVCELPGGPVQDAENLLVMVFPGLRL SREAFLLTAFTGTELRPAQLRLQVYRLLSTAGTPENGSEPESSP DNRTQLAPACMPGGRWCAGANICLPLTPPATPLGRQCCTEVTISTPL EKEEEKIP
1544	A	115	348	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNGILT FSNLVTCSAIYHLPVFPEREPCSMRDLRVA
1545	A	1	513	FHFTPLFRDGETYVV/MLDSTLPRSQYAYILPQVSFTAVGYHKHITL IFNPARKLPEQDIAQGSYIALPLTLLVLLAGYNHDKLIPLLQLTSR LQVGALGQAASDNNGPEDAKRQAKKQKTRRTLRLQEEFQLMWCLVP WRGTLGIHLFSSLPFASEILLETATCIHY
1546	A	1	888	MASLIMMSLPAMRTLAWAMAVSGNCIPEGQFSALSCADFGISPKLIG IEQFRAQRTLIIGNRVGTVTGQREFEITYDERRPDKTRERRIRQSAL LPDAGVNALSGLRRVREFVGLIRRASVASGSRYHCRMRRKRLIRPTE GAGIRRPDKTRKRRIRQSAPMPELPGPPVIETSTRNFKENWEENFCY

				LEFTIAKLGTTTRKRIQENCKGQPLGPAGVQVSLRNTGTEAKIQSTVT QPGGKPKVDKTTKMGKKQSRKTGNSKKQSTSPPPKEHSSSPATEQSW MEDDFDKLRKEGFR
1547	A	1	4710	MGSTGVYKVTTPRSCHRFEQAFYTYDTSSPSILTLTAIRHHVLTGTTT DKMMDVTVTIKSSIDSEPALVLGPLKSVQELRREQQLAEIEARRQER EKNGNEEGEERMTKPPVQEMVDELQGPFSYDFSYPWARVLFCVGTGPA KLKYINYFRSGEKITVTPSSKELLFYPPSMEAVVSGESCPGKLIIEIH GKAGLFLEGQIHPELEGVEIVISEKGASSPLITVFTDDKGAYSVGPL HSDLEYTVTSQKEGYVLTAVEGTIGDFKAYALAGVTLHSQDVLMLPG DLVGLQHDAGPGALLHCSAPAGHPGPQAPYLSANASSWLPHLPAQLE GTWACPACALRLLAATEQLTVLLGLRPNPGLRPLGRYEVRAEVGNV SRHNLSCSFVDPVSPVAGLRVIYPAPRDGRLYVPTNGSASVLQVDSGA SATATARWPGGSVSARFENACPALVATFVPSCPWETNDTLFSVVALP WLGEGEHVMDEVVENSASRANLSLRVTAEEPICGLRATPSPEARVLQ GVPVLLAGSSGYLVGFKFLESHGSDSGSANSFHRLISRNEFKTLP DLTRVPRYSPVVEAGSDMVERWTINDKQSLTFQNVFNVIIYQSAAVF KLSLTASNHVSNVTNINITVERMNRMQGLRVSTVPAVLSPNATLAL TAGVLVDSAVEVAFLWTFGDGEQALHQFPYPYNESFPVPDPSSVAQVL VEHNVTHTYAAPALGGGAVLTRQPSVLLHLCSVPHVAWEPGTLKAG PQVSTVLTVLASNAFENRTQQVPVSVCASLPSVSVCASLTGACWYPR VLIRSGRVPIVSLECVSCKAQAVYEVSRSSYVYLEGRCLNCSSGSKR GGYTFTLTVLGRSGEEEGCASIPLSPNRPPLGGSCRLFLGAVHALT TKVHFECMGWHDADAAGAPLVYALLLQRCRQGHCEFCVYKGSLSGY GAVLPPGFRPQFEVGLAVVQDQLGAAVVALNRSLAITLPEPNGSAM GLTVWLHGLTASVLPGLLRQADPQLVIEYSLALVTVLNEYERALDVA AEPKHERORRAQIRKNITETLVSLRVHTVDDIQQIAAALAQCMRKL EQDIAQGSYIALPLTLLVLLAGYNHDKLIPLLLQLTSRLQGVGALGQ AASDNSSGPEDAKRQAKKQKTRRTLATSINTSREPSTDDQLPAHNQTM PQRHARRSAPPAYDRKTRQEENPHQTRSHAAAKRRERP PHDLQKQA TTRLIPAGPRRRDGTSPRRTPQPPNTRRPAAGHLARFRRAAPGAR ARPPTARRGREELDPAHIYAAAPGLPTPPRAGRTPPTPERDRNTRR RRTREEGEGEFRPVSFLLKTIFFPSQNGHDGSTDVQQRARRSNCRRQEG IKIVLEDIFTLWRQVETKVRKIRKMKVTTKVNHRDKINGKRKTAKE HPSTEKLRPDDDICRRSTSKHYRKFTKGSTEVLSKWQPLGPAGVQVS LRNTGTEAKIQSTVTQPGGNSCLSPLSNPVECSVTGPCCAARIGFMP EILEIKGDVSTPLSDQHMEHPSWHTVPSLFPKPKSSKSLKKNRQFEFA KTLDMHRFTFTFSCFRQOR
1548	A	37	3683	LGLGLSMLVGQAGPLGPAVVTAAVVLLLSGVGPAHGSSEDIVVCGG FVKSDVEINYSLIEIKLYTKHGTLKYQTDCAPNNGYFMIPLYDKGDF ILKIEPPLGWSFEPTTVELHVDGVSDICTKGGDINFVFTGFSVNGKV LSKGQPLGPAGVQVSLRNTGTEAKIQATATQ\PGGKFAFFKVLPGDY EILATHPTWALKEASTTVSVTNSNANAASPLIVAGYNVSGSVRS DGE PMKGVKFLLFSSLVTKE\ALGCNVSPVP\GFQPPIREVWCNLCYTV SREDGSFSFYSLPSGGYTVIPFYRGERITFDVAPSRLDFTVEHDSLK IEPVFHVGMGFSVTGRVLNGPEG\GVPEAV\VTLNNQIKVKTKA*WA HSRLENITTGTYYTHAQKEHLYF\ETVTIKIAPNTPQLADIVATGFS VCCRISIIRFPDTPVKQMNKYKVVLSQDKDKSLVTVETDAHGSFCFK AKPGTYKVQVMVPEAETRAGLTLKPQTFPLTVTNRPMDVAFVQFLA SVSGKVSCLDTCGDLVTLQSLSRQGE\KRSLSGKVNAMTFTFDN VLPKYKISIMHEDWCWKNKSLEVEVLEDDMSAVEFRQTGYMLRCSL SHAITLEFYQDNGRENVGIYNLSKGVNRFCLSKPGVYKVTTPRSCHR FEQAFYTYDTSSPSILTLTAIRHHVLTITTDKMDVTVTIKSSIDS EPALVLGPLKSVQELRREQQLAEIEARRQE\SVYKGEEGEERMTKP PVQEMVDELQGPFSYDFSYPWARSGEKITVTP\SSKELASFIPLSM\E AVVQWEKACPGKLI\EIHGKAGLFLEGQIHPELEGVEIV\SEKGAS SPLD\ITVFTDDKGGLQCLGPLHSDREYTVTSQKEG\YVLT\AVEGT

				MGDF\KAYAL\AGVSFEIKAEDDQPLPGSPFY*TGGL\FRSNLLTQ GQRAFLTFSNLKPLASIYFKPM\MK\EFRFEPSSQMIEVQEQNL\K ITITGYRPAYSC\YGTVS\SLNREPEQGV\AM\EAVGQ\NDCKHFTE KTPVTDEEG\KFRL\RGLLP\CVYH\VQLKA\EGN\DHIERALPHH RVI\EVGNNDI\DDVNI\VFQINQFDLSGKCDLPLEYLP\TLWG SSFYKSE\NLDNPIQTVSLGQ\SLFFHFPPLLRDRELCLCFWDSTL PRSQY\DY\ILPQVFFSPQLGLTIKHITLDFYFPRREAANWRDIRTK DPYIALAIDRCWFCWAGYNP
1549	A	1	474	MDNLSSEEIQRAHQITDESLESTRILGLAIESQDAGIKTITMLDE QKEQLNRIEEGLDQINKDMRETEKTLTELNKKCCGLCVCPCNSITNDA REDEMEENLTQVGSILGNLKDMLNIGNEIDAQNPQIKRITDKADTN RDRIDIANARAKKLIDS
1550	A	1	1554	MLSCYKQKFLAADALVTMDVDFYQAKENAELKNAINQPHHLAQVVT IKQLQTLPLDSWGQICNKNQSLSVSLTSQDAGIKTITMLDEQKEQLNR IEEGLDQINKDMRETEKTLTELNKKCCGLCVCPCNRTKNFESGKAYKT TWGDGGENSPCNVVSQPGPVTNGQLQQPTTGAASGGYIKRITNDAR EDEMEENLTQVGSILGNLKDMLNIGNEIDAQNPQIKRITDKSHLGQ PSVLKLDTSFLRRFHMSAERTVSHPSAAAQVPAGRKRCCHRPVHPV GLPAGAPAPALNSRRSLAPGARPKSDKEESEEHRTARPPSPAFAALR RPGASGSLRKIREPRTRLPLSCRKAPQEMLNMSKKTVSCFVNFTRL QQITNIQAEIYQKNLEIELLKLEKDTADVHPFFLGNPTDAYLDAT MNEAPGPINFMTFGEKLNGLTDPEDVIRNASACFDEEATGTIQEDYLR ELMTTMGDQFTDEEVDLHREAPIDKKGNFNYIEFTSILKHGVKDKD D
1551	A	87	736	FIMDNLSSEEIQRAHQITDESLESTRRI\GLAIESQDAGIKTITM LDEQKEQ\LNRI\EEAWAQIIKDMR\ETEKTLTELNK\CCGLCVCPC NRTKELLSLGQGFIKTTWGRWWEKTSWPQC*YSKQPGP/VWTNGQLQ QPTTGAASGGYIKRITNDAREDEMEENLTQVGSILGNLKDMLNIGN EIDAQNPQIKRITDKADTNRRFVLDYCPMPEQK
1552	A	99	362	FSHIYSLFILFQPLEIRGPYDVANLGLLFGLSSEDAKAAVSTNCRAA LLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKKAKCEG
1553	A	184	360	YVKPPHFKLCLNFKHSGFPVCFTETRKTAFGIISTVKKPRPSEGDE CLPASKKAKCEG
1554	A	3	403	ISSALNLMQICKGKNVISSAAERPLEIRGPYDVANLGLLFGLSSE AKAAVSTNCRAALLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKK AKWSHVSQTAGVQVHNLGSLQPLPLGLQAIPTFTSLPRN
1555	A	1	872	EFGRWDFSMVAFADLLRAGSDLKALRGLVET\AAHLGYSVAINH IVDFKEKKQIEKPVAVSELTTLPIVQKSRPIKILTRLQIMLSH \SPAKVLKNTLKRAGL*D\VGAGFPKAEKAFILLCTHL\DVDL\V CITVTEKLPPFYFKRPPINVAIDRGLAFDLALIPLLSKDSMTMRYTIS PVPLQF*CKSCKGKNVIIS\SACKKRPF*KIRGPILTAN\GLPVW GFSESERQGFQCPNCRAA\LLHGETRKTAFGIISTVKKPRPSEGDE DCLPASKKAKCEG
1556	A	46	584	SRRPWVISQRRTRLLSTSLWCKVNVE\DAGGETLGRLLVVPWTQRF \FDSFGNLSSASAIHQTPKVKAHGKKVLTFLGEMPLKHL\DDLQGA PFAQA*SELALVDKPMWDP*GTSKLPGEILLVTRFGQSLFRQKNFT PGGARVSWGRKMGDLELASALVPSRLPLSSLAHECRAFQ
1557	A	1476	1747	GNFNSLRSLSKTQLCAHCLYPHTFGRQRWVDHLRLGVDR*PGQHGETP SLLKNNNNNTKISWAWWHEPV\IPA\MGEAEAGESLEP\GRRRLQ
1558	A	1	507	MSMLRLQKRLASSVLRGKKKVWLDPNKTNEIANANSHQQIWKLIKD GLIIRKPVTVHSRARCQKNTLAHWKGRHIGIDKRYCESKKIDRHYH SLYLKVQGNVFTNKPILMEHSHKLKADKAHKKLLADQAEARRPKTKE ARKRSEERLQAKKEEIIKTLFKEEDTKK
1559	B	15	400	MSMLRLQKRLASSVLRGKKKVWLDPNETNEIANANSRQQIRKLIKD GLIIRKPVTVHSRARCQKNTLARRKVRHMGIGKRKGTANARMPEKVT WMRRMEILRHLLTRYRECETINRAMHLLNLKVM*

1560	A	15	710	INPPPPAFLSLLRPQPCSMRLRLQK\RLAS\SVLR\CGKKKVWLDPNE TNEIANANSRQQI\RKLIKDG\LIIRKPV*RVHSRARCCKNTL\ARR KGTAH\CGIGKREGYSPMPRMP/TRKVTWMKENEGFWRRLASERYR* NLKKIRFATLLSQALYPEG*RGNVVSKTRRVFHCNTFHKLEGRQRP KKAPWLDQA*G/RRRS*DQKGHGKR\REERLPGQRKEEINQRLYSKE EETKK
1561	C	1791	2183	MNRTVENSTPLQDFVFTSSFTNPKPNPLLKISLAALPR SAYDGGIHI GRAQVCPWVAMARPRAERCLLHFALQLLQLPDRERAKRLQQLAERW RRPPSGHHQIPLFPRRHGDPRTDLRASNVYSSIIC*
1562	A	2	421	MASGRARCTSNLRNWVVEQVESGQFPGVCWDDTAKTMFRI PWKHAG\ WAI FKGKYKEGDTGGPAVWKTRLRALNKSSEFKEVPERGRMDVAEP YKVYQLLPPGIVSGQPGTQKVPSKRQHSSVSFSEKKEEDAIANCTL
1563	A	20	432	GRLSPATAWTATQAWAIFKGKYKEGDTGGPAVWKTRLRALNKSSEF KEVPERGRMDVAEPYKVYQLLPPGIVSGQPGTQNVPSKRQHSSVSSE RKEEDAMQNCTLSPSVLQDSLNEEGASGGAVHSDIGSSSS
1564	A	107	401	FQVLLTLQLLLWQDPLPLSIMGSSLLPPCLWPSLFFLFPEPLTSL SDLVRYFQGLGPPPKFQVTLNFWEEESHGSSHTPQNLITVKMEQAFAR YLLE
1565	A	191	353	PHSSTTCPPAPMLVF*KRDPPSLGPHDALVPPCPVPVEILRSSAKTR CGKKASS
1566	A	553	690	SRRRFPMSGGTKLV*G*GEMESLEEQAQKGGTESCALHPVDLFSSPG PLFNSLCLSKPMAPPTL
1567	A	2406	4031	GGRAGDGPLSATCTYAPSLWLDEGSPCLPGPLVTEADRRGTLGTEYP PQAEVAEGKGPDEGPMACSLRNSSSTNKEASYHGPFLVLLPEFDWY LKSPNMYQVGTGVECRCTGVHSSPEVPGLTPGNWPPWGSBGVQORMA SG\RARCTRKLRNWVVEQVESGQFPGVCWDDTAKTMFRI PWKHAGQ DFREDQDAAFFKAWAIFKGKYKEGDTGGPAVWKT\SLCCALNKSDF KEVPERGRMDVAEPYKVYQLLPPGIL\SGH\PGTQKVPSKRQHSSVS SE\RKE\EKDAMQNCTLSPSVLQ\DSLNEE\EGSGGAVH\SDI\G SSSSSSSPETTRKITDTTE\APFQGDQ\RSLEFL\LPPEPD*SLLLT FI\YNGRVVGEAQVQSLDCRLVAEPSCSESSMEQVLFPPKPGPLEPTQ RLLSQ\LRGILVASTPQGLFRCSAFCPPIFWGIAQP\APPQ\PGP HLLPSNECVELFRTAYFCRDLVRYFQGLGPPPKF\QVTLNFWEEESHG SSHTPQNLITVKMEQAFARYLLEQTPEQQAAILSLV
1568	C	77	325	MSLIQEALHLVLTDPDAPAGDDPKYREWHHFLVVMKGNDISNGTVL SDYXCAAPPKAPSHVPQFSVACIIDFSSSCPPWHG*
1569	A	60	287	ISMFPQKNPPPSWFFQGWFFKGPEGHFYAFLGILNALCWGLTPNPP FGFFGEGPPPKIPLGSLGSGFQQRQRP
1570	A	3	703	VEFFSSQRAELYATPLTPAPGPNNGGIPGWTLLWALPRPGNLRKGPGP LSLQEVDEQPQHPLHVTYAGAAV/DDELGKVLTPQVKNRPT\SISW DGLD/SKGKLYTLVLT\DPDAPKQKDP\KYRE\WHHFLGWSTLKGQ MTSATGTVLS\DYVGLGGLPKGTGLHR\YVWL\YEQ\DRPLK\CDE PHPSATRS\GDHRGKIQRWASLPVKK**SSRAPGGWAPCYPQPEVGM NQCAPKL
1571	A	1749	2411	APSLVSEHSAPGPQRELPOPLLTQAYEQILGITC\GSCP\AQGWG AWSSDAVPOLLARRPPLPHGLPACGEWGRGELGVKPSGLPSHAGPAW GHQVRTVCATAHPQDCISPEGAVEEEIVGG*GC\TEGQSQRVLQIWP \SQGVSSLSALVPLN\MF\TELLIEYEEKIFSTP\EAPGEHGLAPWE QGSRAAPLQEA VPRTOATGLTKPTLPPSPLMAARRRL
1572	A	1	3408	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIGEAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQVRGYTIEQINHM RDVF GTRLRRAEDVFPPIGVAAHKGGVYKTSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIPSCIALHRIETELMGKFDEGKLPTDPLMLRLAIETVAHDY DVIVIDSAPNLGIGTINVCAADVLIPTPAELFDYTSALQFFDMLR DLLKNVDLKGFEFDSAHPPAVHLSNGPGQEP IAVMTFDLTKITKTS

				SSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQLHNHWAQLT VGAGPRLLDDGRWHQVEVKMEGDSVLLLEVDGEEVLRRLRQVSGPLTSKR HPIMRIALGGLLFPASNRLRLPLVPALDGCRLRDSWLDKQAEISASAP TSLRSCDVESNPGIFLPPGTQAEFNLRGSSGSKSVGPLRGLVAVCEA LGLWSQTAGIRMASVRIREAKEGDCGDILRLIRELAEFEKLSQVVKI SEEGPCVVGYGIIYFIYSTWKGRTIYLEDIYVMPEYRGQGIGSKI KVAEVALDKGCSQFRLAVLDWNQRAMDLYKALGAQDLTEAGWHFFC FQGEATRLAGNMQSERQIPFGDVRLPPPADYNKEITEGDEVYVSR ANEQEPGWWLARVRMMKGDQVAQVIHNFSSFTMCQFYVIEYAACDA TYNEIVTLERLRPVNPNPLATKGSFFKVTMAVPEDLREACSNENVHK EFKKALGANCIFLNTNSELFILSTTEAPVKRASLLGDMHFRSLRTK LLLMSRNEEATKHLENCIRVRNIETKLVGTGKVGTONQTLGNTLTGS TAAKGVGVLI EGLATSKNPLMTLKPNDTNSVYIDYETEDDTSQDVYP NQGNVTSQPLHFQATLKQDGNIAIEPGEFKATSTFQAEAKLPSKHPI CSKFRGSLQRMGRGYWIQLFSPVPVHPDYGKQEKADLSFSFVANEV LSERREAFISIDSEEGALLEDNGMLLAHWIYVSEICDYCNLRFQGS SVTGMISMDSYCFDIHVSSSELFSSVTEHLLRTFSSHIIPRLECRS DATTSEKD
1573	A	2	1136	MPGQRIASLAYSLLPYGAGIPAPLTRPRLPRRPPRLPPPRSLRLFRI QVRRPFGKSSCRLRGPGTLVPDSDGPDGFRADPRGQGGRLWRYPEAD SGENCRPVTRGSEWRGQSGVLRGGGRGRGSPWEPARGAAGPFCSNLA SGPTP*ELAEFEKLSQVVKISEEALRADGFGDNPFYHCLVABILPAP GKLLGKSTWPLEVHLSSRPQRSPLRLPEALLPFSLSQG/HCVVGYGI YFIYSTWKGRTIYLEDIYVMPEY/RGYWAEAEAGVGAKHPTDPTVI PCPQSPAGVIF*SPSAQTIAIFCLFLSTTGQIGISKI IKKVAEVALD KGCSQFRLAVLDWNQRAMDLYKALGAQDLTEAGWHFFCFQGEATRK LAGK
1574	A	182	797	LPFARPWDGPRQRGSGWLPCGSREAKEGDCGDIL\RLIRVKTAGE LAEFEKLFSGGERSVEEALESRLAFGDNPFYHLFW*AEILPAPGESY WG/HCVVGYGIYFIYSTWKGRTIYLEDIYVIAGNIGVQIGISQK*S KKV\AEVALGIRGCSNFRRLARPLD\WNPEGPWDLYKAPRSPKI*RK LEGWHFFCFQGEATRKLAGK
1575	A	1	254	STISLCRRCGSKAYHLQKSTCGKCGYPAKRKRKYNWSAKAKRRNTTG TGRMRHLKIVYRRFRHGFREGTTPKPKRAAVAASSSS
1576	A	3	308	RTSEMTKGTSFFGKRRNKHTLTCRRCGSKAYHLQKSTCGKCGYPAKR KRKYNWSAKAKRRNTTGTGRMRHLKIVYRRFRHGFREGTTPKPKRAA VAASSSS
1577	A	1	380	IPTPLIGNFGPRGPRIRHERPQKRDDRREPSSFGKRRQ*DGTLIC\R RCGS\KA\YHLQKSTCGKCGYPAKRKRKYNWSAKAKRRNTTGTGRMR HLKIV\YRRFRAWDFREGTTPKPK*GSLLOHSSSS
1578	A	41	544	APSPRRPWGHFTEED\KATI\TSLWKG\VNVE\DAGGE\TPGKGLV VYP\WTQRFFDSFGNLSSAF\AHHGQTPKVKAHGK\KVLIT\SLGDAI K\HLDDLKGTFAQA*VNLHL*QSCNVDP\ENFQAPGEMLLVTR\VLA IHF\GK\EFTPGGCKASWAEDG*LAVGQWPCSSRYH
1579	A	1207	1369	ILETYIKTLQRYADGSYKSEKVKSVGPRGGAIEKEKNCLTVPFQEK LGSGIVV
1580	A	1	1716	TCIAAVKMEGPLSVFGDRSTGETIRSONVMAASIANIVKSSLGPVG LDKMLVDDIGDVTITNDGATILKLEVEHPAAKVLCELADLQDKEVG DGTTSVVIAAEELLKNADELVKQKIHTSVISGYRLACKEAVRYINE NLIVNTDELGRDCLINAAKTSMSSKIIGINGDFFANMVVDAVLAIKY TDIRGQPRYPVNSVNILKAHGRSQMESMLISGYALNCVVGSGQMPKR IVNAKIACLDFSLQKTKMKLGVQVVIITDPEKLDQIRQRESIDITKERI QKILATGANVILTTGGIDDMCLKYFVEAGAMAVRRVLKRDLKRIAKA SGATILSTLANVEG*ERFEGAMWDQAEVQERICDDELILIKSTKA \RTSASIIISRVPIDSMCEMERSL\HDALC\VVK\RVLESK\SVVPR \GGAVEAALSIY\LENYA\TSMGSREQLAIA\EFARSLSGYSPIPLA

				VNAAQDSTDLVGKN*R/RLFHNEAPGLTPE\RKN\LKWIGLDLSNGK P\RDNDKQAGVFEP/TPIVKVKSCLKFATEAAIT\ILRIDDLIKLHPRK *R*\KHGSYEDAVHSGALND
1581	A	1	514	PRVRNLSREWLCDRHLREKMFSSVAH\LANANPFDTPH\LQLVHDGL GDLRSSSPGPTGQPRRPRNLAAAAVEEQYSCDYGSGRFFILCGLGGI ISCGTHT\ALVPLD\LVKCRMV\DPQYKGFNG\FSVTLKEDGV RGLAKGWAPTFL\GYSMQGLLQVLAFYEVFKVLY
1582	A	2	1296	ALCEPQPFQSGSCVIAILGRKMFSSVAHLARANPFTPHLQLVHDGL GDLRSSSPGPTGKPRRPSQ/HMAAAPVEEQYSCDYGSGRFFILCGLG GIISCGTHTALVPLDLVK\CRMQVDPQYKGF\IFNGFSVTLKEDGV \RGLAKGWAPTFLGYSMQGLCKFGFYEVFKSL\YSNMLGE\ENTYL* RTSLYLAASAS\AEFFADIALAPMEAACKVRIQTQP\GYANT*EGISF PKCIKEGLTSILQGGLPLWMRQIPYTMN*SSPCLERTV\EA\LYK FV\VPK\PRRE*FKRQSRLVVTIW*QVTIARVFCANCFSPLEFLG* PVLDD*GKKVSQCFLWVLQRDGLGK\GV\WKGLFA\RII\MIGT\LT\ ALQWFIYYSVKGYFR\LPRP\PPP\EMQES\LKKKLGVNSVVRIKAN CGLNLLVDPVFEEESAKGTFIYLT
1583	A	127	434	RPLESWIGLVRCNICRSPIAEAVFRKLVTQDNISKNWRVDSAAATSGY EIGNPPDYRGQSCMKRHGIPMSHVARQ\DLNRKSNRVKTCCKAKIELL GSYDPQKQL
1584	A	2	535	QRGGIRKMAEQATKSVLFVCLGNICRSPIAEAVFRKLVTQDNISENW VIDSGAVSDWNVGRSPDPRAVSLRNHGIHTAHKARQITKEDFATFD YILCMDESNLRDLNRKSNQVKTCCKAKIELLGSYDPQKQLIIEDPYYG NDSDFETVYQQCVRCCRAFLEKAHLGRFVPCCGQPD
1585	A	551	1299	PADPPRPSYYRHRTPPQAHWSRLRRSRLRRRGSHTRCPVGVGAGLRR RAGARLAVRLRASACGTPRCLGASARGKMAEQATKSVLFVCLGNICR SPIAEAVFRKLVTQDNISKN/WEGRQRGNFRWVIDSGAVSDWNVGRS PDPAV\SLRNHGIHTAHKARQIT\KEVFPTFDYILCMDESN\RD LNRKSN\RVKTCCK*KFELPWEL*SPQKQLIIED\PYIGE*LWTLET VYQQ\CVR\CCRAFL\EKAH
1586	A	1	1239	MERAEFVFTGIDAYSRYGFAYPACNASAKTTSVDSWNALSTVMVFHT ALPLTKALTLRLKKLVTVSLVDSTVVLWLWLQLOTQLKVAKDRAFSPC PSVGEENPPYESLQISPDVPLRRTSRCQVHNYTKCPAWGQVPAHAE VRGEWADGQLPQPILDQSTPMILTRVLWPYKGGKVLPLSAPGEK GGPCRQGSKSGAAVGGVLQALLWRKSCCPEWRQGWMMVDNQLIGTTO PFMLYVTPLSNENEVIETGPAVQVNAVKFPSKSALTNIYKHLMITAQ RFTVQIEEKLLKLLSFFGYDQAESEVEKYDENLHEKTAEQGGTPIR YYFENLKISIPQIKLSVFTSNKPLDLKELLSQAARILGSVDFLGNP MGLLNDVSEGVGTGLIKYGNVGGILIRNVTHGVNSNAK
1587	A	298	408	SILRCVISYFSSFSVSKISPSWCLGFRSFFFLKTRTG
1588	C	92	244	MRCEIILVLIPIVYFYFYSNKLCSRLXXXXXGGAVLKNPWGGQSLPGL AR**
1589	A	33	191	RDDPRVRPPPNST*PQQEPGL*LIKCTSPQAPAPRTVHGPFYFMR LIKMF
1590	A	3	1285	CFSFVVRHSSRHCREYETLITADFPPEASYLMSLCSWSVTTMVAFL AQSRPSGSAGAHRSRVSSTALGHSKRLADTDLALMKPAWTPAFQH CMQHPNQPCEEKRYEQMVTQOSDTHQKATCRGSTCWALGQPQLLVS HVIMKREQILYSGPCCQMTSPSCQLILSCDKTEFYVLFIPALMDETA FLVKFAGTSLDGLGKTMNDRHQSEREYIRYHAATSGEHLVAGIHGLA HGKSWVTSGSAAAGPQRRLCINLIAAIKKERLQQLSFSLGIIGGLT SVITSTVEGVKTEGGVSGFISGLGKGLVGTVPKPVAGALDFASETAQ AVRDTATLSGPRLKYFQVPLLVGVRWHSKRQPPNFPKPGNPVLR KADEALKSQLGALGLRLRGPYCGMIKWGPADSGLLLRGAKLNGDERG DLKL
1591	A	3	3469	QPGHTIYLLPTVVICNLLPCELDYVKGMPINGTLKPGKEAALHTAD TSQNIELGVSLNFPLCKELLIPPGTQNYMVRMRLYDVNRRQLNLT

				RIVCRAEGSLKIFISAPYWLINKTGLPLIFRQDNAKTAAGQFEEHE LARSLSPLLFCYADKEQPNLCTMRIGRGIHPEGMPGWCQGFSLDGG GVRALKVIOQGNRPGLIYNIGIDVKKGRGRYIDTCMVIAPRYLLDN KSSHKLAFAQREFARGQGTANPEGYISTLPGSSVVFHWPRNDYDQLL CVRLMDVPNCIWSGGFEVNKNNSFHINMRDSLKG\CFPLRVEITLRG ATYRISFSDTDQLPPPFRIDNFSKVPVFTQHGVAEPRLRTEVKPMT SLDYAWDEPTLPPFITLTVKGAGSSEINCMNDFQDNRLYYENFIY IAATYTFSGLQEGTGRPVASNKAITCAELVLDVSPKTRVILKKKEP GKRSQLWRMTGTGMLAHEGSSVPHNPNKPSAARSTEGSAILDIAGLA AVTDNRYEPLMLRKPDRRRSTTTQTSWFREGKLTGCLHGLVVQAKGGL SGLFDGAEVVLGPDTSMELLGPVPEQQFINQKMRPGSGMLSIRVIP DGPTRALQITDFCHRKSSRSYEVDLPVTEQELQKLKNPDTEQELEV LVRLEGGIGLSLINKVPEELVFASLTGINVHYTQLATSHMLELSIQD VQVDNQLIGTTQPFMLYVTPLSNENEVIETGPAVQVNAVKFPKSKAL TNIYKHLMITAQRFTVQIEEKLLLKLSFFGYDQAESEVEKYDENLH EKTADQGGTPIRYFFENLKISIPQIKLSVFTSNKPLDLKALKSTLG FPLIRFEDAVINLDPFTRVHPYETKEFIINDILKHFEELSQAARI LGSVDFLGNPMGLLNDVSEGVTGLIKYGNVGGILRNVTGHVSNSAAK FAGTSLDGLGKTMNHRQSEREYIRYHAATSGEHLVAGIHGPGLMGI I/GVGLTSVITSTSGRV*KQKGGVSGFISGLGKGLVGTVTKPVAGAL DFASETAQAVRDTATLSGPRTQAQRVRKPRCCTGPQGLLPRYSESQA EGQEQLFKLTDNIQDEFFIAVENIDSYCVA/LISSKAVYFLKSG\DY V\DREAIFL\EV\KYDDLYHCLVSKDHGKV\MCR
1592	C	398	655	MMFPLAFSLPLKNAFHISVCRVCPGYTGFAKRALTNLNDTSLSANC CNTPPAEXPVHNPCYMGSLKPARXSKLGSCKGSSXH*
1593	A	1	930	MAMDALAYTQMFLLLMNGGDWVIALANLNTLINHSLQLVSQDANSRE IQLRFTANDTLPEIQADPDRLTQWGVVEGQIIKKYICKNIIIGVGAVE KKMSEWNRKCFKERLQEVKECALRRSAVAASLAEEAAEARLLRLQQA CTSLSQFPNSIAGVRWERTLGAIVRQKNHPMTPEAVKANWKKICDFE NASKPQSIQVYSYSEKELICHNQFSLFLVSGGGFGGKRTSDKVKDHR SSPAIEQSWTKNDFDKLTEVGFRLVITNFSSELKEHVRTYRKEAKNL EKRLDEWLTRINSVEKTLNDLMEPKTMA
1594	A	1	134	SRVDDFVSLQALFMGSPRLRFDGRVVLVTGAVAGEHAKVGGRAPC
1595	A	3	2455	HASVCPAVGVQRLCLFPCVSLQALFMGSPRLRFDGRFF\LVTGAGAGL GRAYALAFARGALVVVNDLGGDFKGVGKGSALADKVVEEIRRRGGK AVANYDSVEEGDKVVKTAALDAFGRIDVVVNAGILR/DINSFARISD EDWDIIHRVH\LRGSFQVTPAAWEHMKKQKYGRSMTSSASGIYGNF GQANYSAAKLGLLGLANSLAIEGRKSNIHWNTIAPNAGSRMTQTVM EDLVEALKPKYVAPLVWLCHQSCEENGGLFEVGAGRIGKLRWERTL GAIVRQKNHPMTPEAVKANWKKICDFENASKPQSIQUESTGSIIEVLS KTDSEGGVSANYTSRATSTATSGFAGAIGQKLPPFSYAYTELEAIMY ALGVGASIKDPKDLKFIYEGSSDFCLPTFGVIGQKSMGGGLAEI PGLSINFVKVHGEQYLELYKPLPRAGKLCCEAVVADVLKSGSVVI IMDVYSYSEKELICHNQFSLFLVSGGGFGGKRTSDKVKVAVAIIPNR PDAVLTDTTSLNQAALYRLSGDWNPLHIDPNFASLAGFDK\PILHG\ LCTFGIFCQGVLLQQFCR*MDVVQGFKN*RARF\AKPVYPGANFYQ T*ECWKE\GNRNSFFKPKVQGNLETLVISKWHMWDLTQHSYFSLR TPSEGPGSFRVPLVFEE\IGRRLKDIG\PEVVK\KVNAV\FEWHITK GGNI\GAKWTIDLK\SGSWEKLYQGPS/KKGAADTTIH/ILSDEDF/ LWEVVLGQA*PSRKAFFSGPG*RPQGGTSMA*AQ\KLSDGFLKDYAK LLKGTPTLLIKMESIKIPPPHPQICLDYSAKS
1596	A	2	289	QHAMFGNDTITCTTHGNWTKLPECREVKCFPSPRDNFGFVNYPAKPT LYYKDKATFGCHDGYSLDGPEEIECTKLGNSAMPSCKEHEFGFLE N
1597	A	1	397	PTRPRTRGVCLPFHAMFGNDTITCTTHGNWTKLPECREVKCFPSPRP DNFGFVNYPAKPTLYYKDKATFGCHDGYSLDGPEEIECTKLGNSAMP

				SKKASCKVPVKKKATTVVYQGERVKIQEKFVNGMLHGDKS
1598	A	1	412	STMISPVILIFSSFLCHVAIAGRTCPKDDLPFSTVVPLKTFYEPGE EITYSCKPGYVSRGGM\RKFCPLTGLWPINTLKCTPRVCPFAGNLR KMGAVRLITDFLNYSPTRFSSLSLLTWGFILEWALDS\AKCIEGG
1599	A	19	1215	CQCDSSMTIFSRCSSLFSSFLCHVAIAGRTCPKDDLPFSTVVPLKT FYEPG\EEITYSCKPGYVSRGGIEESLSCLP\TGTVGPFNTSGNVTP RVCPPF\AGIFRKMGGRTLITTF*NYPNTDPVFSLLTLGF*FWNGALD FWPSCGTGGKGW\SP\ELPGLVAPII\CPP\PSIP\TGFATLHVLLR PFRLGNNSPPIGDTAVFECLAHNMMF\NDTIT\CTTHGKLDLNY ECRGSKMPPFFHQDPDNGIW*TYPCQNPNTLFTRVKAPHLGLPHDGI FSGMGPRKEI\EC*PQTWKGKGSWPLAPSW*KPSLVKGTVPVKKRPTV V\YPQGERVKDSREKFKWEWELHG**KFLSFCNKEKKCSYTEDAQ IDGTIEVPKCFK\EHSSLAFWKT\DA\DVKPC
1600	A	1	282	RCGSQQLGRREEWQRQGSVPSRRLSARRGPQAPGTRLPRRHPARAFP AATMPKRKVSSAEGAAKEEPKRRLSARLSAKPPAKVEAKPKAAAKCR
1601	A	1	453	EFGSQQLGRREEWQRQGSVPSRRLSARRGPQAPGTRLPRRHPARAFP AATMPKRKVSSAEGAA*LEPNRSARLSAKPPAKGEAKPKAAAKDK SSDKK\VQTKGKRGAQKQ\AEVANQETKEDLPAENGETKTEESP\A SDEAGEKEAKSD
1602	A	146	824	TWKGKDPKKPRGKMSSYAFFVQTCR\EEHKKHPDASVNF/ESFSK KCSERWKTMSA*R/EKGKFEDMAK\DKARY\EREMKTYIPPQRGRQ KRKFKDSQLHPRGPPSGLSSSCSEYRPIK\GEHP\GL\SIGDVAK KLGRDVGINTAAD\DKQPYEKK\AAKLKEYEKDIAAYRAKGPDA KKG\VVKAESKKKEEEDEEG\DEDEEEDEDEDEDEDEDER
1603	A	1	223	PIRTSRVDPVRVATRDNCCILDERFGSYCPTTCGIADFLSTYQTKV DKDLQSLLEDILHQVENKTSEAKQAGDV
1604	A	1	400	FADD/PSDK/FFTSNNGMQFSTGHNDNDKFEGNCAEQDGSWWMNKC HAGHLNGVYQGGTYSKASTPNGYDNGI IWATWKTRWYSMKKTMTKI IPFNRLTIGEGQQHHLGGAKQVRPEHPAETEDSLYPEDDL
1605	A	18	365	NILIKVYFNSKNDFKIFHELFKQNYMKNMYKSVINVIDIFMKNFQ/ SEKYPRII/DKGS LNK*MLTILALKSNTVRLIRD TAFYVREHI INV SSKRARIWVCVGF I*ASC*QPPLF
1606	A	212	1645	HYKARSSGHS DIMSWSLH\ARNLILYFYALLFLSSTCVAYVATRDNC C\ILYERFGCYC\PTTCGIADFLSTYQTRVD*DIQSL\EDILHQVEN KTS\EVKQLIKAIQL\TYNPD\ESSKPNMIDAATLSRKMLBEMKY EAS\ILTHDSSIRYLQEI I*FQIIQKIVNL\KEK\VAQLEAQCQEP KDTVQIHDITGKDCQD\IANKGAKQSGLYFIKPLKANQQFLVY\CEI DGSG\NGWTVFQKRLDGSVDFKK\NWIPYKEGFGHLSPTGTTEFLAG EMRKIHFD*GTQS\AIPYGI*GVGTGKTWEWARNQYCRSMPLFKVVH EVD\KYRFTYAYFAGGDAEDAFDGYDFG\DDPSDKFFH IPIAMQFT YLGTMNDKV*KANCA*/QQGWDPGWWDGNKC\HAG\HSSMGVLFTQ GWALYFQKASYLPNGLWIMGI IWA\TWK\TRWVFR*RKPTMKIIP\F NRLTIGEGQQH\HLGGSQTGLETF
1607	A	2	531	GTVAACGACYWLLGLMAVRASFENNCEIGCFAKLNTYCLVAIGGSE NFYSVFEGELSDTIPVHASIAGCRIIGRMVGN\TEEILADVLKVEV FRQTVADQVLVGSYCVFSNQGLVHPKTSIEDQDELSSLLQVPLVAG TVNRGSEVIAAGMVVNDWCAFCGLDTTSTELSV
1608	A	18	889	GVQGTVAACGACYWLLGLMAVRASFENN\CEIGCFAKLNTYCLVAI GGSENFYSVFEGELSDTIPVHASI\AGCRI\IGRMVGN\RHGLL\ VPNNTTDQ\EL\QHSATGLPRHSGRFRAGWKERFLSLWGNFFNHLA IDYVGLGSNQD\LDKGRQEEISGQMLFKGWEVFRQTV\ADQV\LVE S\YCVFSNPGRAWVPSRPFQ*RPRNELSSISFKVPL\VAGTC*TKGS EVICLLGMGEMNWCA\FCGP GTPNPAQSCQVVEECLQS*NEAPALA PIANRACGNSL\IDSLT
1609	A	1	248	GPLIWEWPASPEPPPLPWGKPRMQ/SG*YG*TP*IPKIRFPKKPFP FPQALEPQQKGP N*AHP*EPTPAKYSPQRVOKVPK

1610	A	290	1414	NKRHPSRVYMSLPQG\EKVQAMYIWIDGTGEGLRCKTRTLDSEPKCV EELPEWNFDGSSSTLQSEGFQTVNMYLVPAAMFRDPFRK\DPNKLVL \EVFRYN\RRP\AETNLRHTCKR\IM\DMVSNQHPWFGEQ\EYTL GTDGHPFGWPSKG\FPGPQGQYLLGVG\GDRSLGRDIR\EAHYRACF Y\AGTRIPGTKAGVSPLQ\WEFQIGPCEGIKQGG/HIFWVARFILH\ RVCEDLG\VIATFDP*/RPLLGNWNGA\GCHTNFSTKAMRKENGLKY IEKAI*KLNR\HKSHIRAYDPKRGLDNARRLTG FHETSNDIFS VANRSASIRIPRTVQGEKKGYFE\DRRPS\ANCDPFSVTEALI\RTC LLNETGDEFPQYKN
1611	A	38	396	SSVHDLVAAMSATSEIQDPRGRGDGPGGLPDVVAIPWPPR*ILSQE E/HHPTDNQDIEP\QEREGTPPIEERKVEGDC\QEMDL\EKTRSER G\DGSDVKEKTPT*ILKHAKTKEAGDGQP
1612	A	129	1182	APPSPPSSGCSQPQQLSALTPGTRVLAPSFASFLLPSFFLPPLAPALP LQVALPGPDCLGSPPLPARALPRLSLALPESPAAAVADSPREPQPNPS PTATAPAPAPAPQPAAPARGSPGARGRLQWASAPSPSPAPQPCPARR GRTGKMNNGGKAEKENTPSEANLQEEVRTL FVSGPLD IKPRELYL LFRPFKGYEGSLIKLTSKQPVGFVSFDSRSEAEAAKNALNGIRFDPE IPQTLRLEFAKANTKMAKNKLVGT PNPSTPLPNTV PQFIAREPYELT VPALYPSSPEVWAPYPLYPALAPALPPAFTYPASLHAQLCEGQTV RRSHPLSAPSPDSASLAWFPV
1613	A	1	353	PGTRSFDSRSEAEAAKNALNGIRFDPEIPQTLRLEFAKANTKMAKNK LVGT PNPSTPLPNTV PQFIAREPYELTVPALYPSSPEVWAPYPLYP ELAPALPPAFTYP\ASLHAQETL
1614	A	129	1238	APPSPPSSGCSQPQQLSALTPGTRVLAPSFASFLLPSFFLPPLAPALP LQVALPGPDCLGSPPLPARALPRLSLALPESPAAAVADSPREPQPNPS PTATAPAPAPAPQPAAPARGSPGARGRLQWASAPSPSPAPQPCPARR GRTGKMNNGGKAEKENTPSEANLQEEVRTL FVSGPLD IKPRELYL LFRPFKGYEGSLIKLTSKQPVGFVSFDSRSEAEAAKNALNGIRFDPE IPQTLRLEFAKANTKMAKNKLVGT PNPSTPLPNTV PQFIAREPYEL \TVPALYPS\SPEVW\APYPLLPRRELGACFYLP PG/SFTYPASLAW PRCAGSLPPRLLLRAGSPVSSAEYTLQWLLLEGRTIALLWKYG
1615	A	129	1143	APPSPPSSGCSQPQQLSALTPGTRVLAPSFASFLLPSFFLPPLAPALP LQVALPGPDCLGSPPLPARALPRLSLALPESPAAAVADSPREPQPNPS PTATAPAPAPAPQPAAPARGSPGARGRLQWASAPSPSPAPQPCPARR GRTGKMNNGGKAEKENTPSEANLQEEVRTL FVSGPLD IKPRELYL LLFRPFKGYEGSL*KLTSKQL*GFVSFDSRSEAEAAKNALNGIRFDPE EIPQTLRLEFAKANTKMAKNKLVGT PNPSTPLPNTV PQFIAREPY ELTVPALYPS\SPE\WVAPYPL\YPALGPA\LPP\PAFT\YPASLR CPGNPVEKEIQDSV
1616	A	1	669	MRWLVSPIEDTGHKALLFACLALHRACVSGHCLSPKCVGVDGRSHEM VAPGLFLDWLLDGTGVWDGTSTNVEGAQEHAVLILLIITDGVISDME ETGMPWCRLPSCPCPSSSGRGQCGLRCHGVPGWGRMLRSHTGEEAA RDIVSSFPFESSATMSEEVYDPRSLYERLQEQRTGSSRTARQEAVVG SKVTVSQPGHRQETT VLEHLVQYVGF SICCKELMV
1617	A	267	1057	GRTMMFGAKRRQEWEKVRKPEDPEECPEEVYDPRSLYERLQEQKDR KQQELRGTVSNCKNM\VRG\LDEDETTFLDEVSRQQELIEKQPKR\E ELERT*RNTEITSRRLEFSQENKKEVEKLTCE\VL*KPRTKFSQAN VLGQEL*SMKSSSGHQCEKT*NRTPEPD*QESRALILAKSLGNNLP LSGPFHPLAPSAASMYRHPPRPGWPTLGAATPSPASDSEGTIQCHRK DCSPPCFRTNTFLRGPLSFFRSLHREAPPQG
1618	A	1	641	DTRFLERLRLSISSYVQTPMGHFTTEEDKATI\TSLWCKVNVE\DAGG ETLGRLLVVYPWTQRFFDSFGNLSSASAI\MGNP\KVKAHGKKVLTS FGRLP*KHL\DDLKG\TFAQA*SE\LH\CDKAALLDPE\NF\KLPGE ILLVTRFGQFHFRANKFTPEGCA\SWQERWVTWSWPVPCSSRLPLK LNCP*MQSFSRIRLLFLQAITNNKSISAKRSP
1619	A	1	194	KEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQF

				WRYFAGNLLPVDGRRL
1620	A	98	1136	ASDAFHSLAPGLRLGSRSAARPATMTEQAISFAKDFLAGGIAAAIS KTAVAPIERVKLLQ\QVHASKQIAADKQ\YKGIIVDCIVRIPKGAGG VLSFLEGQPLPTVIRYFP\TQAFNFRPFKD/KSYKQIFPGGAWDKHT QF\W\R*FGGANWASGVAAGADHPSCFVYPLDFARTGLGKGRWKSQA QSASFRGLG\DCLVKIHQVQTASRGLYQGLPVSPFTATIIYPA\AY\ YGVY\DTAKGHASPTPSNT\HILLSRMNRARTVTARGAVGCPNPLKT VRR\RMIDAIRGAKGADIMYTG/TLVDC*RKNLSEDEGGQRPFFKGC VVQTLRLRGHGGRRPSVLVPVRTSSRRVI
1621	A	4	101	VQWNDFGSLQNPFGVSPFFWLSLPNNLGFKGSSSRPGPFLKF**KP /EVFRVNPDPGFPFAP*FGPPGPPKSWGFP*PPPGVSPFFWLSLPN NLGFKG
1622	A	3	1728	GDRTDGVWWLGLSRRYAI PFNSLEPSSLGSCPLSIGTHK\ALHALE LTTTDIQCGKAFNSSSSFRYHERHTTGEKPYECKQCGKAFRSASLLQ THGRTHTEKPYACECKGKPFNSFFQIHERMHREEKPYECKGYGK TFSLPSLFHRHERHTTGGKTYECKQCGRSFNCSSSFRYHGRTHTEK PYECKQCGKAFRSASQLQIHGRTHTEKPYECKQCGKAFGSASHLQM HGRTHTEKPYECKQCGKSPGWASRLQMHGRTHTEKPYCKQCGKA FGWPSNLRRHGRTHTEKPYKCNQCGKKWKDQNI EYEQNPRRNFRS LIEGNVNEIKEDSHCGETFTQVPDDRLNFQEKKASPEAKSCDNFVCG EVGIGNSSFMNIRGDIGHKAYEYQDYAPKPYKQQPKAFRYHPSF RTQERNHTGEKPYACECKGKTFISHSGIRRRMVMHSGDGPYKSSFLR SHPKVPGHGRRFAMNPTLLNKEDERGNKNVVTREHLDRMKNSCIVCN MGHSNTEIDVNVVMGNYERLERDARMTIRKKRKRYSDIRFRIMGRYT VRVEVLTAVNSE
1623	A	1637	5763	KPGNGACAGREWCDDGGGAAWNWRDPGLPVGDGSGVWDRVLELLGPRS PRPLDVGGPAAGTPGVLSRPCPSTAALAPKPFCAAPRPQPDAPACAG ATGGSCADFDGSGVDFVRRRSSGLWGPQPPLSPVKNYTEMFQDPVAFK DVAVNFTQEEWALLDISQKNLYREVMLDTFWNLTSIGKKWKDQNI EY EQNPRRNFRSVTEKVNEIKEDSHCGETFTQVPDDRLNFQKKAS\ LK*NHVTALCVQKLA*VTHL/CNMSIRGDTGHKAYEYQYEGPKPYK QQPKNKKAFRYRPSIRTQERDHTGEKPYACKVCGKTFIFHSSIRRH VMHSGDGTCKFCGKAFHSFSLYLIHERHTTGEKPYECKQCGKSFT YSATLQIHERHTTGEKPYECSKCDKAFHSSSYHRHERSHMGEPYQ CKECKAFAYTSSLRHERTHSGKKPYECKQYRGRAYHMLLGLQPH\ KRMNSGERPYCKICGKGFYAKSFQTHERTLTGERRYKCKQCGKAF NLSSSFRYHERIHAGEKPYECKQCGKAFRSASQLRVHGGTHTGEKPY ECKECKAFRSTSHLRVHGRTHTEKPYECK\ECGKAFRYVKPLQIH ERTEKHIRMPGERPYKCSICEKGFYSAKSFQTH\KKTHTGEKPYEC NQCGKAFRCNSLRHYHERHTTGEKPYECKQCGKAFRSASHLRMHERT HTGEKPYECKQCGKAFSCASNLRKHGRTHTEKPYECKQCGKAFRSA SNLQMHERTHTGEKPYECKEKEKAFCKFSSSQIHERKHGRGEKPYECK HCGNGFTSAKILQIHARTHIGEKHYEFLFDIMKGLTLGRNPINIHER AHTGEKPYECRECGKAFKWPISVRRHERTHSRKKPYECKHRGKVLST LTSFQNLGMHTGEISHKCKICGKGFYSPRSLQRHEKHTTABKPYEC KQCGKAFSSSSFWYHERHTTGEKPYECKQCGKAFRSASILQMHAGT HPEEKPYECKQCGKAFRSAPHLRIHGRTHTEKPYECKECKGAFRSA KNLRIHERTQTHVRMHSVERPYCKICGKGFYSAKTHTEKPYECKQ CGKTFRSTSHLRKHGRTHTEKPYECKQCGKAFRSMKNLQSHERTQT HVIHSGERPYCKKLCGKGFYCPKSLQRHEKHTTGEKLYECKQR/CS SSFSSSSSFYHERHTTGEKPYKCEQCGKAFRVAVSIL*MHGRTHPEE KPYESTRPPAMQGHKLCYAIIDVYTHCMITFILLWPPIAQSSSRRS ADSEKLSPGKQKTHMHTQARTMAQACPTQHVPGVIPVEGCNPQGL APNEIWQMDVTHIAAFGCEKAIATCMPAGLLEGLPRQLMDCILRQIM ACWCASAYQCALLLACSS
1624	A	2	658	APTPTGQVRVATPAQSAPVRLRRRSYDVNPNIPSNLKSEAKKAAKI

				LREFT\EITSRNGPDKI\IPGSTVIAKAK\GLANSCLLNQSPGSLVT FQGGPGVLVARL\PDGK\WSSPFS\ALGIAGFG\GGFEIGI*GIQT LVIILEF/DDPCC*EAFKGGNLTGGNLTVAVGPLGRNLEGNVALR SSAAVFTYCKSRGLFAGVSLEGSCLIERKETNRKFYC
1625	A	141	1307	FHVNNPIPSNLKSEAKKAAKILREFTEITSRNGPDKIIPAHVIAKAK GLAILSVIKAGFLVTARGGSGIVVARLPDGKWSAPSAIGIAGLGGGF EIGI/EDTFTATYSL*ALPWLPSISVECHSSFLRLPSA*HIFLHPFT VNLMSVDLVIILNYDRAVEAFKGGNLTGGNLTVAVGPLGRNLEGN VALRSSAAVFTYCKSRGLFAGVSLEGSCLIERKETNRKFYCQDIRAY DILFGDTPRPAQAEDLYENLDSFTEKYENEGQRINARKAAREQRKSS AKELPPKPLSRPQQSSAPVQLNSGSQSNRNEYKLYPGLSSYHERVGN FYQPIDLTALYSFEGQQPGDLNFQAGDRITVISKTDSHFDWWEGLR GQTGIFPANYVTMN
1626	A	167	402	KYSLPRVTSSLDLPTHVHSQATSPSPSWPFCPYPTHSTPLPPLGKM EQVFGKLPHPPLPLTLSESWGTEAVFLAP
1627	A	133	312	VRVGEKLPKCFWPPEANPDP*CYLHLWILDSQTKSKPVLTS*RP GILGTSVCCTFY
1628	A	1759	1967	SGCKPLTFPPP*SDSPVKEDPCR/SPPSHPRLPPLPALPPTPNP PPPKIYTAVSRIWEMKDRCNIP
1629	A	167	1378	GNTLVNTMTEFWLISAP\GEKT\CQQTWEKLHAATSKNNLAVTSKF N\IPDFKGWARWDVLVGL\SDEL\AKLGCIL*EGSWLKESRLQLHGL DVLEDSKDKVQENLLA\NGSGLGLPYITKVPSGDMAKYPKQSLKNI SEIIAKGVQTIDNDLKSRASAYNNLKGNLQNLERNKAGSLLTRSLAE IVKKDDFVLDSEYLVTLVVVPKLNHNDWIKQY\ETLAEMVVRSSN VLSEDQDSYLCNVTLFR/RAVDDFQDTKPGENKF\IVRDFQYNEEE \MKADKK\EMDRAST\DKKKQFGP\LVRW\LKVNFEAFIAWHVKA LRVFVESVLRVGLPVNL\QHMIFHRNNNPFKPLRQVLHESYIHLDS A\AAIIDAPMDIPGL\NLSQOEYYPVYKIDCNLLKFK
1630	A	569	1050	PLESRRLARSSGGWAGITGTPMNIFTGPDGPGSERSAQPRVWDSTCC LKSNCWFRKVKATTPMSSMMRQIPRMYMNA/WEKVQVVTBGRQHTN EGDHEHDDAQEDDDGWSQEGTFKGFIFLPLNLCIDAHQDQGPNT CNPSTLGGRGQITRPGDRDH
1631	A	1	595	MGTDSRAAKALLARARTLHLQGTGNLLNWGRLRKKCPSTHSEELHDCI QKTLNEWSSQINPDLVREFPDVLECTVSHAVEKINPDEREEMKVSAC SVLGVAQLDSVVIASPPIEDGVNLSLEHLQPYWEELENLVQSKKIVA IGTSDLDKTQLEQLYQWQVKNPSNQVNLASCCVMPPDLTAFKQFD IQLLTHNDPK
1632	A	2	1121	ARGCGRSSRSRSHRCLPFPFPPPSRRPASLGPERRPGSSRAAPAAS RSLSGLSRASGTASGRPPACPPARSPLPAGPWAARAMGTDSRAAKA LLARARTLHLQGTGNLLNWGRLRKKCPSTHSEELHDCIQKTLNEWSSQ INPDLVREFPDDL\ECTVSHAVEKINPDEREEMKVSAKLFIV\ESNS \SSSTRKVQLTWACSVLGS/VAQLGFLWIHWLSPPI*KDGGILFPWE HLQPYWEGI*KNLVQRQKGLLP*GTSDDLKTQLEQLYQWQVKNPSN QVNLASCCVMPPDLTAFKQFDIQLLT\HNDPKELAFWKASFGRLF QGKAFF\DISSGTEWGAAGVLLRYSVIVKSRGIKSKGYILQAKRRG S
1633	B	63	458	SLENTVSTAISKAQNGAPSWGYPYPSIHAAYQLPGTVKPLPAAVQSVQ VQPSYAGGVKSLSSAEHNALLHSPGSLTPPHKSNVSAMEELVEKVT GKVNIIKEERPPEKEKSSLAKAASPIAKENKDFPKTEE*
1634	A	3	2303	EMEGKEDAQKVLKCMYCGHSFESLQDLVHMIIKTKHYQKVLPKEPVP AITKLVPSTKKRALQDLAPPCSPEPAGMAAEVALSESADQKAAANPY VTPNNRYGYQNGASYTWQFEARKAQILKMECGSSHDTLQELTAHMM VTGHFLKVTTASAKKGKQLVLDPVVEEKIQSIPLPPTTHTRLPASSI KKQPDSPAGSTTSEEKKEPEKEKPPVAGDAEKIKEDSEDSEKFEPS TLYPYLREEDLDDSPKGGDLILKSLENTVSTVINKAQNGAPSWGYP SIHAAYQLPGTVKPLPAAVQSVQVQTSYAGGVKSLSSAEHNALLHSP

				GSLTPPPHKSNSVAMEELVEKVTGKVNKKKEERPPEKEKSSSLAKAAS PIAKENKDFPKTEEVSGKPQKGPPEAETWEAKKEGPLDVHTPNGTEP LKAKVTNGCENNLGIIMDHSPEPSFINPLSALQSIMNTHLGKVS KPVS PSLDPLAMLYKISNSMLDK\PVYPATPVKQADAI DRYYYENS DQPID LTKSKNKPLVSSVADSVASPLRESALMDISDMVKNLTGRLTPKSSTP STVSEKSDADGSSPEEALDELSPVHKRKGQSNWNPOHLLILQAQFA SSL\SETTEGKYIM\SDLG PQERVHI\SKFTGLSMTTISHWLANVEV TSLRRTGG\TKFLKEPGTQGHVFF\CNDCASQFRTASTYISH\LET HLG\FSLKDLSKLP LNQIQRQQ\NV*KVLTNKT LGP\LGATEEDLGS TFQCKLCNRTFAKQARSQTAP
1635	A	133	500	YNTVNYKSHPEGQSMCWSMPVITATFGNPRRVDQPLRSGVQD\QPGQ HGKIPSLKIQKLAGHG\GACL*SQLLGR LRKENCLN/SPGGGGCSE PSSRHC\IPAWAIA*DTI*KIKK*KPPKMRN
1636	B	1568	1588	MGDQQLYKTNHVAHSENLFYQQPPLGVHSGLNHNHYGNAV TGGGMDA PQASPI SPHF PQDTRDGLGLPVGSKNLGQMDTSRQGGWGSHAGPGNH VQLRGNLANSNMWGA PAQAEPTDGYQYTYSQASEIRTQKLTSGVLH KLDSFTQVFANQNLR IQVNNMAQVLHTQSAVM DGAPDSALRQLLSQK PMEPPAPAIPSR YQQVPQQPHPGFTGGLSKPALQVQGHPTQGHLYYD YQQPLAQVPVQGGQPLQAPQMLSQHMQQMQHQYPPQQQQAGQQR ISMQEIQTPQQIRPSQPQPPQQQQPPQLQLQQRQGS MQIPQYYQP QPMQHLQEQQQQMHLOPPSYHRDPHOYTPEQAHTVQLIPLGSM SQ YYYQEPQQPYSHPLYQQSHLSQHQQREDSQLKTYSSDRQAQAMLSSH GDLGPPDTGMGDPASSDLTRVSS TLP HRPLLSPSGIHLNMMGPQHQQ LSPSAMWPQYLLSAYCVPSIELGFENAAVNSTDLLPHPMGMVKNOLA KPDKLLKRAVRRLPQELAQM SLSGEAFGGAGLR LTLLEGGQPKGAFGE QFDAKNKLTCSI CLKEFKNL PALNGHMRSHGGM RASPNLKQLPPEAE SLTPMVMPVSVPVKLLPPKPSSQGFTNSTVAAPSARDKPASSMSDDE MPVLTPLLEARMAPWKA EKLREKQKGAEP EALEGEEPRAE EPMQEI PRKHQPSVPKAE EPLKTVQEKKKFRHRPEPLFIPPPPSYNPNPAASY SGATLYQS QLRSPRV LGDHL LLDPTHELPPYT PPMLS PVRQSGSLF SNVLISGHGPGAHPQLPLTPTPTPRVLLCRSNSIDGSNVTVPFGPG EQTV DVEPRINIGLRFQAEIPELQDISALAODTHKATLVALEM LLLR KPVRLKCHPLANYHYADGPGSYITSGVASGKQFGNMKGHASQKSTGL GTEHCFWGQKSGSDKWTSLERKLFNKALATYSKDFIFVQKMWKSKTV AQCVEYYYTWKKIMRLGRKHRTRLAEIIDDCVTSEEEEELEEEEEED PEEDRKSTKEEESEVPKSP EPPPPVPVLAPTEGPPLQALGQPSGSFIC EMPNC GAVFSSRQALNGHARIHG GTNQVT KARGAIPSGKQKPGGHPE WHEKEYLGEMLPKWFLKLYHENIPSYISKARVFFKIKSRNAHMKTH RQEEQQRQKAQKAFAAEMAATIERTTGARGGAGAAVPWTS*
1637	A	2	251	FFFFFLINKTKRLFTP*ALQWGYPSGSCGSVSQSKCILRGRSRATI SIEAEMVDL
1638	A	36	531	NKVLPPAASEHSDCQISKHQVQLCP/PNIITLADIVKDPVSRTPALV FEHVNN TDFKQLYQTLTDYDIRFYMYEILKALDYCHSMGIMHRDVKP HNV MIDHEHRKLRLIDWGLAEFYHPGQEYNVRVASRYFKGPELLVDY QMYDYS LDTWRMGCM LASMI IQKEP
1639	A	1	1833	MRRTQPAVTGGDQIESVRRGMQAASSRKGQSQTTSKEVGTQSYSCK ELNSANSLNECGSKFSPEFPAGNPPTGYPHLALRVIASGVKFHIVTL FCLYGVVKRCIDDDYIVRDSTGIPISLRNODDYQLVRKLGRGKYSEV FEAINITNNEKV VVKILKPVKKKKIKREIKILENLRG GPNIITLADI VKDPVQLYQTLTDYDIRFYMYEILKALDYCHSMGIMHRDVKPHNMI DHEHRKLRLIDWGLAEFYHPGQEYNVRVASRYFKGPELLVDYQMYDY SLDMWSLGCMLASMIFRKEPFFHGH DNYDQLVRIAKVLGTEDLYDYI DKYNIELDPRFNDILGRHSRKRWERFVHSENQHLVSPEALDFLDKLL RYDHQSRLTAREAMEHPYFYTVVKDQARMGSSSMPPGGSTPVSSANMM SGGWYLVLF SRDYKNVASQGRQEERKEGKEGRTQSIGAVDCLLVAY ITLLHKRFSGVILVALVEVCLSYIKMLKIYPKCRQILKTSVHCDWFR

				SGYTGRGLLEKVFWRAEIRRQSTGFKSKERQAQNGRDDMGTYLVNTSGHWTQPGTRNEGNVPAGPTALDDAASSDDTSPRHYLGDAEEDNSGG
1640	A	3	432	GWYLVLFSDYKNVASQGRQEERKEGKKEGRTQSIGAVDCLLVAYITLLHKRFSGVILVALVEVCLSYIKMLKIYPKCRQILKTSVHCDWFRSGYTGRGLLEKVFWRAEIRRQSTGFKSKERQAQNGRDDMGTYLVNTSGH
1641	A	137	1368	FHISLFEENRVLKQGSLLPPPAFLNTVTAQISQTSKSQALSROPCSDHVGDPVPKAGHRV\YTDVNTHRPREYWEYE\SHVVEWGNQDDYQL\VRKLGRGKYSEVFEAINITNNEKVVKILKPVKKKKIKRE\IKILGGIWRGGPNIIITLADI\VKDPVSRTPAL\VFEHVNNITDFKQLYQTLTDYDIRFYMYEILKALDYCHS\RGIMHRDVKPHNVIMIDHEHRKL*LIDWGLAEFYHPGQEYNVRVASRYFKGPPELLVDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGHNDYDQF/VCRMALVLTEDLYDYIDKYNIELDPRFNGYLG\RHSRKPMTALSNSENQH/LLSSPEALDFLDKLLR\YDPPSHGLLAREAMEHPYFLHCCEGPRPRNGFHLAMPGCSTPVQQRPI
1642	A	874	1183	TPMLEQLGNRYLQNIACYPFRNMCTYQLGCSGSR*SQHF\GRPRQVDHLRSGVRDQPGQGETPSLLKVQKFSWAWRTPVIS\ATWEAEAGEVLEPGRRRLK
1643	A	2	498	APSPDAMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFDSFGNLSSASAIMGNPKVKAHGKVLTSGLDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQTIVTGLGNALCFTKHLDFMCMMSFKE
1644	A	49	538	SQTPMGHFTTEEDQGLLSKSLWGK/VLNVEKMLGRKKTPLGKGSPLVVPPTP\WDPKRFL*TSFGKTLSPALLPHQWANPPK\VKGHGKEGCLTFPWEDAHKAPLDDPQRAFPAPA*SELHCDKLHVD\ENFKLLG\NVLVTV\LAHF\GKEFTPGGCRASWAEDG
1645	A	53	394	RETGLPALGTCAVPLARAAPILQRLQSQSPRTSLKARPKTRITGALPMDHTEGSPAEEPPAHAPSPGKFGERP PPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFF
1646	C	116	379	MYLCLSQERIIQFQLNGRWGRQCLNLQGNFTSKFTECGFGGCRKAGNYVTGVGGGVWLLCSSPDISGISEEGWEMGSRXTSSGVPV
1647	A	3	202	CIASGTKVALFNRLRSQTVSTRYLHVEGVDDDESEGEFTVRDGYIHYGQTVKLVCSTGMALPRL
1648	A	1	639	MRSAARGPRQSCSAFNRFRAANSSSPGFGAPCGRQCWIWESLGKERAKEGKDGLQSPRTSLKERPKTRITGALPMDHTEGLPAEEPPAHAPSPGKFGERP PPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPCPPCVYLMGSGWKKKKEQMERDGCSEQESQPGAFIGIGNSDQEMQQL/NTLEGKNYCTAKTLYISDSDKR
1649	A	111	750	GKREGAGERDQGRRRGESREGWSFGESLWKMAPVVTGKFGERP PPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPCPPCVYLMGSGWKKK\EQMERDGCSEQESQ\CAFIGIGNSDQEMQQLNLE\GKNYCTAKTLYISDSDK\RKHFMLSVKMFYGPST\DDIGVFL\SKRIKVISKPSKKKQSLKNADLCIASGTKVALFNR
1650	A	1	519	IISTD/KAET/FYEGMGPVFTPVTPVPVVESLQLNAGGDVAMLELTGQNFTP\NLRV/WFGDVEAETMYRCEQSMLCVVPDISGFR\EGWRWVRQPVPVTL\VR\NDGI\IYSTSL\TFTYTPEP\GPRPHCSAAGAILRANSSQVPPNESNTNSEGSYTNASTNSTSVTSSTATVVS
1651	A	238	1713	STMAWIKRKFGERP PPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPCPPCVYLMGSGWKIKLQMKDCGCEQSQPCAFIGIGNSDQEMQQLNLEGNKYCTAKTLYISDLKQKHFMLSVKVFGNSDDIGVFLSKSSKPSKKKQSLKNADLCIASGKERWALFNRLLSQTV\STRYLHV/EKEGNFHASSQWGAFFIHLDDDGSEGEFTV*DGYYHYGQTVKLVCSTGMALPRLIIRKVDKQTLLDADDPVSQLHKCAFLEDTERKYLCLSQERIIQFQATPCPKENKEKINDGASWAIISTHKAKHTFYRESGPLSLAP/VSCPPALSVELKLNNGGDEPSLKLNRTEFQLPKFYKVWFGDVE\AEAMYRCG\ESMLRVVPDVSAF*EGWR\YSQQPIQVSV

				TLVRNDGIIYSTSLTFTYTPEAGPRPHC\SVAGAILKASSSHVPPNE LNTNSDGSYTNASTNSTSVTSSTPTVVS
1652	A	1	309	FF*DR*A*L\CPPGWSARSQHTVVSTFLGSSKFSLGPPPELPGDHRHA PPCPANFFYFS*RWGLPMLLVSNSQAQAILLPSPFQKGWDYRAWGHH TWGSYLNFE
1653	A	259	331	RNE*LLTRFSPLSLSH*VLGVSMF
1654	A	569	4150	IISLNKGPAEKGGKGGNGGGKPPSGPNRMNGHHQQNGVENMMLFEVVK MGKSAMQSVVDDWIESYKHDRDIALLDLINFQICSGCKGVVTAEMP RHMQNSEIIRKMTEEFDEDSGDYPLTMAGPQWKFKSSFCEFIGVLV RQCQYSIIYDEYMMDTVISLLTGLSDSQVRAFRHTSTLAAMKLM TAL VNVALNLSINMDNTORQYEAERNKMIGKRANERLELLQKRKELQEN QDEIENMMNAIFKGVFVHRYRDAIREIRAICIEBIGIWMKMYSDAFL NDSYLKYVGWMTMDKQGEVRLKCLTALQGLYYNKELNSKLELFTSRF KDRIVSMTLDKEYDVAVQAIKLLTLVLQSSEEVLTAEDCENVYHLVY SAHRPVAVAAGEFLYKCLFSRRDPEEDGMMKRRGRQGPANLVKTLV FFFLESELHEHAAYLVDSMWDCATELLKDWECMNSLLLEPLSGEEA LTDREQESALIEIMLCTIRQAAECHPPVGRGTGKRVLTR\KEKKTOLD DRTKVTELFAVALPQLLAQYSVHAEKVTNLLQLPQYFD*EIYTTGRL EKHL DALLRQIRNIVEKHTD TDVLEACSKTYHALCNEEFTIFNRVDI SRSQLIDELADKFNRLLDFLQEGEEPDEDDAYQVLSTLKRTAFHN AHDLSKRDLFACNYKLLKTGIENGDMPEQIVIHALQCTHYVILWOLA KITESSSTKEDLLRLKKQMRVFCQICQHYLTNVNTTVKEQAFTILCD ILMIFSHQIMSGGRDMLEPLVYTPD\SSLQSELLSFILDHVFIEQDD DNNSADGQOQDEASKIEALHKRRNLLAFCCLKIVYTVVEMNTAADIF KQYMKYNDYGDIIKETMSKTRQIDKIQCAKTLILSLQQLFNEMIQE NGYNFDRSSSTFSGIKELARRFALTFGLDQLKTREAIAMLHKDGI EF AFKEPNPQGESHPPLNLAFLDILSEFSSKLLRQDKRTGYVYLEKFMT FQMSLRREDVWLPLMSYRNSLLAGGDDDTMSVISGISSRGSTVRSKK SKPSTGKRKVVEGMQLSLTEESSSSDSMWLTREQTLHTPVMQTPQL TSTIMREP KRLRP\EDSFMSV/YYPMQTEHHQTPLDYNRRGTS L MED DEEP\ILWEDVMSSEG\RIEDLNEGMDFD TMDIDLPPSKNR\RERT E\LKADFFDP\ASIMDESVLG\VSMF
1655	A	1	2325	MGKKRTKGKTVPIDDSSETLEPVCRIHKGLEQGNLKKALVNVEWNI CQDCKTDNKVKDKAEEETEEKPSVWLCLKCGHQGCGRNSQE QHALKH YLTPRSEPHCLVLSLDNWSVWCYVCDNEVQYCSSLNQLGQVVDYVRKQ ASITTPKPAEKDNGNIELENKKLEKESKNEQEREKKENMAKENPPMN SPCQITVKGLSNLGN TCF FNAVMQNLSQTPVLRELLKEVKMSGTIVK IEPPDLALTEPLEINLEPPGPLTLAMSQFLNEMQETKKGVVTPKELF SQVCKKAVRFKGYQQQDSQELLRYLLDGMRAEEHQRVSKGILKAFGN STEKLDEELKNKV KDYEKKKSMP SFVDRI FGELTSMIMCDQCR TSG KKS VNDKNL KKTVEDEDQDSEEEKDND SYIKERSDIPSGTSKHLQKK AKKQAKKQAKNQRQKIQGKVLHLNDICTIDHPEDSEYEAMSLQG EVNIKSNHISQEGVMHKEYCVNQKDLNGQAKMIESVTDNQKSTEEVD MKININMDNDLEVL TSSPTRNLNGAYLTEGSNGEVDISNGFKNLNLNA ALHPDEINIEILNDSHTPGTKVYEVVNEDPETAFACTLANREVFNTDE CSIQHCLYQFTRNEKLRDANKLLCEVCTRRQCNGPKANI KGERKHVY TNAKKQMLISLAPPVLT LHLKRFQQNVAEENTRVLYSLYGVVEHSGT MRSGHYTAYAKARTANSHLSNLVLHGDIPQDFEMESKGQWFHISDTH VQAVPTTKVLNSQAYLLFYERIL
1656	A	3	128	ATSHNAAFRKL LLSRGHSGVIRRSQFVTRRKTELAAQPKGP
1657	A	203	2698	SANMGKKRTKGKTVPIDDSSETLEPVCRIHKGLEQGNLKK\ALVN VEWNICQDCKTD\NKVKDKAEEETENKPS\VLCL\KC\GPQGFRN FSR/EQHALKH YLTPRSEPHCLVLSLDNWSVWCYVCDNEVQYCSSLN LGQVVDYVRKQASITTPKPAEKDNGNIELENKKLEKESKNEQEREKK ENMAKENPPMNSPCQITVKGLSNLGN TCF FNAVMQNLSQTPVLRELL KEVKMSGTIVKIEPPDLALTEPLEINLEPPGPLTLAMSQFLNEMQET

				KKGVVTPKELFSQVCKAVRFKGYQQQDSQELLRYLLDGMRAEEHQR VSKGILKAFGNSTEKLDEELKNKVQDYEEKKSMPSFVDRIFGGELTS MIMCDQCRTVSLVHESFLDLSLPVLDQSGKKSANDTP\LTKTVTYA ECYSEEKYHTDCCYI*RSDISSGTRKHLQKKATKQAKKQAKNQRRQQ KISGPALHLNDIRTIHDPEDSEYEAEMSLQGEVNITSNHISQEGVMH K\EYCVNQKDLNGQAKMIESVTDNQKSTEEVDMKNINMDNDLEVLTS SPTRNLNGAYLTEGSGEVDISNGFKNLNLNLAALHPDEINIEILNDS HTPGTKVYEVVNEDPETAFCITLANREVFNTGE\CQIOHCLYQFTRNE KLRDANKLLCEVCTRRQCNGPKANIKGE\RKHVYTNACKQMLISLAP PVLTLHLKRFQQAGFNLKVNKHIKFPEILDAPFCTLKCKNVAEEN TRVLYSLYGV\VEHSGTMRSGHYTAYAKART\ANSHLSNLVL\HGDI PQDFEMESKG\QWFHISDTHVQAVPTTKVLNS\QAYLLFYERIL
1658	A	992	1863	GIWRNVHRQPQLESCEPTPACSGRACACCPVSCGWSHGQDWMVPVAG RCTRAQRCCTGGASLPTVHKSTLSSCSAPPADSAACVFYFIIIF*R QSLNSVAQ\AGVQWR\NLKLLQPLPPAFKA\FSCLSLLCNWDYRRVP PGLANFCIFSRDGGFTMLVVRLVSNS*PCDLPASASQSAGIT\ALSH HAW\LLFFETESRSVVQAGVQWCDLGSLOQAPPPGFTPFSCLSLQSSW DYRPPPPRANF/CVFLVETGFHC*PGWSRSPDLMIPPGLSLPKCWD CRDRTKHPASKF
1659	A	318	1681	SPRMHALVLLLCIGALLGHSSCQNPASPPEEGSPDPSTGALVEEED PFFKVPVNKLAAAVSQTSAYDLRYVRIQA*APRPNVLPVSLFKCGPT ALSA\LSLGRSKRNKNPIIHR\ALYYDLIKQAPDI\HGYLIRKLP* HGHPFPQKNLKSASR\IVFEKKLRIKSSFVAP\LEKSYGTRPR\VL GNP\RLDL\QEINN\WVQA\Q\MKGKLARSTKEIPDEISIVLL\GV* AHFKGQ\WETKFDSRKTS\LEGFLGGMKERTREGPP*LSDPKGCIFYA MGLGFRFSACKICPACPLTG\SMIIFFLP\LKVTQ\NLTLI\EESL TLRS*FMTIDPRT*KTVAGGPSLSPKLK\SYEGEEHPKFLAGR*SL QSLV*FHPDFSKI\TGK\PIKLDFRVEHPRLAFEWNE\DGAGNHPPS PRGLQPAHL\TFPLDYHLNQPFIFLLRDTDT\GALLFIGKI\LDPRG P
1660	A	3	340	DLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQ LVSIESEDEQKLIKFIENLLPSDGDWIGLRRREEKQSNSTACQDL YAWTDGSIISQFRETSSSF
1661	A	2	501	GKPD PSTKKQHTIWPSPHQGNPDLEVYNVIRKQSDVSLAETRPDLK NISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVENEIYGY*D I*KTETDNNGKEMISKILLFSIRKIHRRSMNKLRSQPVDEHVVPPTS CWTPTFWLYPLSQPVQLDLMMRYL
1662	A	3	52	GRSKESGWVENEIYGY
1663	C	92	244	MRCEIILVLIPIYVYFYSNKLCSRLXXXXXGGAVLKNPWGGQSLPGL AR**
1664	A	336	413	GPWTVLGAGACGGEVHFISYRPGSC
1665	A	233	401	GGAVLKNPWGGPSLPGLAR**FFPYRGAY*NLPGNFWKEPLFLGGDI LGQPPFGNL
1666	A	194	360	GGAVLKDPWGGQSLPGLARK*FFPYGGPN*NLPGNFWKGPLLWGGDI LGQPPYRN
1667	A	319	391	FFPYGEPYINQPGDFWEGTFLGG
1668	A	313	542	ALKQPT/PQTKEERAFDPRVHAE*IPYVFEIHIRST*KTT*NGNPTA PLPVRAPTPARVRTWPNPGHSCAGSHSSR
1669	A	143	1316	ERLEIGKELQLVWDEPHLTPGNDSLPSSCCVTAASDLDLRGGQPVC RGGTQRPCYKVIYFHDTSRRLNFEEV\KFSCRRDGGQLGSISEDEQ KLIKFIENLLPSDGDWIGLRRREEKQSNSTACQDLAWTDGSIISQ FRNWWYDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWDDRCNMKN FICKYSDEKPAVPSRRS*\GEETELTPVLPEETQEEDAKKTFKESR EAALNLAYILIPSIPLLLLLVVTT\VCWVWICRKRKREQPD PSTKK QHTIWPSPHQGNPDLEVYNVSKTNAKSFLSETRPDLRNISFRVCS EES\PPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQ

				MGRSKESGWENEIYGY
1670	A	18	688	SPPPPPPAREMNFVRAANRRRPRVSRPRPVQOQQQQPPQPPPPQPPQ QQPPHQQPSSPPQ*QQQHPPASSPPPPPLPQERNVGERDDVDPAD MVAEESGPGAQNSPYQLRRKTLLPKRTACPTKNSLEGASTSTTENF\ GHRAKRARVSGKSQDLAAPAE\QYLQEK\ PDEVVLKIFSYLLEQD LCRAACVCKRFSELANDPNLWKRLYMEVFYTRPMMH
1671	B	155	310	MAAIRKKLVIVGDGACGKTCLLIVFSKDQFPEVYVPTVFENYVADIE VDGKQ*
1672	A	162	877	AMAAIRKKLVIVGDGACGKTCLLIVFSKDQFPEVYVPTVFENYVADI EVDGKAGRSLACGDTAGQEDYD\RLRPLS*PDT\DVIL\MCFSIDSP \DSLE\NIPRKS WTPEVK\HF\CPNGGPSILVGELRRVLSGIDGATQ GRGLRPRLKAGSPVET*RKGRDMGKQGLALEGYIGSCSSQRPKDEW EEVF*KWATESLLWQA*TLGKKKSGVPLSLVKPLLQAQPLMLRIFE VLFINLSV
1673	A	1	711	MREEARSRELWAGASRHVPVPVYKNLQLFMENKOPRDDLFDRLTTTS LNKHLQELMDGLTAKVFRYNASITLQEQRLRALTRGLPGGGARAGCS GALTLMCFACRGPQRPVLCPCPDNLGAGAALGLWDAEELAGIQVR APGEETPPPLREAEDSGPCLSAEDSIAAKILSYNRANRVVAILCNHQ RATPSTFEKSMQNLQTKIQAKKEQVAEARAELRRARAETHKAQGDGKS RR
1674	A	1	2647	MGVTSAAAGLVGSAPQCVALPSEGWTAVWPVAACTCSGVGSSPKLT PGSFVHCPWFLLLTEATRAEIKRPFKAELKASVRPMEGSHCWGGEA RRTSQGHEQKELRARRQAQNEDEDVKEVWVGKTKKEESDKLGCQG AWVPPRVPSWIGRFELWVVGWYEQPAVSWQMRVRLRLRAALTLLG EVPRRPASRGVPGSRRTQKSGARTDSAWRRALTIVISTPGTSRMDP VALVAVGGPRRFPGGHTLQRLPVALRTLIPADQAHQAPNSTWLGSR AGLLALAAGLGIRDSAAHGPLQVGGMGGYTGMGSEVRWEKEKHEDG VKWRQLEHKGYPFAPPYEPLPDGVRFFYEGRPVRLSVAEEVATFYG RMLDHEYTTKEVFRKNFFNDWRKEMAVEEREVIKSLDKCDFTEIHRY FVDKAAARKVLSREEKQKLKEEAELQQEFGYCILDGHQEKIGNFKI EPPGLFRGRGDHPKMGMLKRRITPEDVVINCSRDSKIPEPPAGHQWK EVRSDNTVTWLAAWTESVQNSIKYIMLNP\CSLKGETAWQKFETAR RLRGFVDEIRSQYRADWKSREMKTQRRAVALYFIDKLALRAGNEKED GEADTVGCCSLRVEHVQLHPEADGCQHVVFEFDLGLKDCIRYINK\V PGEKPVY*NLQLFMENKOPRDDLFDRLTTTSLNKHLELMDGLTAKV FRYNASITLQEQRLRALTRAEDSIAAKILSYNRANRVVAILCNHQRA TPSTFEKSMQNLQTKIQAKKEQVAEARAELRRARAETHKAQGDGKSRS VLEKKRLL*KLQE\HLAHLVQATD\KEENK\QVALGTSQNLNLD RISIAWCKRFRVPVEKIYSKTQRERFAWALAMAGEDFEF
1675	A	2002	2238	KGDFTKLPLC/C*SVPAFY*RSLKICCSIYLV*YMSVSVIESICYKY TVFCSRG
1676	A	3	430	SAAEVNIQOVSQKEAKHKITSADGHIESSALLKEKQHRHLHKFLCLT VGKPMRKTFSVQASATMQYAQRDKKHEYWFAVPQERTDHLIAFFIQ WSPEIYAEDTGEYTREPFGFIVVKKIEESETIEDSSNQAAAREWEVVS V
1677	A	263	899	ISYQEGTSAIQRK*QEVTLRK*TOESE/SAGNDSASTAPRSTEEELS EDVFTESELSPIREELVSSDELRODKSSGASSESQVTNQAEEVSLT VKSESTGTPGHLRSDTEHSTNEVGTLCHKTDLNNLEMAIKEDQIADN FQGISGPKEDSTS IKGNSDQDSFLHENS LHQEESSQENMPGETAEF KQKQSVNKGKQKQKEQNQDFTGQAG
1678	A	1165	1530	VKNGGNEVIICHFHLTFGIYLLFFETEFCSRPRLEC\NGAILAHCN LRLPGFKRFSCFSLPCC*DYRHLP RPVKFFVVLVETGFHYLGQAGL KLLTPGDL/PPPLGLPKCVSHCAQPRVSTF
1679	A	197	843	RLFSSNQTVDSQKNVDITLKGTPQ*SCKGPRGT\LR\RDEN\HIKC GTSALLGKEKKRGFRVD\KWWG\SRRELGYPGFTI\CSHVQDHDPRG VTTGASRYQDEGPVYASPSPHPTVGLSQENGSSLLKSRNFFGVKKYI

				PQGFRMRPGCLLVSVSQGPKE*INPLKGNDI*ALLQIPAAL\IPAS PTRLKTGIRKFFGWVSMSEKGTVPGLIE
1680	C	27	218	MLMADIRKEERNHLCRSSRRTWTILDRAEYSDHVVLQAGVGWGT SX SPFLYSFEIPYGAQVA*
1681	A	490	773	HPQIFVPGQESFNDRILKQPVEGLVVLREHERHSPSLRLHLEATQRL RHPGLRLRGELLWLIIIRFIQTLPLPFAAKGPTRGAGIYPRGKQPV EGLVVLREHERHSPSLRLHLEATQRLCHPGLRLRGELLWLIIIRFI QTLPLPFAAKGPTWGAGIYPRGKQPVVEGLVVLREHERHSPSLRLHLE ATQRLCHPGLRLRGELLWLIIIRFIQTLPLPFAAKGPTWGAGIYPR GKQPVVEGLVVLREHERHSPSLRLHLEATQRLCHPG/LPQAQGRAPSL AHHQIHNPNTSSFCSSQGTAGGWDLPQQAAC
1682	C	48	80	MGLWLFHEIY*
1683	A	858	1055	PSVPVMPILLEPEGQEEPLSDSPVPETSVPVLLFHERQGLGFPGGVGG EHRTQGRCGFSAGTLFQC
1684	A	1	103	VFFLFGGDGVSLCHPGWSAVA*TQEAEEPFVQII
1685	A	451	785	CSQDGLRWDLVRHPQTFVPGQESFNDRILKQPVEGLVVLREHERHS PSL/PASS*GHTASPPPRSPQAQGRAPSVAPPPTTPQICPTTPSSFS SKRTYAGGWDLPQQAAC
1686	A	1	1335	MNDDIRSDLPDWRDRTPCVQKKAMDRTKTRFRKRQGITGKITTSRQ PHPQNEQSLQRSTSGYPLQEVVDDEVLGPSAPGVDPSPPCRSLGWKR KKEWSESEEEPEKELAPEPEETWVVEMLCGLKMKLKQQRVSPILPE HHKDFNSQLAPGVDPSPPHRSFCWKRKREWWDESEESLEEEPRKVL PEPEEIWVAEMLCGLKMKLKRRRVSLVLPHEHHEAFNRLLEDVPIKRF LAWDKDLRVSDKIPSEPTI/HGSITQNPSSGFSDLHPTFEYPSIPQF PNEYSHNPTEGGCQS*ARDSPLPS/VSGKLTSAAGLSWWCP*APT*F LSSATWPMTWRRTRTPNKTSTSCMRPALAYPWSVTVGSSYAVA* TPCVQKKAMDRTKTRFRKRQGITGKITTSRQPHPQNEQSLQRSTSGY PLQEVVDDEVLGPSAPGVDPSPPCRSLGWKRKKEWSESEEEPEKEL APEPEETWVVEMLCGLKMKLKQQRVSPILPEHHKDFNSQLAPGVDPS PPHRSFCWKRKREWWDESEESLEEEPRKVLAPPEPEEIWVAEMLCGLK MKLKRRRVSLVLPHEHHEAFNRLLEDVPIKRF LAWDKDLRVSDKIPSE PTILGASPKTLPLASQICIRPSNTPPSRNFQMSVTPTLRVGASPEL GTVPYLPLEADLSRRPLLVLSTNLISVLSYLANDMEEDDEDPKQ NIFYFLYGKTRSRIPLVNRNRFQLCRLNPRARKNRSQIALFQKLR QFFCSMGRWVSREELEENTGPRGDVDFQQELYSNANGRQGERGEE PFVQII
1687	A	385	889	LEPTLTEQGYARAVLPIQEVVDVLFGLVLLHVIGQVESQEE MNAL VLPGEAGPAEIRYDHSQEILVRHPQIFVPGQESFNDRILKQPVEGL VVLREHERHSPSL/PASS*GHTASPPPRSPQAQGRAPSVAPPPTTPQ IGPTTPSSFSKRTYAGGWDLPQQAAC
1688	C	1	1869	MDSPTPHDPAAPLLVTVLESVQKTKDRTETSFGIEGQILGKIMTSH QPQPQEEQSPQRSTSGYPLQEVVDDEVSGPSAPGVDPSPPRRSLGCK RKRECLDESDDPEKELAPEPEETWVAETLCGLKMKAKRRRVSLVLP EYIEAFNRL LAPGVDPSPPRRSLGCKRKRECLDESDDPEKELAPEP EETWVAETLCGLKMKAKRRRVSLVLP EYIEAFNRL LAPGVDPSPPRR SLGCKRKRECLDESDDPEKELAPEPEETWVAETLCGLKMKAKRRRV SLVLP EYIEAFNRL LAPGVDPSPPRRSLGCKRKRECLDESDDPEKE LAPEPEETWVAETLCGLKMKAKRRRVSLVLP EYIEAFNRL LAPGVD SPRRSLGCKRKRECLDESDDPEKELAPEPEETWVAETLCGLKMK KRRRVSLVLP EYIEAFNRL LEDVPIKRF LAWDKDLRVSDKIPSEPTI LGASPKTLPPASRICIRPSNTPPPRNFMSTVTPLSYLANDMEED EAPKQKIFYFLYGKTHSHIPLRPKHWFQLCRPMNPRARKNCSQIALF QKRRFQFFCSMRCRAWVSPEELEENTGPRGDVDFQQELYSANGRHQ EGGEEPFVQII*
1689	A	520	1235	WTDFRSIGLMALAGSVLEFSARSKDATPDPP/LGTGKVPSTAPT GAP PPGLPTAAFDVVLHPFRAGRKKYFPSLLFA*WLCQRSSP*RGADPVI

				GLYLVRHGGACQTPTLGNRQTPRLGIHARPRRRATTSLTLLLAFGK NAVRCALIGPSLTSRTRPLTEPLGEKERREVFFPRPERVEHNVES SRWEPRRRGACSGRGNFPSPRGGSGVASLERAAENSTPEAKAIKPI DRKSVHQICSGPVVPSLRPNVAVKELVENS LDAGAH
1690	A	2176	2641	RKTIEEKADPKLQGGFFVCLFVLETESCSASQAGMEWPNLNSLQPPPP GFTQFLC/SQPPE*LGLTGVPPHQAHCIFSRDGASPC*PGWSPTPG LKRSTCFSLKWCWYRHEPPRLAYFL\LFNRDEGLAMLPRPVNSWP QVILLWPPSVLGFQA
1691	A	112	410	LLPPPPMPLRCPFQTLRASRVKEANS LPTGPAGVGRPNCPGSPTQTM TLLPVQSRPRQGPMEHMLRAMGVRAKATEQDAEEPRLGPVLPPEHEP LGAGA
1692	A	2148	2510	SQHFGKLRQEDHLRSGVREQPGQHGTPLYLLKIQKL\AGHGGMCLYS QLLMRLRQENG VNPGGGACNEPRLRHCTPAWVTEQDSVSKKKTVHKK KLNWGS\VRGET*RTSPCVALDTAHL
1693	A	178	730	IFFFFFFFKMESCSVAQAGVQWRDLGSLQAPPRGFTPFSCSLPSSWD YRRPLPRPANFFYF**RRGFTVLATMVIS*PHDLPTLASQAGITG VSHHTQPVYALFFSFETEFCS\VAQAGGQWRDLGSPQPPPPRFKQFS HLSLPSSWDYRHAPPSLANFFCIFS RDRVSPSWSGWSRTPDLR
1694	A	2	780	CWGLRRQRSQDVTMAWALLILTLLTQGTGSAQSALTQPPSASGSL GQSVTFSCSGTSSDIGNYNYSWYRQHPGKAPKLMIEVTKRPSG\V PE\RFSGSKSGNTASLTVSGLQ\SEDEG\DYCCSMARHHS/VGWVF GGGTQVDPSLGQPKRAALGSLCFPPSLGEASSQRPRTLVCVISDFLP GKP*TVA*KA\DSSPVKAG\VETTPTPSKQ\SNNNYAATSY\LTLTP EPLKVPQEATAACRVTP\EGGTLEKTVAPECS
1695	A	103	532	NETQPKACREQNMEGDFSVCRNCKRHTV SANFTLHEAYCLRFLVLC ECEEPVPKETMEEHCKLEHQYAGSGIGKRFWFQERLAVLLRSVKRG CEKGRSWKAVRWSVSRLSMSIPPGAPDLSLWYSSSGSRCQHKGTGL TT
1696	A	112	1158	SCGLGHRKTF SFVSLPARNETQPKACREQNMEGDFSVCRNC*RHVVS ANFTLHEAYCLRFLVLCPECEEPVPKETMEEHCKLEHQV\GCTMCQ QIMHKSSLEFHKANECQERPVECKFCKLDMQLSKLELHESYCGSRTE LCQCGGQFIMHRMLAQRDVC RSEQAQLGKGERISAPEREIYCHYCN QMI PENKYFHMGKCCPDSEFKKHFPVGNPEILPSSSLPSQAENQTS TMEKDVRPKTRSINRFP LHSSESSSKAPRSKNKTLDP LLMSEPKPRT SSPRGDKAAYDILRCSQC GILLPLPLNQHQEKCRWLASSKRKTSB KFQLDLEKERYYKF\KRFHF
1697	A	343	586	KQOKTSFSSLP RRVCN SHLVLL/RCDFKNCNLAFETKICQPIIKST *EYMGFGIFLCFLLYNIPFHICGPRVKSSFCYRH
1698	A	217	360	HYNDSILQIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEBANQNV H
1699	A	1	390	WEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQENKELRTSLEEH QSALELIMSKYREQMFRLLMASKKDDPGIIMKLKEQHSKELQAHVDQ ITEMAAVMRK\PLKLTNRVARNKNEYFNLNKKTKA
1700	A	386	790	NSIMEEQELNEVARHRPRST\LV\MGIQQENRQIRELQQENKELRT SL\EEHQSGLGNL**AKYREQM\LRLLMASK\DDPG\IIMKLK\EQ HSYD*HWYIVTSPKDSSLMHLDTS LKHLNMDWREGTWKQIRMYTK
1701	A	1089	1296	CPPPLFFFETEFRRSCCPGWSNSSLHRPPPGFKQFILNFLG*K/PSYP YLFAQSCARMCVCVCVCIIFTET
1702	A	2	367	RDNTSPISVILVSSSGSRGNKLLFRYPFQRSQEH PASQT/RFS DVILA TILATKSEMCGQKFELKIDNVRVFGHPTLLQHALGQISKTDPSPKRE APTMI LFN VV FALRANADPSVINCLHNS
1703	A	1	452	RCQYSTREAKLI/LALQD/EVSAMAD/GNE/GPQSPFHHILPKCKLA RDLKEAYDSLCTSGVVR LHINSWLEVS FCLPHKIHYAAS SLIPPEAI ERSLKAIRPYHALLLLSDEKSLLGELPIDCSPALVRVIKTTSAVNKL QQLAQDALLPRLP
1704	A	1	468	LSPNASVCLYSPLAEQFSHQFP SHDLPSVLAKFSLPVSLSEFRNPLA

				PAVQETQLIQMVVWMLQRRLLIQLHTYVCLMASPSEEEPRPREDDVP SMDNSSAELLPSGDSPLNQRMTEENLLASLSEHERAAILSVPAQNPE DLRMFARLLHYFRGR
1705	A	2	118	NENTRRSQLMLLFDKFRSVLVVTTTHEDPVIQVQALLP
1706	A	1	672	DADSRFSEVF/LATILATQFEMCGQKFELKIDNVRVGHPTLHRHAL GQISKTDPSPKREAPTMILFNVGFALRANADPSVINCLHNLRRRIAT VLQHEERRCQYLTREAKLILALQDEVSAMADGNEGQSPFFHHILPKC KLARD/PQLWLPNQQR*HDPHQPHGQQLQRRATSQRGLATEPEDDGE PAGQPVGA*TRSHPOQTRSPEP*GPPHVCQAPSLLPRP
1707	A	230	345	TWALKDAASPRDRSPGRPPSSVEMPTRAARTGGKRRNT
1708	A	464	763	LEHSVYGPLLVASLAFNNQLLFRVLAKSEVNSQQCFNKGKLRMYN ENTRRSKLLMLFDKFRSVLVVTTTHEDPVIQVQALLPWPAGGGRKAA RPGNH
1709	A	3	156	GRHHL/EEEIMYNENTRGSQQLMLF*QSFAACWMVTTTHEDPVIQVQ QALLP
1710	A	1	1878	FRGTWAPSASGSVLLRLPPPPAPSSSGPLRPRPRPHGGMRRDNTSPIS VILVSSGSRGNKLLFRYPFQSRQEHASQTSKPRSYAASNTGDHA\ DEQDGSRFSDVILATILATKSEMCGQKFELKIDNVRVGHPTLLQH ALGQISKTDPSPDGKAP\TMILF*CWLFA\LANADPSV\INCLH NLSRRRIATVLQHEERRCQYLTREAKLILALQDEVSAMADGNE\DPK PPFFHHIL\PKCKLARDLKEAYDSLCTSGVVRHLHNSWL\EVSFCLPH KIHYAASSLIPPEAIERSLKAIRPYHALLLLSDEKSLGELPIDCSP ALVRVIKITSACERTCRQLAQDADLA\LLQVFQLAHL\VYWGKAI I IYPLCENNVY\MLSP\NASVCLYSPAGPSSSSHQFPFSWTWPSVLAK FSLPVFLCQNFNPLAPRCARRTQLH/IQMVVW\MLQRR\LLIQL\H TYV\CLMASPSE\EEPRPR\EDDVPFT\ARVGGRSLSSTP\NALSFGS PT\SSDDMTLTKPQAWTTPSAELLPSGDSPL\NQRMTEENL/APSL EHERAAIL\SVPAQNPEKDMFA/RGILHYFRGRHLEBIMYNENT RRSQLMLLFDKFRSVLV/VTTTHEDPVIQVQALLP
1711	A	1	613	PLKRSDBGNDGRPTRPPTRPDPTTVFTSNLQKTRMVHLTPVE\KSAVT ALWGQA*TWMKVGGKALGK/RCWVVLWDPKRSFEVLWGNLSQLP\D AVNGANP*R*KASMAKEKVLGCPLSEWPLAHL\DN\LKGHPLPHTEV NLNCDK\LHRGSLKNFR\LLGQTCVLCVPGPINFWQKNSTPTSCAC LIKKSWLAWCWLNALGPTSIT
1712	A	208	748	ENGTTGEREGSLRTHPGYPRSPGLGHDPHCKPFLLSTAGOPPNYEM LKEEQEVAK\LGAPQKPCLEPCPRVINIRNE\TSWPDHVRVLPVQ\H PLHEHLLRLGFI RFA\YSVKSLRDRK\MVGDNVRGPKA*CLHRQ\VP E\NLGPDFGHL\HDHFCSS/HH/HPVLGRP\GPAIDQEASLRP\GAL PVTICPRTLSSIPRPAPRGQELCP
1713	A	243	850	NHTVQTLFFPCHQWPAPPTMKMLQGRSQQLAVLGAPPKPLLPPTS\T VIPHPASENLRCPD\HVVLVP\VSTPFFNETPGCLGLQ*DSPYSVK\ SRDRK\MVGDNVRGARAYASPAKVPEHLGP*F\GHPHDHSAHRHPSA DLARPI/AIDQEASLRPGALPMT\CIPRTPTSIPRPAPRSRVLYQPF ILTRFSTMAFNKVHVFLVLL
1714	A	97	424	SPALWEAYDGWITLRSGVQD\QSGQHGEPPSLLKIQLAGHDGECL* SQLLRRLRRENHLNLGGRGCSELSRYCIPAWAPEIAPLHSSLGDLN KTLSQKKTKTVSFYI
1715	A	83	1259	KMAEEVVVAKFDYVAQQEQELDIKKNERLWLLDDSKSWVRNRMN KTGF\VPSTYVGR\ENSARKASIVKNLKDITLGIGVKRKPSVPDSAS PADDSFV\DPGERLY\DLNMPA\YVKFN\YMAEREDELS\LIKQ\TK VIVMEKCS\DGWWRGTYNGQVGFPSNYVTEESD\SPGLDHVGSLS KLAUVNNLNTGQVLHVQALYPFSSNDEELNFEK\GDVMDVIEKP ENDPEWWKCRKINGMVGLVPQKLW*PLLQSIQLTSGLTTLTFQCGFI RPYIPGKFVGNPWYYGKVRHQAEMALNERGHEGDFLIRDSESSPND FSVSLKAQGGKKNHFKVQLK\ETVYCIWQRKSCCTME*LVEHYK\KAPN FYNVNKGEKLYLVKHLSMILLTQK

1716	A	18	367	SPPPPRTRRWPLRRPRLSLGTRAASLRFSSRKPCQNKPDYGLRSE KFR*SRK/A*GRQRP/PREKFPLPFPKPIEPGEAKPGEIVNGSVRP PNMPLYIPTSIALPYFTFLAVLTL
1717	A	47	409	NSYIYMCIIYSYINTIYIHIYLESNISLPLNIYISTPT/HIY*RHTV* VHTKAYVHML*HVYIHFCLCVHKSFKGTIYRDASFLESCSKVNTech KLRKVKRKYSRIHHTGIHQSSFIMRKMS
1718	A	89	1560	IMKHTNPEPGSFSRFYSLKVAPKVATAAP\AGAPPQPDLEFTKLP NGLVIASLENYSFVSRIGLFIKAGSRYEDFSNLG\TTHLLRLYIQS* RTKGASSFQDNFVGIGRQLGGQIKC*PQQENMGLYWWECL\RGDVD I\LM\EFLLI\TT\APEFRSLGK*VNLQPQLK\IDKAV\AFQNP\Q TH\AIGNLHAAA\YTGNALANPLYCPDYRIGKVT\SEELHYFVQNH TSARMALIG\LGVSHPVLKQVA\EQFLNMRG\GVGLSGWQRANYRGG EIREQNGDSLVAHF\VAKS AVAGSAKPNASFVLQH\VLGAGATMSR GAATTS\HLHQ\AVSQATQQP\FDVSAFNARYS\DLGLFGI\YTIS QGHQLAGDCIK\AA\YNQVKPIRSKPPFPPTQGVSA\KNKG*KAGI PLMVQWKSFLKCSGPRKSGSPGLLV/GLVPYMPHTPTVPSSQMDSSG LMLDIIN/ARAKKFVFWARSSMGSKFGKFGDITPFCMEL
1719	A	53	421	DTMALTSDLGKQIKLKEVEGTLLQPATVDNWSQIQSFEAKPDDLIC TYPKAASGTTWIEIVDMIEQNGDVEKCQRAIIQHRHPIEWARPPQ PSVLVLRRCFLLSYFKGVEKAKAMPSR
1720	A	1	1260	MALTSDLGKQIKLKEVEGTLLQPATVDNWSQIQSFEAKPDDLICTY PKAGTTWIEIVDMIEQNGDVEKCQRAIIQHRHPIEWARPPQPSAP LAPLAFEEEEKMTSYCPMEETNADDITSMEGYWGEGNMANEPFLE LVGLGMGPAAWAVSCTLSTLCPSTLSLSNHRGIPGGICRCVINRDL HNVAQATMSPAVKVLGETLEECFLLSYFKGVEKAKAMPSRILKTHLS TQLLPPSFWENNCKFLYVARNAKDCMVSYHFORMNHMLPDPGTWEE YFETFINGKVVWGSWFDHVKGWEMKDRHQILFLFYEDIKRDPKHBI RKVMQFMGKKVDETVLDKIVQETSFEKMKENPMTNRSTVSKSILDQS ISSEMRKGTVGDKWKNHFTVAQNERFDEIYRRKMEGTSINFCMEL
1721	A	403	1334	DTMALTSDLGKQIKLER/EVEGTLLQPATVDNWSQIQSFEAKPDDL ICTYPKAGTTWIEIVDMIEQNGDVEKCQRAIIQHRHPIEWARPPQ PPQPSGVEKAKAMPSRILKTSFHFWSLPPSF\ENCKF/LFMLA SEIAKD\CMVS*\YHF\QRMNHMLP\DPVTWKYF\ETFINGK\VF GSWF\DHVKG\WW\EMKDRHQI\LFLFYEDIKRDPK\HEIRK\VMQ MGKKVE*TVLDKIVQETSFEKIKENPMTNRSTVSK\SILD\QSIFPP FMRKGTVG\DWEN\HFTVA\QNERFDEI\YRRKMEG\TS\INFCMEL
1722	A	2	645	HGIQAHGQIPSYKTIGGRDDSFHTFFSETGAGKHVPRLLL*NBKPTV MDEVRTGTTCQLFHLEQFITARKIAANNYARGHYTIGKEIIDLVLD IRKLADQCTGLQGFLVFHSGGGTSGGFTSLLMERLSVDYGGKSKLE FSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMEEGEFSEAREDM AALEKDYEEVGVDVSVEGEEGEEGEEY
1723	A	87	1531	SLATMRECISIHVGQAGVQIGNACWELCYLHGIQPDGQM/TQVTRP LGGGDDSFNTFFSETGAGKHVPRAVFDLEPTVIDEVRTGTYRQLFH PEQLITGKEDAANNYARGN\YTIGKEIIDLVLDRIKLADQCTGLQG FLVFHSGGGTSGGFTSLLMERLSVDYCKKSK\LEFSIYP\APQVCT AVVEPYNYILTDHTT\LEHSDCAFMDNEAIYDICRRNLDIRPTYT NLNRLISQIVSSITASLRFDGALNFTLTNFGTKLVFPF\RIPLPFCP IMPPVHFA*ERPPMNSFSV\REITQMLCFEPSPTRLVK\CDPRPWK SWPCCLVATGGDVVPKRCQMLPIAHPSKPKR\TIQFVDWCPTGFKV\ GINYQPPH\WVPGGNLA\KVTREAVCMLS KHSPFAEAWARPGPTSF DLMLCQACPFVHWYLG\EGMEEGEFSEGRER*GCPFRKDYEKV\GVD SVEGEEGEEGKGILIIHSLFG
1724	A	84	1560	EATTSPLRLRHQLGSREAATMRECISIHVGQAGVQIGNACWELCYL HGIQPDGQMPSD/RKPLGEGDDSFNTFFSETGAGKHVPRAVFDLEP TVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLV DRIRKLA\QCTG\LQGFLVFHSLGGGNWVLPVPPCLQLGGGGAGK

				RLSVDYQGEVPSWEFSIYPGAPRFPQPVVEPYNFHPTNPTPTL GAL* LCPSWVDNEAIYDICRRNL DIERPTYTNLNLRLIGQIVSSITASLRF GALNVDLTFEQTNLVPYPRIHFPPLGHIMPPVIFAE\KAYHEPAFL*Q RSQMLCFEPAN\QM\VKCDPRPG\KYMLCC\LLYP\GDVVPQRISFL PLPTIKTQ/RLTIHFLDWSPTDFKLVINYPPTVPPG\DLTKVQRA VCMLSNT\TAIAEAWARLDHKFDLMYAKRAFVHWYVGEEMEEGEFSE AREDMAALEKDYEEVGVD SVEGE EEEEEEEY
1725	A	153	380	EEYKTQNR FELRSPRLDCSGAISAHCNLCPLGS\SN SHAS\ASK*AG ITGMHHHAWDNFCILFSRRWGFCHVGQGW
1726	A	14	322	IFSSEPLEGRPGRPGGARAACGQEGAGK\AGAAGD*PSP/PG*GHAA APKCREFGHNQIDAGWNQRP/GKPGLVPMWEP CQPQSCPLELSEFP GAHSSWTSNSIY
1727	A	605	3135	DSRGQEG*RTGAPHMGDKGPGVSGPPGFQASIKFGCGQN\FSPITLG PGPG/PWGGCGQALSPSGVPGLEGVSPTRAKGW\RFPKAPETLNER QIYP\NAPPS*AG*\GHADTEGQDRTPHLLGANSSGHLGQLPF*SA SIGGAGR\SQGLSRAFSSASKHSVPASAGTF*HSFSKG*VSKTTTT NAGNALFPMPGSSSKTKPN SHQRGQMS*GRNPPSLGRAPAPLPERE APIPAPQLGPSAAGTSRQVGQKSSTSP/PPGRGGNIEP*TQEERRKE KMKKATGLSKHQ PAGFIQNE*NLKGAGEF/GP/SGLAGSQNPSSKL QGLGGKC*EURL**GAGPDCSPLGKHTP*RSPSPLPRTGDASRG\ S* GFSGKEASFGPGQPSTCLSGIRPSLGS*PLGQ*RTL/PCSNLPAGK /RNCLG/PPGLGRGHGRCDLSQHGSQT*AGANWRKRQ/PPVPAGLL DPGPLTAQQA VTRSPWEGAQGRGGEGPVGLCWG*ACAKCRLQGSRT FAGGRQGSRSRGVWVGSEVMAPRKRPAGPPGHKEGTAEAVSSQTVTG GRIPEAVWPHHHQKGTEQEPC*DVTKASAPGVSGDTG/MRGPLQ PQASPNI*GAAACPFSSQRAGSSLQRRSLPAPSCPQAA/RGPPGLPG LPSSGSEENIHSGAWALVGQEGPSMDGRGNMMLRGVWTVGHGGMD EMWRRGDLKGKVP HGMIVWTP/G/DKQDSSPARTPAPQWLSITTGS *TPE/GDPGGKLDAAQRGRAIAAHEQEVAVLGVA/GHL*SPGSARS SPRWHPHRSACRPPRS GGSPPSPSSA*KSDRTDAGAGVAAAASPGAG APAHCPQGP RSCQGPQR
1728	A	1096	1748	ELFPPTSTSI ALAQLRAL TQAGQPLTQVNQGA FMSPLWVLDPRERGD LKIKPSFLLWGWALHGFQHEALWALGCAPIEERGGEREAF LGPEMF SWGGFAHPCP*THQFWGEPQ/EV*GGRHCGKAPREKWPALAPTQK EKPVPVPTPEAIPVCQEGAPPGTAKSIHCPPEIHTKEACPVPGKEEN VPGKRKIWSKKRDRQGRAQESRIQGEIP
1729	A	162	788	QKLFFLAENIIRSFRTVKTLSFVLNQMMCFISVFDVFSFFSPGFTS FVISLCFGFAANLIGLGLAAKALDSGAFFSFVVLSPSFPPLPSCPHHF TLLKVINMTRSEIPFLAPSTLGFFEMESHCVTQ/CSGA/ISAHCSLH LPG*SNFPVSAS*VAGTTGASHDNWLI FLFLVETGFHHADQGG LKF* PQIIHPLGLPKWLGLQCEPCGWL
1730	A	158	468	TGAGHGLMPVIPSHFGRPW RADHLRSGVRDQPGQH*NPVSTKNTK IGWA*WRAPVIP\AT*EGLRQGESLEPGRAEGARRCHYIPAGGDRVR LCLKKKKLN
1731	A	1	1161	MSSF EKCLFMSFAHFLMDAEKAFDKIQPFMLETLNKL GIDGTYFKI IRAIYDKPTANIMLNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLRLIS NFSKVS GYKINVQKSQAFLYTNNRQTESQIMNELPLTIASKRIKYL IQLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMPFFTELEKTTLKFIWNQKRAHIAKSILSOK NKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNRTKDMNRHFSK EDIHAAKHKMKCSSSLAIREMDIKTTMRYHLTPVRMAIKKSGNNR CWRGCGEIGTL
1732	B	1	1380	MDKFLDTYTLPRINQEELES LNR PITASEIVAI INSLSSKKSPPGPDG FTAIFYWSVGSAGQAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLEN PIVSAPNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIMSEL

				PFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPC SWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTEILEKNTLKFOWNQ KRARIAKSILNQKNKAGGITLPDFKLYYKATVTKTWWHQNDRIDQ WNRTEPSEITPHIYNYLIFDKPEKNKQWGKDSLFWKWCENWLAICR KLKLDLFLTPYTKINSRWIKDLKVRPKTIKTLEENLGITIQHIGMGK DFMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNREPTWEKI FATYSSDKGLISRIYNELKQIYKKQTPSKSGRRT*
1733	A	1	293	MIISIDAFAFDKIQQPFMLKTLNKLIGIDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTROGCPLSLCTSFCQCLGRASERRNISIGMHE ETF
1734	A	1	1185	MKLKRNNEMSGKALDPREGFCDASYBIQTTIREYYKHLIYANKLENLE EMDTFLDITYTLPRLNQEEVESLNRPIGTAEIVAIINSLPTKSPGPD GFTAEFYQRYKEELVPFLKLFQSIEKEGILPNSFYEASIIILPKPG RDTTKKENFRPISLMNTDAKILNKILANRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVIQHINRAKDKNHLIISIDAFAFDKIQQPFMLK TLNKLIGIDGTYFKI/Y/RDRHFSKEDIYAAKHKMKCSLSLAIREMQ IKTTMRYHLTPVRMAIIKKSGNNRCWRGCGEIGTLLHWCWDCKLVQP LWKSVMRFLRDLELEIPFDPAIPLLGVPKDYKSCCYKDTCH/IMF IVALFTIAKTWNQPKCPTMIDWI
1735	A	66	1394	QVLLSFGTPLVLTTKREKNQIDAINDKGDITDTPTEIQITSIEYYK HLYANKLENLEEMDKLLDITYTLPRLNQEGVESLNRPIGTSEIEAIIN SLRPISLMNIHAKILNKILGN*IQQHIKKLIHHDQVGFIPGMQGWFN IRKSINVIEHINRTKDKNMIILIDAFAFDKIQQPFMLKTLNKLGI DGYTLKIIIRAIYKPTVNIILNRQKLEAFPLKTGTROGCPLSPLLFN IVLEVLAKAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIISAQ NLLKLTGNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELPTIAS KRIKYLGIQLTRDVKDLVKENYKPLLKEIKEDTNKWKNIPCSWVGRI NILKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKFOWNQKRACIA KSILSQKNKAGGITLPDFK
1736	A	1	432	MSELPTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKN NIPCPWVGRINIVKMAILPKVATITVLTQVRFRLCNMPKVTQLDT AEPRFSAQLSVLHVYVWVPLKEFVFEALGKWLKGDQLQATMRVCLI SST
1737	A	1	413	MSELPTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKIIYRFSAPIKLPMTFFTELEKTTLKF IWNQKRACIAKSILSQKNKAGGITLPDFKLYHKATVTKTAWYW
1738	A	1	1401	MGQHDKQOYLEVQSNKIIIAIWISDDHEDIISELGCLHIPERQKMSIL FPSSATSGWARAQDRFVAGSARPALLSGRLAPPALGSERLSTRAS SCGGLPRATPRGRAPPPATRHVPVSTAQRRLRSAAARQLLAGSSARGR DALGKASWAPESVLEVLARAVRQEKEIKGILLGKEEVKLSLFAGDMI VYLENPIISAQNLLNKINVQKSQAFLYTSNRQTESQILSELPTIAS KRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLPMPFFTELEKTTLKFIRNQKRARIA KSILIQKNKAGGITLPDFKLYYKATVTKTAWYQNRDIDQWNTTEP SKIMPHIYNYLIFDEPEKNKQWGKDSLFWKYWENWLAICRKLKLDP FLTPFTKINSRWIKDLNVRPKTIKTLEENLGITIQDIGMGKDFM
1739	A	1	512	MLEVLAWAVRQEKEIKGIQLGKEEVKLSL*LMSNFSKVSQYKISVQK SHAFVYTNNRQSESQIMSELPFTVATKRIKYLGIQLTRDVKDLFKEN YKPLLNEIQEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTK\FIWNQK\RAHIAKTIL
1740	A	1	2052	MIISIGAFAFDKVVQPFMLKTLNKLIGIDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIP IKLPMTFFTELEKTTLKFOWNQKRARIAKSILSQKSKAGGITLPDFK

				LADNMTVYLENPIVSAQNLLKLISNFSKVSQVSGQKSQALLYTNN RQTESQIMSELPFTIASKRIKYLGIHLTRDVKDLFKENYKPLLKEIK KDTNKWKNIPCSWVGRINIVKMAILPKDIIQENFPNLRQANIQIQE IRKTPQRYSSRRATPRHIIVRFTKVEMKEKMLRAAREKASHHTYSKI DPILGSKPLLSKCKRTEIITNYLSDHSAIKLEFRIKNTLQNCSTTWK PNNLLNDYWVHNEMKAEIKMFFETNENKDTTYQNLWDTFKAVCRGK FIATNAHKRQERSKVDTLTSQLKELEKQEQTSHKASRRQEITKIRA ELKEIETQKTLQKINESRSWFFERINKLDRPLARLVKKKREKNQIDA IKNDKGDITITNPTEIQTITIRDYKHL
1741	A	1	764	MNIDAKILNKILAKQIQQHIKKLIHHDQVGFIPGMQGWFNIRKSINV IQHINRTEDKNHMIISIDAFAFDKIQQPFMLKPLNKLIGIDGTYFKI IRAIYDKSTPNIIILNGQKLELMSNFSKVSQVSGYKISVQKSHAFVYTNNR QSESQIMSELPFTVATKRIKYLGIQLTRDVKDLFKENYKPLLNEIQE DTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELE KTK\FIWNQK\RAHIAKTIL
1742	A	1	1057	ATATSLPTSSSENFSGEALCSLKPLPKQLPKRLIRKVQHENGQELS LRPYPIIGVRVWGKGLRNPQDFANLNSTNCLYGYTFQKPRNAPFPW KHINRAKDKNHMIISIDAFAFDKIQQPFMLKPLNKLIGIDGTYFKI RAIYDKPTANIIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKGIHLGKEEVKLSLFADDMIVYLENPIISAQNLLKLISN FSKVSQVSGYKINVQKSQAFLYTNDRTQTESQIMSELPFTIASKRIKYLGI QVTRDVKHLFKENYKPLLKEIKEDTNKWKNIPCSWVGRINIMKMAIL PKVIYGFNAIPIISFNWYGVQPGH
1743	A	1	1380	MGFNTPLSTLDRSTRQKVNKDTQELNSALHQADLIDIYRTLHPKST EYTFSSAPHHTYSKIDHIVGSKALLSKCKRTEIITNYLSDHSAIKLE LRIKNTLQNRSTTWKLNLLNDYWVHNEMKAEIKMFFETNENKDTT YQNLWDAFKAIIIESLIFHNRAEIVAIIDSLPTKKSPPGPDGFTADFYQ RYKEELVPFLLKLFQSIEKEGILPNSFYEASIIILPKPGRDRTTKKEN FRPISLINIDAKILNKILAKRIQQHIKKLIHHDQVGFIPGMQGWFI RKSINVQIHINRAKDKNHMIISIDAFAFDKIQQPFMLKPLNKLQAN LLKLISNFSKVSQVSGYKINVQNSQAFLYTNNRQTESQIMSELPFTIASK KIKYLGQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGRIN IVKMAILPKAMLCLDVAYPTDDTRWYKLYTQKWTHTFS
1744	A	1	862	MDTFLNTYTLPRLNQEEVESLNRPIITGSEIVAIINSLPSKKSPGPDG FTAKFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEGSIIILPKPGR DPPKKENFRPTSLMNIDAKILNKILATRIQQHIKKLIHHDQVGIIIPG MQGWFNIPKSINVQIHINRAKDKNHMIISIDAFAFDKIQQPFMLKT LNKLIGIDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTROGCPL SPLLFNIVVEVLARAIRQEKKIKGIQLRKEEVKLSLFADDMIVYLEN PIVSA*RLNQEEVESLNRPIITGSEIVAIINSLPSKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKEGILPNSFYEGSIIILPKPGRDPPKK ENFRPTSLMNIDAKILNKILATRIQQHIKKLIHHDQVGIIIPGMQGW NIPKSINVQIHINRAKDKNHMIISIDAFAFDKIQQPFMLKPLNKLIG IDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTROGCPLSPLLF NIVVEVLARAIRQEKKIKGIQLRKEEVKLSLFADDMIVYLENPIVSA
1745	A	1	1551	ATATSLPTSSSENFSGEALCSLKPLPKQLPKRLIRKVQHENGQELS LRPYPIIGVRVWGKGLRNPQDFANLNSTNCLYGYTFQKPRNAPFPW KHINRAKDKNHMIISIDAFAFDKIQQPFMLKPLNKLIGIDGTYFKI RAIYDKPTANIIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKGIHLGKEEVKLSLFADDMIVYLENPIISAQNLLKLISN FSKVSQVSGYKINVQKSQAFLYTNDRTQTESQIMSELPFTIASKRIKYLGI QVTRDVKHLFKENYKPLLKEIKEDTNKWKNIPCSWVGRINIMKMAIL PKVIYGFNAIPIQNLLKLISNFSKVSQVSGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIHLTRDVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLTMTFFTELEKST LKFIWNQKGARIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWY

1746	A	1	947	MDTFLNTYTLPRLNQEEVESLNRPTITGSEIVAIINSLSPKSKSPGPDG FTAKFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEGSIILIPKPGR DPPKKENFRPTSLMNIDAKILNKILATRIQQHIKKLIHHDQVGIIPG MQGWFNIPKSINVIOHINRAKDKNHMIISIDAFAFDKIQQPFMLKT LNKLGIDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTRQGCPL SPLLFNIVVEVLARAIRQEKKIKGIQLRKEEVKLSLFADDMIVYLEN PIVSAPAAFLQSLWSSTMAGTLEKGEPLSGKEQ
1747	A	179	887	LLKRDVKDLFKENYIPLLNEIKEDTNKWKNIPCSWVGRINIVKMAIL PKVIYRFNAISIKLPMFTFTELEKTTLKFTWNQKRAHIAKTILSQKN KAGGIMLPDFKLYYKATVTQTAWYWYQNRDIDQWNRTEPSEIIPHIY NHLIFDKPKDKKKWGKDSLNFNKCWENWLAICRKLKLNPFLLTPYTKI NSRRIKDLNVRPKTIKTLEENLGNTIQDIGMGKDFMSLLNDMSFTEC K
1748	A	1	1074	MDKFLDITYTLPRLNQEEVESLNRPTITGAEIVAIINSLWNRTEPSKIM PHIYNYLIFDKPKDKNRKWKDSLNFNKCWENWLAIRKLDPLFLTP YTKINSRWIKDLNIRSKTIKTLEENLGNTIQDIGMGKDFMSKTPKPM ATKAKIDKWDLIKLSFCTAKETHSSWRPACLCRLHLWGQWTGKQKD SSNLCKLKCPLTALKRAVVLPAWSRSEKQGTASQSWTENDFDE LREEGFRRSNYSELREDIQTKGKEVENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLSRSCDELEERVSAMEDEMNMKREGKFR EKRIKRNEQSLQEIWDYVKRPNLRLIGVP
1749	A	1	1060	MDTFLDITYTLQRLNQEEVESLNRPTITGSEIVAIINSLPTKSKSPGPDG FTAIFYQRYMEELVPFLLKLFQSIEKEGILPNSFYEASIIILIPKLGR DTTKKENFRPISLMNIDAKILNKILAKRIQQHIKKLIHHDQVGFIPG MQGWFNICKSINVIOHINRAKDKNHMIISIDAFAFDKIQQRFMLKT LNKLGIDGTYFKWKNIPCSWIGRINIVKMAILHKAIFYRFNAIPIKLP MTFPTTELEKTTLKFIWNQKRACIAKSILSQKNKAGGITLPDFKLHYK ATVTKTAWGPYDR/DID/SWNQTDLMCAVLPSRYVTLQDSSIL*KMR *VKKLQKKSLLQADLVQGLRKDVST
1750	A	1	1402	MSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAIMPVIYRFNAIPIKLPMPFFTELEKTTLKF IWNQKRARIAKAILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNR DIDQWNRTEPSKITPHIYNYLIFDRPEKNKQWGKDSLNFNKCWENWL AICRKLKLDPLTPYTKINSRWIKDLNVRSKTIKTLEENLGNTIQDT GMGKDFMSKTPAMATDKIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELQQIYKKTNNPIKKWARDMNRHFSK EDIYAAKHKMKCSLSLAIREMQIKTTMRYHLTPVRMAI IKKSGNNR CWRGCGEIGTLLHCCWDCKLVQPLWKS VWRFLRDLELEIPFDPAPL LGVYPKDYKSCCYKDTCT/R/MFIVALFTIAKTWNQPKCPTMIDWI
1751	A	1	1410	MSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMPFFTELEKTTLKF IWNQKRARIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNYLIFDKPEKNKQWGKDSLNFNKCWENWL AICRKLKLDPLTPYTKINSRWIKDLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMATEDKIDKDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKEIYKKTNNPIKKWAKDMNRHFSK EDIYAAKHKMKCSSSLAIREMQIKTTMRYHLTPVRMAI IKNSGNNR CLRNTFRSVPDSASVIAQGTGTHPRGDTPSHKAGVLVVGMSFPEEPV LQDRSDDFSLAHGSKQGSVLCVGQWKTQGPCSRNEQYRPITGPGSH
1752	A	1	1559	MDTFLDITYTLPRLNQEEVESLNRPTITGSEIVAIINSLPTKSKSPGPDG FTAIFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEASIIILIPKPGR DTTKKENFRPISLMNIDAKILNKILANQIQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIOHINRAKDKNHMIISIDAFAFDKIQQRFMLKT LIKLGIDGTYFKIIRAIYDKPTANIIILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADNMIVYLEN PIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSEL

				PFTIASKRIKYLGIQLTRDVKDLFTSVISQVWVGS�DTSLILQLWVG SLDISVILQLWVGSLDTSVISQLWVRS�DTSVISQLWDIAFLSHVPG MLS*KSQVSLATLMQRMSSHGLGQLQPCGSAGYSSHGCFHRLALNAC GSSSAQCCKLLVDLPFWGLDGGLLLTAAARGHSPGALCVRVPTPHFPSM LP
1753	A	1	1576	MNTDAKILNKILANRIQQHIKKLIHHDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIVSTDAEKTFDKIQQPFMLKTLNKLIGIDGTYLKI IRAIYDKPTANIILNGQKLEAFPLKTGTRQGCPLSPHKLFDTYTLP RLNQEEVESLSSPITGSEIVAISS/FTNEKESRTRWIHSRILPEV* GGT/RIKYLGIQLTRDVKDLFKESYKPLLKEIKEDTNKWKNI PC*WV GRINIVKMAILP/KELEKTTLKFIWNQKRACIAKSILIQKSKAGGIT LPDFKLYYKATVTKTAWYWYQNRDIDQWNSTEPSEIMPHIYNYLIFD KPEKNKQWKGKSLFNKWCWENWLAICRKLKLDPLTPYTKISSRWIK DLNVRPKTIKTLEENLGNTIQDIGMGKDFMSKTPKAMATKANIDKWD PIKLKSFCTAKE TTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQ IYKKK\TNNPIKKWAKDMNRHSSKEDIYAAKGHMKCCSSSLAIREMQ IKTTMRYHLTPV
1754	A	468	4080	RVRSGTDSIASGPRVLCSTRTERRRRRSYLVHRRVCVPCGP\AVDGVF NLTNIDRWFLHINRAKDKNHMIISIDA EKA FDKIQQPFMLKTLNKLIG IDGTYFRIIRAIYDKPTANIILNGQKLEAFPLKTGTRQGCPLSPLLF NIVLEVLAIRAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIVSA QNLLKLISDFSKVSGYKINVQKSQTFLYTNNRQTESQIMSEL PFTIA SRRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGR INIVKMAILPKVFYRFNAIPIKLPMTFFTASCPSAKSVEQYQYGNIG KRRAAEWQRAMTRKVLQEILEKNPRFHHLTPLKTKHIAHWCRCHGY TPDPESLRNDGDSIEDVLTQIDSEPDHGS LGDGKSSSVGPTAVVTL LACHLECPSSFSSADNLCKRLEDLQQFQKREPENEEVDILSLSEPV KINIKKEQEEKQEEVKFYLPPTPGSEFIGDVTQKGGMLVWREAVSKA AIRTNGFLLLFQIGITLQPVALHRNVYASVVEDMILKATEQLVNDIL RQALAVGYQTASHNRYYYLCSLWCEAYTSFLTVELPMKV FYTYINPV GDGGSKTCDTMVFNHPAIKKFLES PSRSSSPANQRAETPSANHSED SLSQHNDFLSDKDNNSNMDIEERLSNNMEQRPSRNTGRDTSRITGSH KTEQRNADLTDETSRLFVKKTIVVGNVSKYIPDPKREENDQSTHKWM VYVRGSRREPSINH FVKVWFFLHPSYKPNDLVEVRYKIVVTRYVLG SGRDKGTVMKSTGFWLWETKKVFLPLRIKYLGIQLTRDVKDLFKENY KPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKTERGEEASEEKY EASRCWFVRFKEGCRLHNIQLQGEAASADGEAAASYPEDPAKIDE G GYTKQHIFTVYVVG YDGNRLSSVECYDSFSNRWTEVAPLKEAVSS PAVTSCVGKLFVIGGGPDDNTCSDKVQSYDPETNSWLLRAAPIAKR CITAVSLNNLIYVAGGLTKAIYCYDPVEDYWMHVQNTFSRQRGELGV FVVP SAGFPASTE AERHTPFYALPSSLERTPTKMTTSQKVTFCSHGN SAFQPIASSCKIVPQSQVPNPESPGKSFQIPITMSCKIVSVLLSSVMF NKRKFITVDWQSCHKAKTKLIHTEMNGGDK
1755	A	1	2882	MDKFLD TYTLPRLNQEEVESLNRSITGSEIVAIINSLPTKKSPPGPDG FTAEFYQRYKEELVLLLLKL FQSIEKEATLPNSFYEASIILIPKPGR DTTKKENFRPISLMNIDAKILSKILANQIQHIKKFVHHDEVGFIPR MQGWFN IHKSKNVIQYINRTKDKNYMIISIDA EKA FDKIQQLFMLKT LSKLIGIDGTYLKIIRAIYDKPTVKIILNGQKLEEFPLKTGTRQGCPL SPLLFNIVLEVLAIRAIRQEKEIKGILLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQFTRDVKDLFKENYKPLLNEIKEDTNKWKNI PC SWVGRINIVKMAILPKPPLIPRQTGSGVDLQOTPTDLQLSVLTVRR KINKQKGHPHQYLIWTS PSSKTKGRQLLASNRTTNGEIRPED*KGE VSSCCWRR I*YTAENKIPRNPTYKGCEGPLQGELOTTAQGNKRGYKQ TEEHSMLMGRKNQYRENGHTAQ\VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWYWY

				QNRDIDQWNRTEPSEITPHIYNYLIFDKPEKNKQWGKDSL FNKWTWE NWLAI CRKLKLD PFLTPYTKINSRWIKDLNVRPKTTKTLEENLGITI QDIGMGKDSMSKTPKAMATKDKIDKWDLIKLSFCTAKDTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELKQIYKKTNNPIKQWVRDMNRH FSKEDIYAAKHKMKK\CSPSLAIRETQIKTTMRYHLTPVRMAIIKKS GNNRDIDEGVNHHSQQTITRTENQSLHVLTHTWEFNNENTWTQGGEH HTLGPVMGYVFISSVKMDQYTKLVSEEWGVAENQATNAFLHRIGKNY FKVHMEPKKSPHCQVNPKE
1756	A	1	1746	MIISVDAEKAFDKIQQPFMLKTLNKLIGIDGMYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLARAIQEKEIKGI HLGKEEIKLSL FADDMIVYLENPIVSAQNLLKLISNFSKVSQYKINA QKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFK ENYNPLLNEIKEDTNKWKNIPCSWVGRINIVKM\AILPKNWKKTTLK FIWNQKRACIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEIMPPYNYLIFDKPEKNKQWGKDSL FNKWCWENW LAICRKLKLD PFLTPYTKINSRWIKDLNVRPKTTKTLEENLGITI IGLGKDFMSKTPKAMATKAKIDKWDLIKLSFCAEKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNELKQIYKKTNNPIKQWVRDMNRHFS KEDIYAAKHKMKKCSSSLAIREMQIKTTMRYHFTPVMAIIKKS RDMDEIGNHHSQQTIAMTKNQTPHVLTHRWELNNENTWTQEGEHHTL GPVVGNLKLLRKPISLS
1757	A	1	2866	MDIDAKILNKILAKRIQOHIKKLIHRDQVGFILGMQDWFNIQKSINV IHHINRTKDKNHMIISVDAEKAFDKIQQPFMLKTLNKLIGIDGYLV TRAIYDKPTANIILNGQKLEAFLLKTGTROGRPLSPLLFNIVLEVL RAIRQEKKIKGIQLGKEEVKLSL FADDMIVYLENPIISDQNLRLIN NFSKVSQYKINVQKSQAFLNTNNRQTESQIMSELPFTIASKRIKYL IQMLNQEEVESLNRPIITGAEIVAIINSLPTKKSPGPDGFTAIFYQRN SVEEELVPFLKL FQSIEKEGILPNSFYEASIIILIPKGRDTTKKEN FRPISLMNIDAKILNKILAKRIQOHIKKLIHRDQVGFIPGMQGWFI RKSINV IQHINRAKDKNHMIISIDA EKVFDKIQQPFMLKTLNKLIGID GTYFKIIRAIYDKPTANIILNGQKLEAFPLKTGTQGCPLSPLLFN VLEVLARAIQEKEIKGIQLGKEEVKLSL FADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSKLPFTIA SKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGR INIVKMAILPKIGYCVQDTSANTTLVHQTTPSHVMPNNHHQLAFNY QLEHLQTVKNISPLQILPPSGDSEQLSDGITVMHPSGSDSDDTMMLES EQAPVQKDIKIKNADSWKSLGKPVKPSGVMKSSDEL FNQFRKAAIE KEVKARTQELIRKHLEQNTKELKASQETHRDLGNLTVESFSNKIQN KCSGEEQKEHQSSQAQDKSKLWLLKDRDLARQKEQERRRREAEQGW APPPPPNGEAAGLPAPPDAPVALLVPGLLLLRALRLHPPAQTFV EPRQGAGADLPAARPGSTLPACLSDP SLGTHCYVR IKDSGLRFHYVD GAGICLASGEASGSF
1758	A	1	1285	MLEVLAWAVRQEKEIKGIQLGKEEVKLSL FADNMIVYLENPIVSAQN LLKLISNFSKVSQYKVSQKSQALLYTNNRQTESQIMSELPFTIASK RIKYLGIHLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGRIN IVKMAILPKDIIQENFPNARQANIQIQEIRKTPQRYSSRRATPRHI IVRFTKVEMKEKMLRAAREKASHHTYSKIDPILGSKPLL SKCKRTEI ITNYLSHSAIKLEFRIKNLTQNCSTTWKPNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDTFKAVCRGKFIATNAHKKRQERSKVD LTSQLEKELEKQEQTHSKASRRQETKIRAELEKIEQKTLOKINESR SWFFERINKLDRPLARLVKKKREKNQIDA IKNDKGDIT\TDPTBIHT TIREYYKNLYAKKLENLEEMDKFLETYTLP RPNOEEVESLNRPIITGS EIVAIINSLPTKKSPGPDGFTAIFYQRYKEELVPFLKL FQSIEKEG ILPNSFDEASIIILIPKLGRTDTTKENFRPIPLMNTDAKILNKILANR IQQHIKKLIHRDQVGFIPG\MQGWFNICKSINV IQHINRTKDKNHMI ISIDA EKAFDKIQQPFLLKTLNKLIGIDGYLVKIIRAIYDKPIANIIL

				NGQKLEAFPLKTGTRQGCPLSPLLFNIVLEVLARAIRQEKEIKGIQL QKEEVKLSLFADDMIVYLENPTVSAQNLLKLISNFSKVSGYKISVQK SQAFFYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKPPLLI PRQTGS GVDLQQTPTDLQLSVLTVRRKINKQKGHPHQYLIWTSPPSSKTKG\GS SSPATELYYKATVTKTAWYGYQNRDIDQWNRTEPSEIMPLTYNYLIF DKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGVGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVKNQPTTGEKIFTTYSSDKGL\ISRIYNEL KQI*KEIKGIQLGKEEVKLSLFADNMTVYLENPIVSAQNLLKLISNF SKVSGYKVSGQKSQALLYTNNRQTESQIMSELPFTIASKRIKYLGIH LTRDVKDLFKENYKPLLKEIKKDTNKWKNI PCSWVGRINIVKMAILP KDIIQENFPNLARQANIQIQEIRKTPQRYSSRRATPRHIIVRFTKVE MKEKMLRAAREKASHHTYSKIDPILGSKPLLSKCKRTEIITNYLSDH SAIKLEFRIKNLTQNCSTTWKPNLLNDYWVHNEMKAEIKMFETN ENKDTTYQNLWDTFKAVCRGKF IATNAHKRKQERSKVDLTLSQLKEL EKQEQTHSKASRRQBITKIRAELEIETQKTLQKINESRWSFFERIN KLDRLPLARLVKCKREKNQIDAIKNDKGDITNRSRNTYHQRIIL
1759	A	2	231	PPSAS/CVQTGPPCHSLAFPPSAPGQEQEGHQLP SHVIPCHLALGTA FPQPAAMAGWGV SQATYCQELEPQFPVSSS
1760	A	1842	2096	CHSQKPQVPPPKPWGSLERP\ PNT*VPACVLPA PAPAQRPGQIARQ* PWVAPGTSGQSRVGRTPGVSSGHGQTLTCPMALLQPLL
1761	A	37	288	WGNTGSQVMTTVLNTALLPPKPSPMLPIKHAIIPPPSY/SPHP*PPI PSPTANLESAPPASAP/PPPLPP\PAQLGEAHAPPE*YAIIPPPSYSH TRSHPSPAQQOTLSQRHQPLHLSSSASTLPSWGKLMHHLNNIPQ
1762	A	397	506	SFLEDLTGLSNQPATAGANWITRLCTGSP*NV*PPWHMSSGHPEAVS RVCIFNLVGFGI
1763	C	291	491	MGADRQTHPQDRWFSHLHLIKLLRRSYRIEQPASHSRGRLDNTSLHRL SLCPCHPPLFLTLFLGIMF*
1764	A	630	1159	SFYALMLSDRKNRGRGRHGLSRRIKRQRKLVEAEAAASQACLAGKP GPTPASHP/PGDGLPCPLSAPTLSPAT/ALPLP/SP*RSPNHSAN/P NPLSPTSSVKHSRCSPPHSALPLSTPKATPPSPNHRAGLFSSSLPLAP MSTS*LLQKNCVLVRAPAPTSYIPVFFMTPAQCPVFLSAQ
1765	B	1	1359	MGIKNSKRGSPLAAPALLKPDTLWSCIFGEGDLGEEDMPPDPQAPS PAILPPNHAFGLWPFRTYTQTHPQEAADPAAYHEPPPLILAGVRF RSNPALPENGKGAWRGDGV AEGHAALWVLGRCSRVTAALAARTRE HDGRWREGAEKGPRRRWVRAIQTPRLGKAL IHCWTTGRSLWVNSSV SAGSERDQRADHAAQTSCAAGAVACGLLLLLLVRGQAWVKQNLSP TRTKELVVSIMPLPHPGQGHNLASRAKARTQPVPSGPTHGAGAGESC PCEGRQAGVQTFGLIPFAKPPLVRCDLHPLSPNLGVVWGWNHPSGH IYTPAHSHEGSNLPHWRQARNRQLGYLDQVAALRWVQQNIPTLEATL TVSPFLASLRWHECVFACCVPHIPRTFHGAIMESGVALLPGLLPAQL MSSPRFPGPCVFYEFQHQPSWLKNIRPRT*
1766	A	2	597	RWLIPKVMRIYDTQKMDREASQAALQKMLTLLMLPPTFGDLLREEY IGDNGDPQTLQAQFQEMMADSMFVIPALQVAHFQCSRAPVYFYEFOH QPSWLKNIRPPHMKADHVKFTEEEEQLSRKMMKYWANFARNGNPNGE GLPHWPLFDQEEQYLQNLQPAVGRALKAHRLQLW\KKALPQKIQEL EEPEERHTEL
1767	A	3	1867	IHPSAPRLGKALIHCCSFPGQPLGEQQRVRRQRTETSEPTMRLHRLR ARLSAGACGLLLLLLVRGQG\QDSASPIRTTHTGQVLGSLVHVKGANA GVQTFGLGIPFAKPPL\GPL\RFAPP*SPLESWGVRDGTTHPA\MCL QDLTAVE\SEFLSQFNMTFSPDSMSMEDCLYLSIYTPAHSHEGSNLV MVWIHGGALVFGMASLYDGSMAL\AL\ENVVVVI IQLPPGGVLGFFS TGDKHATGNWGYLDQVAALRWVQQNIAHFGGNPDRVTIFGESAGGTS VSSLVSPISQGLFHGAIMESGVAL/LLPGLIASSAD\VISTVVANL SACDQVDSEALVGCLRGKSKEEILCN*TSLFKMI PGVGGMGVFLAQQ

10020

				TPRELLASADFQPVPSIVGVNNEFGWL\IPKVIEDLIDNPEGKLGQ ERASQG\VLQKMLTLLMLPPTFGDLLREVYIGDNGDPQTLPKRKF\Q KMMADS\MFVIPALQVAHFQ\CS\RAPVYLPTSSQH\QPSWLKNIRP P\HMKADHG\DELPFVFRSFF\GGNYIKFTEEBEQLSRKMMKYWANF AR\NGNP\NGEGLP\HWP\LFDQGGAITLQLNL\QPAVGPGL*KAH\ RL\QFWK\KALPQKIQ\ELEPEERHTEL
1768	A	2	288	CPNSSPGSASEVGCARSGQSSLLRSLPRCDGWPWAEAGA/MCAGRNL TSCSVGRY\YSSR*QDEES*TARHLLCAPQTGHQRRRRCRGQRNFCH IPC
1769	A	1017	1463	PRGPWSQGEPKWLARQAAGCCPPGACLWGHSPAGACSPLCAAKGSR YSRVPASSGTGAGK\GWQLLAREGEQEAGLCIEASQIGVPNSSPRKR PQR*DVPDRGSPVC*EVFPRCDGWPWAEAGASVQGGTSPVFSFNRMT SASTPNIW
1770	A	1	1181	MAAYKLVLIQHGESMWNPENRFSSWYNTDLSPAGHKEAKCGRQHS LIGLNKAETAACHGEAQVKIWRHSYDVPPLMEPDHFPYNISKDRRF ANLTEDQLPSCESLKDTIAKALPFWNEEIVPQIKEGKQPKYPFEKRL EUVNHYFTTDDGYRIISARFGVPRTQVVRTWVALYEKHGEKGLIPKPK GVSADPELRIKVVKAIEQHMSLNQAAAHFMLAGSGSVARWLKVYEE RGEAGLRALKIGTKRNIATISVDPEKAASALESKDRRIEDLERQVRF LETRLMYLKKLKALAHPTKKAIEIPRSTFYHLKALSKPDKYADVKK RISEIYHENRGRYGYRRVTLSLHREGKQINHKAVQRLMGTLSLKAAI KVKRYRSYRGEVGQTAPNVLQORDFKATRPNEKWTVDVTEFAVNGRKL YLSPVIDLNFNEVISYSLSERPVMNMVENMLDQAFKKNPHEHPVLH SDQGWQYRMRRYQNILKEHGKQSMRSGNCLDNAVVECFGTLKSE CFYLDEFSNISELKDAVTEYIEYYNSRRISLKLKDLIASCLTVQLFG VSTLEGLSEEAIMELNLP TGIPVYELDKNLKPIQFLGDEETMRKAM EAVAAQVEDEYNLYGDVTTVSSLTPEKLAPEVKENVPERLNILLQVG GRSRTNLNRVRVP IHHKPSIRDPNSQASLNKLTDKMDSLWLKSKNRP KGPWKGEAVKLFVSLNAAKPVFLQPSQRRVPGNNGSWEFPS*SRK SGISIGAVKRPTH*GS*KASSIS*NAAYVSKKAESLSSSHEKGC AQYVLLSSKGSQQA*QVCGR*KAY**DLSRE*RPRIIP*GNAVSSSR RETD*P*SCSAPDGNPLT*SSD*GQAIPLLRGRANRP
1771	A	362	552	DRLDPHSAAH*GAKSSPLAATSDQWHLALSRGSGSLYKCTEVKQMSN S*PASRSACPPSPPR
1772	A	2318	3201	FMPHLHDGGYCSPAEGFSSRYEHGLMKDLSRGSLSPGGERACEGVPS APQNPPQRKKVSLLEYRKRKQEAKEENSAGGGGSDAQSKSKSAGAGQG SSNSVSDTGAHGVQGSARTPSSPHTKFFPSHSSMSHLEAVSPSDSR GTSSSHCRPQENISSRWMGSHISRTTP/SKEGASPRSEAA*G/SAQ KGEPSPTWESNITEKSDPADGEGPETLSSALS*RSNSFTALSRYSY QT/PLAPFTGTGPYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPS DSPTSDSVQSSTGTL
1773	A	53	1025	GTRHLEAVSPSDSRGTFLSHCRPQENISSRWMVPTSVERLREGGSIP KVLRSVRVAQKGEPSPTWESNITEKSDPADGEGPETLSSALSKGA TVYSPSR\SATSSCSVIVLGQNHKASFVRVPPPSEDIPTQSPGYSYR TTALRPGNPPSHGSSSESLSTSYSSPAHPVSTDSLAPFTGTGPYFS SQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTSVFSFVPAQEL *ASTS/SSSEI/PRSSLAIRLTD*SVCPLVQGSAGYQGLQGICGFQF TALPHTVGVGFSTQYRIPSPLOQGSRSQDSRRGLFLGLLGFQGGKQ
1774	A	1	415	AENTILSLMFSGKSWGSLSSSECGALLPGTPTATRLQSLTRRSSLKRG T*GPQIPAARPREGSRIGTCTSS*\PGLRTEAHRSLRNRQAGVSSPF QLSPALKPRKSPSQATGQRP*GQWGQKSGSALLPTNTTHVEA
1775	A	1	458	ENTILSLMFSGKSWGSLSSSECGALLPGTPTATRLQSLTRRSSLKRG *GPQIPAARPREGSRISQNVGDGGKENRYRGFGGPPGTKSDPGHQH G*\GGEGLWGSWSKSGPAIATGAIASPATQLLRVNPDTGDWDVYFL LTLVSGLRLTGA
1776	A	1	1387	HSMGWKEHVDRGHTKGMVFSVLQACWLPFRERPFQLRLCLIEDPLL

				RLCGQGRGRGQETTSGLILLSHVGTFLRDRWTLTSLWPCPRALLVFL SHSCEVMGAGAPGVSLPEGQLSPLPWLVQGRSSRRAPDSGQGPLGPP GLADVSMRGRAPGTSMCGS/RSTPVPPQSPGG*VSMPATPGIGFLCR LPHKSAPEGP/GGFGFLFFIKHLKQHCSLPSRGLSITASTCVVLVG SKADDPDFCPCPHPGPLTSSSLRGAFSR/PSEQGRAGRGLESSRSLSV SQGSCEASVLRPESRGSTHP/ISPVSGFTLRSWVAGEAIAPVAIAGP AGAGLR/GLRGALRPAHGHPRL*SPGNPISPSSTSPCLMPQGHSC PAGPPNPRCLSSFPSPTLVLTNPASLSGPGCRDLGSLKSLSLKNFC GSDSEAEELLVGVPGRAPHSLLKLPQLFPENIKLRIVFSAKKKKK
1777	A	46	591	LSPPKPQKQSQEQNPFCQRWALGKQLGPPQGGQEG/QGPPDSLVLPG V/PPVPLFVGGNLPHPPPP/PQPQRNKGRTQESCSPPFKGQHNS/P CGPQPS*AHPLRHGSGDQAQPTSAP/PPCR/PES*PQADEMPTPCCH NTGKAL/GPPSQEGMEPGGPQPGPSRSTQSSVAHLTSGTAVRPGGLGS PP
1778	A	1412	1673	KRCPINRFPLECLPLPHLMGIPPEGHFH\HPLMGE**NPPCSIQDPH CVTYFETPPVNLCPSTRPPEVWEGGPSSPPAFEAPGLKG
1779	A	646	1100	MVELLVTFPPFSQQLQYFQLTYASFTELLKVPLMLVLYFGMPMKKHFL KPTVSDQWENNRLKRRRI\SR*FSCRKV*V*IAHCHKFCLVLREA/H MHWLILCAKKRF/PPLKLTWLGMSHTCNPSTLGG*GR*TA*TQEF KTSLDNMVKPHLF
1780	A	109	943	WAKLGKGPAPK*PQALGASAPSALYPRHVAPARAPGRTKGAGSSCRN SPRQV\RPQPWQWGGGAQSDVSP*QOTPRGGSFERSSSCSGHTGLVG KERRPLSLEGP*/SPEDPPRARHGGPQGREHPPWFSRPLCPEAGPE PRAPAWTSDSIGERSTGG/PSRPASKGPVPSAQRAQTGPNPEAAGS LSLPCRALPQGREAPQPQPPPYLPLKLERGILVFALSKI FKN
1781	B	98	195	GLCLGQEVGQEDLVMQTLPGYVLGLDRDEEVTG*
1782	A	2	1556	KHSSGEQDTSTLPSPLLTTVEDVNQDNKTKTWPPKAPWQHPSPLPS TLPSAPSAPLYAVTSPGSQWNDTMQMLQSPVWAATNDCSAAAFSYVQT PPQPPPPPAHKAAPKGFKAFFPGKAMYNGENVFKHLAKDSRGSGNEAP KRQDWIAQGRANTRDKPPASWGRAVSRVPGGRERTLDKTVAVES PAM AALTRDPQFQKLQWYREHRSELNLRRLFDANKDRFNHFSLTNTNH GHILVDYSKNLVTEDVMRMLVDLAKSRGVEAARERMFNGEKINYTEG RAVLHVALNRNSNTPIILVDGKDVMEVNKVLDKMKSFCQVRVSGDWK GYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDG THIAKTLAQLNPESSELI IASKTFTTQ\ETITNAETAKEWF/LQ\AA KDPS\AVGEDFLFALSTNTTKVKEFGIDPQNMFEFWDVWGGRYSLWS AIGLTSIALHVGFDNFQELL\SLAHWMDQLFRTDAPGRKNAPVLLAL LGIWYINCFGCETHAMLPYDQYLH\ALLRTSSRA\TWSPMGNTSPNL EPVWTTROAPLCGGS/QGPMASMLF\TSCIHQGTMI PC\DFLIPVQ TQHP IRKGLHHKILL\ANFLAQDRGP**GGKSTEEGPKGASRVAGKS PED\FERLLPHKGL*KGNRP\TNFYVFTK\VTPIQLGAWSPMYEHKI LRFV I IW\DINSF*PSGELELGK/QPGLRKLPELGD\SAQVTF/Q DVSTNGLINFIKAAARGPRVPINSVLICSLCDSHFFFSLSFSPKPE LIVP
1783	A	2	1928	ARGAPRLLRAAGAPSSSARVSLVSPSSPAMAALTRDPQFQKLQWYR EHRSELNLRRLFDANKDRFNHFSLTNTNHHGILVDYSKN/LLVTED VMRMLVGLWPKSRGVEAARERMFNG\EKINYTEG\RAVL\HVA\LRE TGFKTHPI LG*NGKDV\MPEVNKVLDKMKSFCQVRVSG\NLKGYTG QRPFTD\VINIWIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTH IAK\TLAQL\NPESSELI IASKTFTTQ\ETITNAETAKEWF/LQ\AA KDPS\AVGEDFLFALSTNTTKVKEFGIDPQNMFEFWDVWGGRYSLWS AIGLTSIALHVGFDNFQELL\SLAHWMDQLFRTDAPGRKNAPVLLAL LGIWYINCFGCETHAMLPYDQYLH\ALLRTSSRA\TWSPMGNTSPNL EPVWTTROAPLCGGS/QGPMASMLF\TSCIHQGTMI PC\DFLIPVQ TQHP IRKGLHHKILL\ANFLAQDRGP**GGKSTEEGPKGASRVAGKS PED\FERLLPHKGL*KGNRP\TNFYVFTK\VTPIQLGAWSPMYEHKI LRFV I IW\DINSF*PSGELELGK/QPGLRKLPELGD\SAQVTF/Q DVSTNGLINFIKAAARGPRVPINSVLICSLCDSHFFFSLSFSPKPE LIVP
1784	C	127	435	MAASXNPEVLDITEETLHSRFLGVRNVASVCLQIGYPTXASVPHSI INGYKRVLALS VETD YTFPLAEKVKAFLADPSAFVAAAXLGCCHHSC SXCCCSPS*

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1785	A	112	1161	RTAVMPREDRATWKSNYFLKIIQLDDYPKCFIVGADNVGSKQMQQI RMSLRGKAVVLMGKNTMHAQAPFEGTL*NNPSLWRKLLP\HIRGEFG LLFHPGRTLTEI\RDMLLAQ*GCPAAA\RPGAICPHVKVTVASPRTL GLG\PEKTSFFPGL*VSPTKNLQGAPIENPEVNVPAESRTGDQSGEP SESHGWLNML\NISPFLLGWVIPARCSTNGQHS TKPLKVLGLFTGG KLLQFSAFLGGVSRKCLPSVCLPELAYPNCCNQYPSIING\YKR\V LALSCGDGITPPFLAEKVK\AFLADPSAFVCCCNLWVAATTACFA/A AAAAPAKVEAKEESESEDEDMGFGFLD
1786	A	2	355	RSITCKTKEARMLLAWVQAFVLSNMLLAEAYGSGGCFWDNGHLYRED QTSPAPGLR\CLNWLDAQSGLASAPVSGAGNHSYCRNPDEDPRGPWC YVSGEAGVPEKRPCEDLRCPGGRI
1787	A	1	771	MLLAWVQAFVLSNMLLAEAYGSGGCFWDNGHLYREDQTSPAPGLRCL NWLDAQSGLASAP\VG YCRNPDEDPRGPWCYVSGE/AGVPEKRPCED LRCPETTSQALPAFTTEIQEASEGPGADEVQVFAPANALPARSEAAA VQPVIGISQVRMNSKEKKDLGTLGYVLGITMMVIIIAIGAGIILGY SYKRGKDLKEQHDQKVCEREMQRITLPLSAFTNPTCEIVDEKTVVWH TSQTPVDPQEGTTPLMGQAGTPGA
1788	A	48	375	KGLIKPFHRTPERKK*LAQGRKQATGMARAQLPDGAQHFSALC*Q LSRASNL*CHTQEALAAPSHKASFSEPFLPMGRRVNGAFYGAIWFG DLNLKWSSCGNDAG
1789	A	6	902	LQGWDEAEPPRGPRLNTGRSITCKTKEARMLLAWVQAFVLSNMLL AEAYGSGGCFWDNGHLYREDQTSPAPGLRCLNWLDA\QAGLASAPVS GAGNHSYCRNPDEDPRGPWCYVS GEGG\VPEKRP\CEDL\RCP\ETT \SKALPAF\TTEIQGNVLKGPSADE\VQVFAPANALPARSEAAVQP VIGISQVRMNSKEKKDLG\TLGYVLGITMMVIIIAIGDGIILGYSY KRGKDLKEQHDQKVCEREMQRITLP*SAFTSPTCEIVNEKTVVWHTS QTPVDPQEGSTPLMGQAGTPGA
1790	A	1	1995	LGRPTRPAPTFWAVAVRTRCLAEKRRQELMGALCYPPQGDRLFQKSW IFFRPVMADKLTRIAIGNHDKCKPKRRRQECKKSCPVVRMGK\LCIE VTPQSKIAWISSETLCIGCGICIKKCPFGALSIVNLPSEKETHRY CANAFKLHRLPIPRPGEVLGLVGTNGIGKSTALKILAGKQKPNLGKY DDPPDWQEBILTYFRGSELQNYFTKILEDDLEAIKPKQYVDQIPKA\A KGTVGSILDRKDETKTQAIVCQQLDLTHLKERNVEDLSGGELQRFAC AVVCIQKADIFMFDEPSSYLDVKQRLKAAITIRSLINPDRIIVVEH DLSVLDYLSDFICCLYGVPSAYGVVTMPFSVREGINIFLDGYVPT\B NLRFRDASLVFKVAETANEEVKKMCMYKYPGMKKKMGEFELAIIVAG EPTDSEIMVMMLGENGMGKTTFIRMLA\GSLKPDEGGEVPLNVSYK PQKISPKSTGSRVQLLHEKIRDAYTHPQFVTRL**KPLQIENIIDQE VQTLSGGELQRTV\LA L*LGQNLDPVYLI\DEPPA\YLDSEQRLMA ARVVKRFIPHAKKTA\FVVGTTWTFIM\ATYL\ADRVIVFD\GVPSTK NTVANSPTQLLQWA*INFWSSAWKFTFQEELQNTY\W\PRI\NKLISL EDVDQKKSGN\YFFLDD
1791	A	3	367	VVGLLD\WPLRVRADPVSGCGKMAELRVL\ELSRGSSTTP*RSE*S LTADLRLNEPRYATLPNIMKAKKKKIEVIKPGDLGVDLTSKLSVISV EDPPQRTAGVKVETTEDLVAKLKEIGRI
1792	A	3	404	RLKEKKLVKEVIAVSCGPAQCQETIRTALAMGADRGIHVEVPPAEAE RLGPLQVARV\AVVTADLRLNEPCYATLPNIMKAKKKKIEVIKPGDL GVDLTSKLSVISVEDPPQRTAGVKVETTEDLVAKLKEIGRI
1793	A	1	1044	MEQCVVTETLLHLHQLWGLPGSHILSQIPCGEMRETIRTALAMGAD RGIHVEVPPAEERLGLPLQVARVLAKLAEKEKVDLVLLGKQVAVVSP PCAPLLIPAREEGGDTSTPPLPPYGPDPPTITVSSDRDAAPARFV TAGSNVTLRCAAASRPADITWSLADPAEAAVPAGSRLLLPAVGPGH AGTYACLAANPRTGRRRRSLLNLTVAGGPGKRVHGVVERIRCVPMT ARTCEERHEHCHPAQDVGP GKAPVPKAAAQEAADGDSSVDGQGQHDEK GWGERAGGCSPTSAQGYPTAPECPYMTVQVLDITHQPFYVDLHHQ IPDPWILILRVFETHGASH

1794	A	11	364	SGASRVGAFCSASWPTSSWCSPRPPTTGPANKRATVACGRNATTASA PASPARVRLRPPRCQRAFQTPRARDTQLGFWRDAPFHPGLSCSCPL SAEAATNPAPRLVGLSPTSPSPW
1795	A	54	868	WDCGFGATRASCARPRAPSSSSAIRVKPDRGTGVVTDGVKHSMPF CEIAVEEAVRLKEKKLVKEVIAVSCGPAQCQETIRTALAMGADRGH VEVPPAEAERLGLQVARVLAKLAEKEKVDLVLLGKQA\IACDNCQ \TGQMTAG\FLDWPTGQIRPPQVTLEGDKLKVEPGKSIGGLETPCA* KLP\AVGDSLTLRFNGGPRTPRPVNIHESPRRRRSKVIK\GD\LG DLT\SQLSVISVEDP\PORTAGVKVETTEDLG\AKLK\EIGRI
1796	A	1217	2829	GARSEAAEFQQSASCRRLRGGGGPGTPGRGGALLASLLPPCPTPPDP PDGSCRCRPLLSPLGKLSAPPRPRPLFVVAQAGHAPQGLLPTSRPA APATAGSRNMSTTLISAFYDVDFLCKTEKSLANLNLMNMLDKKAVGT P/VAAAPSSGFAPGFLRRHSASNLHALAHAPSPGSCPKFPGAANG SSCGSAAAGGAVGGRRRTALLNKENKFRDRSFSSENGDRSQHLLHLQOQ QKGGGGSQINSTRYKTELCRPFEEESGTCKYGEKQFAHGFHELRLT RHPKYKTELCRTFHTIGFCPYGPRCHF IHNADERRPAPSGG/ASGDL /RPTSRTPPPPSCSSASSSCSSASSSCSSASAASTPSGAPTCCASAPA AAAAALLYGTGGAEDLLAPGAPCAACSSASCANNAFAFGPELSSLIT PLAIQTHNFAAVAAAAYRSQQQQQQGLAPPRAP/APPSATLPAGA AAPPSPPFQPRRLSDSPVFDAPPSPDLSDRDSYLSGSLSSGS LSGSESPSLDPGRRLPIFRLSISDD
1797	A	731	2553	GARSEAAEFQQSASCRRLRGGGGPGTPGRGGALLASLLPPCPTPPDP PDGSCRCRPLLSPLGKLSAPPRPRPVIRGGSSPATPPQGLLPTSRP AAPATAGSRNMWTTLVSAFYDVDFLCKTEKSLANLNLMNML\DKKAV GTPV\AA\APSSGFAPGFLRRHSASNLHALAHAPSPGSCSPKFPGA ANGSSCGSAAAGGPTSYGTLKEPSGGGGTALLNKENKFRDRSFSSENG \DRSQHLLHLQOQKGGGSPDQIPTRYKTELCRPFEEERARAQYGE K\CQF\AHGF\HELRLT\HPEVQDRSCAAPFHTIGFCPYGPRCHF IHNADERRPAPSGGASGDLRAFGTRDALHLGFPREPRPKLHHSLSFS GFPSGHHQPPGGLE\SPLLDSPTSRTPPPPSCSSASSSCSSASSCS SASAAST\PSGAPTCC\ASAAAALRLLYGTGGA*DLLAPGAPCAAC SSASCANNAFAFGPELSSLITPLAIQTHNFAAVAAAAYRSQQQQQ QQQGLAPPAQPPA\PPSATLPAG\AA\APPSP\PFQPRRLSDSP VFDAPPSPDLSDRDSYLSGSLSSGSL\SGSES\PSFDPGRRLPIF RLSISDD
1798	A	146	405	RKLDVYFEYEEKIMSKTTLDKSLDDIISDPDAGTPEDKMRVFLIYYI STQQAPSE\AFTKMASAPASYGSTTTKPMGLLSRVMTG
1799	C	47	235	MXVXCNQIKXLVSRAINRPDITDTEMETVMDTIVDSLFCFFVTLGA VPIIRCSRGNSKKW*
1800	A	48	2100	PAPGLPVLPRVEVFLEEPGSGSWEPRWRRRRRQRRQQQ\QPSFRKDSQ LLSCVYCLSMCLILKTAQEHYPYGRYSLMHRFGQDIFSPLLSVRELDR MGITLHLLHSDRDPIDVPVAVYFVMPT\EENIDRMCQDLRNQLYES YYLNFISAI SRKLEDIANASVRGLSA\VTQVAKVW\DOYLNFTILE DDMFVLCNQNKELVSRAINRPDITDTEMETVMDTIVDSLFCFFVTL GAVPIIRCSRGTAEMVAVKLDKKLLENL\RDARNSLFYRVDTLGAG HF\SFQRPLLVLVDRNIDLATPLHHTWTY*ALVHVDVDFHLNRVNLE ESSGVENSPAGARPKRKNKKS YDLTPVDKFWQKHGSPFPEVAESVQ QEL\ESYRAQE\DEVKRLKSIMG\LEGEDEGAISMAF/SDNTAKLTS AVSSLPELLEKKRLIDLHTNVATAVLEHIKARKLDVYFEYEEKIMSK TTLDKSLDDIISDPDAGTPEDKMRFLIYYISTQQARS\EADLQYK KALTDAGCNLNRSYIKQ*RAFT\KMASA*AGYG\STTTKTMGLLS RVLN\TGSQFVM\EGVKNLVLKQQLPVT\RILD\NLMEK\KSNPRK LMDYRYFDPKNACGGNDSS\VPQKLKIPFPRGHSFFVGGEENYI\E YQNL\CDYIKGQKGKHL\YGC\SELFN\ATQFIKQLSQLGQK
1801	A	1	394	AGGRAASCLQSLTARGPSLQSRGAFAGCGGISFCLRLGLLFLFADV DPLSFRDSGTPVVFSSSNDPEGMEFSSPSREECPKPLSRV SIMAGSL

				TGLLLLQAVSWASGARPCIPKSFYSSVVCVNCATYC
1802	A	3	538	RIYIFRV/PMASCD/FSIRT/YTNADTPDDFQLHNFSLPEEDTKLKI PLIHRALQLAQRVPVSLASPWTSPTWLKTNGAVNGKGS LKGQPGDIY HQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGLLSGYFPQCLGFT PEHQGGS LKAAAGVPRHPDDSYGTSQEKWQLLKEKMFEPKK
1803	A	192	2035	GRYLHPCFCLVDPLSFRDSGTPVVFSSNDPEGMEFSSPSRECEPKP LSRVSIMAGSLTGLLLLQAVSWASGARPCIPKSFYSSVVCVNCATY CDSF\DPPTFPALGTFSRYGE/STRSGRTGWSLSMG\PIQANHTGTG LLLTLOPEQKQKVKVGFGGAMTDAAALNILALSPPAQNLLLSYFSE EGIGYNIIRVPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLQD TPGFHRLAQLAQRVPVSLASPWTSPTWLKTNGAVNGKGS LKGQPGDI YHQTWARYFVKFLDAYAEHKLQFWAATAKNESAGLLSGYFPQCLGF TPEHQQDFIARDLSPTLANSTHNVRLMLDDQRLLLPHWAKVVLTD PEAAKYVHGIAVHWYLDLAPAKATLGETHRLFPNTMLFASEACVGS KFWEQSVRLGSDWRG\MQYSHSIHQQTSWYHVVG\WTAGNLALNPEG \GPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFKQSS IPEG\SQR VGLVA\SQKNDLDAV\ALMHPDGS AVVVVLNRSSKDVPLTIKDPAVG FLETISPGYSI\HTYLW\RRQLDGADYSRRHWGSAGAFKGTESAHTL SVTKEGTAGPV
1804	A	113	1799	PSAYSYGRYLHPCFCLVDPLSFRDSGTPVLFSSSSDPEVMEFSSPSR EECPKPSGRVSIAGSLTGLLLLQAVSWASGG/RPCIPKSF/SYSSV VCVNCATYCD\FDPPTFPALGAFSRYKSRSSGHWMELSTG/PIQANC TGTGLLLILQPE\FQKVGFGGAVTDAGALNILALSPPAQNLLLKWY FSEEGIGYNI IWVPMAS*DFSIRTYTYADTP\DDFQLHNFSLPEEDT KLKIPLIHRALQL\AQRVPVSLASPW\TSPTRLKTRGAGNGKGPLKG QPRDIYHQTWARYIVKFLDAYAEHKLQFWAVTAENEPSAGLLSGYFP QCLGFTPEHQQDFIARDLGPTLANGTHNVRLMLDDQRLLLPHWAK VVLTDPEAAKYVHGIAVHWYLDLAPAKATLRETHHLFPNTMLFASE ACVGSKFWEQSVRLGSDWRGMQYSQ\SIKKLPVPMWVGWEPNW/IT PSL*NITQATRFNKQP\MFLPPLANFSKFIP\EGS\QRVGLVA\SQK ND\LDAVALMHPDGS PVVVVLNRSSKDVPLTIKDPAVGFLETISPGY SIHTYLWRRQ
1805	A	22	424	ALGMAHITLFFFFLLFCDSLALSPRLQCSGTISAHCNLVPPGFKQF SCLSLGSDYRCMPPC/RWLTFLVETGFFHVGQAGLELLTSGDP PALA/FPKC*DYRR\DPRAWALFVFLT*FFSKLYHKAKEKWS
1806	A	14	253	LIPCGPQLFNCLSL*PGFWAMVKFAWVQYVRSCLSSSGCLKESRSSC SESGGDHHLPLSSTSLPLSLFMLCKEVLLELSGR
1807	A	318	455	GGLPLGVETLAGEHLRPCSSPATSLPGASLSQEWWSPPDSETRRS
1808	A	1960	2150	CFVT\SNLKCSK*GRAWWFIPVISTLWEAKVGSLEPRSLRLQCAMI APLYCSLGDRVRPYLLK
1809	A	2	1345	GVVPPGLLAGGVQCQLLRHSSPGRCLLKSRARGSVIMSRYGRYGGET KVYVGNLGTGAGKGELERAFSYYGPLRTVWIARNPPGFAFVEFEDPR DAEDALRGLDGKVICGSRVRVELSTGMPPRRSRFDRPPARRPFDPNDR CYECGEKGHYAYDCHRYSRRRRSRAENLRR*SP*Q*IWLTIGAPLRF RKRNTRLTTFPTRKI FLRQSSLTWLIWLSV*SSLD*RKHLDAAGYR YF*IV* IY*TMQQRGSTCKLARFMLNTHYSVLYYVMLSCNSAFNKSF FR**KKYSTTNRPVYFQMRH*I*IVLRFDFSRGTQTLKNELLSDI LFFL*LEK*\SRSRSHSRSGRRYSRSRSGRRSRSSASPRRSRSI SLRRRSASLRRRSRSGSIKGSRYFQSP\SRSRSGRRSISRPRSSRSK SRSPSPKRSRSPSGSPRRSASPERMD
1810	A	1	840	VVPPGLLAGGVQCQLLRHSSPGRCLLKSRARGSVIMSRYGRYGGETK VYVGNLGTGAGNGELY\RVIR*YGPLRTVWIARNPPGFAFVEFEDPR DAEDAVRGLDGKVICGSRVR\VELSTGMPPRRSRFDRPPARRSFDPN GCYECGEKGHYAYDCHRYSR\RRRSRSGRRYSR\SRSGRRYSR\SR RSGRRSRSSASPRRSR/SPI SLRRSR\SASLRRSRSGSIKGS\RYF IPRRRSRSGIPGLFHGPRSSRSK\SRSP\SPKRSRSPSGSP\RRSAS

				P\ERMD
1811	A	20	701	DHASGQSTASSGPDSVSGQLQPSQPNADQGKLTMMRIAVICFLLGI TCAIPVKQADSGSSEKQLYNKYPDAVATWL\NPDPSQKQNLAPQ GCVL*RNQ*L*TR\TLPSKSN\ESHDM\DMDD\EGD\DDHVDSD SIDS\N\DSDDVDDT\DDSHQSDESHS\DESDELVTGFSTDLPA VFTPVVPTVDTYDGRGDSVYGLRSKSK\KFRRPDIKYPDATEDI
1812	A	121	1206	LIAGSTHACAHASGRAQHRRDQTRLKASCILLSQTPTKENSPLREL VICFLLGITCAIPVKQADSGSSEKQLYNKYPDAVATWLNPDP QNLAPQ\TLPSKSN\ESH\DHM\DDM\DEED\DD\DHVGTARDS SNDS\DDVDDT\D\DSHQS*WSLHHS*WNLD\ELVTGFFPTG RSGSIPVCSPTVDTYDGRGD\SVYGLRSKSK\KFRRPDIQY EDITSHMESEELNGAYKAIP\VAQDLNAPSDWANRGKDSYGT *QSAETHR\HQQ\SRLYKRKANDESNEHSDCDW*ARTFPKVS S\HEFSS\HGDFACL*PPKSKEEDNTPLEFRYSPGIRMWHFWG SI
1813	A	171	461	GSLDLWRGAELSPGHSTLFTLCACAKVKAAYKALSVGYRHIDCA YGNPEIGEALKEDVGPGLKAVPREELFVTSKLWNTKHHPEDVE PALRKT
1814	A	1	235	EEAPRNSRKVISIPKSIPTSRILQNMVDFDFTFSPEEMKQLNAL KNWRYIVPMLTVRMYQPPRLGECEIWGGILAQV
1815	A	292	1396	AQATGPYSRICACAKGAMAAS\CVLLHTGQK\MP\LIWSWGTW K\SEPGQVKAAYKVLPLALGYRHI\DCG\VIYNELEIG\EAL KGRVTG\PGKAGCLRGRKPGFVTSKLW\NTKHHPGEMWSL PLRKDSGLTFQLE\YLDLYLMHW\PYAFERGDNPFPKKCDW NIWLDSPH\YKET*RALKALVAKGLVQA\VGLSNFSNRQI \DDILSVASVRPAV\LQ\VECHPITGLKMRLIA\HCQGTW AWR*TAFNPLGLPLNRAW\RDP\DEPVPAGGNPVVLGIGLKK YGRSPSSSCLRWPGPSGKVI\CIP\KSITPFSNPFRTFKV FDF\TFSPEE\MNQLNA\LNKNWRYIVPMLT\VDGK\RVP \KDAGHPLYPF\NDPY
1816	A	133	402	LLTSLVNSRILILFINSKKIFAIIFSTRGGILRITAVIW\NNIS VT HGNGDMALAQYSMPVPA*AIGRRILVMLYPSRTEAFEKFL IRC
1817	A	356	463	NFFFFSFRPDAPVPDGESEKTVEESSDSESSFS
1818	A	81	728	TRGPPPAEEMDEDGLPLMGSGIDLT\VP AIQQRT\VAFLNQF VVHT\VQFLNRFS\TVCEEKLADL\SLRIQI\ETTLNII\DA K\LSSIPG\LDDVTV\EVSPFKLSPSVTNG\AHP*RPLSE\Q PQPEPVPGLLDLQES*SIQAGNFL*L*PKDP\RYARYLKMVQ \VGVP\VMARN\KMI SEGL\DPDLLERPDAP\VPDGE\SE \KTVEESSDSESSFS
1819	A	1214	1565	LKEITDEMVRITLLHSHRIKMVSPIFPFSTNTVPFFPCYNP FFMNIQEMTKVTASRLFFVDLLQGVQPCFLCCCLSIWFCNE HLDL**ASDFVMCMCVMHYIYTPIHV*YIHYIYVDY/MEVC IHLVII*CV
1820	A	1	1044	MAEKFDCHYCRDPLQGGKYVQKDGHHCCCLKCFDKFCANTC VECRKPIGADSKEVHYKNRFWHDTCFRCAKCLHPLANET/FC GQGGQDP\CNKCTTREDSPKCKGCFKAIVAGDQNVYKGT VWHKDCFTCSNCKQVIGTSFFPKGEDFYCVTCHETKFAH CVCNKAITSGGITYQDQPWHADCFVCVTCSKKLAGQRF TAVEDQYYCVDYKNFVAKKCAKCKNPIT/GEKDCVKSEPP SL*S*EAPSVPRETLASHPVSQRQPPGQASGWREDLSLV GGSL*KKSKLSSSSWPGFGKSSVVAYEGQSWHDYCFHCKK CSVNLATKRFVFPQEQVYCPVCAKKL
1821	A	235	1119	GPSSYKVGTMAEKFDCHYCRDPLQGGKYVQKDGHHCCCLK CFDKFCANTCVECRKPIGADSKEVHYKNRFWHDTCFRCAK \CLHPL\ANETFCG\QGGQRSCATSCTT\REGLPPSAKGC FKAIVA\GDQNVYKG\TVW\HKD\CFTCSN\CKQVIGT\GS FFP\KGKDFYCVTCHETKFAHCVKCNKAIASWGVY*DEP WHAEGFVCVTCSKKLAVQHFTTTVEDQ*YCVDCYK\NF VAKKCAKCKNPITGFGKSSVVAYEGQSWHDYCFHCKKCS VNLANKRFVPHQEQVYCPDCAKKL
1822	A	222	622	KCSSSKHFTKEDSQITNKHIEKCSS*LLVREMQUIITKSV SAIHONG* NENTKQTCQ/DIDNDMQQWEFMR*EWANW*N* KTNWQ*LLRLDKCV

				S\YDPAIPFLDISPTERHIYAYHKTCIRMFKATLFKIPNI
1823	A	75	1402	VRRRTLSSRRWHLRSHGPRWLPQVLTASPPQLQARGAFRSFPHSWGED FLASLMFKIQLEPLKLRATWLNFGVVKFRNKETSAGPVAVMGKDYYKI LGIPSGA\NEDLIVCAYRTMALKYHPDKNKEPNAAEEKFKEIAEAYDV LSDPK\KRGLYDQYGEGLKTGGGTSGGFRGF\FHYTF\YGDPHATF ASFFGGSNPFDFIFASSR\ST\RPFSGFDDDDMDVDEDEDPF\GALF GRFGFQWG*VGGPR\RAPGTIVTLGRQGCRRDPVV\HELRSLEEIY HGSTKRMKITRRRLNPDGRTVRTEDKILHIVIKRGW\KEGKITFPK EGDATP\DNIPADIVFVLKDKPHAFRRDGTNVLYSALI\SLKEALC GCTVN\IPLFD\GRGIPLPCNDVIKPGTVKRLRGEGLPFPKVPTQRG DLIVEFKVRFPRDLTPQTRQIL\KQHLPCS
1824	A	245	487	TPPISQLLKEEEDLSKAMSQDGASQFQEVIRQELELSVKKELEKILT TASSHEFTKKOLDLTVQQIEHLNKTNTDVP
1825	A	63	1820	RVDKGGLAAGLRPLGRGSRACVREERERERGLRGDFQPASLLSRGA INAPNFPACLKEEEDLSKAMSQDGASQFQEVIRQELELS\VKKELEK ILTTASSHEFEHTQKKTWMDFRKLFHR\FLQRKGAFLWNLGEKFQRP P*DSIQPYEKIKARGLPDNISSVLNKL\VVKLNGGLGTSMGCKGPK SLIGVRNENTFLDLTVQQIEHLNKTNTDVPVLVLMNSFNTDEDTKKI LQKYNHC\RVKI\YTFNQSRYP\RINKES\LYFPVAKDVSYS\GEN\ TEAWYPP\GHG\DIY\ASFYNSGLLDTFIGEKEYIFVSNIDNLGAT VDLYILNHLMPNPGKRCFVMEVTN\KT\RADVKGGDNSLQYGRA NLRTWWEIAQVPK/AHHVDEFKSVSKFKIFNT\NNLWISL\AAVKRL QEQNAIDMEIIVNAKTLDGGLNVIQLET\AVGAAIKSFENSLGINVP RT\RFLP\VKTTSDLLLVMNSLYSLNAGSLTMSSEKREF\PTVPLVKI RPVLFERKQVD\YLGFEK\IQNRLELDHL\TVSGRCDHLEKNGFIKG EPVIHPLQIHGDR\MDIPTWEPVFREPRLVSGNL\RILDH
1826	A	48	239	GRAETMSDIEEVVE\BY\EEEGQEEAAVEEEDWREDEDEQEEAAEE DSEAEA*D/TRETRAEEDE*YEDASD\AEDGPMEESLKP\WS*RPN LVL*P*VLI*FIVVYVDLHRLCME*DE
1827	A	78	359	RSNVTITRGCEPGASACSRCCPQAGAPALLTLDPPQKPPTFTMSDEEVE QVEEQYEEEEEAQEEEEKPRPKLTAPKIPGEKVDFFDDIQKKRQNK
1828	A	3	327	CEKTTEGEKVDFFDDIQKKRQNKDLMELOALIDSHFEARKKEEELVA LKERIEKRRARAQQRIRAEKERERQNRLAEEKARVQMLAKFSKKA GTPAKGKVGGRWK
1829	A	1	429	RAEVALKKKKALSSMRAHYS\SYLAKADQKRGKKQTAREMKKKILAE RRKPLNIDHLGEDKLRDKAKELWETLHQLEIDKFEGEKLKRLKYDI TTLRSRSDSTSSSPHNVPVRSGLTVLGVERPSRGVPRVCVLAAFIPW GL
1830	A	3	986	HTPATQSLANGLLGRSNVTITRGCEPGASACSRCCPQAGAPALLTLDP QKPPTFTMSDEEVEQVEEQYEEEEEAQEEAAEVHEEVHEPEEVQEE KPRPKLTAPKIPGEKVDFFDDIQKKRLNKDLMELOALIDSHFEARKK EEBELSALLERIEKRRAE\RAEQQRIRAEKERERQNR\AEKARRE \REDATRAEDDL\KKKKALSSMGAN\YSSYLGRPLDQKRGKK\QTA \REMKKKILAE\RRKPLQPSIHLGERQN*GDQGQSFWEHL\QLED LTKPEF\GEKLR\QKY\DITTLQEPECRCWPESTSKEGLGPPAKGK V\GGRWK
1831	A	7	1382	PPGLEARPAPARLAGSGVCSGGRGRGAGRRSRRQSMRGAARAAGRA GQPWP RPAPAGPPPPPLPLLLLLLAGLLGGAGAQQSSDRCSWKGSGL THEAHRKEVEQVYLPCAAGAVEWMPYTGALIVNLRPNTPSPA\RHLT VCIRSFTDSSGANIYLEKTGELRLLVPDGDGRPRVQCFGLEHGG\L FV\EATPQS/QDIGRRTTGQYELVRRHRASDLHELSGECPARSSSS SSSSSSSSPPARAANSHLKWRSQRCLDVTLPDLALLSVRIL*RW WAAFQSLSRPGCFLTLPFFS\APCRPCSDTEVLLACTSDF/A*VSP RQLLSSSSSSSSSSSSSPHLLPRTAVRGSIQQVTHEPERQDSAIHL RVSRLYRQKSRVFEPVPEGDGHQGRVRTLLECGVRPGHGDFTLFTGH MHFGEPR\LRCAPKASRTFQRMVYR\DA\QERGLNPLVGWQRN

1832	A	1	433	NNPDFKAGV/MALPTL/LQIQRHDDYLVMLKAIRILVQERLTQDAVA KANQTKGELPVALDKHILGFDTGDAVLNEAAQILRLLHIEELRELQT KINEAIVAVQAI IHFWHVWKSCHILGGGSPENWVCSRDLPLLLIAF FFNKV
1833	A	1	459	YLRDVDCPFKIQDRQEAHLLGLAVRLEYGDNVNNPDFKAGVMALA NLLQIQRHDDYLVMLKAIRILVQERLTQDAVAKANQTKGELPVALDK HILGFDTGDAVLNEAAQILRLLHIEELRELQTKINEAIVAVQAI IAD PKTDHRLGKVG
1834	A	2	1108	SFRSDSAPARPLAASPVPAPPAPPRFFSPGRGPGDQSEKRWTFRRK LTGSSTTY\SPFVFNRRDETEFRNFI\ VWLEDQKIRHYKIEDRG\NL RNIHSSDWPKVL\EKYFK\DVNCPFKIQD\RQE\TIDWLLGLAV\RL EYGR*WLKNTKDLVP**FQNLNDNATKN\AEPFDPFWDVNNP*F*GL VLLALG*TWLQI\QRHDD\FLV\MLKANSGFVWQEP*PPGMPVCLR ANSNKRGA*PVAFRQTHILGFD\TGDASSLMKLEILRIACT*EELR ELTDQKSTKAIVAVQAIYC*SKRQDHRLGKSLEDEHFEDLQLLTYFR YMLGNHTLLACFGKSKCHNSRGEPSPEKLGYSRGFYHHWLIASCF L
1835	A	1	891	MYQYQONQATQQECSCICLEHGMKIKSESQVLAKGRKVKAGGESEWVEG EGGREEKKHRSRNIYQRPVAVSVVAVYGTLSDDL SVASSKLGIKATSV YNGKGGGLIDDIALIRDDVLFVCEGESFIDPQTDSKPPEGLLGFTD WLTNLVGGRYFTTTRITPTRQIFAVQILNELISGSVLNANLQGVKM LCSNAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRV ATLKDACLKNCNLRGATLAGTDLENCDSLGC DLQEANLRGSNVKGAV FEEMLTPLHMSQSVR
1836	A	1	984	MAEPVEDNCINFVAMKFIDNTLYFIENLES DYFGKLESKLSVIRNL NDQVLFIDQGNRPLFEDMTDSDCRGQKGEGERRIQVGGGGEGREEKK VGGGPGGRVVAHSGSPGSGSVMMRMTLFLNGSPKNGKV VVYGTLSDL LSVASSKLGIKATSVYNGKGGGLIDDIALNRDDVLFVCEGEFFIDPQ TDSKPPEGLLGFTTEWLTNLVGGRYFTTTRSTLVNKEPDSMLAHMFK DKGVWGTNLGVLNKGVDMEGSQMTGINLRVATLKNACLKNCNLRG ATAGTDLDNCDLCCGDLQEANLRGSNMKGAI FEEMLTPLYMSQSVR
1837	A	1	1917	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQVRGYTIEQINHM RDV GTRLRRAEDVFPFVIGVAAHKGGVYKTSVSVHLAQD LALKGLRVLLV EGNDPQGTASMYHGWVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIPSCIALHRIETELMGKFDEGQLSTDPHMLRLAIETVAHDY DIVIDSAPNLSIGTINVSSRCTRCCIVLYVWSTALDYDSSSSSSTY YRQVTVTVDVTVLAMALTS DPSSANDPSVRLYHVHWHPLSIYLRRP DLRSINPCALDRIELSYLAIAHKINSLSGLQCSKESLIDTRLATREK KFLKSVPLKAQRLRFFKDNLHRSRNIYQRPVAVSVVAVYGTLSDDL VASSKLGIKATSVYNGKGGGLIDDIALIRDDVLFVCEGESFIDPQT SKPPEGLLGFTDWTNLVGGRYFTTTRITPTRQIFAVQILNELISG SVLNANLQGVKMLCSNAEGASLKL CNFEDPSGLKANLEGANLKGVD MEGSQMTGINLRVATLKDACLKNCNLRGATLAGTDLENCDSLGC DLQ EANLRGSNVKGAVFEEMLTPLHMSQSVR
1838	A	2	1411	FVGKGRQAEDSRCGAGRRTGRTLGEQQRACVWCVPKGRKVKAGGES EWVEGEGGREEKKVGGGPGGRVAAHSGPTGGSAMRRVTFLNGSPNN GKAGAGYGTLSDDLSSGSSKPGIKATNVYNGKGGGLIDDIALIRDDV LFVCEGEFFIDPQTDSKPPEGLLGFTDWTNLVGGRYFTTTRSTLV NKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNLYLRHG QLIVNDGINLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISR KEFVRFLATPTKSELRCQLNFGADLSRLDLRYINFKMAQFKPL* \FAHANLC*ANLERTDLYGSVLDCANLQGVKMLCSNAEGASLKL CNF EDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNACLKNCNLRG ATLAGTDLENCDSLGC DLQEANLRGSNVKGAI FEEMLTPLHMSQSVR
1839	A	1	320	PRRRWALLLSESSGLGGVHVLSLGRVRAAARVGPAGVGVCSVEMGRK

				LEPGSSSSSLPAPAPRHLLVGSALMPQLSLQRDLDFITIDLDLDFKGQL CELSCSTDYMR
1840	A	1	1430	MAAAEAANCIMELPRAFGIRPSGGSYPSSHVEEGWGRFRPGPHVAAA RPPPRGPGHTPWGVIDLGPSTMWGVSWEEQCFSALYQPPSELRGHLL GYRTRFCAFWVSCGQAESSEKPAEDMTSKDYI *LHTHTFGIHEEM LKDEVRT\LYRNSMFHN\RHLFKDKVVLVDV\GSGTGIL\CMFCCQG PWPRKVIGIECSSYSS*LWR*RCVQA\NKLPRRGTSIKGKGGRKVE LPVGERWDIIHQRVGWGYCLFLTESM\LOHRALMPRDKWLAP\DGL\ IFPD\RAQLYVTAIRGTGRYKDSRSHLLGENVY\GFDMS\CIK\DVP IKEPLVDVDPKQLVTQRLAFIKEY\DIYT\VKVEDL\TFNLPRFCP CKLKRN*LCTALVTLLSTFEFTHCHKRTGGTGFFHQPPRSP\YTHW KQ\TVFY\MED\YLTRERRAEEIFGT\IG\MRPNAKEQPGTLDFTID LDFKG\QLCELS\CSTDYMR
1841	A	1	45	RIDYDEFLEFMKGVE
1842	A	2	580	GRVGGRVGCEPPAWIDIYKAAGRSSFEEQ*ARKMSS*AAFRTSFVLG A\EDGCISTQSGWGKVMRMHGPEPHMRELQEMIDEVDEDGSGT\VD \FDEFLVM\MVRCKMDDSK\GKF*GRSLDLLPACFDQKMLDGYI\D L\DELED*LLQATGRDPFTEDDDIEEL\MKDGDK\NNDGRID\YDEF L\EFMKGVGUDA
1843	A	481	1479	EERLGEDI FRSGTLWPNAGGRAFSQAVYCLNGFIDTSVRLLDKIERN TLTROSSLPKDRGKRSRAFVFELSGEHWTELPDSLKEQTHLREWYIS NTLIQIIPTYIQLFQAMRILDLPKNQISHLPAEIGCLKNLKNELNVGF NYLKSIPPELGDCEENLERLDCSGNLKLMELPFELSNLKVQTFVDISA NKFSSVPICVLRMSNLQWLDIHRHNLADLAEDIDRLEELQSFLLYKN KLTYLPYSMLNLKLTLLVVS GDHLVELPTALCDSSTPLKFVSLMDN PIDNAQCEDGNEIMESERDRQHFDKEV/TESLY*SP*RKRICSQLYH QSVF
1844	A	2	369	VKDLEHTKMITPTVKMHTMSSSHLFYLALCLLTFTSSATAGPETLSS SSPFRSCDL RRLEMYCAPLKPAKSARSVRAQRHTDMP
1845	A	28	479	PIHFQTLSSSEAMGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYLA LCLLTFTSSATAGPETLSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSPFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMP KTQKYQPPS
1846	A	4	458	NHSIFRLCTSEAMGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYL ALCLLTFTSSATAGPETLSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSPFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDM PKTQKYQPPS
1847	A	90	769	HCSQHLPSLWISFCFIIPANQFIFRLCTSEAMGKISSLPTQLFKCCF CDFLKVKMHTMSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQ FVCGDRGFYFNKPTGYGSSRRAPQTGIVDECCFRSCDLRRLEMYCA PLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNQTSQRRKGWPKTHP GGEQKEGTEASLQIRGKKKEQRREIGSRNAECRGKKGK
1848	A	231	909	HCSQHLPSLWISFCFIIPANQFIFRLCTSEAMGKISSLPTQLFKCCF CDFLKVKMHTMSSSHLFYLALCLLTFT\SSATAGTGDSAGAE\VD ALQVPCVEDRG\FYFNK\PTGYGLPAVRRAPQTG\IV\DECCFR\SC \DLRRLEMYCAPPQACPSQLRSVRA\QRHTDMPQDPERKYI*RTQVE GVQETRRTTGLLEDPPGGVKS DMPPQDPLLCTSYLLNFGTPTKK
1849	A	65	396	RPLKPRRTFCK*V\CKAPT PHKSDHSTKKGKDSSVRPQGKRRYDRKQ \SGYGGHTKPIFRIKAKTTEKIVLRLECEVEPN\CRSKRMLAIKWQA FLNLGGDKKRKGPSASKF
1850	A	141	441	IQTFLGLGKNWATCTDLYLINIRSMSTCYLCSISDQVDATLIPITN FSCGIFAGILASLVTQPADVIKTHMQLYPLKFQWIGQAVTLIFKDYG LRGFF
1851	B	851	1807	MAIKSIYAALRSIYHSEHGRGLFSGLTATLLRDAPFSGIYLMFYNQ TNIVPHDQGPPLGMLGQAIHKAQRSCKPALPGPEELPTQGNWK*

1852	A	913	1375	SIFPGVIEHLTLTFIYYHFIINRTSQGIDSQILSLFLFF/CFFET ESRSVTQAGVQ\WRHLGSLQPPPPWFKRFSCLSLQSSWGVRHVPHP G*FLVFLVGDDGFTMLGQGSQNSCTSRSTRRLRLAQPLFSQFKNCF KNCKSSIGLIPLYYY
1853	A	1295	1679	KCINCKVYFTGVFFLIPTCQMQUIHIFVCLCLVIISIHISFFYFIYFY DIIS*MCNL*\ILLDYFNPLEITIHAFCIQFM**LIYL/CFKCILFC GFLGFCFLCFLKIRF**S*FSFSLKCIYSFYSLV
1854	A	2	410	SCREFCLSCPRLSLRSLTAVTCTVWLAAYGLFTLCENSMILSAAIFI TLLGLLGYLHFVKIDQETLL\IDSLGIQMTSSYASGKESTTFIEMGK VKDIVINEAIYMSAKPRLDCLIEVYRSCQEILAHQKATSTSP
1855	A	3	322	ALQRRYSPFCREFCLSCPRLSLRSLTAVTCTVWLAAYGLFTLCEVM ASRPLPALEGGGSLGSLVEPGPLVGPSSYSDRTGGRELTSQSGD DIPLLDSSSLNDV
1856	A	1	666	SGRDDQGRRAQCSAARCGRPSGGVMEDERSFSDICGGRLALQRRYYS PSCREFCLSCPRLSLRSLTAVTCTVWLAGYGLFTLCENSMILSAGIF ITLLRPLGVSPSVKNDQETLL\IDSLG\IQMTSSYG\SGKESTTF\ IEMGKVK/EIFVNNEAIYMSI*KHKAIYYLWNLFKIPV\EPHGD PKYVPVFQSAKPRLDCLIEVYRSCQEILAHQKATSTSP
1857	A	1	1158	MELKAKARELREECRLSRSDQLEERVSVMENEMNEMKREGKFKREK RIKRNEQSLQEIWDYVVRPNLHLIGVPESDGENGTKLENTLQDIIQE NFPNLARQANIQIQEIQRTQORYSSRRATPRHIIVRITKVENMEKML RAAREKGRVPHKGPRIRLTADLSSETLQARREWGPINILKRIFSP QRRGTGGRMVKLTAELIEQAQYTSAVRDRELDLGRYKIPVNIENLG ATLDQFDAIDFSDNEIRKLDGFPLLRRLKTLVN/NNRIC/RVLDFO KVK/LKERQEAEMKFKGRGAQLAKDIARRSKTFNPGAGLPTDKKKG GPSPGDVEAIKNAIANASTLAEVERLKGLLQSQQIPGRERRLGPTDD GEEEMEDTVTNGS
1858	A	2	433	RKLDGFPLLRRLKTLVNNNRICRIGEGLDQALPCLTELILTNNSLV ELGDLDPASLKSILTYLSILRNPVTNKKHYRLYVIYKVPQVRVLDFO KVKLKF\NPGAGLPTDKKKGSPSPGDVEAIKNAIANASTLAEVERLK GLL
1859	A	208	293	LLLLWWFPLGPTDDGEEEMEE\DTVTNGS
1860	A	22	907	ARNPWSTHASGWREATGFPQRRGTAGCTMGKLTAE\LIEQAQYTN VRDRELDLGRYKIPVNIENLGATLDQFDAIDFSDNEIRKLDGFPLLR LKTLLVDTRI\CGIGEGLDQA\LPCLTELILTNNSLVELGDLPLA SLKSVAY\LYLRNPVTHKKHYRLYAIYKAPHVRVLDQFQNVKLK\ER QEAE\QIFKAKRRAQLAKDIA\RRS\KTF*FPGAGLPN*PKRKGPP/ SLPGDVEAIQEC*QNAFNSGLKVERLKGVCCKSCSRSPGRERRSG\ PT\DDGEEEM\EEDTSHQTGS
1861	A	20	466	VACCVRIPGPPRRSGPAMAVTITLKTLLQQTTFKIRMEPDETIVKLKE KIEAEKGRDAFQNMQRVIQONPALLPALLQQLGQENPQLLQQISRHQ EQFIQMLNEPPGELADISDVEGEVGAIGKEAPQMNYIQVTPQEKEAI *RLKALG
1862	A	6	450	VPAEVACCVRIPGPPRRSGPAMAVTITLKTLLQQTTFKIRMEPDETIVK VLKEKIEAEKGRDAFPVAGQKLIYAGKILSDDVPIRDYRIDEKNFVV VMVTTKKAGQTSAPPEASPTAAPESSPAQPSWQDLEATDGPLL GSVQLS
1863	A	391	1610	VAMCVEIPGPAASLGPRHWPVTITLKTLLQQTTFKIRMEPDETIVKLK EKIEAEKGRDAFP\VAGQKLIYAGKILSDDVPI\RDFAFDGGRNFV VRSWVTK\TKAGQGYLQAPPGGSPSHSLPQSPLTSFPFPCPHLQACSI PPLAQRRHKSPSEE\SGPKTFPESV\SGSVSSG\SGSGREEDA\A STL\VNGAFY*GRWLTEIMSG\YERERVAAALRASYNPN\HRA\V EYLLTGIPGSPEPEHGSVQESQVSEQATEAAGENPL\EFL\RDQF\ QFQ\NMR\QVIEEPLRCCPALLPASWAQENP\QLLTAKSARPPRSQ FI\QMLERSPPGEAWADI\SDVEGEVGA\IGEEAPQ\MNYIHGDARR RKEAIER*KALGFPE\LVIIQPYF\ACEKNED\LAANFSLSQNFDD

1864	A	2	354	PSTFVEHSI\SCKEKLNKKNKIGAAFTDD/GFAMGVAYILKLLDQYR EFDLSLHWFQSVREKYLKEIRAVAKQQNVQSASQDEKLLQTMNLTQKR LDVYLQ\ARIFFRADKTAABENQEK
1865	A	1	1353	MLQYWKLFECHRNAQWKCSLEHFGFQIRDAELGFLYAYSISTIKTT MNLVMSMQPMTKTSVKALCRLVELLKKRVISDKKYSEQRLDVL VLAENTLNGPSTKQRR\IVSLALSVGTQMKTFKDEELFPLQVVMKKL DLISELRERVQTQCDCCFLYWHRAVFPIYLLDDVYENAVDAARLHYMF SALRDCVPAMMHARHLESYEILLDCYDKEIMEILNESGLIQLDRDCL KIHRTKTHSVPGGRLPSRLRKGLRCRWLIITSGLSVRSNLNRMQCEK SGSDDGQGHSSPQAVVQVLDQTSSHGSPGLTHEIPALGEEIKPLPGG GDQPCFAVSCVLKSPVPESTSGHLQVLLPRYGYWVHFRNNVFLYIV KAKLPIQVERAAEGYNLAGMIWEIMGSASKGDTSPRADSPHHSHMLT TKPGDATRMSPTPLRTEHLENHPSDTWS
1866	A	1	260	YMFSA LRDCVPAMMHARHLESYEILLDCYDKEIMEILNESGLIQLDR DCLKIHRTKTHSVPGGRLPSRLRKGLRCRWLIITSGLSV
1867	A	2	401	FVPDLEDIVNFEELVKEEGLAEETLKAASWLRSQSOPGATRRSAWAS WSLWALTLPRAHPVPGTAPLRCLDFPPIPAKVQTKTAYPLSSTFPY KGQGIYSQDNCFSIATASDSGIANCTRCRAATSSAKTFV
1868	A	1	2694	MQEKQYLMFLKVERTEFLKRRARFMRHLDSVLSDHTRNSAEGTEY FKMLVDVFAPEFRPKNIHLRNFIIVPPLMSFLASETDRKPDKVSL TPFLPSSSPFLAEVPLPFASVPKCLVHLLNEMCLATQQLSKQLLAYE KQTGTCSLLEAQNSALNRADQQQEVNEILSGKCCLPDSLLQQMFI VRFLGSMVKTDTSTTEVIYEAMRQVLAARAIHNI FRMTESHLMVTSQ SLRAPGGRGCGRSFSRLKCSCLPALKRAAGLPAQRLSSAKGQTASS SESLTLVVPDGETPPSRNRQTPTHTGEFQLASALAAEKDGTVPVFKLPK WRVKGKTIKEVAEAYRSVGAELNVLPFCTQFIPMDIIDSPKHGSIY HPSILPRHRGASAINWTLIMGDKKAGFSVFWADDGLDGTGPILLQRSC DVEPNDTVDALYNRFLPPEGIKAMSIREDRNGRSQKT VHTEGDMNMN IKKIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSHTRH DMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQADGT VAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDNSIDSWKNAGRVP KDSDFDANDPILKQDTQEWSGSATFTSDGKIRLFYTDYSGVAYILK LLDQYREFDSLHWFQSVREKYLKEIRAVAKQQNVQSASQDEKLLQTM NLTQKRLDVYLQHLDDKLCKEIEKDLRLSVHHLKLDLDRNPFVGMK DLALFFSLNPIRFFNRFIDIRAYVTHYLDKTFYNLTVALHDWATYS EMRNLATQRYGLVMTEAHLPSQTLQGLDVLEIMRNIHIFVSRYLIN LNNQSPLLKTTPRVSVSFYPIRRETRALVFFTHQSHINVYHEKHPRN QKLV
1869	A	1	3754	MAAAFHGGGLAFPGAPAVAGATSPAGPRERRRRGRGRKSRVTVAGV RPSSPHGLVGAVSVGGAGVMAKKTLSPDWEFDRVDDGSQKIHAEVQL KNYGKFLBEEYTSQLRRIEDALDDSIGDVWDFNLDPALKLLPYEQSS LLELIK TENKVLNKVITVYAALCCEIKKL\KFEAGTKFYNGL\LFYG EGATDASMVEGDCQIQMGRFISFLQELSCFVTRCYEVVMNVVHQLAA LYISNKIAPKIIETTGVHVFQTMYEHLGELLTVLLTLDEI IDNHITLK DHWMTYKRLLKSVHHPNSKFGIQEELKLPFEKFLKLEGQLLDGMIF QACIEQQFDSLNGGVSVSKNSTFAEEFAHSIRSIFANVEAKLGEPSE IDQRDKYVGICGLFVLHFQIFRTIDKKFYKSLLDICKKVPAILTAN IIWFDPNFLIQKIPA\SVTLDRKSLQAIKIHRDTFLQQAQSLTKD VQSYVVFVSSWMMKMESILSKEQRMDF\AEDLTNRNCNVEIFQGLHA YSIRTIKTTMNLVMSMRKPMKTLAKALCRLVELFKAI EHLFYRRS MVDVSVSHITQHLQHQALHSISVAKKRVISDKKYSEQRLDVL LAENTLNGPSTKQRR\IVSLALSVGTQMKTFKDEELFPLQVVMKKL DLISELRERVQTQCDCCFLYWHRAVFPIYLLDDVYENAVDAARLHYMF FSALRDCVPAMMHARHLESYEILLDCYDKEIMEILNEHLDDKLCKEI EKDLRLSVHHLK\DDRNPFI VGMKDLALFF\SLNPIRFFQSVS IDIRAYVTHY\LDKTFYNLTVALHDW\ATYSEMRNLATQRYGLVMTEA

				HLPSQTLEQGLDVLEIMRNIHIFVSRYLYNLNNQIFIERTSNNKHLN TINIRHIANSIRTHGTGIMNTTVNFTYQ\FLKRKFYIFSQFMYDDHI KSRLIKDIRFFREIKD\QNDHKYPF\DRAEK\FNRGIRKLGITPEGO SYLDQFRQLISQIGNAMGYVRMIRSGGLHCSSNAI\RFVP*SLKIIV NFWKNLVKEEGLAEGTIKSSQGHLLGFQSLSDHTRN\SAEGTEYF\KM LVDVFAPEFRPKNIHLRNFYIIIVPPLTLNFVEHS\ISCCKLNKKK KIGAAFTDDGFAMGVAYILKLLDQYREFDSLFWQSVREKSLKEIRA \VAKQQNVQSASQDEKLLQTMNLTQKRLDVYLQEFELLYFSLSSARI FFRADKTAEEENQEKKEKEEETKTSNGDLS DSTVSADPVVK
1870	C	293	448	MXKTLQELRAHENEITXVRKVTFNGLNQMIVIGLPPSLTELHLGWQQ NQQS*
1871	A	1	475	SYIRIADTNITSIPQGLPPS/LTELHLDGNKISRVDAAASLKGLNNLA KLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHKYIQ VVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS/LFKNPQYWEIQPS TFRCVYVRSAILGLNYKKK
1872	A	1	636	MKATIILLLLAQVSWAGPFQQRGLFDFMLEDEASGIGPEVPDDRDFE PSLGPVPCPFRQCCHLRVVCSDLGLPPSLTELHLDGNKISRVDAAASL KGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGL AEHKYIQVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQ YWEIQPSTFRCVYVRSAILGLNYK
1873	A	196	1274	IMKATIILLLLAQVSW\AGPFQQRGLFDFMLEDEASG\IGPEVPDDR DF\EPSLGPS\VCPPFR\QCHL\RVV\QCFLILGL\DKVTGIFSP NTLLDLQNNKITEIKDGDfKNLKNLHALILVNNKI\SKVSPG\AFT PLVKV/EERLYLSKESA*RELPEKMPKTLQELRALED*/EFTKVRKV TFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSI PQGLPPSLTELHLDGNKISRVDAAASLKGLNNLAKLGLSFNSISAVDN GSLANTPHLRELHLDNNKLTRVYLHNNNISV\VGSSDFCPP\GHTP KRASYSGVSLFSNPVP/QYWE\IQHPTF\RCVYVRSAILGLNYK
1874	A	248	1393	IMKATIILLLLAQVSWAGPFQQRGLFDFML*DEASGIGPEVPDDRDF EPSLGPMPFPPLQCHL\RVGQGSCLCLEQMPK\DLPPDT\TLL\DLQ NNKIT\EIKDGDfKNLKNLHALI\LVNNKISKVSPGAFTPLVK\LER LYLSKNQK\ELPEKMPKTLQEL\GAHEEWDH\QWRKS*LFNG\LNP MIVHRNWAPIPLKSS\GIENGAF\QGM\KKLSYIGI\AD\TNITSIP QGL\PPSHTKLHL\DGKQKSSRV\DA\ASLKG\NNL\AKLGIEFSN SISAG*TNGLSGPTRPH\LRHLHLGQQALPRVPWWGWAH*VHPRL S*PFITNQYLCRLGSSDF\CPPG\HNT\KKASYSG\VSLSNPVQYW EIQPSTFRCVYVRSAILGL\NYK
1875	A	81	137	TMAFPAGFGWAAATAAYQVEGGWDADGKGPCVWDTFTHQGGERVFN QTGDVACGSYTLWEEDLKCIKQLGLTHYRFSLSWSRLLPDGTTGFIN QKGIDYNNKIIDDLLKNGVTPIVTLYHFDLPOTLEDQGGWLSEAIIE SFDKYA\QFCFSTFGDRVKQWITINEANVLSVMSYDLGMFPHARSHF GTGGYQAAHNLIAHARSWHSYDSLFRKRQKGMVSLSLFPARLEPAD PNSVSDQEAAKRAITFHLDLFAKPIFIDGDYPEVVKSQIASMSQKQG YPSSRLPEFTEEBKMIKGTADFFAVQYTTTRLIKYQENKKGELGTL QDAEIEFFPDPSWKNVDWIYVVPWGVCKLLKYIKDTYNNPVIYITED GFPQE*PSAFWMDTSTLGSIFRQTFQELFKAIQLDKVNLQVYCAWSL LDNFEWNQYSSRFGLFHVD FEDPARPRVPYTSK*YAKIIRNNGP* RTRGAWLLWPKGALLLAAEDPSRQLLKPWLSLQDLIDGRQPLQLIK
1876	A	243	1126	FQORLYRAARRFTMVKIAFNTPTAVQKEEARQDV\EALLSRTVRTQI LTG\KELRVCHPGKKEGSSGEMLWFTLFRFQFILG\GLYLFGGACI YK/YTFMPKRHHFTVGEMCFDSED PANFPFGGGE*LSCLVT*/EE ADIREDNIAI IDVPVPSFS\DS DPAANYFMTFEKGMTA\YL\DLLL G\NC\YLMPLQYFYLLWPPKKIWVELFGQTGRVGRY\LP\QTYVVR\ EDLVA VSRKIRDVSNLGIFYQLCN\NRKS FRLRRRDLLLGFNKRAI DKCWKIRHFPN\EFIVETKICQE
1877	A	985	1401	DFA*V*RDRVKFKGTCFLFV*WFLKFFFKMEFLLPRLCENGKI\HCN

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				LLMGSSNSPTSASQVAGDYRHVLIWWFLIEMEGFPMPLVRAGLKLLY LEWIGSAF
1878	A	184	481	SPRCNPSPLPQAFQSGDCPLPCTAAGLMCAWRSAREPCLLPHPCLP RVWHRRDP/CSQPTSQG*TEALPILCK*KPPWPWPQEISPSQWIHQ PADPAL
1879	B	148	194	XNILSVIAVRKLFATA*
1880	A	2	1508	PESVGGGKTLQEEKQLQPCMQMDNRLPPKKVPGFCSFRYGLSFLVH CCNVIIITAQRACNLMTVMVMNS\TDPHGLPNTSTKKL\LDNIK\NP MYNWSPI\QGIILSS\TSYGVIIQVP/VLGYFSGIYSTKKMIGFA LCLSSVLSLLIPPAAGIGVAWVVVCRAVQGAAGQIVATAQFEIYVKW APPLERGRITSMSTSGFLLGPFIVLLVTGVICESLWGPWVFYIFGAC GCAVCLLWFVLFYDDPKDHPICISISEKEYITSSLVQQVSSSRQSLPI KAILKSLPVWAISIGSFTFFWSHNIMTLYTPMFINSMLHVNIKENG LSSLPYLFADWL/CGNLAGQLSDFFLTRNILSVIAVRKLFATAAGFLL PAIFGVCLPYLSSTFYIVIFLILAGATGSFCLGG\VFINGLYCSP DILGFIKACSTL\TGN**GGLIAS\TLTGIL\KQ\DPESAWF*NLQ SLMASPLMVTGP*FSPYRLPTARNSRDW\AKEKQHHTSPEV
1881	A	90	458	HFSRGYLEAFSEISNIRFVPPHSVTVVVFGACFLCILGIWPWACL PGGEGSGGFGEGRGSEAGRLGSELTP\ATPLQAPAEAYPVFEPVP PVPEAAQGDTEDEGAPPLKRICPNADP
1882	A	15	796	PGSTISWRPGLARSLSPDGRPRRGLGPGSPASMAGRTVRAETRS RAKDDIKVMATIEKVRKWKRWVVAATPFRILNWVA\VVDPQEEE R/RREAGGAERSRG\RERRRGASPRGGP\LILDL\NDENSQON FHSEG\SLQRGTE\PSPGGTPK\PNRPCVTLPDPPEGGP*EGLSPPR \LGQEERSPGGITV\GSTYEPP\MLTKEEPPVELLEAEAEPEA\YPVF ETVPPVHETAQGDTEDEGAPP\LKRICPNADP
1883	A	566	831	ARSFFLITILIQRTDWRKKNFFPSNFPNLRNFTLDQFLKETILRK H/RVGLGVLAHTCNPSTLGGRGWSP*QEFENSLTNMNVNHS
1884	A	534	1835	GSSYMHFQGEWVIAQCFKKLHRGVVCVCL/CLYTHICIF*YITKAI LMNY/ACI*KNSCHLAHRFVCMCIYICMYVWCGYIVLKITQ*CMY
1885	A	60	397	DMEEASEGGGNDVRNRLQSEVEGVKNIMTQNVIRILARGENLEHLRN KTEBLEATGQPSINVCQEGLLSCLPLQRMLLGPPTPLPEALLPRCMP QKAGIELERCQQQANEVT
1886	A	1	193	FRLARGENLEHLRNKTEDELEATSEHFKTTSQKVARKFWWKNAKMIVL /VFIIILFIVLFATGAFS
1887	A	1	280	NIMTQNVIRILARGENLEHLRNKTEDELEATSEHFKTTSQKVARKFWW KNVKMIVLICCHVVCPRRYLGPPEGEKKERWTVA AFLGSLEWAGET
1888	A	1	396	MEEASEGGGNDVRNRLQSEVEGVKNIMTQNVIRILARGENLEHLRNK TEDELEATGNFYDIWSTDVLEIKEEGVLKFLAAGSHLGSTNLDQFMEQ HIYKRKSNIGIDIINLEKLLLAACAIENPADVSIILQEY
1889	A	85	410	DMEEASEGGGNDVRNRLQSEVEGVKNIMTQNVIRILA\RGENLEHLR NKT\EDLEKPTS\EHFKT\TSQKGGSEKFWWK\NVKDDCPLICRDCF *SSLLQLWLFA\TGAFS
1890	A	122	975	AARPTRHLCCGQQQVLCVGPSPAVGRPLQWGLGLGPTMSSLGGGSQ DAGSSSSSTNGSGSGSGPKAGAADKSAVVAAPASVADDTPPP \GVGTRAVSSVSPSTRACA/GSRPLSHYSSFGSGSGSGGSMGGES A*QGHCGCSRGLPVGQWA*PGGGHGGGQKPYLKAQKWCCGQPAEQ RAGHGAGSRGTADAAVFAVHRDAEARGAGASPADERGGLLACLDME AVAGAEALNGQSDFPYLGRFPSTQGLLSLLTPAGVVSWA EKRAAHG RAWA
1891	B	1	8736	MPGQILVKAQFLQKAKSFHRMVLEQLGIYWETNKPFPFHPI THEN EFEMNHRGECKTKNYKTSRRKYRRTSLTPRGQSFRLRIQKIGQRYLQ YIYQAKASNPECTKNCKPKDKQPDNMGKKTLESDEGLRKPAPIP APDPVAGRTLIGKEHVPILWGGVLAGTSCSLSPAGSPVHPTTLRDH QLGPPQPLWSCLELQPHQTHNKFVGRGGAKERDRNLARACPPLSQGQ WQRPGLNTTINI PAGENLNLVEGPRDPGLALDPARTPTSHQREWAGP

				<p> LMGQEPGPPTLTQLLGAGDPTLSAHPQPEQLTAEQTALSHTASPV CPLSPNSQRPPHLEAPGYLPGGSSRTQPAVLRVAPLGSQCASVPPIA WIENDSIYTEAGKLATSAPGTLPDSSHLGTLFTVYHLTPTLSQAGQG WLSQRRRTQRPSLLEWDRKETLAQSGAVMPDALTTPARAFAGAPTPAT PTSQQPEGGALHSWPQRWPRKFPDPKCSAASVVRQALEHMTBESSW CTLPNADSHGNAPHPAPGFLQTLSTCHWLCLGHPPSSDPGLAPPPGT QNRALGSRAPGGRLGLPLALRDGCVHWACPLAKKWSQNQPQLLSR NFASALHGAHFQVYFTEMMGEDPLTSWVPVSGLGIVPRSTSSAPTQ LGSGNVAVVGHVRVLPFSFSDGFLQPMSSSSGLAQQSVWASLGSEQQ QVPMLEPPASPGTPAARAGPVQFEQCLLQSPTWKYPQLVPFRLCHRA GWSAQKLAQEASSGLAATWAAPTSSCNQGWAPDVKGRRLGSPGRPA PRRACILSSCPSGLCWPGGSKMQRRRELGGEPPLSDLQEEAASASLRV APERLSDDSLLEWRRTCPDLLLLSDGKASISMPREGGSTCTARCPDPGE HSSTWGEFEGFRESSAKSGQFSQSLLELEGTEPQPRTTSAPKES SHQPCQGGPWVTGTSVAPPSEPILSYENILKCAFQBITVQQAEDVS TIDHFLEISSEKPGVERVHKLCHESRKLWRLQSIHTTSTSQRLLWS ESRQENFFLVLGIDAAQKNLSGGQGHIMEDCDLKEPEGLLTVSSFC LQHCKALIQTKPQQAQFVPHGCGQEVAPLACESLWVRHKSAGAEIR EGRGCEAPLDCEQAQVRQVRSTVGVQGGTGPASTKMSATSWFLVSS SGARHRLPRELIFVGREBCEMLQCPAQCKPGTELVPSEALNDAG TWTQAGLPVAVTVPVVAQAVVQETTAWAGPDLLCPVHRAGLLRPVVA ANGELGDCHWGGQEPSCGCGQLRRRNLRVDLESRSVDKQHAVINYD QDRDEHWVKDLGSLNGHACLMKRLSLNGCTASGRSSACVDCVTHMGF ERTFVNDMRI PDQKYVTLKLNDRVIRFGYDILPLSVPPPGLLLSPQDH SHPVTPEAGLSLLGKRPLLCPLRWALELAHLLLGVDIFSAGLLALLC VRLNTPCHSNMYVLERVQHRVPEEALKHEKYTSQLQVSVKGLAPKRS EALPEHTPYCEASNPRPEKGDRRPGTEAASYRTPLYGQPSWWGEDDG STLPDAQRQGEPPYPERPKGPVQDQDGLHGFRAPEPQGCFSRREPSY FEIPTKETPQPSQPPEVPAHEMPTKDAEAGGGGAAPVVQSHASFTIE FDDCSPGKMKIKDHITKFSLRQRRPPGKEATPGEMVSAETKVADWL QNDPSLLHRVPGDDRHSTKSDLVHTRTLKGHKHEDGTQSDSEDP AKAASAAGVPLEASGEQVRLQRIKRDPELLHNNQAFVIEFFDEDT PRKKRSQSFTHSPSGDPKADKRRGPTPADRDPSVPAPVQAGGRSSG PQRAGSLKREKTEERLGSPSPASRTPARPFGSVGRRSRLAQDFMAQC LRESSPATRPSPEKVPVLPAPLTPHGTSPVGPPTPPPAPTDPQLTK ARKQEEEDSLSDAGTYTIEAQDTEVEEARKMIDQVFGVLESPELS RASSATFRPVIRGDRDESDDGGVAQRMALLQEFASRPLGAAPQAEHQ GLPVPGSPGGQKVVSRWASLADSYSDPGLTEDGLRRGSGPEGLPV RMRRRLPQLPSEADSPAGPESSRRSGPPELDSESGSRLFGQEEL DPDSLSDASGSDGGRGPEPGVEPQDSRRRSPOEGPTWSRGRSPRAP GEPTPASFFIGDQNGDAVL SRKPLAAPGDGEGLGQTAQPSPPARDGV YVSANGRMVQLRPGRSPEPDGPAPAPLRQESFTKEPASGPPAPGKP PHISSHPLLQDLAATRAARMDFHSQDTHLILKETETALALEARLLS NSVDAECEGGSTPRPPEDALSGDSVDVTASTVSLRSGKSGPSPTTPQ PLRAQKEMSPSPAAQDPGGTALVSAREQSSERQHHPGLGPTDMGRGE PVRRSAIRRGHRPRGSLDWPSEERGVPVLAHLPSDDVMASNHETPEAT GAGRLGSRKPAAPPPSPAAREEQSRSSASSQKGPQALTRSNLSLTP RPTRASRLRRARLGADSDTEAADGERGSLGNPEPVGRPAAEQAKKLS RLDILAMPKRAGSFTGTSDPEAAPARTSFSGRSVELCCASRKPTMA EARAVSRKAANTATTGPRQPF SRARSGSARYTSNTRRRQGSFTTS TSEEEYGSRHGSPKHTRSHTSTATQTTPRAGSSSRARSRAPGPRD TDD EEEEDPYGFIQTAETAEIARVSSLPSPRLAVPTCSDSLGLFAL GSHLQRLPARPGSRFPFAASAPCPSWLAVPTCSDSLPLVLADGSHL QRLPARPGSRFPFAASAPCPSWLAVPTCSVSSLPVLADGSHLQRL PARPGSRFPFAASAPCPSWLAVPTCSDSLPLVLADGSHLQRLPARP GSRFPFAASAPCPSWLAVPTCSDSLPLVLADGSHLQRLPARPG* MVGENNTQWGRSGSRWLGFSPXPRPGXQPV </p>
1892	C	377	463	

1893	A	753	3000	KLEPCGGTTPGPRAGSGPCQDPHIPPEGVGGSPDGPAGWAPAPNTHSAS WSWGPHECPCPPA*AADCRGTDRES\PASVPCPLSPNSQRPPHLEA PGYLPGGSSRTQPAV/PTCSPPGIP/AVPALCP*PG*KTT/PIYTEA GKLATSAPGT/PPRQLSPGNAVYCLPPDTHTQPGRAGLAESAPYPEA QPAGVGQEGDAGTE/PGPSCQTOH*PPQEPLLGPPQQL/PPTSQQPE GGALHSWPQRWRKPPFDP/PL/PVRPVWSAKPWNT*RRSPPGAPSP TRTAMGT\TTPCPRPSPDSKHVPLALPGAP/VPAQILDLLPRQALRT EPSAPEPLAGYGDSPWLCGMAVSTGVPVLPWLRNGPRTNHSC/CRSRN FASALHGAA\PSKSFIRR*WGRTP*PAGCPF/PGLGIVPRSTSSAPT QLGSGNVAVVGHVRVLPFHSDBGFLQPMSSSGSLAQQSVWASLGSEQ QQVPMPLPPASPGTPAARAGPVQFEQCLLQSPTWKPY/PAFAQAVP *SRMVCPEAGPRSQQ/PA*QPPGLPPPPATRVG/PPDVKGRGRGLGS PGRPA/PPACMSPEQLPIGPLLAWGLQDARPAAGAGGRAFE*PPGGSS QRFPPSGT*EAE**QF/VNGDGPAPTFCMPGKPPASPCPVRAVPPAL PDVLTGNTAALGGSLKAFGNLQPSLDNS\VPV*\LLEGPTQPQPR TTSAPKECSSSPTMPGVGPWVTGTSGRPTFLSPFFSYBEHFKVLLFK EITVQQAEDGFHHRPFPNRKQ
1894	A	3	576	LTRIPFLGAKYAPVIFA/EGA/YQ*QRS*TEIQMACFKQATRWVKC/ DPRHGKYMA\CCLLYRGD\VFPKDVNAIATIKTKRSIQFVDWCPTG FKV\GINYSPPTVVPGGDLAKVQRAVCMLSNTTAAIAEAWARLDHKFD LMYAKRAFWHVYVGEEMEEGEFSEAREDMAALEKDYEEVGVDSEVEGE GEEEGEY
1895	A	58	1636	LVGDGNPGPGVCSCRLRLIIPYPLCGECT\SI\HVGQAGVQIGNAC\ WELSCL*HGIQPDGQMPK*PKPLGEGDDSFNTFFSETGAGKH\VPRA VFVDLEPTVIDEVRTG\TYRQLFHPEQVITGKEDAANNYARGN\YTI GKEIIDLVLDRI\RLK\ADQCTGLQG\F\LVFHSFGGGTG\SGFTSL LDE\RLSVDYWQESPSLEFSIYPGAPRFPQPVVEP\YNSILTTHT\T L\EHSGLCPSWVENEAIYDICRRNLDIERPTYTNLNRLI\SIQVSSI TASL\RFDGALNVDLTFEQTNLVPLPRHSTSLRPTYAPVNPSS*EKP TH\EQAFCSRRSPKCAFEPSPQRLKCDPSPMGKY\MAC\CLLYR\ GDVVPK\DV\NAAIAHPSKPKRS\IQFVDWCP\TGFK\VAINYQPP\ TVVPVGDLA\KVQKTV\CMLSNT\TAIAEAWARLDHKFDLM\YAKRA \FVHWYLG\EGMEEGEFSSKA\REDMAAL\RKDYEEVG\VDSEVKG\EG EEEGKGLI\HSLFGPCSMSCSQNFSFSLTDRR
1896	A	491	1068	VSRIQONISTR*ROACLALV\NLYLQGLPPPTSLWGFYFD\RDDV \ALE\GVS\HFFRRIGPRKCR\EGYERSS*QMOKTSRGRPALFFQDN QDSQLED\EWGKTPQTPMK\AAMALEEKA*TOALFGSFIALGFLPAR TPMLL*ASLETHF\LDE\EVKLIK\KMGDHL\TNLHR\LGPEAGAG AKYLF\ERLTLKHD
1897	A	2	350	SQVDR*QSEPEsirICREDHMERLQAFDANSRKQEAWEKEKAIKELE EWYARQDEQLQKTKANNRVA\EKLSTNNPSLT*LVMSEAFVNDIDE SSPGTEWVARLCDFNPKSLD
1898	A	2240	2492	AVACVARQPPGCSKGVHLKPTYFVVASRAAEAFVNDIDESSPGTEW ERVARLCDFNPKSSKQAKDVSRMRSVLISLKQAPLVH
1899	A	1	906	ATAVSVSGRLVVFVSTGCVRAVQLPMAELDP\FGAP\AGAPGGPALG NGVAGAGEEDPAAFLAQGESEIAGIENDEA\FAILDGGAPGPQPHG EPPGGPDAVDGVMNGEYY\QESNGPTDSYAAISQVDRLQSEPEsirK WREEQMERLE\SLDANSPESSKQSWKEK\AIKGA*KEW\YARQDE\Q LQ\KTKANNRVADESFLQTTLR*RDWLCHKHKPSLLQPRGTGQPEEAL FK\DLGLSPSNEWE\RVARLCGL*PPSLSKQA\KDVSPHGASVLI\ SLKAGPRWGHKSHPVETLHLQYLNPTQ
1900	A	29	852	PSRSLVRVVEFAPQRWLPVGVSVGRLVVFVSPVGVRAVQLPMAELDP FGAPAGAPGGPALGNVAGAGEENPAAFLAQGESEIAGIEN\DRAF AIL\DGAPGPQPHGEPAGGPDAVDGVMNGEYYQESNGPTDS\YAAI SQVDRLQ\SQPES\IRKWREEQMERFGKPFDAANSRKQEAWEKEKAIK ELEEWYAR\QDEQLPENQKANNR/AQTEARPL*NDID\ESSPRPLKW

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				GNGWPRAV*TLNPPKS*AKQAQKMSPPHDASVLILPLKAGPRWCH
1901	A	1	585	MKTIRSNQTVDIPENVITLKGCRVIVKGPRTLWRDFNHISIELSLL VKKKKRLRLNNTWGENMIKGVTLGFHYKMRSVYAHFPINIVTRENGS FVEIRNFLGEKYIRVRMRPGVACSVQCQTQKHELILEGNDIELVSNS AALIQQATTVKXKHIRKFLDGIYVSEKETAQHIRKFLDGIYVSEKGG SYRATRQ
1902	A	2	537	GTLRRDFNHIN\VELSLLVKKKKRLRVDTMLGQQKRNWPTRSGLFGS HVQDHDQGVLPPLGFPLPRMRVLCMPHFPPQSTVVIPGRMGSSLLKI\R NFLGVKNTI\RRVR\MRPGCCLVQYPQAQKDELILEGN\DIEL\VSN SAG\LIQQATTV*KQGISGNFLDGIYVSEKGTCSCLRMNKI
1903	A	560	898	KCNTECFGSLMHFVVVLFIIIIIFLRQQGRSVT\RLECSGAILAHCN LRLPGLSNSPASASRVAGTTGTCTYRIQLIFVFLVETGFHYVQAGHK LLT*VIHPPQPPKVLGLQV
1904	C	224	379	MYLHMLPPPGSTQXXXXXXXXXXXXXXXXXHADLTRVGKIIINRMING LGVRV
1905	A	1249	1642	LGCPGPFPIHPVKWMIFFDPCEISVTGVCVC/G/GVCSCGVCG/CG/ CGCLPGGKGICKYI*ICSQIL
1906	A	415	656	SLPRSPGLRGTPSPQHLSSNLNLASLYHPHEITPWIIIFSSSGSSI*T PI/TPSFYPSPTNCDPQIFDPQTPVSGCRCLASSQGPSLSNPTSNLSG PQIPFASYPCLLLAPHPSLPASRPQSCPCSPKTWAPPS
1907	A	1	419	TISWNTGPRARSRARGSSSTGLDGCVGGSGGNSGLPCPDLEPLGGLQ SKCRLCAPTEARGLWS/KVPLFRQVRHLALHACGCREAWPPPGPPPL LVALCFHLKALPSRGSRAGREAVSKHLKFAMLAGGRVCGSRRVLSM
1908	A	1	438	QCTPSSAADCELTACYGFSS*PS*GPSPLPWRPRMCESWVLHLPPPT PQCFSWDIGPSEVMVRPLGWDTLRGSMLPW*GAGERAGKPLPAPADA SPHRSGTGFDRAAGGRRRRCNRSEEGVIFFAAPRLLPPHAFWRVFP HWETT
1909	A	113	704	MAASGAGAEVSGRYGREPPPALPPAPCGPRRRRSPYPKTYRFFSL WQRGRPDRESSAPIGNGLPCPDLEPLGGLQSKCRLCAPTEARGLWKK VPLFRQVRHLALHACGREGLGLPQGPPLLVLCGFHLKALPTRGSR AGREAVIKLPLSVVPQDMYRKSHAAHLREMSSKAAQLSWNNAYFGS SKGLSCVWP
1910	A	317	470	NYPMSVVP\QD\MWRKSHAA/HILREMSSK\TAAQL*WNNAYFGSSK GLSCVWP
1911	A	147	850	MAASGAGAEVSGR*GREPPPALPPAP\CGP\RRRRSP*LPKTYRFF SLWQRGRPDRESSAPI\GNGLPCPDLEPLGRAARSKCRLCAP\TEAT KACWK*GPSCFRQV\RH\LALHACGCR/EG/LGLPQGPPTSAGLLCA FTLKALPSRGSPCKEEKLASTSNFSSHAGCRVCGSRRVLSML*FSG LKLP\LSVVPQDM*RK\SHAAHLR\EMSSKACRSAFDGNALFLEVS KGLSCVWP
1912	A	119	1001	GSRTKGRAVPEACAPVGAGEGRPAGVAVSDGVIKVFNDMKVRKSST \PEEVKKRKKAVLFLP*VRTKNIIIL\EEGKEILVG\DVGQT\VDDP YATF/VSKMLPKDCRY\ALY\DATY\ETKE\SKKEDL\VFIFLGGP ESAPPLEQNGFMPSSQGRPSKKGSWTGDSSHEFAKPNCLPKQGT CTLAREAGGQVPVYSPGRAKPFVSPFWPPCLGASGSPQHLAPWGFA CPPFLQRPGRAGGSPAGGGEIPLNPSCPQTTPNPPGNFPSPSNPL DGFWPFPKLLFESFDSSWG
1913	A	361	1785	LPLPRWKVLLPRDILGPRKINEVSSDDKDAFLCEQTSKDILKKTSE VVKSSPLGVTPLFMQSNVINSTAIVKTLAATGTGFDCASKTDIQLCA ESRGVPPERIIYGKSFVKQVSQIKYAANNGVQM\MTF\DSEVELMKV \ARGTFPKAKVWLRI\TDDSKAVCRLSVKFGATLRTSRLLLERAK ELNIDVVGVSFHVRSCTDPETFVQAISDARCVDMGAEVGFMSYLL DIGGGFPGSE\DVK\LKFEEITRP*STQPLDKYFP\SNWN*KS*LE PG\RYYVASTFDALQLISFAKKICIKRNQTGS**PKIESELSRPLMY \YVN\DGVGSGFNCILYDHAHVKPLLQK\RPKPR*RRYSSSIWGP CDGLDRIVERCDL\PE\MHVGDW\MLFENMG\AYTV\AAASNPMLP

				RGPTIYYVMSG\PAWQ\LIQQFQNP\GFPPGSRRRQPGCPAPCPVFCA W\ESGMKRTRASVPVPSG
1914	A	501	746	ARSSVLVLLFIYIFRDRVLLCHSGWSAVVQSWFTAALISQA*VILK*F SHLSLPSSWDYRQVSPHPANF/SYILFCRDR/SFTMLPRVGWNSWAQ VLLLIQPPKVLQL*AGCHGSCL
1915	A	156	166	VLFLKRPYLVDQAVLWLF\AIISHSTLELLGSSYPTTSAS*VKHSN SNIMKFKVPVLNECTMQLGTKTMIKVLVKSYP
1916	A	452	1017	SLHGISRPHLPTGRLLGPETCAGFSRFGQNESLTPFVTSR\SKNR\ KRHFKAFFPHFEGKIMSSPLSKE\LRQDVQLCGSDARS*KD\DEVQV V\RGHL*GSAKLAKVVQ\VYRKKYVIYIER\VQREKA\NGTTV\HVG HFTPSKQVVIT*G*NWDQRPAPKRSRGTGPKPSR\QVGKGKRGKYKER T\IEKMQE
1917	A	3	474	PLHSHARSHFLFAIMNRPAPVEISYENMRFLITHNPTNATLNKFTEE LKKYGAATLVRVCDATYDKAPVEKEGIHVLDPFDDGAPPPNQIVDD WLNLLKTKFREEPGCCVAVHCVAGLGRKRRGAFNSKQLLYLEKYRPK MRLRFRDTNGHCCVQ
1918	A	1	246	MNRPAPVEISYENMRFLITHNPTNATLNKFTEELKKYGVTTLVRVCD ATYDKAPVEKEGIHVLKKGVSQFQTAALFGEIPT
1919	A	373	560	SQLKNAKFNLRLPPLPNVY*DKGQVTSQLYQNAAQPIFKQAFETC AHHTNTIQDQAPRI
1920	A	837	1441	IFFFHLSPSHSHARSHFLFAIMNRPAPVEISYE\DMRFLITHNPTNA TLNKFTEGT*GSMGVTDGFGVCGWLHMDK\APVWKKEGFHVL\DW\ PF\DDGSSTPLIQIVGWIGFKPV*KTGFSCSHGCCV\AVHCVGRVG EGAPVL/VLALALDWNVGMK\YEDAVQFIRQKRRGAFNSKQLLYLEK YRPMRLRFRDTNGHCCVQ
1921	A	2	1059	GRVGFFFAGNPGSDSFGGLLLGLTPVLRWVADGGTIPKRHE\LVKGP KKVEKVDK\ETELVAQWNYCTLS\QEILRRPIVACELGRLYNK\EPV IEFLLDKSAEKALGKGSISH*NALTNC*QS*KLSDNPCPGKIGKNT KGDK\HDDLQAGASFI/CP/LVGGPGRWNGRHRFLPSGGCGLCCFS *AEPWKEIKAEFCHTCGAGLSRRMMIIVLNGTKEDVDVLKTRME/AE KAVERSFKRISKPKAAESVSKTQMSVEGSPRAHQKLRLPGKP*RSPA LDSREKKTNLAPKSTAMNESSSGKAGKASVWSHKEVHR*PVKNRKP KSLFTTHSFRQSAPKEGVCPTGVHPTRPTCF
1922	A	272	468	GEIEFASCSQASLLLSFVWMPALLPVASRLLLPRVLLTMASGSPPT QSPASDSGSGYVPGSVS
1923	B	131	268	XFVTCPNKVAKEIARAVVEKRLAACVNLIPIQITSYEWKGKIEEDX *
1924	A	2	353	GSPPT\QSPASDSGSGYVPGSVSAAFVTCPNKVAKEIARAVVEKR LAACVNLIPIQITSYEWKGKIEEDSEVLMSVHPYEVAEVIALPVEH GNFPYLQWVRQVTEVSIDSITVLP
1925	A	70	357	DQLSCTSVCRMSSGRAPAVLLGGVASLLLSFVWMPALLPVASRLLL PRVLLTMASGSPPTQSPASDSGSGYVPGSVSAAFVTCPNKVAKEI AR
1926	B	120	839	MSGGRAPAVLLGGVSDRPRPAPSGPRSLDRYPHPKSQRRFAKEIAR AVVEKRLAACVNLIPIQITSYEWKGKIEEDSEVLMMIKTQSSLVPAL TDFVRSVHPYEVAE*
1927	A	259	935	GASLLLSFVWMPALLPVGLPAFLFANPESLLTMG/SLGSPSDPSRP ASDSGSG\YVPGSVSA\AFVT\CPNEKGS PREIAR\AVGGRRLA\A CVQPSSPQITIPSMKWK\GKDSREDS*GCWMDGFKTQKFPWVPSFWT DFV\RSVAPYEV\AEVI\ALPVEQG\NFPYLQWVRQVTEVSIDSITI LAMMSVPVPAHHEDPRDTSKAFLTQVMTWAPNKSRLWVKKKKSR
1928	A	285	476	LLKHLINMMVSKTTWLGVLHTCNPS/TNFLGGRGGRIS*GQFEA SLGNMGRPCLYKNRQKTN
1929	A	218	602	NGGQAVAHACNPSTLGGQWRVDHLRSGVRDQPGQRGETPSLLKIQKL AGRGARLWSQLLRLRLQENRLNLGGGCSEPRWH\HCI PAWGNKKB *NGNYAQRMGERWLTGLKHQRNGEDRTVRELGR

1930	A	1	628	FFYKSVLAQKEVRCVLDE/ISPLGPPELKPVRFADL/LPHESRRDS SVPELAEKMSRSVDVPTPPSLLMAASIYLHDQNPDAALRALHQGDSL ECTAMTMQDAYYIFQEMADKCSPTLLLLLNGQAACHMAQGRWEAAEGL LQEALDKDSGYPETLVNLIIVLSQHLGKPPEVTNRYLSQLKDAHRSHF FIKEYQAKENDFDRLVLQYAPSA
1931	A	1	354	TFLDMAASIYLDKPNDAALRALHQGDSLECT/ARKELKRMQDLDED ATLTQLATAWVSLATDSGYPETLVNLIIVLSQHLGKPPEVTNRYLSQL KDAHRSHFPIKEYQA\RLVLQYAPSA
1932	A	29	1061	EDSEMAPPAPGPA\SGGSSEV\DELFVDKNA\FYIGSYQQCINEAQR \VKLSSPERDV\ERDVFLYRAVPGAEESSGVALDEQSPPWTLDFQG RAQLFADY\LAHEN\RRDKHRWPSLDRE\MSRSVGR*PKPTFL\LMA PFI*FQEPEPRIGPLRGLHQGN\SLEFTPMTVEVLAESGTALNFAGK ELKRMQDLDE\DATLTQ\LATAWVSLATG\GEKQ\EMPYYIFQGDG CTSASPQPLLLAQLGKAA\CHNGPRARW\EPAEGLLQ\EAL\DKDSG \YPETL\VNLIIRPVPSNLGKPPE\VTN\RYLSQ\LKDAH\RSHPFIK EVPRPKENDF\DRVLQYASQAPEAGPELSGP
1933	A	2	355	TSMLGCTVLFRL/YCVYS\YCNVLATVWSSLV*RLRICHLHVS/WS FVTDCKACYNLTGMLFYSDY**FVYYP*YCYFFCLCSLFFSICLLMYFN IFFF/CNFMFDCYILLLSFYFIILYHYF
1934	A	194	9967	KMWPTRLVTIKRSGVDGPHFPLSLSTCLFGRGIECDIRIQLPVVSK QHCKIEIHEQEAILHNFSSNTPTQVNGSVIDEVRLKHGDIVITIIDR SFRYENES\LQNGRKSTEFPRKIR\DRRPARRVSRSSFSDDPEKAQ DSKAYSKITEGKVSNGPQVHIKNVKEDSTADDSKDSVAQGTINVHSS EHAGRNGRNAADPISGDFKEISSVKLVSRYGELKSVPPTQCLDNSKK NESPFWKLYESVKKELDVKSQKENVLQYCRKSGLQTDYATEKESADG LQGETQLLVSRKSRPKSGSGHAVAEPASPEQELDQNKGKGRDVESV QTPSKAVGASFPLYEPAMKTPVQYSQQQNSPQKHKNKDLYTTGRRE SVNLGKSEGFKAGDKTLTPRKLSTRNRTPAKVEDAADSATKPENLSS KTRGSIPTDVEVLPTETEIHNPEFLTTLWLQOVERKIQKDSLKPEKL GTTAGQMCSGPLGLSSVDINNFGDSINESEGIPLKRRRVSFGGHLRP ELFDENLPPNTPPKRGEAPTCKRSLVMHTPPVLKKIIEKQPPSGKQ ESGSEIHVEVKAQSLVISPPAPSPRKTTPVADQRRRSCKTAPASSSK SQTEVPKRGGERVATCLQKRVSISRSQHDILQMICKRRSGSEANL IVAKSWADVVKLGAKQTQTKVIKHGPQRSMNKRQRRPATPKKPVGEV HSQFSTGHANSPTIIIGKAHTEKVHVPARPYRVLNNFISNQKMDFK EDLSGIAEMFKTPVKEQPQLTSTCHIAISNSENLLGKQFQGTDSGEE PLLPTSESFGGNVFFSAQNAAKQPSDKCSASPPLRRQCIRENGNVAK TPRNTYKMTSLETKTSDTETEPSKTVSTVNRSRSTEFERNIQKLPE SKSEETNTEIVECILKRGQKATLLQQRREGEMKEIERPFETYKENIE LKENDEKMKAMKRSRTWGQKCAPMSDLTDLKSLPDTELMKDTARGQN LLQTQDHAKAPKSEKGIKMPQCQSLQPEPINTPTHKQQLKASLGK VGKKEELLAVGKFTRTSGETTHTHREPAGDGKSIRTFKESPKQILD AARVTGMKKWPRTPKKEAQSLEDLAGFKELFQTPGPSEESMTDEKTT KIACKSPPPESVDTPSTKQWPKRSLRKADVEEEFLALRKLTPSAGK AMLTTPKAGGDEKDIKAFMGTPVQKLDLAGTLPGSKRQLQTPKEKAQ ALEDLAGFKELFQTPGHTTEELVAAGKTTKIPCDSPQSDPVDTPSTK QRPKRSIRKADVEGELLACRNLMPSAGKAMHTPKPSVGEEKDIIIFV GTPVQKLDLTENLTGSKRRPQTPKEEAQALDLTGFKELFQTPGHT EAVAAGKTTKMPCESSPPESADTPTSTRRQPKTPLEKRDVQKELSAL KCLTQTSGETTHTDKVPGGEDKSINAFRETAKQKLDPAASVTGSKRH PKTKEKAQPLEDLAGWKELFQTPVCTDKPTTHEKTKIACRSQDPV DTPSTSSKPQSKRSLRKVDVEEEFFALRKRTPSAGKAMHTPKPAVSGE KNIIYAFMGTPVQKLDLTENLTGSKRRLQTPKEKAQALDLAGFKELF QTRGHTESMTNDKTAKVACKSSQPDLDKNPASSKRRLKTSLGKVG KEELLAVGKLTQTSGETTHTHTEPTGDGKSMKAFMESPKQILDSAAS LTGSKRQLRTPKKGSEVPEDLAGFIELFQTPSHTKESMTNEKTKVS

				<p>YRASQPDLDVDTPTSSKPQPKRSLRKADTEEEFLAFRKQTPSAGKAMH TPKPAVGEEKDINTFLGTPVQKLDQPGNLPGSNRRLOTRKEKAQALE ELTGFRELFTQPCDNTADEKTTKKILCKSPQSDPADTPTNTKQRP KRSLLKADVEEEFLAFRKLTPSAGKAMHTPKAAVGEEKDINTFVGTP VEKLDLLGNLPGSKRRPQTPKEKAKALEDLAGFKELFQTPGHTESM TDDKITEVSCSPQDPVKTPTSSKQRLKISLGKVGVEEVLVPGKL TQTSKTTQTHRETAGDGKSIKAFKESAKQMLDPANYGTGMRWPRT PKEEAQSLEDLAGFKELFQTPDHTESSTDDKTTKIACKSPPPESMD TPTSTRRRPKTPLGKRDI VEELSALKQLTQTTHTDKVPGDEDKGINV FRETAKQKLDPAASVTGSKRQPRTPKGKAQPLEDLAGLKFQTPVC TDKPTTHEKTTKIACRSPQDPVGTPTIFKPQSKRSLRKADVEEESL ALRKRTPSVGKAMDTPKPAGGDEKDMKAFMGTPVQKLDLPGNLPGSK RWPQTPKEKAQALEDLAGFKELFQTPGTDKPTTDEKTTKIACKSPQ DPVDTASTKQRPKRNLRKADVEEEFLALRKRTPSAGKAMDTPKPAV SDEKNINTFVETPVQKLDLLGNLPGSKRQPTPKKAEALDLVGFK ELFQTPGHTESMTDDKITEVSCSPQSPESFKTSRSSKQRLKIPLVK VDMKEEPLAVSKLRTSGETTQTHTEPTGDSKSIKAFKESPKQILD AASVTGSRRLRTRKEKARALEDLVDFKELFSAPGHTESMTIDKNT KIPCKSPPELTDATSTKRCPKTRPRKEVKEELSAVERLTQTSQGS THHKEPASGDEGIKVLKQRAKKKPNPVEEESRRRRPRAPKEKAQPL EDLAGFTELSETSGHTQESLTAGKATKIPCESPPLEDVDTTASTKRH LRTRVQKVQKEEPSAVKFTQTSGETTDADKEPAGEVDGKALKBSA KQTPAPAASVTGSRRRPRAPRESAQAIEDLAGFKDPAAGHTESMTD DKTTKIPCKSSPELTDATSSKRRPRTRAQKEVKEELLAVGKLTQT SGETTHTDKEPVGEGKGTAKFKQPAKRNVDADVIGSRROPRAPKEK AQPLEDLASFQELSQTGHTTEELANGAADSFTSAPKQTPD SGKPLKI SRRVLRAPKVEPVGDVSTRDPVKSQSKSNTSLPPLPFKRGGGKDG VTGKRLRCMPAPEEIVEELPASKKQRVAPRARGKSSEPVVIMKRS RTSAKRIBPAEELNSNDMKTINKEEHLQDSVPENKGISLRSRRQDKT EAEQQITEVFVLAERIEINRNEKKPMKTSPEMDIQNPDDGARKPIPR DKVTENKRCRLRSARQNESSQPKVAEESGGQSAKVLMOQKKGGEAG NSDSMCLRSRKTSQPAASTLESKSVQVTRSVKRCAPENPKKAEDNV CVKKITTRSHRSDSI</p>
1935	A	194	1026	<p>KMWPTRRRLVTIKRSGVDGPHFPLSLSTCLFGRGIECDIRIQLPVVSK QHCKIEIHEQEA I LHNFSSTNPTQVNGSVIDEVRLKHGDVITI I DR SFYENESLQNGRKSTEFPRKIREQEPARRVSRSSFSDP/G*E*GN TFEKKACVLWWAPKT*TI**KLAS*YASQKGRSPNQKPKVSGNAHSTC PEENHQGTASTIRKTRVFRNPGSGEGLGYKPPSSS*S*ENSSCQ* STP*VLQNSPCFQQQISDKGS*ERRR\KSGNLPSKESVYQPKST*YF TDDMFQKKKWCFGSKSDCKIMGRCSKTWCKTNTN*SHKTWSSKVNE QKAKKTCYSKEACGRSSQSI*YRPRKLSLYHNNRESSY*K\STCACS TLQSAQQLHFQPKNGL*GRSFRNS*NVQDPSEGATAVDKHMHSRYFK FREFAWKTVSRN*FRRRTSAPHLREFWRKCVLQCTECSKTAI**MLC KPSLKTAVY*RKWKRSKNAQEHLQNDFGDKNFRY*DRAFKNSIHCK QVRKVYRVQEYTEATCGK*E*RNKYRNC*VHPKKRSEGNTTTTKERR RDEGNRKTF*DI*GKY*IKRKR*KDESNEEIKNLGAEMCTNV*PDRP QELA*YRTHRHGTWPESPPNPRSCQGTKE*ERQNH*NALPVITTRT NKHPTNTHKTTVEGIPGESRCERRAPSSRQVHTDVRGDHAAHQAASRR WQEHQNV*GVSKADPGPSSPCNWNNEEVAKNA*GRGPVTRRPGWLQRA LPDTRSL*GIND**ENYQNSLQISTTRISGHSNKHKAMA*EKSQESR CRGRILSTQETNTISRESHAYAQTSSR**ERH*SIYGNSSAETGPGR NFTWQKKTATDS*GKGPGSRRPGWL*RALPDSWSHRGISGCW*NH*N TLRLSTVRPSGHPNKHKATTQEKYQESRCRGRTLSVQESNAISRQSH AHA*TISR*RERHHHICGNSSAETGPDRELN\RQOETATNS*GRGPG SGRPDWL*RALPDPWSY*RSSGCWQNY*NALRIFSTRISRHPNKHKK AAQDTFGEKGRTEGALSPEEAHTDIRGNHTHR*STRR*G*KHQRV*G N\CKTET\GPSSKCNW\EQEAPKN*GKGPTPRRPGWLERALPDTSMH</p>

				<p>*QAHSRENYQNSLQITTRPSGHTNKLQATVQEKSQESGRRRILRT QETNTISRQSHAHTQTSSKW*EKHLRIYGNSSAETGPDRELNWQOET ATNS*GKGPGSRRPGWL*RALPDTRSH*GIND*R*NCQSSLQIFTTR PRQKPSKLQATAQDIPGESGRERRAPSSWQAHTDIRRDYTHTHRANR RW*EHESIYGVSKADLRLSSKSNWQEEAAENS*GKV*SP*RPGRHLR ALPDTKSH*GIND**KNYQSILQSFTARPSGHPNKLQATAQEKSQES RH*RRIFSI*ETNAISRQSHAHTQTSSR*RERHQHVFGNSSAETGPA RKFTWQQ*TATNS*GKGPGSRRTDWLQRAF PDTMH**PHS**ENYQK NTLQISAIRPSGHPNKHKATAQEKQESRRRGRIFSIQETNTISRQS HAHA*SSSR*RERHQHICGDSSGETGPARKFTWQETATNS*RKGQG SRRSGWLQRALPDTRSH*GINDR*QNHR SILQISTTRPSQNPKNLQA TTQDILGESRCERRGPTSRQAHTDVREDHTDQDRSRRWKEHQSV*G ICKADAGPSKLNWDGEVAKNT*GRGPITRRPGRLQRALPDTRPH*G INN**QNYQNSLQISTTRINGHSNKHKEAAQNTFGEKGYSGRALSPE AAHTDHTHRQSTRR*G*RHQVQGNCKTETGPSSKCNW*QEAAKNS* GKSPTPRRLGWLERALPD TSMH*QAHSRENYQNSLQISTTRPSGY NNLQATVQEKSQESRRRGRIILSTQETNTISRQSHGHPKTSSK**EYQ ESIYGNSSAEIGPARKFTWQQKMATNS*GKGPGSRRPGWLQRALPD RH*QAHD**ENYQNSLQISTTRPSGHPNKHKATAQEKQESRRRGRI FSTQETNTISRQSHGHPKTSSK**EYQHICGNSSAETGPARKFTWQ QETATDS*GKG*GSRGPWLQRTLPDTRSH*GIND**QNHR SIL*IS TARVIQNLKKLQAKAQDTPGESGHERR\SLTSQQAHTDIRGDYANTH RANRR**EHQSV*GVSKADPGPSSKCNW*QEAAENS*GKGPCSRRPG *LQALLSTRSH*RVNDY*QKHQNSLQISPTRTNRHCHEHKEMPQDT SQERSKRGALSS*EAHANIRAKHTHTQRTS\KR**GHQSI PATCKEE TKPSRKGTQOEKAKST*GKGPTPGRPGRLHRL*NIRSHGITDCWQ SH*NTLRISP\TRSGRHHSKPKEASQDTCAEGTSKRRAFSSQVHTNI RGNHGCRQRTSR*/EIKGHQSI EGICKTDG\SSS\QCNWQQ\KTAK ST\QKGCPSHRRPSWLQRPSSRSH*RIND**QNH*NTLQIITRT\R RHRNKLKETAQDTCPESTRSEGGAVSSWQAHTNLRGDHAHRQAGR*G Q\KHESI*ATCKAEAGRRRCNWQOETAKST*GKGPTPGRSQGLPRAL SNTRPH*GTGWCC**LYKRSKANT*QWKTSKNIQKSSSGP*SRTRG RRGKHQRPKITKQKQHFPAPTALQEGRWQRWRHGNL/KQAALHAS TRGNCGGAAN\QOEALRGCSQGKRQIIRTRGHHEEKFEFCKKN*TC GRAEQQRHENQQRGTQITRLSP*K*GNIPALQ\TPK*D*GRTANN* GLCISRKNRNKQK*KEAP*RTSPQRWTIPEFPDDGSPGNPHPLETKV H*E\QKVLEVL/A*TE*EL\PA\QGGRGERRAECEGSHAESERERR SRKFRHLVPEIKDKKPACSKHFGEQICAESNAECQEVCRKSKEG*G QCVCQENKNQKS*GQ*RYENESLQNGRKSTEFPRKIREQEPARRVSR SSFSSDPDESEGIPLKRRRVSFSGHLRPELFDENLPPNTPLKRGEAP TKRKS LVMHTPPVLKKI I KEQPQPSGKQESGSEIHVEVKAQSLVISP PAPSPRKT PVASDQRRRSCKTAPASSSKSQTKVLKRGGEKSGNLP ESVYQPKST</p>
1936	A	139	784	<p>GLHHGCSLGMEEAAGRGDRSRRCRAPQHHRPPPLSCQQPRLG GRGGVRGKHGSL*KQAPPPRGRAETPGLANHTLPPRVPP/SEGQHP REGQGLHGGPGEKGP HRRKLKASVPCVSAERVNGPKGSS LQTAR PTGGHRKPTGAVCVCAAAHTSAARGPLRPHHTACPAHVCTRRCRRE HTPPSLCTRVP LSGPGGSSLLHVLSRA</p>
1937	A	1	1878	<p>MVSQAHCATLHAPTPAAATLTGRRSLGTAGRAPPLGTRDHAPAG RRVSGGEGSRKAAAAAALAAVAAAPGPVRRCSQSCFSSSGSSHYSAR TSPVRVRPRRSLSSRSAAGNRAEATESAMEKTLETVPLERKKREKEQ FRKLFIGGLSFETTEESLRNYEYQWGKLTDCVVMRDPASKRSRGFGF VTFSSMAEVDAAAMAARPHSIDGRVVEPKRAVAREESGKPGAHTVVK LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRSQGKKRGFGFVTF DDHDPVDKIVLQKYHTINGHNAEVRKALSROEMQEVQSSRSRGDGY GSGRGFGDGYNGYGGGPGGNGFGGSPGYGGGGRGGYGGGPGYGNQGG</p>

				GYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGSRNMG GPYGGAEASQVI INKAFLGSFSGVGSKMGMKGKQNGKSKKVEEAEP EEFVVEKVLDRRVVNGKVEYFLKWKGFADANTWEPEENLDCPELIE AFLNSQKAGKEKDGTGRKSLSDSESDDSKSKKKRDAADKPRGFARGL DPERIIGATDSSGELMFLMKWKDSDEADLVLAKEANMKCPQIVIAFY EERLTWHSCPEDEAQ
1938	A	345	558	LYMLIRMRLKEGRAKMVESIFR**FILE*SVLS/RIMKPGMYPVLNR WVKCGNSSSVSYPEEKVVGWLLKFI
1939	A	345	511	ARDATFVNGLDYLIITLPYCGWKDCCKKCPLRQFP*PFNCCFFLVVVFV RV*KHSLP
1940	A	827	2660	CCHCFQDLISINGEVVEQKRAVAREESGKPGAHVTVKCLFVGGIKKN TEEHLTDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKI VLQKYHTINGHNAEVRKALSRQEMQEVQSSRSRGDGYGSGRGFGDG YNGYGGGPGGNGFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNY GGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGIWK NTSITERKKSRLDLIQSKKGSRTKEAPQPPVASLCMHLGHWSRLMV SPGAQLTGKNSHGLSVSSVRKSNVGPRLCAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTDRPHFPLSWPTWISLALLLKTIDGALE RMPQQLPSLHPSQGTQSIHPDPSSTSSFLLPFPPTLKRAAFPCPPS IVNPAVWDTSTPSVAEHHTPIRITLKEPTQFLSQKQYPIPOAALVGL QPIISHLLASHLLRPTDSPFNTPILPVKKPNGTYRLVQDLRLINQAV LPRHAGLGRDLGSRRARGPASASVAARGRLSRGCGDRPVNVAAAGQ KMGKKQNGKSKKVEEAEPPEEFVVEKVLDRRVVNGKVEYFLKWKGFTE
1941	A	478	1150	SMPWQIGRSSVSAPPTITPTSTASWTIVSSTIWSHPVATTKVSTL HWTVVRRLVLIISKIIVISTSISSSIIVITTSVAPTLVAISRSTT ISSSSSITGATSKIATSRSSSSAGSRAEVLALFLQEQFSLQRO DESGSCSSAEISLISLGCGKSG*SD*VRDGERKRNSSVSSLLVA*AL KPQKKV*GTTTNNGESLQTVW**GILQAKDQEDLVL
1942	A	123	734	LFKSAIKNGLQHELHCRKWEKKQNG\KSKKVQ\EAEPVESGVEKVL DRRV\VNGKVE\YFLKWKGFADANTWEPE\ENL\DCPELD*SRFLN FSRKAGQRKRWVPKRKSLSD\SESDDSQIHRKRDAADQPKEDFARG \LDP*KK*LGHRPASGE\LMFL\MKWKDS\DEADLVLAKEANMKC P\QIVIAFYEEKPTW\HSCP\EDEAQ
1943	A	1092	1286	IDVCVCLALLLRLECSSVISAHCSLCS/SGSSDPPTSAS*VAGTTTA CHHAQLIFGFFFLKRWGF
1944	A	76	533	LPRPRSRALTALPPPPSFLQTPKSRALMAGLEVLFAASAAPAITCRQDA LVCFLHWEVVTGHCGLGVGDQPGPNDKKSELLPAGWNNNKDLYVLR YEYKDGSRKLLVKAITVESSMILNV\RTYKNSEELSRIVSGIITPI HEQWEKANVSSP
1945	A	109	1008	ALPPPPSFLHTPKSRALMAGLEVLFAASAAPAITCRQDALVCFL\HWE VVTHGYFGLGVGDQPG\PNDKKSELLPAGW\NNNKDLYVLRYEY*GW GPESFLVESHSPWESSIDSSMLLGIMGSQQSWQI*PLNLG*LFSMAE HLGDFHRTYKNSEELSRIGA\GIL\TPIHEQWEKANVSSPHREFPP ATAREVDPLRIPPHHPHTSRQPP\WCDPLGPFVVGEDLDPFGPRRV G\MNV\DPLRSLP\RAFNDP\SSGLPNRL\PPG\AVPQGAGFDPFG PIG\TSPPG\PNP\DHLPDPG\YDDMYL
1946	A	152	991	RKTKCVTRPAVVVFQSPLTSSSRASACEVAFPRGQPRKGPKRDNWIL GTRPSWVAVCSSPRLGLSR\EYKLVMLGAGGVGKSAMTMQFISHRFP EDHDPTIEDAYKIRIRIDDEPANL\DILDAGQAEFTAMR\QYMR GEGFIIC*LLSRIRRSF\HEVPESLNQLIY\RVRR\DDTPVVL/VW GNKSDLQTA*DRFTKGRKGLALAPENSSCPLFWRTSGCHTR\YYIDG CFPHAP\VREI\RRKEKEAV\LA\MEKKS*APKTSVWKEAKNHPFRK KKDSVT
1947	A	305	406	VTLNKQSNLLSSHFLSCNSWIKSPRSGKNQETS
1948	A	372	501	RPGAVAHSCNS\STLGGRGRWIT*GLEFETCLANMVKLCFLHLY
1949	A	441	812	ITTHLYISKPLLCTPMKTYNYLSIAKIKF*FSLRQGLALSPRLEC

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				TSTITAHCSLNLPGFKQSSHSQPSE*LGTTDTHHHIQLVFLIL/AET EFCHVAQGG/LNIS*VQLIHLPPQTSKVLGLQM
1950	A	2	370	RVAHASGASQLPDYSISPPSLPPRISFHPSPTLARVAMAEPSTAATQS HSISSSSFGAEPSPAGGGGSPGACPALGTKSCSSSCAGTDLGNSSDY KCHTDQLEESLLIGAVLKGLLVFGLHSI
1951	B	209	524	MLLSLAAFSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPF KAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLK LAVFMWLMITYVX*
1952	A	3	465	GRIPCRFRRLGAGGVKGLERASCRIILFPLPLSRPVSFLTLLPPFAR VAMAEPSEATQSHSISSSSFGAEPSPAGGGGSPGACPALGTKSCSSS CADSFVSSSSSQPVSLFSTSQVHDLIFWRDVKKTGFVFGTTLIMLLS LAAFRVISVGSY
1953	A	49	1129	RDLIEFSCRIILFPLPSLPPRISFHPSPTLARVAMAEPSTAATQSHSI SSSSSFGAEPSPAGGGG\SPGSLPRPWGPKSCSSS\CAVHDLIFWRDV KKTGFVFGTTLIMLLSLA\AFSVISV\VSYLILAL\LSVTISFR\IY KFVIQAVQKSEE\GHPFQKPNWNVDITLSSKSFSINNMAAILHINM FLKLIIRLFLVEDLVDSLKLAVFMWLMITYVGAVFNGITLLILAEFPI FSVPVIL*RYKTQID\HYVGIARDQTKSIVEKIPSKTPLGIKAKKG RIKYMETRATSYLKHHLISYNVVTCTMKENTQCQLEPAFAQFFLIW CFLPSFPFNPQSSSTKIDGLIKDLFLDLRRRKNQIS
1954	A	46	519	SQTPMGHFTTED\KATI\TSLWGK\VNVE\DAGGET\LGRL\LVVYP MGPQRFL*PALGNLSSASAIHGQPPKSRAGHQEGC*RSLG\DAIKAP GIDLQRAFFAQ*SELALVDKLA MWDSL RNF KASWGKFC LVDPFLAI PFSAKEFHPLRCQVFLGQKDG
1955	A	1	747	MNSLLGLIIRRTFIEHQPYTTNDVLENSANESARVHLVLANENS DPC AGPPNGAQATRYLNPGLTRQLQRRRSPALARRAVLTAPRTLVSLLPSP RPSLGRAGTLAFVPVPHGAAPTDPGECARGPLSEASPSAPQLPCRFSH LLRASPSQPGLLFSSPELTASPASLALRPVLSGPPFPVWIPSPNPS LPRGGRSVGKRFRDGACQVSSDLENIDTGVNSKVKSHVTIRRTVLEE IGNRVTTTAAQVAK
1956	A	1	813	MKEENLCQAFSDALLCKIEDIDNEDWENPQLCSDYVKDIYQYLRQLE VG\LQSNPHPLDGRDINGRM/RAILVDWLQVHVKFRLQETLYMC VGIMDRFLQLSLPAEDREALGTSSPQHSGALGDVGYKSGFILSPHPC MSKIEPEDEKLSFLFIGPFLKNPSPRANGDPMFLCLNEDEAQLEET KWTGCQKQLCDPLSEEVKTGEKLVQTKGERTSRIREVQFLAQNHTR RWQSWDLGTSSLTPEPVFSLEINVREQRDEDNIQVLRG
1957	A	1	1390	EATASKIPSAAGSESSPNGASYASVPPFSVRVPPWAGLALLPSPSLM ALLRRPTVSSDLENIDTGVNSKVKSHVTIRRTVLEEIG\NRVTTRAA QVAKESSTGPKFQVQPTKTINVNKQL\KPTASCQTQYQMGKVLWPKG PSPTP\EDVS\MKGRESLPKLFSDALL\CKIEDIDNEDWENP\RLCS DYVKDIYQYLRQLEVLQSNPHPLDGRDINGRMR\AILV\DWLVQVH SKFRLQETLY\MCV\GIMGSDF*QVQPVSRKKLQLVGITALLLAPK YEKMFSPIEDF\VYITDNAYPS\SQIREMETLILKELKFELGRPLP LHFLRRAS*AGEVDVEQHTLAKY\LMELTLIDYDMVHYHPP*G*PAA AS\CLSQKVLDKGKME*SQYYHKDTQENEVLEVHASTMAQECGAK *MENLNLNSIGHQRIKYAKQTP*KISMIPQLNSKAVKDL\ASP\LI GRS
1958	A	3	269	VGGGTGFIGTALTQLLNARGHEVTLVSRKPGPGRITWDELAASGLPS CDAAVNLAGENILNPLRRSARALKLIPTRAQGGQCPTDENL
1959	A	3	253	CRTL VHPPQEAGGRAELGGARRGRGTVCFLRQDELAASGLPSCDAV NLAGENILNPLRRSARALKLIPTRAQGGQRPDENL
1960	A	283	1208	TIFHFPIQVAGTGFIG/RQP*PSCLNARGHGITFGFPESPGPAGFTW DELAASGLPSL\DAAVNL\AGENILNPLRRWNETFPKRGSRAAA*ET TQLLG*SHSPKAPQPPK\PGVLVTGVSFTTSPV*LRSID*RQPREGT LTFFSNLLTKW/EKLAAKAFLGDSTRQVGWCRSRLCLGPLGAGSMG HMLLPF\SLGLGGPIGSGHQFFPWIHIGDLA GILTHALEANHVHGV

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				NGVAPSSATNAEFAQTLLGAALGRRAL/LPLPSAVVQAVFGRQRAIML LEGQKVI PRRTLATGYQYSFPELGAALKEIVA
1961	A	698	1240	GLKDSHTAHFCYRPKVSMGRVRKGKQKPGGAVGSFKAECTPVPSLFP ALGVVLGRGGGAMGHMLLPFRLGLGGPIGSG/HQFFPWKHIVALARN LDPGP*SKPRARGPEW/MLAPSSATNAEFAQTLLGAALGPPSL/LPLP SAFGASCLWGDSVPSCSLSGGPER*SPRAEHLATWLPSPISQS
1962	A	494	1068	EFIFPSPLVLPFIRIMKMGLLCEVSAAPVAVLFLTDLVGLGPCLKAK NVSFFFFFVFLVMCNLSLITVEQISLTQITREGKGASARNTNLFLF CFGEQKWSKGKVRDKLNNLVLFDKATYDKLCKEVPNYKLITPAVVSE RLKIRGSLARAALQELLSKGLIKLVSKHRAQVIYTRNTKGGDAPAA EDA
1963	A	1	573	KYSQRTVVFGPVSEQRFLFVPTILTRLRCLLLILPELRNAALRTDQE GRKDAGKVGPRKGQRPQ*TKSGGQKQKEGRNKTSLKETREVVQKAKV RDKLNN/LVLFDKA/TYG*TLVKGSSPTY*TLTTPAVGLLRRL* EAPWGQGPALSR/GFL*LKGFYSKLGFFKRHRSSKLFYTRNYQGWM LPAAG
1964	A	33	515	SAWNSWDKSSPEEALKGLVDKLOALTGNEGRVSVENIKQLLQCLVP GSTTLHSAEILAEIARILRPGGCLFLKEPVETAVDNNNSKVKTASKLC SALTLSGLVEEKELQREPLTPEEVQSVREHLGHESDNLFLVQITGKK PNFEVGSSMQLKLSITKKS
1965	A	1	503	GHESDNLFLVQITGKKPNFEVGSSRQLKLSITKSSPSVKPAVDPA AKLWTL SANDMEDDSMDLIDSDELLDPEDLKPPDPAS/LRA/ASC GKKRKACKNCTCGLAEEL/EKEKSREQMSSQPKSA/CGNCYRGAMPS GCASCPYLGMPAFKPGKVLSDSNLHDA
1966	A	29	1270	FPFWPAVFQVCQYCTARMADFGISAGQFVAVVWDKSSPV/EALKGL/ VDKLQAF/TPGNEGRVSV/ENIKAAVAIPLTKNPSFGHYFVQ/CLVP GKAPLWHA*DFWAGNPPGFLRPGWMFFFLKEPVETAVR*Q*AKWKT ASKL/CSAL/TLGLV/EKLELQREPLTPEEVQSVREHLGHESDNL LFVQITGKKPNFEVGSSRQLKLSITKSSPSVKPAVDPAAL/WTL SANDMEDDSMCIFCGCSLTHRWPLEHVQVE/IMMDQPKRRTRVDT/ FFTPTPKFPPSRSPASHFSFSIKQKT/TRPVSLIALNTL/QDLIDSD ELLDPEDLKPPDPSSLRAASCGEKGRKACKNCTCGLAEELKEKSR EQMSSQPKSACGNCYLGDAPFCASCOPYLGMPAFKPG/EKVLSDSNL HDA
1967	A	3	498	LANRAIMSHKQIYYSDDKYDDEFEYRLVLAREQLATGRELWPLRAQ ISNRN*GDRIGACVRDMSCCPKDIAKLVRTH/LMSESEWRNLGVQ/ QRSQGWVH/YMIHEP/EPHILLF/RRPLP/RKPKMKLGKLTQPS FYTAGPYLPNIFLDNIIYVGLLVFFTFDI
1968	A	1	690	RRKAFPKRLPKMAEVQVLVL/DGQG/HLLG/RLA/AIVAK/QVLLGR KGGCSYACEGIHI/SGNFLQNQVCSTLAFPLQA/RMNTNP/SQGP/Y HFG/APSRI/WR/VRGM/LPHKTKAEARPLD/RLKVFDDGIPPPY D/KKKR/MVVP/AALK/VVRFEAYTESFAYLGR/LAPEVGNNAIRPV TAPPGGERGKRKAKIH/YRKKK*L/MRL/RKQAREETWRKKIDKYTE VLKTHGLLV
1969	A	2064	2561	KRFWSFALFYLLILKLL/CIDSIVRIGTILYSTVLFFIFLKFV*LV LITFIQIFAIFGSETF*QGV*FLLIPNFFSRVLLILSEGKVI*VC QLIVLLGLNFHIVFTVYGEVVGIIYYSILNK/AVIHFFIKV/YFHVKF LFLYVLLLSYITQFLF*KSSFVEVLVKN
1970	B	49	754	MAGAAPRLPWSRPHGSCGWPMQPLQGPGRRAVAAAEVATPVFMPV GTQATMKASRPNSWTLWVAASAWEYLPSSGSKAGGTAAPFDGAVGSV RGDGGGLRFRSPYDGNETLLSPENPCRSRMRWAPGVVTGALLQVNPL AGPVHAAHQRPDKQNLFAIIQVGWQISGPPALKRFGSAWHSRAFLT HCCTVTTRPRCTTSRPPQHRLELMSAVRTSIVEKRFDPSCGTSWAP X*
1971	A	1	1498	RQSRWREQLPRLSWRLVPRIMRLVAECGRSRARAGELWLPHTVATP VFMPVGTQATMKGITF/EFLDALGCRICLG/NTYHLGLRPGPEL/IQ

				KANGLPRLS*IWPSLILLNGTAAVFQMVSLVSLSEVTEEGVRFRSPY DGNETLLSPEKSVQIQNALGSD\IIMQLDDVVSSTVTGPRVEEAMR SIRWLDRCIAAHQRPDKQNLFAIIQGGLDADLRATCLEEMTKRDVPG FAIGGLSGGESKSQFWRMVALSTSRLPKDKPRYLMGVYVVDREARA LPVGSGFLGTPYPAWGGGIWKGRTQV*SEETRKTWLSLGGHSEGIWP SLGQCEGWEGPWEAPEVLCPLPSWLQPQL\ATDLVVCVALGCDMFDC VFPTRTARFGSALVPTGA\LQLRKKVFEDFGPIRPGVHLPPRPKST SRAFLHATAAQ*QHGPRTTTLTVHN\IAYQLQLMSAVRTSIVEKRFP DFVRDFMGAMYGDPTLCPTWATDALASVGITLG
1972	A	786	1502	PPPTKKEMFVPYSPEQRIETSIPPPFKGTGRP/PGQRTWERPPFSL EGKAGALPPLLSPTTKGEDPSETLAQSGSQEGDCINRWQHLH*SAF RPSSAEPFTRKRLEGGPAPLRYPGAGNEPGRDAEGRP*GALAGRPRW PPSHGRPPPAPCHPASRGGTARKTP/GRSTKPPRFPPLPLGDATSGK AIPANGRKGGAMSPHRGAGPASPSRFFSHIKQGRAIPHVSSRLHFSP SSSGSR
1973	A	8	234	SAQMAVTTADPRVRPRVRTQQLCSLASLIQTLLVHLT\PEEKSAVTAL WGKVNVD\VGKALGRLLVVLWPDPKRSFQSPLGESVPTP*MKVGG KALGRLLVVLWPDPKRSF
1974	A	1	169	NLYISNLPMSDEQELENMLKPFQVISTR\ILRDSSGTSRGVGFAR MESTEKCEG
1975	A	2	219	IRHKEESPRGNPKVSATLHGMLPSSFMGKVWKQMQYPQYATYYYYPQ YLQAKQSLVPAHPMAPPSPRHLQF
1976	A	17	796	HSTAKLY*HSTFAKRSHRNPOHPYV\PI*ISKSLTSSI\NSSTSSNSG WDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTNAILHKTNNKC KGYGFVDFDSPAQAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLP LSMDKQELENMLKPFQVISTRILRDASGTSRGVGFARTESTEKCEA V\MVQSPSWTQPPYILQHGPVLTSPMEHTMSLQPASMISPLAQOM SHLSLSTGTYPATSAMQGAYLPQY
1977	A	3	1421	CLRRLEHFGTRPPPTPLPSSPERERQESPRGNPKVSATLHGRLPS SFMGKVWKQMQYPQYATYYYYPQYLQAKQTLVPAHPMAPPSPSTTSND NHR\SISSNSRWDQLSRTNLYIRGL\PPHTTDQDLV\KLCQPYG\KI V\STKGNFGIRTTNNCKGYGFLFDF*QPMQQLKKA\ALKASGGSS SKWAKQQGD\PTNLYI\SNLALSMD\EQELENMLKPF\QGVISTR\ ILR\DSSGTSRGV\GFARMESTEKCEAVIGHFNGK\FIK\TPPGVSC PHRNL/CVLSFAGWEGQEKGDRTPNKYIPNG\RPWA*EEGRGETLL GLTLT/YTDPTTAAIQNGFYSPYSIATNRMITQTSITPYLAST\XH AFQVQSPSW\MQP\QPYILHDPGAVLTSPMEHTMSLQPASMI\SPLA QQMSHLSLCSTGTYPATSAMQGAYLPQYAHMQTTAVPVEEASGQQQ VAVETFNDHSPYTFQPNK
1978	A	2	1440	NSGPSSFMGKVWKQMQYPQYATYYYYPQYLQA/KVWKAFGNTK*KGRV KNRKMVLVGWQTL*TLFLVGQKNQSLVPAHPMAPPSPSTSSNNNSS SSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILD KTTNCKKGYGFVDFDSPAQAQKAVSALKASGVQAQMAKQQEQDPTNL YISNLPMSDEQELENMLKPFQVISTRILRDSSGTSRGVGFARMES TEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCKFADGGQKKRQNPKNY IPNGRPWHREGEVRLAGMTLTYPDTTAAIQNGFYSPYSIATNRMIT QTSITPYIASPVSAQVAKETRENTYRGSIAKVQ\SPSWMQP\QPIY FYQHPGAVLTP\SMKHTMSL\QPASMIQPFWPQMSPSVH*GQHPPEP YHALQPSLCKGALLGPQYCTYCRLTAVPC*GRQSGQTGRLAVRGRL NDPFSIYRFNPKN
1979	A	104	340	TGQSYKKRKFVKWLKQINRYLTSFLF/VFKEIRSHSVA*TLHSGAIM AHCSLKFLGLSNPPASASQVAGTSGVQYHTSLI
1980	A	118	528	TFFSVLISYYPLSSWAFELYMLLDNVYKSSSMNPETKAVKTEPE KKSQSTKLSVVEHKKSQEGKPKHETEPKSLPKQASDTGSNDAHNKA VSRSAEQPSEKSTBPKTQDMISAGGESVAGITAISGKPGD
1981	A	1	864	MFPGDKKRASRRAAANSPOGARGQGEAHRPGRVHAQAGPRAVAGQA

				RAQGAQARPKRPKLEGGGRMGVTSWGSQQGLGRNGGKPGVHTGRPW LATGTHATWGSCSTRAWQVMQVTAAPPAGAEGSAHLAPPWDVRSSVP ARSRPSECEPGASNATPRALAGSPPCGSEFAGCCHGIRQWWYKTVNR SGCWAGPEGSVLEGSVFALPFWAWDEALSGVWRGRGADRVDLLADL QRAIVGRTSPTQRRGSCNVRQGENPNIKGQKQLRSETKTLERAVEGW RKESEK
1982	A	3	4258	SDKTSRSEAQALVHTFFVVEWSDALFVGIDENILAVQRIVRKAVETD LQTSRESIGVAAGASPKLHQREKKRRRGEAVGCQRLQLDIGDKQPS TDSKAKRALTGTFLSGASGIAGTSLDAAMAPTEFASWWRPKALASAP APPTCAPRPTDLAAIPDFQSGAMENWGLTTYRESALLFDAEKSSAS SKLDITMTVAHELAHQWFGNLVTMEWWNDLWLNNEGFAKFMFVSVSV THPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDV SYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMA SICPTDGVKGMDGFCRSRQHSSSSSSHWHQEGVDVKTMMNTWTLOKGF PLITITVGRNVHMKQEHYMKGSDGAPDTGYLWHVPLTFITSKSDMV HRFLKTKTDVLILPEEVEWIKFNVGMNGYIVHYEDDGWDSLTLGLL KGHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIM PVFQGLNELIPMYKLMEKRDMEVETQFKAFLIRLLRLDLIDKQTTWD EGSVSEMLRSQLLLLACVHNYQPCVQRAEGYFRKWKESNGNLSLPV DVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALCRTONKE KLQWLDESFGDKIKTQEFQILTLIGRNPVGYPPLAWQFLRKNWNK LVQKFELGSSSIAHVMGTTNQFSTRTRLEEEIKMKLNIKILIDDIS GVRPWPWGCKRAPLESYR IAAVKTEPEKKSQSTKPKSLPKQASDTGSN DAHNKKAVERSASAEQQPSEKSTEPKTKPQDMISAGGESVAGITAISGK PGDKKKEKSLTPAVPVESKPKPSGKSGMDAALDDLIDTLGGPEET EEENTTYTGPEVSDPMSSTYIEELGKREVTIPPKYRELLAKPIGPDD AIDALSSDFTCGSPTAAGKKTEKEESTEVLKAQSAGTVRSAAPPQEK KRKVEKDTMSDQALEALSASLGTRQAEPELDLRSIKEVDEAKAKEEK LEKCGEDDETIPSEYRLKPATDKDGKPLLPPEEEKPKPRSESELIDE LSEDFDRSECKEKPSPTEKTEESKAAAPAPVSEAVSRTSMCSIQSA PPEPATLKGTVPDDAVEALADSLGKKEADPEDGKPVMDKVKEKAKEE DLEKLGEKEETIPPDYRLEEGKEKDGPPLLPKESKEQLPPMSDFLL DALSEDGSGPQNASSLKFEDAKLAAAISEVLSQTPASTTQAGAPPRD TSQSDKDLDDALDKLSDSLGQRQPD DENKPMEDKVKEKAKAEHRDK LGERDDTIPPEYRHLLDDNGQDKPVKPTTKKSEDSKKPADDQDPIDA LSGDLSDCPSTTETSQNTAKDKCKKAASSSKAPKNGGKAKDSAKTTE ETSKPKDD
1983	A	44	1360	VWDCPGLRWASFYLRLSWRAHRPQCGTISFVTVNAEEQEKQFVSSRT KQKAKEEKLEKCGEDDETIPSEYRLKPATDKDGKPLLPPEEEKPKPR SESELIDELSEDIDLSECKEKPSPTEKTEESKAAAPAPVSEAVSRT SMCSIQSAPPEPAT\LKGTVP\DDAVEALADSLGKKEADPEDGKPV DKVKEKAKEEDREKLGEKEETIPPDYRLEEVKDKDGKPLLPKESKEQ LPPMSDFLLDALSEDGSGPQNASSLKFEDAKLAAAISEVVSQTPAS TTQAGAPPRDTSSDKDLDDALDKLSDSLGQRQPD DENKPMEDKVKE KAKAEHRDKLGERDDTIPPEYRHLLDDNGQDKPVKPTTKKSEDSKKP ADDQDPIDALSGDLSDCPSTTETSQNTAKDKCKKAASSSKAPKNGGK AKDSAKTTEETSKPKDD
1984	A	159	2467	EKKGSYEEKKAASLGSSQSSRTYAGGTASVTKVSFSGATSKSYSMNP TETKAIPVSQMEGPHLPNKKKHKKQAVKTEPEKKSQSTKLSV\VHE KKSQEGKPKHETEPKSLPKQASDTG\SNDAHNKKAVERSAS\EQQP\S EKSTEPKTKPQDMISAGGESVAGITAISGKPGDKKKEKSLTPAVPV ESKPKPSGK\SGMDAGL\D\DLIDTLGGPEETEEENTTYTGPEVSD PMSSTYIEELGKREVTIPPKYRELLAKKEGITGPPADSSKPIGPDDA IDALSSDFTCGSPTAAGKKTEKEESTEVLKAQS\AGTVRSAAPPQEK KRKVEKDTMSDQALEALSASLGTRQAEPELDLRSIKEVDEAKAKEEK LEKCGEDDETIPSE\YRLKPATDKDGKPLLP\PEEEKPKPRSESELI

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[illegible]

				FDAGELITQRELVSQVSNLME*AATFGLIILDDVSLTHLTFLKELT /EQVAPQEAESARFVVEKAAIISAEGDSKAAE\LIANSLATAGDGQS ELCKLEAAEDIAQQLSCSRNITCLPAGQSVLLQLP
1999	A	3	417	RLITRRELVSQRQVSDDLTERAA\TLGLIL\DDVSLT\HLDGKGVSQ KRVEAKQVAQQAERARFVVEKAEQQKAAIISAEGDSKAAELIANS LATAGDGLIELRKLEAAEDIAQQLSRSRNITYLPAGQSVLLQLPQ
2000	A	546	882	CHVPPTLGTGQTHQDPPFPFPHSPGAPAPCPPPA/LLGPPRPFPPSP PVPGPGENRKPFTSAP*A*VFPRTPLGALSRG*GSPVVGRGATPSP PTPSPACGPLKCWWHLIKN
2001	A	43	311	TMRWNSLVQTAQQVAEDKFVFDLPDYESINHVVVFM LGTIPFPEGM GGSVYFSYPDSNGMPVWQLLGFVTNGKPSAIFKISGLKSGNY
2002	A	178	817	SPASGHCRNLNGAAMVFGCLVAGRLVQTA*QQVAEDKFVFDLPDYE SINHVVVFM LGNNP\FPEGMGGSVYF\SYPDNSNGMPVWKLGL\SVTN GKPSAIFKISGLKSGEGSQHPFGA/NEYCPNLHLLRLGISGELLDS MAQQTPVR*CCWYPQFDSFTQFTQKMLDNFYFNC\SSFAVSQAQMT S/SI*KCSFRPNVVLKWYEA FSVSNIAFYN
2003	A	283	840	TLPAGFTDVISIHKTGENFCLICGINGRFAVHCITLEEAKYKLCCKVR KIWFHDAHTIHYLDSFVKVNDTV*TGKITDFIKFDTGNLGRIGVITN RKKHRGSFDDVHVKDANGNRFAFWLSNIFVTGKCNKPWISLPRGKI RLTIAFHSDKWFCSDISVQNLCKRFSQDGTGIKNSAARRCSNLQV
2004	A	1	966	GRPAPEDGGPLSLPNAAMARGPKHLKRVAAPKHWMLDKLTGVFAPR PSTGPHKL\RECLPFIIF\LRNRLK\YALTGD\EVKKI\CMQR\FIK I\DGQVRN*YNLPLLGFMDVI\SI\EKTGENFPF*SN*HPRGPLLL* HRITP\EEAKYK/VCAKMRKIFCGPTKGIP\HLVTS*CPAPHPAYPR NPLIQGEMNTHSRILETGQD/ITDFHSKFDHLVTLC\MVT\GGA\N LGRNWVLITQRRGTPGSFDRWFT*KDANGNKLATSDFSNIWFLLG KGNKPW\ISL\PRGKGI PHHLLLEERDKRLAAQSSWVKWGPWVTWS DLLVP
2005	A	1	383	RIRKLCNLICVGESGDRLTRAAKVLEQLTGQTPVFSK\VREYELRKN NFSDTGNFGFGIQEHIDLGIKYDPSIGIYGLDFYVVLGRPGFSIADK KRRTGCIGAKHRISKEEAMRWFQKQYDGIILPGK
2006	A	3	226	GGRFKEPLGGPKLTRAGKEKVFSLWGADLKPGPGPCFNNAGRGKFT WEFLERTLILGGGHIGPTSLQKLKALG
2007	A	176	384	CVSLVHLLLTLSWLGDWFLGQVLGRPGFSIADKKRRTGCIGAKHR ISKEEAMRWFQKQYDGIILPGK
2008	A	2	669	IMAQDQGEKENPHAGNFAFRKLVNLIC\VGESGD\RPTRA\AQVLEP AQQKTPCVFPA*HTPVKSLWASRR\NEKIAFPPTATSEGA KARN LCRRGLKRFSEYGVQDNTTFSGYWETPGFGI\QEHIDLGIKYDPSIG IYGPSTSYV/LGVRPGFQHPQTKKPQGQCIG\AKHRI\SKEEA\M RWF\QKQYDGIILPGQINSPFLSKSNKKFSVNKKNNKKITL
2009	A	688	884	CSCVWNLSFHGNAFHLKTPYSRIKKAKH/WMAHVYSPITLGGRGWI T*SQEFETSLSNIIKPCLY
2010	A	442	780	IEFVIKIFFPFSHCLICLAIDLQLQ*YMGVPR\MQLKTCYVRGKYR GVVLEEQNILWK*IHIPLQVREDGRPCPLRLKLGKGGGGGEPLNQH GDPVQGNPPYFLFCHMRNP
2011	A	136	219	DPAREGHPVCCAGQRPCVDGHGQEKGFLLKAALELEVELGASNPSW*DTE VKPQSALPQASALTIVWSYQQGVLSATILYEILLGKATLYAVLVSAL VLMAMVKRKDF
2012	A	3	762	TLRGAVLRGAAGRLGGGLLVLAGRAMGLSAVGRTRAESGTAERAAP VFVLGLQAVSTDTQMFGPGTRLTVLEDLKNVFPPEVAVFEPSEAEIS HTQKATLVCLATGF\FPDHVELSWVNGKEVHSGVSTDPQPLKEQPA LNDSTRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAK PVTQIVSAEAWGRADFGFTS\VKSYQQGVLSATILYEILLGKATLYA VLVSALVLMAMVKRKDSRG
2013	A	1	1010	RYSFFKAVMGIRLLCRVAFCLAVGLVDVKVTQSSRYLVKRTGEKVF LECVQDMDHENMFWYQRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSV

				SREKKERFSLILESASTNQTSMYLCASSLFNSGYQETQYFG\PGTRL LVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATG\IFPDHVEL SWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATP\WQN PRNHFRQCQVQFYGLSGNDEWTQDRAKPVTOIVSAEAWGRADCGFTSV \SYQQGVLS\ATILYEILARGRPTLYCLCW*APLVLMA\MVKEKGFL KAALEVELGAF
2014	A	344	463	ITSKRWHLKFSTQIKKRVIIAPHLLTSLAKLIFCFRT
2015	A	1075	2102	QQKPGQPLFLGSI SPKKSFKTRKQKSSSKAEYNLTACKCLCKRKYS SQIMLKRMHI/RPQDNSFWNKL*KRKR**YCQQFRNKS*S*TSRF CRIFTPFHYPFSTE/CN*REQIIQMKKRTHRQHRKIKNKTLK/CPK STSPSAAGGQKTRKPKLSAGFDFKQLYCKLCKRQFTSKQNLTKHIE LHTDGNNIYVKFYKCPCTYETRRKRDRVIRHITVVHKKSSRYLGKIT ASLEIRAIKKPIDFVLNKVAKRGPSRDEAKHSDSKHDGTSNPSKKY EVADVGIEVKVTKNFSLHRCNCKGKAFKKTYLEHHKTHKANASNS PEGNKTQGRSTRSKALV
2016	A	1	624	GPAVPRWMGQRP GSGGWTA VAKPGELGLPHPLSTGGLPVASEDGLR APESQSVTPKPLETEPSRETAWSIGLQVTVPFMFAGLGLSWAGMLLD YFQANTGQIDDPQEQHRVISSNLALIQVQATVVGLLAAVAALLGVV SREEVDVAKVELLCASSVLTAFLAALFALGVL MCVIGARKLGVPND NIATPIAARPGDLITLSILA
2017	A	216	1520	EPKRGPPSHWRTEPSRETAWSIGLQVTVPFMFAGLGLSWAGMLLDYF QHWPFVFEVKDLLTLVPPPLVG\LKGNLEMTLASRLSTAANTGQIDDP QEQHRVISSNLGLIQV\QATVVGLLAAVAALLGVVSREEVDVAKVE LLCASSVLTAFLAALFALGVL MCVIGARKLGVPNDNIATPIAASLG DLITLSILALVSSFFYRHKDSRYLTPVLCLFAV\ LTPVWVLIQKQS PPIVKILKFGWFPPIILAMVISSFGGLILSKTVSKQYKGMATFPI CGVGGNLVAIQTS\RISTYLHMWSAPGVLP\SR*RNSGPTRVLLFVR QKLNSMSCSRLLLLLLGGSGQHILIFFYIYLGGGVSSQS*TSQTFVGAL TCWAGPDPG*QILLYL/VKK*MVRLTWHQAL\DPDNHCIPYLTGLGD LLGTGPPGDSAFSLTGY
2018	A	1	408	SNPRVRGGGTHRSQQAFAFANMCRGGRMFAPT/KTWRRWHRRVNTTQK RYAICSALAASALPALVMSKGHRIEEVPELPLVVEDKVEGYKKTKEA VLLKKLKAWN DIKKVYASQRM RAGK GK/RCGR*ERKEGCCWC
2019	A	28	1437	BERGCFSLPLACARPL\ISVY\SEKGESSGKNVTLP\AVFKAPI\R PDIVELCSNPNLRLKNNRQPYAVSEL\AGHQTK\AE\SWGTGRAGGSK FPEVRGGGTHRS\GQGAFG\NMC\RGG\RMF\APTCTLGRRWN\RRV NTPP/QKRYAICS\ALA\ASALTSNWVMSK\GHRIEEVPE\LPV\V EDKVEG\YKK\TKEAV\LLLKKL\KAWN DIKK\VYASQR\LRA\SKG KMRNRRIIPGAGGPCIIYNEDNGI\IKAFRNIPGNYSAM*AKLNIL K\LAPG\GHGG\RFCI\WTEKCFSGKL\DELYGTWR*S/RASPQRSN YHSFPLHK\MINTD\LSRILEKPQRSQRAPPGHAKKIHR\RVLKKN PTEKTLR\IMLKLKPHMQKTHAAGTTHSSPRPRNHK\LR\VDKGLL HQRHLQAKSDEKAAVAGKKPAVG\KKGKKAP\VGKK\QKKPLVGKK \AAATK\KPAPEKKPAEKKP\TTEKKPAA
2020	A	1	2196	MSRKGPRAEVCADCSAPDPGWASISRGVLVCECCSVHRSLSGRHISI VHGLRHSAPPTLLQM VHTLASNGANSIWEHSLDPAQVQSGRRKAN PQDKVHPKSEFIRAKYQMLAFVHKLPCRDDDGVTAKDLSKQLHSSV RTGNLETCLRLSLGAQANFFHPEKGTPLHVAAGQTLQAEALLV YGADPGSPDVNGRTPIDYARQAGHHELAERLVEQCQYELTDRLAFYLC GRKPDHKNGHYIIPQADSLDLSELAKAAKKLQALSNNRLEELAMD VYDEVDRRENDVWLATQNHSTLVTERSAPVFLPVNPEYSATRNOGR QKLARFNAREFATLIIDILSEAKRRQGGKSLSSPTDNLELSLRSQSD LDDQHDYDSVASDEDTQEP LSTGATRSNRARSMDSSDLSDGAVTL QEYLELKALATSEAKVQQLMKVNSSLDELRLRLQREIHKLQENLQ LRQPPGPVPTPPLPSEAEHTPMAPGGSTHRRDRQAFSMYEPGSALK PFGGPPGDELTTTLQPFHSTELEDDAIYSVHVFPAGLYRSKLSRHGSG

				ADSDYENTQSGDPLLGLEGKRFLELGKEEDFHPELESLDGDLDPGLP STEDVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIHLAVTEMAS LFPPKRPALPEVRSSRLRLNASAYRLQSECRKTVPPPEPGAPVDFQLLT QQVIQCAVDIAKAAKQLVTITTTREKKQ
2021	A	1	207	SMDSSDLSDGAVTLQEYLELKKALATSEAKVQQLMKVNSSLDELRR LQREELEDDAIYSVHVPAGLYR
2022	A	1	1062	MTWQRGNRSFVFRGQDTSADVMEIDHRRVVYTETLALAGQDRELL AAAQPTTEEQVLSRLTAPVVTQLDTKNISFERNKTGILGWRSEKTEM VNGYEAKTGRVDKNYPLVTGHTAPVLDIDWCPHNDNVIASASDDTTI MGAASSAEQRPEPGPKERRESNHPAAPLREPEGQQAQWQRLSPAHTL FGTASLYRGVSGEGAPERLSQLEGKRFLELGKEEDFHPELESLDGD LDPGLPSTEDVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA VTEMASLFPPKRPALPEVRSSRLRLNASAYRLQSECRKTVPPPEPGAPV DFQLLTQQVIQCAVDIGKELGNNGF
2023	A	171	476	LPRFQTLRNTETEDHSCCCSGRRRFAAAVASRSQ*GNPASLAGSSTT GARSCAPVARTQRCPRCAACGCWRWRTRWICSAGWFAHSQFSARID WLQFLEW
2024	A	1	781	GILDYLDNISPPQIRKLFYVLSTLAFSKQNEASSHIQQLHSSVTRGN LETCLRLLSLGAQANFFHPEKGTTPHVAAGQTLQAEELLVVAAKN PEKREYTTENGSPAETPTCSAGKRGTPRTKMSDISSEDLREIQAVL KDADLATISAKRVREQVEGKLNCSSLSRKKEFDKIVMEVINEQDEE DEDDDEGKDPDADPDESEPESEEDPSSSEEEAAKKKKQTPKKRPQP TKHKAPKKKRTLNADDSGTADERL
2025	B	1	1602	MGYRARIRNHVWLATQNHSTLVTERSAPVFLPVNPEYSATRNQGRQK LGRFNAREFGNLIIDILSESKRRQQARAEQPHSAAAADGVTFSPVPT PHTFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEVEYTKVFALDVAA RHRQPTRRKAPAVLQGCRAIATRETPGWFHVAEVRASRRGRSPTPQC ADPGWASISRGVLVCDECCSVHRSLSGRHISIVKHLRHSANPPPTLLQS GFPGPSRRAAPRAARGPTPRTEEAWAAMALTFLLVLLTLATLCTRL HRNFRGESIYWGPTADSQDTVAGSPDHGLLAFAYHRLVRFLLWVLC PGWAFFLVNSSRGGVFNPILHPCPRHGQARFAGVGRAEDVTFLYHPC AHPWLKLQALALAYACMANPSLTPDFSLTQDRVDIEQLDPRGRTPH LATTGLHLECARVLLAHGETWARENRSGWTVLQEAIVSTQDLELVQLV LRYRQYQYVVKRLASIPVLEKLRKQSYLPGRPLARLRSSVNSSGA VGMIKSESMGRWVFGP*
2026	A	2	692	ENRSGFQSRRIYSISKQKKLTFFDVKDNT*SWNAVASREECYLG IT*SRTLSGRS*TKDRLRRT*SMPCYSDSM/ISMQELEFRHLNTIQK MRCELIRLQHQTETLQLEYNKRRELRKRVMEVROQPKGLKSKE LPNKKSSFQGYLQNSQTRQYKALRNHLLLETPKSEHKAVLKRLEEQ TRKLAILEAQYDHSINEMLSQAVSLLFLGQNKFSAPFLPPPE
2027	A	1	2933	MDDIPQEARQYRHNAQAYAYSIOGDGAEDDDERIVRFHTRVINHKRK NSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSVHINPYLIPFFIGLQNRFTQFRLSET KEITNPHYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRM PDFRRRFLQHIFVLRERPETVLIDLIQRTKDAVRELDNLQYRKMKKL LFQEAHNGPAVEAQEEEEEGWNLDRAVDYVKERRTVTKPNPSFMRQ LEEYQGILLARPKRTAYIYGSVYRRCGYADHKVEIKHPGWASISRGV LVCDECCSVHRSLSGRHISIVKHLRHSANPPPTLLQM/VHTLASNGAN SIWEHSLLDPAQVQSGPALKQTPKDKV/HPFKLEFHSAGAKLPDCWD FVAQVFLCRDD*WELTAKDL/SKAN*HSSVR/TGKPKWTCRLRLS/L GA/QANFFHPEKGT/TPLHVAAGQTLQAE/LVVGADPGSPDVN GRTPIDYA/RQAGHHELAERLVEC/QYE/LTERLAFYLCGRKPDHKN GHYIIPQMADRSRQKCMSQSLDLSELA/KAA/KKKLQALSNRLFEEL A/MDVYDEVDRRENDVWLATQNHSTLVTERSAPVFLPVNPEYSATR NQGRQKLARFNAREFATLIIDILSEAKRRQQKSLSSPTGNLESLR

				S\QSDLEDQHDYYSVASDEDT\EHEPLRSTGATRSNRARSMDSSDLS DGAVT\LQEYLELKKALATSEAKVQQLMKVNSSLSDEL\RRL\QREI HKLQAENLQFRQPPG\PV\PTLPFPS*TGREHTPLGARRGEQHRIR QAFSMYEPGSALKPFGGPPGDELNTRLQPPHSTLEDDAIYSVHVHA GLYRPVGSEPPQVGLGVLNSGLKMIRLTWSLILVATSTLGSRRSPMK TRSP
2028	A	6994	7054	LISTSDLYFL*DL*VRCKQTGVLPWFHTTTIPRSSLEVNPRFPTYHL CEL/SASYLTSWYLSFLIWTMG*LLHLHHTELL*G*SNKSC*VLCME PDTVTAHSAVCTQFW/SNVDKNNVVISLRKSFLFF*QSFALVTQAGV QWRDLGSLQAPPPGFTPFSCSLPSSWDYRRPLPRPANFLYF**RQG FPETGFHHVHVGGQADLELLTSGDPPTLASQSAG\ITGVSHHVQPGE GFCNCCCIVESGPFKERVG
2029	A	411	713	TNSLYGLNIYLEIDQHFRNMKIY\RSNSLILILILLHLYCIFALS DL/CSH*PQVAI*KEINWPGAVAHTCNPSTLGNRGRWIV*GQEFETSLV NMAKARLY
2030	A	3	84	SGSTHASGGLQASRWRRAGTSRCSVSSLTSTSTASLRGLPTVATGLR SGSWTSHHGAVAG*GRPTRPVGSRRRDGGERVVRGALCQA
2031	A	3	519	SRWRAGTSRCSVSSLTSTSTASLRGLPTVATGDYPPPDQASSNLT SPPPGHTHCGNRGQWPVLRGGANAAASSSSRVEQGGGS/SSFARL SSTHGTPGGGEGVKAVSSA*GP\GGLPGTLNLVGGGDVTDASLSALT GGLEGILEKP*AGRCPI TDGNPREEGREPRAG
2032	A	212	394	RWRGHSLSHEIFKRSVTQNNLIEYRIPIMSLCCASDTRQ/SFNTTSVP AVKKLTVTVNTISIF
2033	A	726	908	LGSFGYGLNHISSPAHSEPQTSPLVGLSVTCN*KSLVHPHSRGHQGS EK*GSLDPCISWR
2034	A	1	1092	AKRKKINQNSSKEKINNGQEVKIDQRNVKKEFTSHALDSHILDYEN PAIKEDVSTLIGDDLASCCKDETDSSKEETEPQVLKFRVTCNRAGEK HCFTSNEAARDFGGAVQDYFKWKADMTNFDVEVLLNIHDNEVIGIA LTEESLHRRNITHFGPTTLRSTLAYGMLRLCDPLPYDIIVDPMCGTG AIPIEGATEWSDCFHIAGDNNPLAVNRAANNIASLLTKSQIKEGKPS WGLPIDAVQWDICNLPLRTGSVDIIVTDLPFGKRMGSKKRNNWLYPA CLREMSRVCTPTTGRAVLLTQDTKCFTKALSGMRHVVRKVDTVWVNV GGLRAAVYVLI RTPQAFVHPSEQDGERGTLWQCKE
2035	A	711	2257	GRRRAGLQADLVAEPILLPLPGLYPLPRIPGPCRWELGDDSTAFKET VLGILEAQPTWCDIEEAT*\HLLDVNLIEQKSVQVTESDLGSESEL LVTIGATVPTGFEQTAADDEVREKLGSCKISRDRGKIYFVISVESLA QVHCLRSVDNLFVVVQEFQDYQFKQTKEEVLKDFEDLAGK\LPWSNP LKVWE\INASFKKKK\AKR\KKINQNSSKEKINNGQEVKIDQRNVK EFTSHALDSHILDYENPAIKEDVSTLIG\DDLASCCKDETDSSKEE TEPQVLKLRVTCNRAGEKHCFTSHEAARDFGG\AVQDYFKWKADMTN FDVEVLLNIHDNEVIGIALTEESLHRRNITHFG\PTTLRSTLAYGM LRLC\DPLPYDI\IV\DPMCG\TLGEPIEGATEWSDCFHIAGDNNP LAVNRAANNIASLLTKSQIKEGKPSWGLPIDAVQWDICNLPLRTGSV DIIVTDLPFGKRTIILTRCKMDQKITLKTETAIWKLSHRHLRSVTNW ATPRDPS
2036	A	247	1294	MPNTAMKEKRCLLMGERSGSGKNQAM\RSIIFAKLPFARDTRR\LGA TIDVEHSHVRFL\GNLVLNLWDCGGQDTFMENYFTSQR\DNIF\RVN GSFDFKVFVDESREL\EKDMHYQSCLEGHPPRTLPAKI\FCL\VH KMD/LLVQEDQRD\LIFKEREEDLR\RLS\RPLECACF\RTSIWG*G RFYKAWVQAFV\YQLDFPNVSAAGRLNLRDF\AQII\EAD\EVLLFE RS\TF\LVISHY\QCKEQRDVHRFEKISNINK\QFKLSCSKL\PASF QSMEVR\NSNFA\AFMRHLFT*NTYVM\VVMS\DPVDPFLGPLLINH SQCPGNHFEETGRELNGPQATVFPYGYEYCNALSEKA
2037	A	32	959	ALRQSHSQKLRLRLWTAASQGSMPDKACVVTLATIAW\MVSF\VSN\Y SHTANILPDI\ENEDFIKDCV\RIHNKF\RSEVKPTSQVICLYMTWD PALAQIAKAWA\SNC\QFSHNTRLK\PPPQAWHPNPHFWGENI\WD

				LGLLPPIF\SVSSAITNW\YDEI\QDY\DFKT\RIC\KKVCG\HYTQV \VWAD\SYKVG\CAVSILALKVSGFDRSPNGAHFYMQLPGPGGNYP \TTWPYKRGATL/CSACPNNNDK\CLDNLCVNR\QRDQVKRYYSVVYP GWPIYPR*QRR/SSLFLIGNSVILILCVIITILVQHKYPNLVLLD
2038	A	311	459	HEHMLLSFLFFFFVFLVEMAFHVGQAGLELPTSGDLPTSASLSVGI TG
2039	A	1271	1540	ARGCKRPCRQIASLMLQLCILHACWALVPQLHAAPGLAIQRLCICPY LGSWPSTLGPVPPLSPSTSPRPSPAFGASLNPFRHSSGPLR
2040	A	176	552	MRSSKQMKPNFPRCSSITVLSVRGMVLFITLACPRFKMSSRTDFRFG NPQVT*GSTICSIFRLPSILSMRTTK/DQGMFIWQFQGMRFHF*SSE THLVTFLLPPGIM*E*FQSLKPEPFSSFLSCYCH
2041	A	204	401	WHEFTGAENHCKTLPKENF*WCLCKSHPSEPKNAAYNRTLCDLGISK SEVSLGTSFEMWTSQOQE
2042	A	123	311	PSRRLLGHPRWALSPHLLLPQRFCSWVSFAPASCPC/DLFISRDRSS VSVGLMKHRMLGLAELL
2043	A	2459	3031	TSPSTSLRPAPIPSPSPSSRPSSSSQTSAASSPSSAWPKAASRQGA *RCRE*LPSWTSQSSPPLKSWGLDSAPPPPLSTCLSASTTRGAGAAA TPQCSAPCLHR/CDKVPGFAVAQCINQHSSPSL\PHSRHPPAGAPA AAGAPATATLEAPARPPPPQPRVQQSGVAGKDADECSACRRPTVMA ATGF
2044	A	1125	1695	DFFSKIDDSHLQVLFENQLLILFFPHFHLNDCSNSFLFFFSEMESRS VAQLECTG/AILAHCNLRLLGSSDFPALASRVAGTTGTCHHTQLIFV FLVETGFHHVQGAGTCMQSQLIKGLRENHLNPGGGGCNEPRSRPLRS SLGNRVRLSQREKQNP*DAQVSEKGLNTLELQAKF*GVSHVFPGER/ VSLISQNP*PFWKVKIKQVSRLRFKKPQDPFRASQSLRIFQSHH*KS WNTYSQQRQVILFLCLSSYVYFKSFSKQGPRTLQIQLCPAWSTCC RSLREPCTNARVTHLPTLNPRIEDATKQDSFLHGMVPIVRQQQHRM* ENAGEFFPWELGLWMRGCPAHGTIRLLSFL*PFLSSF*R*SRK*SSL KMLDKNSQNNKTHASTSLIKNLP\HLAPKSMATATKSNFKELRFLQQ NR*FTSSSP/CLKISY*YYSSLISI*MTAAIVFCF/CFSEMESRSVA /QAGVHCNGLSLSLPPGFKRFSCLSLSSSWDYRHAPHPAHFCIF SRDRVSPCWPGWSQSPGPHGLPAWASPKCWDYSREPPRPGQQYSFSV TRTSLSPITLRLCIAPCPNQAFDTPSRVLHLFVPASSIPPNLKVTLK Y
2045	A	1	577	PLKRS DGCNDGRPTRPPTRPDTTVFTSNLKQTRMVHLTPEEKSAVTA LWGKVNVD\VGKALGRLLVVPW\TQRF\FESFGDLSTPDAVMGN PKVKAHGKKVLRGAFSDG\LAHL\DNLKGTFATEVSLHC*QACTWD PGELQGSWGNVLCVAGPITFGKRISTPPVAGLPNQENWLAWCWLNA LGPQVIT
2046	A	16	370	ACRIAARAYLDLLRTWVFQVGSSGSQRDVNCSVMGPQEKKVYYLQK LDTAYDDLGN SGHFTIIYNQGFIVLNDYKWF AFFKDVTDFISHLFM QLGTVGIIYDLPHLRNKLAMNRRWG
2047	A	1	1125	MASRGVHAEDWMQDPWWHQCADEQIVTDCHWVIKGTNRSEPSSMKVK RIIPISTNWFYRIQTSSLLNKLWKDSDEVLNCRAFEEKGPQEKKV VYLQKLDAYDDLGN SGHFTIIYNQGFIVLNDYKWF AFFKYKEEGS KVTTYCNETMTGWVHDVLRNWACFTGKKVGTASENVYVNIHLKNS QEKYSNRLYKYDHNFKAINAIQKSWTATTYMEYETLTLGDMIRRS GHSRKIPSKYKHYAKKLENLEEMDKFLDAYTLPRLNQEEVGSINR SITSYESEAVINSLMKKSPGPDGFTVEFYQRYKEELIPFLKLQFQ IEKEGLLPNSFYEASIIILIPKGRDTTTRKRLQSNIPDELRRKKSQ
2048	A	1	1943	MWKHLWNWVIGSGWKTLDVLEEDRKTENLVLDRFSSGCDQSIDRN MDSEVQADEFSRNEEVIGNWSKGQPCYTTLAKDLSALCPYPKALWKV ELKSDDLGEIPLQLRLVHGGQVNLDMEDHQDQEIYKPRLRFKAFSG EGQKLGSLTPEIVSTPSSPEEEDKSILNAVVLIDDSVPTTKIQLA DGSRLIQRFNSTHRRRAVNGPSNQLPDKPGSPSPFCLAPLITVCPAA DDPSPALWLHLVAARSTSQRNGQVLCYLPRKWGAVAVCTSVEACCVW

				FWLLERQNDSGMQLGGPPPSAIFRWLAAPADAPAATSGAGCLATAG GAKTRKLALAELEDEVKCKSSKSNRPKATVFKSPRTPPQRTVKNWF QLIAPNAGEDAEQQELAFIAGGTAKWYSHFGRPFGLNLRATWNVSR KLLRTTQISGLRYWGFPGFQAKVAATLAKQEVIPYLSLGRGAEFK GLSQNSLQAPLHGTSQGGKNDYPETAVLPKLPREKVSRRERKLASSR CLSLGTKCMSEEAFLVITNSSSCSCGEGFPYLIAGKYAQDFGLVEEA CFPYTGTDSPCKMKEDCFRYYSSSEYHYVGGFYGGCNEALMKLELVHH GPMVAFAFEVYDDFLHYKKGIYHHT\GLR\DPFHPFEL
2049	A	1	2077	MTYPENIQIKKITGVQVMVPLKYKEEGSKVTTCNETMTGWVHDVLG RNWACFTGKKVGTASENVYVNIHLKNSQEKYSNRLKYDHNFKVKA NAIQSWTATTYMEYETLTLDGMIRRSBGHSRKIPSSVPLCSSAPLD VQLLVSVPAKILGLYGGRMGGMAGQKAPFLRAPVIGVSFADSFQPSR LQDSPQLFNQGLLSAAQVGSSGSQRDVNCSVMGPQEKVVVYLQKL DTAYDDL\NSG\HFTIIYNQGFIVLNDLQVGLPFFKYKEGGAARV TTY\CNETMTGWGA*CVWGRNWA\CFTGKKVG\TASE\NVYVNTAHL K\NSQEK\YSNR\LYKYDHNFKV\AINAIQKSLTATTYMEYETLT\ LGDMMIRRKWATSRKIPR\PKPAPLTAEYSQKI\LLHLPTSWDWRNV HGI\NFVSPVRNQASCG\SCY\SF\ASMGMLE\ARGIRILTNNSTP ILSPQEVVSC\SQ\YAQGCEGG\FPYLIAGKYAQDFGLVEEAFCPYT GTDSPCKMKEDCFRYYSSSEYHYVG\GFYGCNEALM\KL\ELVHP WGPWEVCFLEVYDDFLHYKKGDPTPHTGLKRPFFSTPFE\LTNHAV\L LVG\YGT*LKPLGMEY\WIVKNKLGAPAWGLRNGYF\RIPRGTDCA IESIAVAATPQFLNFRGLPSIFINGSASSCKGGIGIFTDCRLSTSI FRSLQIDFP
2050	B	59	466	MSAAMRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVAL YLVIWLPSSLHLCGFLWCMAPSPSNGAELLYKRIIRPFLLKHESQMD SVVKDLKDKAKETADAITKEAKKATVNLLX*
2051	A	1	915	MVDQVKVADDQAPAEQSLRRNLNRHILQIAIGGAIGYFTGWTYWF CWVVTGMADVVAITAYAQFWFPLSDWVASLAVIVLLLTNLATVKM FGVIGLVALYLVFGYGASLLCNLIGFGYPAYISECPPTYGVKPGLVV GLIAGGEYAIQHAVEGAEDSREGGVNDLKNINLTAQDVVVGIAASGR TPYVIAGLEYARQLGCRTVGISCNPGSAVSTTAEFAITPIVGAEVV GSSRMKAGTAQKLVLNMLSTGLMIKSGKVFGLNLMVDVVATNEELHVR QVNIVKNATGCSAEQAEALIEW
2052	A	1	3180	FRAVAAPVYPALGTAPGGETVPE\MTAAMRERFERILHDKNCMTDL LAKLEAKTGVNRSFIALGVIGLEALYLVFGYG\ASLLCNLIGFGYPA YISIKAIESPKNKEDDT\QWL\TYWVV\YGVFSHC*NSFSDI\FLSW\ FPF*LG*KGFLVGC\MAPEPLNGG*NCSKRIIRSFSFPGSTK SQIGQVLVKDP*RRPKETADANH*KKPKKSLP*ILLG*KKKKKGG
2053	B	171	256	XVDPASSQAMELSDVTLEGVGNEVMVAX*
2054	A	187	437	PWS*LGSLPT*QTAQVQAPGRYCVSRRHIRPPPGACGPPGGTANGNP EPTLPHPSEGNDKAEAGEGRGDSTWGGWSWGC
2055	A	2	165	NQHHTLPPSPHYHPQ*G*HQRAPWPGCWQGPCRCRNGGQHQAEP EGLQPGL
2056	A	1	506	SPASQCHHYPLMMGSSVVRGAFGLPPVGPAPGVGRMCRLLTQ*RP GAGCYRCLLR*RAKLGPRLESAPPHLPPSPHYHPQ*G*HQRAPW PGCWQGPRTAR*GGVPHPFSEAKVPLLDGPIPSALDWGPWAHPNRR AAWPQPP**DQLSRPVRSRVG*GGHKP
2057	A	496	1092	QPAPGQLLCHLATHP\PPPGACGPPG\AGQKGPEPTELPHPSEGND KAEAGEGRGDSTGEAGAGGGVEP/RP*ASP*HPRPAQKTSRCRQQ SRGPPEI*G*HLPPSQWPHHCAAQIPQ*YRGAGCG*ARGYGCPEE QILPWTRKPDETDLPGPPATRPSPTAFSEHYRQLCDSLPLTPRVS CSRPLSLLGLGH
2058	A	155	701	PGLFRRGLPHPGTGPVQSPFNFP*/PPR/GPEAPPP/RSPAPPRSLR GVDGL*PP*PTLLLTGRDNWSY\PEAGARQFGSGGPMDPSPAPRE* DHPKAEPSPQKKGAGPLLTVRSSRYGQGRSQAECQSKDP*GRTPGVLP

				GPSPREFPVSVPVIVFVFLCRRFFSCKSWIMTLTFLPSGVSCGCDK
2059	A	1	506	DRDAEFYKFLQENDQSQLNFSDDSDSSEEEEESEFHSPLPYVLEEA\AFR AAVATT/RGDQESAEANKFQVTDSAVFNALVVFNALVTFCIRDLTGC LQKLLIGKVAKSSRMLQPSSSLLWGKLRVDIKAYLGSVIQLVSCVA ETVVLA AVLWHISVLVPCFLTTPKQCSRE
2060	A	9	2295	VGCTLRVGVMAAAGSRKRRRLAELTVDEFLASGFDSESESESESESPQA ETREAREAARSPDKPGSPSASRRKGRASEHKDQLSRLKDRDPEFYK FLQENDQSQLNFSDDSDSSEEEEEGPFHSLPDVLEEAASEEDGAEEGED GDRVPRGLKGKQNSVPVTVAMVERWKQAAKQRLTPKLFHEVVQAFQA AVATTRGDQESAEANKFQVTDAAFNALVTFCIRDLIGCLQKLLFGK VAKDSSRMLQPSSSPLWGKLRVDIKAYLGSAIQMNSCLSETTVLA AV LRHISVLVP*FLTTPKQCHMLLKRMVVVWSTGEESLRVLAFLVLSRV CRHKKDTFLGP\VLKQMYITYVRNCKFTSPGALPFI SFMQWTLT\EL LALEPGVAYQHAFLYIRQLAIHLRNAMTRKKETYQSVYNWQYVHCL FLWCRVLSTAGPSEALQPLVYPLAQVIIGCIKLIPTARFYPLR\MHC IRALTLLSGSSGAFIPVLPFIL\EMFQQVDVFNKRPGRMSSKPINF\S VILKLSNVNLQEKAYRGGLGWSSCYDLNPGSYLHSAHCIGFPELV PVVLQKSLFLECKVANYCRVQQLLGKVQENSAYICSRQRVSFGV SEQQAWEAEWKL TREEGTPLTLYYSHWRKLRDREIQLEISGKERLED LNFPEIKRRKMADRKDEDRKQFKDLF\DLNSS\ EEDDTGEGF SERGIL RPLSTRHGVEDDEDEEEGEEDSSNSEDGDPDAEAGLAPGELQQLAQ GPEDELEDLQSEDD
2061	A	203	1383	MSSFGYRTLTV\ALFTLI\CCPG\SDEKVF\EVH\VRPKEAGRLSPK GSLEV\NC\STTC\NQP*SGVGLGDL S*D*GFCWDEQVQLGNNYLGL KHFPIDTVLQ\CHFTL\SGKQE\SMNSNVSV\YQPPRQVILTLOPTL \VAVG\KSFTIECRVPTV\EPLDSL\TLF\LFRG\NEILALWRTFRG RAAPAPQGGPQPHSNST\ADRRGLAHRKLSPSLAVL\DLMS\RGG\N IFHK\HSAP\KMLE\IYETCVRTSPDWSSSLVTGGVGVACPLFVTSV\ LLC\FIFG\QHLRPASGMGTYGVRAAWRRLP\QAFRPIATHGVAWPH TTVVTGTQCDSSGLRYQPWLKDCDRQORLGTLPFLARIQTPGLSPVP TVSPPGITMAREGSHHGGLSLDASLPTLSFTGWHEA
2062	A	503	1808	TTVQEESTVDSQPVPNIDHLLTNIGRTGVSPGDVSDSATSDSTKSKG SWGSGKDQYSRELLVSSI FAAA SRKRKKPKKAQPSSEDELDNVFF KKENVEQCHNDTKEESKKESETLGRKQKII IAKENSTRKDPSTTKDE KISLGKESTPSEEPSPPHNSKHNSPTLS CRFAILKESPRSLLAQKS SHLEETGSDSGTLLSTSSQASLARFSMKKSTSPETKHSEFLANVSTI TSDYSTTSSATYLA*PGLQSTEP*GA\SVAESKGDEADDERSELISE GRPVEDTSESEFPVFPPTSLDFREAFPRKTARS\TKSSRRNSEGSELS CTEGSLTSSLD SRRQLFSSHKLIECDTL SRKKSARFKSDSGSLGDAK NEKEAPSLTKVFDVMKKGKSTGSLLTPTRGESEKQEP TWT KTIADRL KL RPAPADDMYE
2063	A	2	527	DPEADSIRAEMSRVALAVLALLSLSGLEAIQRTPKIQVYSRHPAEN GKSNFLNCYVSGFHPSDIEVCLLKN GK\RIEKV\EHSDLSFSKDW SF \YL\LPYTEFHQP LKKDEYALPV*THVTLSPAQR*FKWDRGHVKQHH GGLKMPHLGWND SKFLLACFFNIDMLITLTLCTKM
2064	A	3	163	ARELTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTEFT EDEVSL
2065	A	611	1434	TPLHLAVITNQPEIAEALLGAGCDPELRD FRGNTPLHLACEQGLAS VGVL TQSC TTPHLHSILKATNYN/GYVCLPALPHPLGGQVTWRGRW ANLRSPGKSLNS*HLEG*ENMCAKCLLDAFIKFFQNPDCGFLKFRR* DYL FHKRIGERSEG*NRWVYFFPVLPGHTCLHLASIHGYLGIVELL VSLGADVNA/QGWCFLPPTH*VRLVLML*AEIPNAAISISNSFWFQ EPCNGRTALYLAVDLPNPDLVSLLLKCGADVNRVTYQGYSP
2066	A	1	1332	MVQLSPHYRGDSEDGRKRMVRQRTKPVLF FWSDWLGNSPSLTTPPORN PQPAFIGRRGGA AEPTAVRAAVPPASAPARKQRAARGPAHPQQR PQL VRAMF\QAAERPOEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYE

				QMVKEIQEIRLEPQE\VPRGSEPWKQQLTEDGDSFLHLAIITHEEKAL TMEVIRQVKG\DLAFL\NFKTNLQQTPLHLAVITNQPE\IVEALLGA GC\DELELRDFRGNTPL/L*SLACEQQCLASVGLDSSLAPPPQL\HSI LKGYPTTMGHTCLHLAFYPMGYWGHRSFLVFLGLVDVKCSRSPPCKW PGLPIHLAV\DLQNPEPGCSLLFESVGADVQQLSPTQGYSPPTQPHP GPPQAPRIQQQLG\QLTLENLQMLPRE/SPDEESYDTRVQSSTGVSP EDELAPMDDCGVFGGPRSDVMSAKGLKET
2067	B	169	251	XPQKEPYVIPFTGCVTQKGQVAGDAGWQ*
2068	A	33	445	SVARFTGIKTAILVGGMSTQKQRMNLNRRPEIVVATPGRLWELIKEK HYHLRNLRLQRLCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPKRQ TLVFSATLTLVHQAPAVPATVYGEPEQVSVSHVWQAAPACTTS
2069	A	1	1428	MGMFGCVTRHGRITVLTNMNGPGSFTRACKDLHGVESWNGKMARGL DVMAFQEQGGFRPCAELKFSGARVAYPMLPMPWNRLRFEPISGGAN SITVPLRRVAVLPRCSGGRCDSARVRHNTGLHFASSGSGLPSPWPK ERAGCPTVAEVSRRRVRTVRLVVAHRDPYDLRVSGKVPRTSEIYVHR SGRTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTKY MDVVKGRKVPFKPLGPGVKAQALDSERIPLFPMYVLQHGRLGLGLPLR RVSLALVRPPGMVGSILGEKDDVTYAIKPTCWPGLDIIPSCALHRI ETELMGKFDEGLPTDPHMLRLAIETVAHDYDVIVIDSAPNLIGIT INVVCAADVLIPTPAELFDYTSALQFFDMLRDLLKNVDLKGFEPPDV RILLTKYSNSNGSQSPWMEEQIRDAWGSMLKNVRETDEVGKAACA EVSKRG
2070	A	1268	2807	LPLESLAVQVKQHIDAVARFTGIKNCFYFGFGGMSTQKPARGC*TRRP \EIVVATPGRLWELIKEKHYYL\GNLRO\LRCL\VVDEA\DRMV\EK GPFWLELLHSCFRDASND\QYNPKRTKRLFFLATLTL\VHQAPARN PFHK\KHTKKMDYTAQL\DLLMQKIGHEGASPKVIDLTRE*GPRWET \LTETKIPL*DLIEKDFLLVTTFLMQYSRAAA*CFANSIS\CIKRL\ SGLLKV/LLDIMALGPWHGLVWHQEGRLRLNLSILPRL\EDCVLL\ ATDVGSSGVWDIPKV\QHVHPFTRVPRT\SEIYVHRSWSNLLRSYQL TGLKS*LLIWGLKDVINFKKIYKTLKKDEDIPLFPADINTWDVV\K ERIR\LARQI\EESEY\RNQF\ACLHNSW\IEQAAAAL\EIEL\EED MY*GEGKA\DQGEERRRQKQMKVLKELRHLLSQPLFTESQKTKYPT QSGKPPLLV\LAPSKERVCFLSCLSQGRKEEGRTKEARGGPQPGTAT AKLQVQFNCPGQVCQ
2071	A	3	495	ASGSVITSGIOWASRPRIRTIA/PSETPSSSFVVFRRKRKRKSHLAS LKRDDNMNTSEDEDMFPIEMSSDEAMELLESSRTLNDIPPFQDDIP EENLSLAVIYPQSASYPNSDREWSPTPSSLVDCKRTAPHLAVAAEGG LSSSCPQSSSLFHPSESPPSGSRPS
2072	A	36	481	RQGEIFLVCLFFEMESCSVTQAGVQWCNLGSLQRPFPFGFKQFSCLSF WSIWDYRCAPPCCPANFCIFSKGGVSSCWGWA*TPGPQMICPPWSPK VLGLLV*ATTPGQRCFFVLFCFVLFPPQQTCEEDLVQGITPSSLCL ECYKLFA
2073	A	2	2737	RADDFVARRRS\VQTMNYVGQLAGQVFVTV\KELYKGLNPATLSGCI DIIIVIRQPNGNLQCSPPFHVRFKMGVLRSEKVVDEIEINGESVDLHM KLGDNGEAFFVQETDNDQEVIPMHLATSPILSEGASRMECQLKRGSV DRMKGLDPSTPAQVIAPSE\TPSSSSVVKRRKRKRKSQLDSLKRDD NMNTSEDEDMFPIEMSSDEAMELLESSRTLNDIPPFQDDIPEENLS LA\VI\YPQSASYPNSDREWSPTPSPSGSRPSTPKSDSELVSKSTER TGQKNPEMLWLWGELPQAAKSSSPHKMKESSPLSSRKICDKSHFQAI HSESSDTFSDQSPTLVGGALLDQNKPTQTEMQFVNEEDLETGAAAPL LPMIEELKPPSASVVQTANKTDSRKRDRKSRHLGADGVYLDL\T DM\DPEVAALYFPKNGDPSGLAKHASDNGARSANQSPQSVGSSGV\ SGVESTSDGLRDLPSIAISLCGGLSDHREITEDAFL\EQAV\SYQQV LGNPAI\IGDP\NFVVKIGSKYYNWTAAPLL\AMQAFQKPLPKAT VESIMRDKMPKKGGRWWFSWRGRNTTIKEESKPEQCLAGKAHSTGEQ PPQLSLATRVKHSSSSDEERAAAKPSNAGHLPLLPNVSYKKTLRLT

10054

				SEQLKSLKLNKGPNDVVF\SVTTQYQGTCRC\EGTIYLNWDDK\VI ISDI*WGQLPR*DTLGHILPTLGKDWTHQGIKLYHKVSQNGYKFLY CSARAIGMADMTRGYLHWVNERGTVLPQG\PLLLSPSSLFSALHREV IEKKPEKF\KVQCLTD\IKNLFFPNTEPFYAAFGRPADVYSYKQVG VSLNRIFTVNPKGELVQEHAKTNISSYVRLCEVVDHVPPLLKRSHSS DFPCSDTFSNFTFWREPLPPFENQDIHSASA
2074	A	1	408	SNPRVRGGGTHRSQGAFANMCRGGRMFAPT/KTWRRWHRRVNTTQK RYAICSALAASALPALVMSKGHRIEEVPELPLVVEDKVEGYKKTKEA VLLLKKLKAUNDIKKVYASQMRAGKGGK/RCGR*ERKEGCCWC
2075	A	3	1434	FPVAAAGLRGAWLSPLSAMACARPL\ISVYSEKGESSGKNVTLPAVF KAPI\RPDIVNFVHTNLRKNRQPYAVSEL\AGHQTK\AE\SWGTGR AGGSKFPEVRGGGTHRS\GQGAFG\NMC\RGGRMF\APTQNLGRRWN \RRVDT\TONRYA\ICS\ALA\ASALTSNWVMSK\GHRIEEVPE\LP LV\VEDKVEGLQEEPRLFLLLKKL\KAUNDIKKV\YASRRMRGGQR QNGETVRRIPGAGGPCIYNEDNGI\IKPFNIPGNYS*A*AKLNI LEALLPG\GHGGTFLAFGT*KLPFRK\LDELYGTWR*S/RASPQRSN YHSFPLHK\MINTD\LSRNLEKQRSQRAPPGHRGKREDPIRRV\LK KNP\LKNLRIMLKNLPICKGPCCR/RHPFFAQAESQSSGVDKGGKL HQRHLQAKSDEKAAVAGKQPVVG\KTGKGCCLLVFKNQKKPLVGKK\ AAATKKPAPE\RSLQRRNATTEKKPAA
2076	A	275	652	TVNLCFSTFLWTVLYFTFFFAKCFQIHLRLIYLR**LKTNSWFMLY A\IMHVLLVQGN*NKIFSVKQIYLLCTFIYTGIF\W*YHTKG*NKT FTM*NSMYIFGYLHTLKPKGKIKRHLFATTIC
2077	A	63	292	GGILLSISRPYKTKPTHGIGKYKHLIKAEPP\KKKKGKVAVRAINLG TDYNYGVNLNIH\LT\AYDMTLAESYAQYVHN
2078	A	315	1092	RPRSSKRMSGTSEKVLCLRNNTIFKQAFSLLRFRSSEKPIYSVGGI LLSISRPYKSK\PTHGIGKYKHLIKAEPPKKKGKVE\VRAINLGT YEYGVNLNI\HLTAYDMTLAESYAPLFSTTFCSNLSH*KSEESYAMPT QNHKKWLPVCRDQGPCKLLGLKCLPHE\RV\VQISGLSATFARKF SWKIIPKPVLP*RESGLFS*REHTERKTSRGRFQRFDPDELGRTFWAK FEVATVDPFHCCQWSYLSAKEKSLLS
2079	A	127	993	SNLILRNLFCPHLALASSAFDKCQEETVEKTELLAERRGLTENPSR LPPITAGLRSDTMNHIVANLLSCQQRPRLPNYEMLKEEHEVAV\LG APQKPCLPCEPPVIHYPQARPPWPDHVLVP\VQTPSSMNPMPWAS *AFA\YSVKSRLDRK\MVG DVEPGPQGLMPPPAKVPEKSGPVILGHL HEPILAH\HHPPPSVG\RPGPNG*IKEGITEGQG\ALPR*TCNPTVL QLSIPRPAPRGQEVLPNCIPLTPPSIPRPVPTAESICISPLSSHAF QWHSIKCICFW
2080	A	61	346	LSLFFETEFCSYPCGLECSGVILAHCNFR\LPGFK*FSCLSLPSSWV YRYPDPANFLVLVETGFHHVGPGLVINDPLIFNLDTCYSAKRQFL E
2081	A	88	386	PHRFGKRRNKT\HTLCRRCGS\KAYHLQKSTCGKCGYP\AKRKRKYN WSAKAKRPKYHPEPGRMRHLKIVY\RIQGMGF\REGTTP*QEGQA VASIQVHL
2082	A	187	913	STNKRSTRPPLGFEMASPHQEPKPGDLIEIFRLGY\EHWALYIGDGY VIHL\APP\SEYPGAGSSGVFSV\LSNSAEVKRG\RI\EDVVGCCY RGQQTAWDHGVPSPRALEG*SFSSAKEMVWFRRLK\YSIV\SRNCEA LCSPSLRYGQVPAVKQVGKGRFEVG/VLATALGILVAGCSFAIRR YQKKS DSLKQPQNPVLEAAVGVPVEMSLPRCLQQPDPRALSQAFSRS FPLFPSLAGSMI
2083	A	1	423	MGIRLLCRVAFCLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMD HENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFS LILESASTNQTSMYLCASSLYGATYGYTFGSGTRLTVVEDLNKVFP PP
2084	A	2	390	PRVRYRGVITDPQPLMEQPLGDSRYWLSSRLVSATFWQNPNRNHR CQVQFYGLSENDEWTHDRAKPVQTQIVSAEAWSKADCGFTSGN*QQGV LSATILYEILLGKATLYAVLVSAVLVLMGMVKRKF

2085	A	2	1027	HLPDAAMGPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTDKGDVPE GYKVSKEKRNFPILILESPSPNQTSLYFCARSFEQGYEQYFGPGTRL TVTEKRNFPILILESPSPNQTSLYFCASSSSQGRSLPGFNYGYTFGSG TRLTVVEDLNKLFPEVAVFEPSEAEISHTQKATLVCLATG\IFPDH VELSWVNGKEAHSGVSTDQPPLKEQPALNDSRYCLSSRLRVSATFW \QNPRN\HFRQVQFYGLSENDEWTQDRAKPVQTIVSAEAWGRADCG FTS\VKSYQQGVLS\ATILYEILARGRPITYCLCW*APLVLM\MK EKGFLKAALEVELGAY
2086	A	1921	1991	SFVIFDANIFFQFIG*SLLSLWM*ALLCLLVTEHLYLVLSIGHLWCVC VCVCVCVCVYDFLIPSHFSIDCFKAIYILRILIIF\VIFDANIFFQ FIGCLLILCFR
2087	C	105	392	MQISPPPGHTQNQPYLLFSIASRKCLHPVLLVHYFFQLFLIPIIHSI FFKFFISCINVNTSLFTFSLQSQVMGELPLISFSTLSLLEESTYRL GI
2088	A	38	230	LYWQKRKGKLLNLTQGIVADPVR*KKPHFKCPSNCPKIHNTESAYA VSFMKYSAHVLGSLYEM
2089	A	487	747	LPSGPEYSAGLSTSRLKARHRGSRSPERRSGRPRGPRRSRAAAEKPS PKCARDAPKAVATSPAPARRPVPGPRLRAPKLGRSLLG
2090	A	1	1350	MVGAADTAVSIMVLALVGLDESEFRDKLTPITIFMEYRLDYRTAADT TGLQPIILNQFTPANISRQSGFVLLTCSQKKIYIGDDNPLTLIVKAQ NQGEGAYEAEIIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQV VCDLGNPMKAGTQLLAGLRFVHQSEMDTSVKFDLQIQSSNLFDKL RNNGPSFSKAMLHLQWPKYNNNTLLYILHYDIDGPMNCTSDMEIN PLRIKISSIQTTEKNDTVAGQGERDHLITKRDIALSEGDHITLIEIA ICYDWYVGSVIGKIRHVLGLMKLMFYSLLTLCSHRISKQWGNPDSK DDGFFRRQDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQILEGQW AARSMPPSFGYSMKGATDIDKNGYPEELAVSAGLKRKMCSSVVEKRHG GQYGLVEQNMKQNNPGYSPKFEIKVTF
2091	C	179	649	MFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPIEFDATELHRE LKENQNHSYSLKSSASFNVIEFPYKNLPIDITNSTLVTNTVWTG IQ PAPMPVPVWVILAVLAGLLLLAVLVFVMYRMGFFKRVPPQEEQER EQLQPHENGEENSET*
2092	A	274	423	VCKHFLEAIENNKYGWFWVCPGGDIDCMYRHALPPGFVFNKDKKKEE KKD
2093	A	1	3849	MCGGVFATEELAVSAGLKRKMCSSVVEKRHGDFQVELLLDKLKQKGA RRALFLYSRSPSHSKNMTISRGLMQCEELIAYLRDESEFRDKLTP ITIFMEYRLDYRTAADTTGLQPIILNQFTPANISRQSGFVLLTCSQKK IYIGDDNPLTLIVKAQNQGEGAYEAEIIVSIPLQADFIGVVRNNEAL ARLSCAFKTENQTRQVVCDLGNPMKAGTQHLLSPCTQFSMQVFLFHY TASSSVVALDSHRSPKPYCVNPAVKACKGSRLHASYENLIPGDPSWT VSSRKHPPLCPGKESRMFLLVGAPKANTTQPGIVEGGQVLKCDWSST RRCQPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPL YHWRTEMQEREPVGTCTFLQDGTKTVEYAPCRSQDIDADGQGFQGG PSIDFTKADRVLLGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYN NQLATRTAQAFDDSYLGYSAVGDFNGDGDIDFVSGVPRAARTLGM VYIYDGKNMSSLYNFTGEQMAAYFGFSVAATDINGDDYADVFIGAPL FMDRGSDGKLQEVGVSVSLQRASGDFQTTKNGFEVFARFGSAIAP LGDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQILEG QWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRARPV ITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGV PRKLNQVVELLLDKLKQKGAIRRALFLYSRSPSHSKNMTISRGLMQ CEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTGLQPIILNQF TPANISRQAHILLDCGEDNVCKPKLEVSVSDQKKIYIGDDNPLTLI VKAQNQGEGAYEAEIIVSIPLQA*SGKCAQWLRNGMEISRWNFFWIN SSKREQ/YRRALFLYSRSPSHSKNMTISRGLMQCEELIAYLRDESE FRDKLTPITIFMEYRLDYRTAADTTGLQPIILNQFTPANISRQSGFVL

				<p>LTCSDQKKIYIGDDNPLTLIVKAQNQGEAYEAEILVSIPLQADFIG VVRNNEALARLSCAFKTENQTRQVVC DLGNPMKAGTOHLLSPCTQFS MQVFLFHYTASSSVVALDSHRSKPYCVNPAVKACKGSRHLHASYENL IPGDPSWTVSSRKHPPLCPGKESRMFLLVGAPKANTTQPGIVEGGQV LKCDWSSTRRCQPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQD KILACAPLYHWRTWKQEREPVGTGTCFLQDGTKTVEYAPCRSQDIDAD GQGFQCGGFSIDFTKADRVLLGGPGSFYWGQQLISDQVAEIVSKYDP NVYSIKYNNQLATRTAQAI FDDSYLGYSVAVGDFNGDGIDDFVSGVP RAARTLGMVYIYDGNMSSLYNFTGEQMAAYFGFSVAATDINGDDYA DVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTKLNNGFEVFA RFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNA VPSQILEGQWAARSMPSPFGYSMKGATDIDKNGYPDLIVGAFGVDR ILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFL KADGKGVLPRLNFQVELLLDKLKQKGAIRRALFLYSRSPSHSKNMT ISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTG LQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVDSDQKKIYIG DDNPLTLIVKAQNQGEAYEAEILVSIPLQADFIGVVRNNEALARLS CAFKTENQTRQVVC DLGNPMKAGTQLLAGLRFVHQSEMDTSVKFD LQIQSSNLFDKVSPVVS HKVDLAVLA AVEIRGVSSPDHIFLPIPNWE HKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKYNNTL LYILHYDIDGPMNCTSDMEINPLRIKISSLOTTEKNDTVAGQGERDH LITKRD LALSEGDIHTLGCGVAQCLKIVCQVGR LDRGKSAILYVKS LWTETFMNKENQNHYSYSLKSSASFNVIEFPYKNLP IEDITNSTLVTT NVTWGIQ PAPMPVPVWV IILAVLAGLLLLAVLVFVVMYRMGFFKVRP PQEEQEREQLQPHENGEGNSET</p>
2094	A	1126	2034	<p>RCWRPRTLGFASPPTRPCSPHAPGCEMTPRDWHRVLSFASPLRIE IFQGYDKTFGLKNKKGAKQKFIKAVTHQVKFGQ/SKSTSGSTE*SW KRKLKDDKKELQELNELFKPVVAAQKI/RVKGADPKSVV\CAFFK QGQCTKGDKCKFSHDLTLGKEM\EKRSVYIDARDEELEKETKSSLIQ ADTMNDWDEKKLEEVNKKHGEAEKKPKTQIVCKHFLEAIENNKY WFWVCPGGDICYMRHALPPGFVLKDKKKKEEDEISLEDLIERER SALGPNVTKITLESFLAWKKRKRQV</p>
2095	A	1	213	<p>ERAAQRRLKAELGIPLLEVPPEEINYLTRIHYKAQSDGIWGEHEIDY ILLDGEQRPSHVTPTVMPDVARCP</p>
2096	A	2	170	<p>MPEINTNHLDKQQVQLLAEMCILIDENDNKIGAETKKNCHLNENIEK GAALKQSFL</p>
2097	A	3	764	<p>PAVVCGRRLISVLEQIRHFVMMPEINTNHLDKQQVQLLAEMCILIDE NDNKIGAETKKNCHLNENIEKGLLH\RAFSVFLFNTENKLLQLQ\RS DAKVTFPG/LVLRNTCCSHPLRQSSRALRESALGS*/GARQHRGL ESLSLGIPLLEVPPEE\LI I*HRIHYKAQSDGIWGGHEIDYILWWRK NVT\LNPD PNEIKSYCYVSKEELKELLKKAASGEIKITPWFKIIAAT FLFKWWDNLNHLNQFVDHEKIIYM</p>
2098	A	1	299	<p>GIPDQEVIGTGYGILDQKASGVKYTKS/DFRSPRPDDLSSFQL*VTS HWDLRLEIETETICKRLL\IIACTRRGPAAIDLPRACQRPLRHYTTW YTKGSRW</p>
2099	A	1	631	<p>MDSMPASRCLLLLPLLLLLLLLPAPELGPSQAGAEENDWVRLPS KCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDL RLIEVTETICKRLL\IIACTRRGPAAIDLPRDGLSFI RSGVRPAC ILVCLLVHRQKCSTVAAPVGT*RH*NGENSARSTMCRKGV*ARCQR TPRACQRPLRHYTTWYTKGSRW</p>
2100	A	171	825	<p>RANPTKPIGCAVRGPWSALKAGCGCQRRAGGR LAVVVVARRHVCSPG SGEGKLLRARPREEEPPGPLGSGPGRAMDSMPASRCLLLLPLLLL LLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAFEET\ GKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLL\IIAC TRRGPAIDLPRACQRPLRHYTTWYTKGSRW</p>
2101	A	2	527	<p>PGRAMDSMPASRCLLLLPLLLVMLVLLPAPELGPSQAGTDENDWV</p>

				RLPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYT KSISDPDQDDLSSFQL*VTSHWDLRLIEVTETICKRLL\IIACTRR GPAADLAKVGFIVLHPLWGPGLQCNLSVSAGL
2102	A	3	1203	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPOWRALARLGWEDCRDSR VREKPPWRVLFPGTDQFAREALRALHAARENKEEELIDKLEVVTMPS PSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVSFGRLLNEALI LKFPYIGILNVHPSCLPR\WRGPAPVIHTVLHGDTVGT\VTIMQIR\P KRFDVGPILKQETVPVPPKSTAKGIGKAVLFKDWGANMLI\SVLEKF GLESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTF\EQKFRLYRAI GNIIPLQTLWMANTIKLLDLVEVNSSVLADPKN*REQALIPGS\VIY HKQSQILLVYCKDGWIGVRSV\MLKKSILTATDFYNGYLHPWYQKNSQ AQPSQCRFQTLRLPTKKKQKKNCCYATMH
2103	A	3	215	EELHEKFDRLKKLHQDEKKNKLEDKKKSLDDEVNAFKQRKTAELLQS QGSQAGGSQTLKRDKEKKNLGL
2104	A	2	341	SKPFSLOQTYEAKRNEFLGELQKKEEEMRQMFVQRVKEKEA/ELKEA EKELHEKFDRLKKLHQDEKKNKLEDKKKSLDDEVNPFKQRKTAELLQ SQGSQAGGSQTLKRDKEKKN
2105	A	1	130	EVNAFKQRKTAELLQSQGSQAGGSQTLKRDKEKKNPWLCTE
2106	A	2	3449	YKPIVEFIDAQFEAYLQEELKIRRVLHTYHDSRIHVCLYFIAPTGH LKSLLDLVTMKKLDSKVNIIPIIAKADAISKSELTKFKIKITSELVSN GVQIYQFPTDDESVAEINGTMNYTRDVVITITILDKSGSRAHLPPFA VIGSTEELKIGNKMMRARQYPWGTQVQVENEACDFVKLREMLIRVNM EDLREQTHTRHYELYYRCKLEEMGFKDTDPDSKPFSLQETYEAKRNE FLGELQKKEEEMRQMFVQRVKEKEAELKEAEKELHEKFDRLKKLHQD EKKKLEDKKKSLDDEVNAFKQRKTAELLQSQGSQAGGSQTLKRDKE KKNASKARSRHWRKSTSRILRRDLLEVREQPRRKRTGLTTPDGTRS ASSLGSLLGGGEDGWRTSAVGGRLPVAPPLPPLPPLPPLPPLPPE PVLEQWRYSHESDWQWALRRSFICRHLHSYPGAALDQLLALSAAWNTN HVFLGCRYSPRLMEKILQMAEGIDIGEMPSYDLVLSKPSKGQKRHLS TCDASSSKDERQEDPYGPQTKEVNEQTHFASMPRDIYQDYTQDSFSI QDGNSSQYCDSSGFIITKDQPVNTANMYFDSGNPAPSTTSQQANSQSTP EPSPSQTFPESVVAEKQYFIEKLTATIWNKLSNPEMTSGSDKINYTY MLTRCIQACKTNPEYIYAPLKEIPPADIPKNKLLTDGYACEVRCQN IYLTGTGYAGSKNGSRDRATELAVKLLQKRIEVRVRRKFKHTFGEDL VVCQIGMSSYEFPPALKPPEDLVVLGKDASGQPIFNASAKHWTNFVI TENANDAIGILNNSASFNMKMSIEYKYEMMPNRTWRCRVFLQDHCLAE GYGTTKTSKHAADAELKILQKTQPTYPSVKSSQCHTGS SPRGSGKK KDIKDLVYENSSNPVCTLNDAQFNRMTVEYVYERMTGLRWKCKVI LESEVIAEAVGVKKTVKYEAAGEAVKTLKKTQPTVINNLKKGAVEDV ISRNEIQGRSABEAYKQKIKEDNIGNQLLRKMGWTGGGLGKSGEGIR EPISVKEQHKREGLDVERVNKIAKRDIEQIRNYARSESHTDLTF SRELTDNERKQIHQIAQKYGLKKRLTATLHYSFHTVWMCSTSKATTA VVELGKRLKIHWCDFEKNQV
2107	A	2	1609	FVPPPFVEAYGWGCRKNWNWAGHRGKRRVKSAPSPYPTFKGWAVEGR LGLEQRRGGPSLAPPPTGLGRARSVTLSLCRRSSSVSCAVAPVAAAP VAALADAGAMAATDISRQVGEGCRTVPLAGHVGFDLPDQLVNKSVS QGFC\FNILCVGETGLGKS\TLM\DTLFQHQISKGEPAHTQPGVQL QSNTYDLQESNVRCLKLTIVSTVGFQDQINKEDSYKP\IVEFIDAQ\F EALLQ\EDPKVR\RVLQTYHDSRIHVCLYFIAPTGHCLKSLDLVTMK KLDSKVNIIPIIAKADAISKSELTKFKIKIT\SELVNGVQIYQFP\ TDESVAEIQLN*TPHLP\FAVIGSTEELKIGNKMMRARQYPWGTQ QVENEACDFVKLREMLIRVNMEDLREQTHTRHYELYYRCKLEEMGF KDTDPDSKPFSLQETYEAKRNEFLGELQKKEEEMRQMFVQRVKEKEA ELKEAEKELHEKFDRLKKLHQDEKKNKLEDKKKSLDDEVNAFKQRKTA AELLQSQGSQAGGSQTLKRDKEKKN
2108	A	1	618	MVRTQCLLGLRTFVAFAAKLWSFFIYLLRGQIRTVIQYQTVRYDILP

				LSPVSRNWLAQVVIDKHSVRFFVRKRPVDFVLEVVVSQWYELVVFTE SMEIYGFVAVAGKLDNSRSILKRRYYRQHCTQLQSSYIKDLSVHSDL SSIVILDNSLGAYRSHPDNAIPIKSWFSDPSDTALLNLLPMLDALRF TADVHSVLSRNLHQHRLW
2109	A	1	427	HPVRFFVHRGPH/VDFSLEVVSQWYELVVFASMEIYGSVAVADKLDN SRSILKRRYYRQHCTLELGSYIKDLSVHSDLSSIVILDNSPGAYRS HPDNAIPIKSWFSDPSDTALLNLLPMLDALRFTADVRSVLSRNLHQH RL
2110	A	2	835	WNSAELGRGGPGAGGAGVIGMMRTQCLLGLRTFVAFKLSWFFIYL LRRQ\IRTVIQYQTVRYDILPLSPVSRNRLAQVKRILVLDLDETLI HSHHDGVLRTVRPGTTPDFILKVIDKHPVRFFVHKRPHVDFFL\E V\VSQWYELVVF\TASM\EIYG\SAVGRNLWDNSRSIL*GGRY\YRQ HCTLELG\SYIKDPLLWFHRDLS\GIVIL\DNSPGAYRSHPGYGGGR\ DNAIPIKSWSVTPS\DTALLNLLPMLDALRFTADVRS\VLSRNLHQ HRLW
2111	A	91	744	TPHFHQGTGKRAAWPTCFKPAGPGKIRQT*RPRKAQRRRIAPRPRV GVPIRP\IVRCPT\VRVHTKV\RAGPRLPALRKL RVAGIHKK\ VART FGI\SVDPRKPDQVPRSSFKA\NVQRLKEYRSK\LILFPQRSRPPK KGD RS\AEELKLA\TQL\TGPV\MPVRNVQ\KKEKARVITEQ\EKNF KAFASLRMARANAPALRHTGQKEPREAAEPGC*KAHNK
2112	A	2	846	RFPLGCFPAQEPQGPVQPMGAPAGNGHGS*SPHFHQGTGKRAALAT WF\NQPAPERSPDVKAPAKPRARRIAP\RPRVGVPIRPIVRCPTV\R YHTKV\RPGRGFSLEELRVAGIHKK\ VARTIGISVDPRRRNS\TES LQAKRAAG*REYRSKLILFPQRSRAPKKGDSS\AEELKLAHPG*PG PGHAPSGTVY\KKEKARVITEEKNFKAFASL\RMARANAPALSAYR AKKS PRKPQKTDVEKPTIKPCLGTWNQSGSHAGSPRGVFRGNNWAWD GASLL
2113	C	714	1010	MKSLNPHLDKIFPHKPLSSLASPSKTLVPGHLCDSTFPFKFSPNYLL FPQNHPTSPHLPSPPKDKGISPIYTPHCLGGVITLILCMHFYRFVC HLSY*
2114	A	2	227	ERFRPPIARVIDVSNGKVHVAE/SCLEETGGLGVDIVLDAG\LDPPD SHCLFLKGATLAFLNDEVWNL SNVQQGRYL
2115	A	3	489	KVQAVGAAQRQSSTDEEITFVFQEKEDLPVTEDNFVKLQVKACALSQ INTKLLAEMKMKDLFPVGREIAGIVLDVGSKVSFFQPDDEVVGILP LDSEDPGLCEVVRVHEHYLVHKPEKVTWTEAAGSIRDGVRAYTALHY LSHLSPGKSVLIMDGASAFG
2116	A	1	489	MKMKKDLFPVGREIAGIVLDVGSKVSFFQPDDEVVGILPLDSEDPGL CEVVRVHEHYLARVIDVSNGKVHVAESCLEETGGLGVDIVLDAGVRL YSKDDEPAVKLQLLPHKHDIITLLGVGGHWVTTEENLQVKKQKHRDV DTSRTQQVAEQESHSGSLSPF
2117	A	2	221	GRVGDEPAVKLQLLPHKHDIITLLGVGGHWVTTEENLQLDPPDSHCL FLKGATLAFLNDEVWNL SNVQQGKYL
2118	A	353	512	QSFQRLILKDVMEKLSTGVFRPQLDEPIPLYEAKVSMEAVQKNQGRK KQVVQF
2119	A	1	1706	MPRAAIAQTPAPTAPAAAAAGPGRRLAALSSPHLRAAEHDGRCSSE TGCHGVLDLSASPTPPFRSDERPDQWEQGAGSLTKDWKVAVVKVQAV GAAQRQVSPGKRVLC LGKRAFKRKVERCPTPEPCSPGEDGGSRRTLTW DLFGPRPSLAEEAEGHFFLPHHFAVFGQLVVICMWLLSQIGPLHY AKRRNHLE RDVTMKG LYFQSSSTDEEITFVFQEKEDLPVTEDNFVKL QVKACALSQINTKLLAEMKMKDLFPVGREIA\GIVLDVGSKVSFFQ P\ DDEVVGILP\ LDS* KTPGL\CESLLRVHEPLLGFINPEKVTW\TE AAGSISGMVRAYYSFLHLSFFIFSPGGNQCLIMDGAKCHLRTIAIQ LAHHRGAKVISTACSLQCLERFRPPIARVIDVSNGKVHVAESCL EETGGLGVDIVLDAGVRLYSKDDEPAVKLQLLPHKHDIITLLG\VG GHWVTTEENLQLDPPDSHCLF\ LKGATLAFLNDEVWNL SNVQQGKYL *QSFQRLILKDVMEKLSTGVFRPQLDEPIPLYEAKVSMEAV\QKNQG

				RKKPSWFQF
2120	A	230	535	KLFFPPSLLFTLATGIFLDLMLHKKPGGFDISLFYRDIISIAEDEDL RVHFEESSKLEDLLRKVRACKETRKRALSRCALSPGQLPTLPLNQQA GRGGSHL
2121	A	344	2631	GDREGTGRAHTEEGAGAGMHFYDVEGVWDVRVQGPMMRGLSSSVQVG RFPAPKVSGPLSICVVRQLGLASSRFARSVPFGVWKKDLPLCLLSQ SEDELTPFDMSIQVRLPFNLRI*QYWLGMVAHAHAGTEKDKNSVNF KNIYVLQELDNPGQ*YFKISFSLIYENISTLIKEDMGHGS DYSLSEV LWVCANLFSVDVQFKMSHKRIMLFTNEDNPHGNDASAKASRARTKAGDL RDTGGHISPFS*IGT*LLFFYFLFF*IISIAEDEDLRVHFEESSKLE DLLRKVRACKETRKRALSRCALSPGQLPTLPLNQQAQGRGGFPFPIK LYRETNEPVKTKTRTFNTSTGGLLLPSDTKRSQVGRDAFCCCCF*DR VSLCRPGWRGLMLMGFKPLVLLKKHHYLRPSLFVYPEESLVIG\SSV DHG*VTLTHSAVYGAALC/RYTPRRNIPPYFVALVPQEEELDDQKIQ VTPPGMWQRYFQGF*TLPLWNHPWTPQGGGTURLALDVSKKLETGT NCRQVKGLCWGNTGRNSKYRAATTVLLSAVSVTHSATPEQ/VWGKM KAIVEKPRFT\YR\SDSFENP\VLQQHFRNL\ALALDLMEPEQAVD LTLAQCSQ*IKRLGSLV\DESKGASLPQPDYNP\EGKSYPKRKNTN K*KGLGKKRPGWK*FKKEGA*RPHIKKGVRWGKVCAPC*KEACR GLRG*KSGLK\KQELLEALT\KHFPGLDQRPAPPAALPAVLPGCPGL VLSQLKCVSPELGRVYPT
2122	A	599	1063	SCSEGLNAVNNLKASRKPKCLSLKWLFLFYFP**IDSQAFYPLISKI VKRKMTHFWTLYFMYLFLRQSLALLRPGWSAVAQSQLTVALGLL/V LRQSSYVSPPGTWNHRYMPPCPAF*NYFCRDGGLPILFRLVLNSWV* AVLSRPLKMLRLQA
2123	A	559	1450	ACAPLVAASGSEVRRSSAAWAMVQLRPRASRAPASAEAMVDEGQLAS EEEEAEHGLLLGQPSSGAAAEPL\BED\EEGDEFDDGGPEEHNLF SA\QAEAREEERRVRETVRDKTLLKEKRKT/REELFIEQKKRKL\ LPDTILE\KLTTASQTNIKKF\PRKR*KKVNLOKKNE\CEKGN\DS KKVKVQKVS\VSPE*KLASAVRLKGPRFWRDSR\QQAQAF\IHNS LYGPGT\NRTTVNKFSL\ANKRLPVKRDCTSFNN\AWGIQKK\Q N\AKRFKRTVGWVRKGWKTKEVNPMLK
2124	A	142	461	KTVSEGFIFSHRTPSLPTFLVLPSSPNFYILDEPTNHLDMETIEALG RACNNFRGGVILVSHDERFIRLVCRELWVCEGGGVTRVEGGFDQYRA LLQEQRREGFL
2125	A	145	904	VINLVYLISPRPELKPVDKESEVVMKFPDGFKEKFSPPILQLDEVDF YYDPKHVIFSRLSVSADLESRICVVGENGAGKSTMLKLLGLD\APV RGIRHAHRNLKIGYFSQHVGAGT*TFACGNLLGTQVFLGRPEEE Y\RHQLGFGMGISGELGHASSLPACLGQKEAEVAFCSGDLPCPNF L\IL\DEPTN\HLGHGRAIEALGPCLQTISGVGVILVSHE*SALSRL VCRE\LWVC*GRRRHPCGKEGF
2126	A	39	2220	GASFPGVPEWNMATCAILRSEFPEIDGQVFDYVTGVHSGSADFES VDDLVEAVGELLQEVSGDSKDDAGIRAVCQRMNTLRLAEPQSQGNS QVLLDAPIQLSKITENYDCGTKLPGLLKREQSSTVNAKKLEKAEARL KAKLRKRSEKDTLKTSNPLVLEEASASQAGSRKESRLESSGKNKSYD VRIENFDVSFGDRVLLAGADVNLAWGRRYGLVGRNGLGKTTLLKMLA TRSLRVPAHISLLHVEQEVAGDDTPALQS\VLESDSVREDLLRRERE LT\SQIAAGRAEGSEAAELA\KIYAKLEEIEADKAPARASVILAGLG FTPKMQQPNPGVSQVAVRMRLALAGAL\FARPDLLLDEPTNMLDV RAILWLENYLQITWPSTILVSHDRNFLNAIATDIHLHSQRIDGYR\ GDFETFIKSKQERRAQ\QREYEAQQYRQHIQVIFDRFRYNANRAS QVQSKLMLEKSELKPVDKES*VVMKFP*WV*EALRRPFCSLDEVD FYYPKHVIFK\RLSVSADLESRICVVGENGAGKST\MLKLLG\DL APVRG\LRHAHRNLKIGY\FSQHVEAAWT*TSVLVELLARKFPGRP EEYRHLGGRYGISGELAMRPLASLSGGQKSRVAFQMTMPCPNFYI LDEPTNHL\DMETIEALGRALNNFRGGVILVSHDERFIRLVCRELWG

				MRRRR\VTRVEGGFDQYRALLQEQRREGFL
2127	A	45	339	PPRTPSPVAG*LRAS/STPPRSSSSSSSSSPRKGLSLRPQEALPPP PCPSCRSSAPSAPRGGRGETPNKGTGGSLLCQSCHHPVDVQAVLNKC FEADE
2128	A	484	1879	FQQORMAGELKPCSNLLEQSILLAKGTS\GSSLTALISQVLKAP*VY VFGELLELCNVHELAE*ANAAYLQLLNLFAYGTYPDYIANKESLP*L STAQQNKLKHLTIVSLASRMKCI PYSVLLKDLEMRNLRELEDLIEA VYTDIIQGKLDQRNQLLEVDFCIGRDIRKKDINNIVKTLHEWCDGCE A\ALLGIEQQVLRANQYKENHNR/TLQQQVEAEDVYILPQSGNDCRG LRFVSSSLIGGVRCVHLKHKGDVWWEAIEEGEALPGKYRLKGGRSVW AAAVRAVCMDQVTNIKKTLKATASSAQEMEQQLAERECPPHAEQRQ PTKKMSKVKGLVSSSPLGPAGAAGTHQAWVRWGGDTKGPPPLSTCS EFQTCPSPHQRLPTLLVLFQKNCYSPSPTPSPFSCSLQQTGLHQCHP KTGSDTAQLPSRRFLSLCKGLVSLPVFLLPRHFVRLVISRRQL
2129	A	225	415	RMWWESNNYQSFCLPSESEPEDLENGEESSAELDYQDPDATSLKY VSGDVTHPQAGAEDAL
2130	A	356	1024	GRAEPEDLENGEESSAELDYQDPDATSLKYVSG*CHPPSGWG/HEDA LIVHCVDDSGHWGRGGLFTALGKA/SPLKPRKIYELAGENEKTLSLG GVLLFPV***KIQDTKGKICWP*LWLSIVNRSNVLSGI*DGSPIRRA *RRY/CLAAKAGKSSVQPPHVLDMPRKGFKRVGPPEPTLFGKHPGL QRGHPQPYHILFPLEGKSACPFHSQFFILPSLKDSWCP
2131	A	3	205	ERSAAETVTKGGIMLPEKSQGVQLQATVVAVGSGSGKGGGEIQPVSV KVGDKVLLPEYGGTKVVLDD
2132	A	3	205	ERSAAETVTKGGIMLPEKSQGVQLQATVVAVGSGSGKGGGEIQPVSV KVGDKVLLPEYGGTKVVLDD
2133	A	1	428	SFTSAGRLEKPRNSSFFLPPPSLRVSVLRRALGANRGARRGDRPPSL GGARGLAATAGASAPARWVIFSRVARAGLRVSLRRYTRAEBESEAEGB VMGGEIQPVSVKVGDKVLLPKYGGTKVVLDDKDYFLFRDGDILGKYV D
2134	A	36	417	QAFRKFLPLFDRVLVERSAAETVTKGGIMLPEKSQGVQLQATVVAVG SGSGKGGGEIQPVSVKVGDKVLLPEYGGTKVVLDDKVKCP**F*KEV RYLQLVVLVTNGFFHLQDYFLFRDGDILGKYVD
2135	A	496	751	ISLLNKHPSFFKGGEIQP\VSVKVGDKVLLPEYGGTKVVLDDK/DV* T**F*KEVRYLQLVVTNGFFHLQDYFLFRDGDILGKYVD
2136	C	92	265	MSLVIIRFIIKGEIWEIIYMTERISGTSSGMGRHHVDAISNSDLFQS TVLSKNCNNL*
2137	A	330	875	AYAAGFGDSCLIAMSGRGKQ*GKVF\AKAKSRSSRAGLQPPGGRVHR LLRKGNYAERV\GAGAPV\YL\AAVLEYLTAEIL\ELAGNAARD\NK KT\RIIPRHLQLGHPATTEELNKLA*GRVTICFRGGVPS*TSRAVL\ LPKKTESSPQGGQSDFDRYLELPRKRYSNPKGSFSEAPLPFQRKS
2138	A	25	414	LKLVAPCRPSRSLRSSPISRRASTTRCLTIEKAKPIKCGTFGATSLQ QRYLATGDFGGNLHIWNLEAPEMPVYSVKGHKEIINAIDGIGGLGIG EGAPEIVTGSRDGTVKVWDPRQKDDPVANMEPVQGE
2139	A	1	65	RTRGRTRGNLSFI*NHM*QIA
2140	A	293	445	SPSGYGR*SEASRRPTWCSQFQLRQPPHPEPPKSATWNQTPNIGNLS LPL
2141	A	544	1553	CQMRSCDRTECSFTTARICLSPLPTAFRTHTYGPKSCRS PACDVLGK GRSCRGGWLRRLASAWCSCARVSAGSALRFGMESEMETQSAGAEEGF TQVTRKGGRRAKKRQAEQLSAAGEGGDAGRMDTEEARPAKRPVFPPL CGDGLLSGKEETRKI PVPANRYTPLKENWMKI FTPIVEHLGLQIRFN L\KSRNVEIRTCKETKDVSDSKRQTD FVK\AFILGLSGWKE*HLTL IRL\DDLFLF\SFEITDVKPLKG\DHLSRAIGRIA/GAKEGKTKFTI E\NVTRTTIVLADV K V H I L G \ S F Q N I K M A R T A I C N L I L G N P P S K V Y G NIRAVASRSADRF
2142	A	1055	1223	SSPGNLNVQEGFRITGLICY*KQYQY*MCFLFLL/SLYVCVVFDFLL LLLFCGHPLH

2143	A	2	258	SPGRTAMRSWSCRPCGGGGLG/SSQGRSEPGSSRLGPAPS/CGLTHP CRRGPSCPHPCPAGCRTCGGICPGPHPTSRCPSPSRNCGQT
2144	B	1	2848	MARRPRNSRAWHFVLSAARRDADARAVALAGSTNWGYDSQGQLLQVT CLSLTGSWLWDAGVPAGSAVFDTCACPVSPNGPAVCCGQEHSDSDS DPEYSTLPPSIPSAVPVTGESFDCACQSEASFCSLHSAHRGRDCR CGEEDEYFDWVWDDLKSSATLLSCDNRKVSFHEYSCTAAIRGTK ELGEGQHFWEIKMTSPVYGTDMVMGIGTSDVDLDKYRHTFCSLLGRD EDSWGLSYTGLLHHKGDKTSFSSRFQGSIIIGVHLDTHWGTLTFFKN RKCIRIKEAWSPLTRLPQPCLPQMALRKGNVSFGGRRSRVPTCPP TAVPRSPPAAPDQGLDAGRRPGPGAAAALVGGTGPPQLEGNKPPKRG ATMTTRMSSASSAAPGTSRACMMESRAATQALWLDGNNLSSVPPAAF QNLSSLGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGT FAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNLSLAVLPDA AFRGLGSLRELVLGNRLAYLQPALFSGLAELRELDLSRNALRAIKA NVFVQLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVAGLL EDTFPGLGLRVLRLSHNAIASLRPRTFKDLHFLEELQLGHNRIQRL AERSFEGLGQLEVLTLHDHNLQEVKAGAFGLTNVAVMNLSGNCLRN LPEQVFRGLGKLHSLHLEGSCLGRIHPHTFTGLSGLRRLFLKDNGLV GIEEQSLWGLAELELDLTSNQLTHLPHRLFOGLKLEYLLLSRNRL AELPADALGPLQRAFWDVSHNRLEALPNSLLAPLGRRLRYLSLRNNS LRTFTPQPPGLERLWLEGNPWDCGCPKALRDFALQNPSAVPRFVQA ICEGDDCQPPAYTYNNITCASPEVVGLDLRLDLSEAHFAPC*
2145	A	3	630	RSGGSASSGRAEARDCWGRRSLPGDRTLEPCGGCNSCSGSPACCV APA*GPAAAADPPACLPSLAAAGAGGGSTGTGGK\CAGTG/GG*PSC CSGPPWSTPSGRISC/CCSLVAATPGREGPSLYTSCS*KR*VCRARC PGARQ*WSPGRTATRSWSCRPCGGGGPCRRGPSCPHPCPAGCRTCGG ICPGPHPTSRCPSPSCRRRERS
2146	A	16	716	SVLESKGQRNKGQRKGPVPAQEGSSTGKSVRSGGSASLWQGGQSRTA GVGGGRCPGDRTLEPCGGCNSCSGSPACCVAPA*GPAAAADPPACL PSLGSR\CAGGGSTGTGGKWRWHRSG*PSCCSGPPWSTPSGRISC/C CSLV/CCHTY/ITSCS*KR*VCRARCPGARQ*WSPGRTATRSWSCR PCGGGGPCRRGPSCPHPCPAGCRTCGGICPGPHPTSRCPSPSCRRRE RSS
2147	A	260	1384	ELVPRSLGNLLRPPMPTPHEAEKQITGPEEADRPPSMSSHDTASPA PSRSP\CCLCWC*CCNCSWNQORRRRAWQASRESKLQPL\PICEVCAT PSPPEVQSWAQSFDKLMHSLAGLSVFRAFLRTEYSEENMLFWLACEE LKAEANQHVVDEKARLIYEDYVSILSPKEVSLDSRVREGINKNMQEP SAHTF\DDAQLQIYTLMRDSYPRFLSSPTLPVPCLLQGPFVLP GLRPPPSSTDPAASYGRLWVPFRCWCRCQCGTCLAGWGPHPKTVL RPSWEVLCLLGLPTRGQAGTPGAGRASRCRAGQKPPHRPAAGWPSAP GWGLLRGESKSPQEPWCWTHEPRWGLLHRQPMGPRQAFGGEQNLRI V
2148	A	123	489	LKCNFRLDKYCGGTAMSGGEQKPERYYVGVVDVGTGVSRAALVDQSGV LLAFADQPIKNWEPQFNHHEQSSEDIWAACC/VCHKGDSHRNVIMWL DHRAVSQVNRINETKHSVLQYVGGVMSVE
2149	A	2	321	ASLIDAHAGGLGVIGADVRGHGLICEGQPVTSLAVICGTSSCHMGI SKDPIFVPGVWGPYFSAMVPGFWLNEGGQSVTGKLDHVMVQGHAAFP ELQVKATARSPD
2150	A	257	565	INKDPIFVPGVWGPYFSA\MVPGFWLNEGGQSVTGKLDILSTNTPHP ITILGNTNSILKTQLQHQPFLITSPHIPKTPQTSRTDQASFLCSPS SDSLQILSL
2151	A	1	291	VADLTCLKGMTGLKLFQDLEYLAILYLATVQAIALGTRFIIAMEAA GHSISTLFLCGGLSKNPLFVQMHADITGSNGKNEQSWESCVPETTG* KIL
2152	A	1	1690	FRDDPRVRARLRAESVYLKFNFRLDKYCGGTALSGGEQKPERYYGV DVGTGVSRAALVD\QSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAA CCVVTKKVQIDLNQIRGLGFDATCSLVLDKQFHLFVNQEGDHS

				RNVIMWLDHRAVSQVNRINETKHSVLQYVGGVMSVEMQAPKLLWLKE NLREICWDKAGHFFDLPDFLSWKATGVTARSLCSLVCKWTYSAEKGW DDSFWMIGLEDVADNYSKIGNQVLPPGASLGNGLTPEAARDLGLL PGIAVAASLIDAHAGGLGVIGAHVRGHGLHL*GAASDVT\LAIVCGT SSCHMGISKDPIFVPGVWGPYFSAMVPGFWLNEGGQSVTGKIDHNV QGHAAPPELQVKATARMPEYILHI*TVTWDL*GRVQPVGFSFTV*F YMFGPDFHGNRSPLADLTCLKGMVTGLKLSQDLDDLAAILYLATVQAIA LGTRFIIIEAMEAAGPL/ESSTLFLCGGLSQE/YPLFVQMHADITGMP VVPVARGGSPFLCGAAVLGACASGDFASVT\EAMAKMSKVGVVFP LPE
2153	A	1	479	AATSWGAAQTISSPILDKSLPADISIEDQQCLVFRDVPAPVHFLV IPKKPIPRISQAEEDQQLLGHLLLVAKQTAKAEGLDGYRLGE*LL ALGPSMPNHSYFSI*SSFFDLCHDPDSLTPSSISVINDGKLGASV YHLHIHVLGGRQLQWPPG
2154	A	284	604	RERRDIGCWSSSSAWGNPREWGFLGNDQGRCTGSLRGPTSREHKT AGPHKRIVSWGSCPRIRGEDGWGCSPRSWSLAGALATFIP*KAPFPR ITPG*RRRPAATYVPPLSL*LLGHLTPMWLSRQRLRGLGDGYRLVI NDGKLG\QSVYHLHIHVLGGRQLQWPPG
2155	A	496	1579	NCLNSFSCSMNQMYLLIALMTIEYNLAYDSYYICIHFIKIVYKLT FFLQML*ILMQIFW*GSLFLL*FQLIRDLPPAFSLR*KLCPHLLK YKGILWKQIILVLC*R*ILIILMCDLFALSGIIVFLSFIMRKFSHL* VTVKFIYMSIPRRPVQIL*EHLGLQDIIGI*ILISCY**ENRYSIVI PLF/CF/VILITHFGFFSLF*I*LLVFV**F*FNNPNQQYI*FI/CF LSNLTTFFLCFLVGG*/CFVKGIIIV*DHCFTCTFLHVF*STFIY*A F\GLE*FHQMNTFW*FVMSSSNCTLLGT*Q*ICKGRNNFLYSANL NFI**IIHFFLKIVWIDCF*NTNLWLWFFFSSAFPASK
2156	B	302	451	XEFLFKHPKRTATLSMRNTSVMKKGIFSAEFLKVFLPSLLSHLLA IGLG*
2157	A	1	765	PPLSPGAHVGRGAPTSAPPPAAEAHPAARRGLRSPQLPSGAMSQNG APGMQEEESLQGSWVELHFSNNGNGGSPASVSIYNGDMEKILLDAQH ESGRSSSKSSHCDSPPRSQTPQDTNRASETDTHSIGEKNSSQSEE\D DIERRKEVESILKKNSDWIWDWSSSAGKIFPPKEFLFKHPEAARPTL QA*G\NRAVMKKGIFSA/ENFLKVFLPSL\LLSHFAGPSGLG\IYI GKGVLTTSTSTFWMKELGVLTLVR
2158	A	1	381	HRQHPCIPHTTPTLSHCRRGGHKARFPRAQNPKREIQKILEFVGRSL PEETVDLMVEHTSFKEMKKNPMTNYTTVRREFMDHSISPFRMKGMAG DWKTTFTVAQNERFDADYAEKMAGCSLSFRSEL
2159	A	2	312	TGRIPGHASGDSKILEFVGRSLPEETVDFMVQHTSFKEMKKNPMTN YTTVPQEFMDHSISPFRMKGMAGDWKTTFTVAQNERFDADYAEKMAG CSLSFRSEL
2160	A	1	576	MRRARAMAFGPPRPQGTAVPPLAPSPSLSRTRGPRGLCALRALEL QGRNMELIQDISRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDL STYPKSGTTWVSQILDMIYQGGDLEKCHRAPIFMRVPFLEFKVPGIP SGMETLKNTAPRLLKTHLPLALLPQTLDDQKVVRGLTVVHTRNLS TLGG
2161	A	2	313	VSYHFRMEKAHPEPGTWDSFLEKFMAGE/VWA*LEECCAEAGWW L*RTATLCRCPLPASLVSYGSWYQHVQEWELSRTHPVLYLFYEDMK EVRPTVMLPPM
2162	A	901	1848	RRNMELIQDTS\RP\PLEYV\KGVPLIKYFAEALGPLQSFQARPDDL LINTYPKSGTTWVSQIL\DMIYQGGDLEKCN\RAPIYVRVPFLEFKA P\GIPLRMETL\KDTAP\RLIKSHLPLA\LLPQTLDDQKVKVYVA AQRKRSVAVSYHFIY\MAKV\HPEPG\TW\DSFLGESSLV*KVVL ADSWYQHVQEWELNRTHPV\YLFY\EDMKENPEKGRFQKDPWSLG GRSLQEKTGDFQ\VQ\HTSFKEMKKNP\MTNLHPTVPPGSSMDH\SI SPLP*GKGMAGDWKT\TFT\VAQNER\FDADYAEKM\AGCS\LSF\R SEL

2163	A	3	287	HEEGSIEIDIPVPKYLSVSSQETQGGPLAPMTGTIEKVFVKAGDKV KAGDSLMVMIAMKMKLSSQKDKVRQFMIFTQSSEKTAVRLSFSK
2164	A	75	301	AHKKLRAAPLAPMTGTH*K\VFVKAGDKVKAGN\PSWVMFPMKMEHT IKSPKDGTVKKVFYREGAQANRHHSFSRV
2165	B	63	368	MKGGRSPASPAKADGSHCDPKTAPKAKEAPAPPKAEAKAKALKAKKA VLKGVRSHTQKRRSACHSPSGGPRHCDSGGSPDILGRAPPGETSVAT MLSSKFR*
2166	A	153	372	LIAGAFRKASGGNNIFRRPKTL*LRRQPR*PQKSTPRRNKLGHYAI KFPLTTESAVKKIEETNTLVFTVLV
2167	A	842	1770	CTPEKCLPAVHRRNWLRNAEPPVWKRHLSPICRKRQGRATKPKRRPW YTPPTRRVRDVALRPYSRH/GRQPHAKKKIRMSLTFRRPKTLRLRR QPRYPRKSTPRRNKLGHYAIKFPLTTESAVKKIEENNTLVFTVDVK ANKHQIRQAVKKLYDSVAKHTEERRHDEQNNILTREAKNRNDNTRN RARTETNTETQKNSGYQALISFHSYSDTS DNKAHLVSYQSGQCTYD RLGWNLLIRMTCRSLQHTYDIQSTQIASCFHPVSVRVNLRLYCANYG GISAVFMPLRKELLILTRSSNSKVSQRLI
2168	A	3	281	KAKKEAPAPPKAEAKAKALKAKKAVLKGVHSHKKKKIRTSPTFRRPK TLRLRRQPKYPRKSAPRRNKS VLPVPMKRFSGYSLVIWKFTSHA
2169	A	353	605	EMAPKAKEAPAHPKAEAKAKALKAKKAVLKGVRSH/TKKKIRMSLT FRRPKTLRLRRQPRYPRKSTPRRNKLGHYAIKFPLTT
2170	A	301	946	PGSYLKPLSWTVALSLRPGFMSRWPCQRLTWQRRSVTQASGASGASL CASRLPRDKTAPKAKEAPAPPKAEAKAKALKPKKAVVERCPHTHAKK RIRMSPTFRRPKTLRLRRQPRYPRKSTPRRNKLGHYAIK\FPLTTE \SAGKKNNKNTPLVHCGC*RPTRHQI\QOAVKK\LYDSDV\AKVTT LICPDKEKKAYVRLAPDYDALDVANKIGII
2171	A	1	1602	MHLIPPATNCDTLVECCLPGLTRDLVCTAFTGFGTSYSPQENSHNH SALHSSNSHSSNPSNPSKTS DANILSQTSRHNDRDYRLPRAETHSS STPVQHPIKPVVHPTATPSTVPSSPFTLQSDHQPCKSF DANGASTLS KLPTPTSSVPAQKTERKVLQQLSKHNRKVMIRSALITSII LDLLYIE KDLRYQKNIESTSGDKPVSHSCTTPSTSSASGLNPTSAPPTSASAVP VSPVPQSPIPPLLQDPNLLRQLLPALQATLQLNNSNVDISKINEAQP SNQSPMSLTSDASSPRS YVSPRISTPQINTVP I KPLISTPPVSSQPK VSTPVVKQGPVSQSATQQPV TADKQQGHEPVSPRSLQRSSSQRSPP GPNHTSNSSNASNATVVPQNSSARSTCSLTPALAAHFSENLIKHVQG WPADHAEQASRLREEAHNMGTIHMSEICTELKNLRS LVRVCEIQAT LREQRILFLRQIQIKELEKLNQNSFMISASKTGSTKGLF FMLDINVN VTTFS DANINFEIALVL
2172	A	243	620	LLTSSKVMNLSLLEVFS/VSSSQRSPPGNHTSNSSNASNATVVPQ NSSARSTCSLTPALAAHFSENLIKHVQGW PADHAEQASRLREEAHN MGTIHMSEICTELKNLRS LVRVCEIQATLREQR
2173	A	3	688	QRSFLRVPQSPIPPLLQDPNLLRQLLPALQATLQLNNSNVDISKIN EVLTAAVTQASLQSIHKFLTAGPSAFNITSLISQAAQLSTQAQPSN QSPMSLTSDASSPRS YVSPRISTPQINTVP I KPLISTPPVSSQPKVS TPVVKQGPVSQSATQQPV TAG/PGPRS/SEPVS PRSSALK*PEKSI TWVPIHTS\NSSNGIQMATVVPQEFFLARSTCSLTAGTSSTLQ
2174	C	1	1038	MEDFTTPLSTLASSMRQKVNKDIQDLDSALQQADVIDIYRTLHPKST EYTFFSALHCTYSKSDHVGSKALLSKCKRTEITTCNVSDHSAIKLE FRIKKLTQNRTTTWKLNLLNDYWVDNEMKAEIKVFFETTQHDQNF TKARCIQEHRTPYSQSFKLKAETRDPSFTKNVQKMKRVRDADLAVA ALSRLRGKVWVKAWPPLRGCRVLGCCFLAFCIRSLMDVKHSCPVCQ RELFFYYHRLPRSPRSAYLAVRDIGPKMARDTVNLWPQARDPENAS PALLQTHAEKVLVRRVSGSLGTTLPRRGDDPTPERQISFLKCLLKKL SHGFGSEGAMPEEISH*
2175	A	1	1312	MGRNQSRKAENSKHESTYSPPKDHSSSQAMEQSWTENGFEKLGFRRK EALYYLDLTASCQSQELFQLYAGMSVVGTSMPVQAVCPYCGNRIITV TTFVPGALTWLLCTTLFLFGYVLGCCFLAFCIRSLMDVKHSCPVCQR

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				ELFYHRLRQMECLASSARTVVAPSRPCAGREGRGDANGKNSSPTAGS AMSSEPPPPPPQPPHQA\GVGLDTPRSRERSPSP\LRGNVVP\SPL PTRRTRTFS\ATVR\ASQGPVYKGV\CKFCRSQRAIGFNYPPAGWA GPDIF/LWHIS*LWKGGVIVPSGKGDEGHPNKMCSHPHPKE*R/IAA RPVKVVHHLTLAPQAPKHET\WS\GHVISSLGGLVESTPLSLCFVGD FAGRRQQTLEDDILPHETGLQRNGGPSQVSPGGKGYGGAGVGCVFPP AISTAYGPLQQPLHHLKSIKSI
2176	A	75	413	PIITKEHLFYVILVPSSGLDGIQG*SQKEGRGLAVPTPVSVAAGLPA ASMAEEAADQVGRAALAWLCPAGRRRGFGGEVMRALVASRPDLLTIS ASSGVALGSEGRVKASAD
2177	A	1	361	GIKRRSGREATRALITSPNPFRFPAGQSQARAARPTWSAASSAMEA AGSPAATETGKYIASTQRPDGTWRKQRRVKEGYVPO\RRSQYMKTSM *SFSRVNQSCPQG*ALRPLLLSPHPGPEGGEPLQGGQPNVNLEGER EKEAAAGKRKERAEGLSKDS*LRCPWEETAQLPSAPQGSRAAPTAAS DQPDASAATTEKAKKIKNLKKLRQVEELQQRQIAGEVSQPSKEQLEK LARRRALEEELEDLELGL*GLSPEATAPVTPSRA
2178	A	24	405	GGKNN*NCKRD*WNCKL**CQF*QL*AKDI*KSNREHK\LTNGSNGR NTESPAAIHPCGNPTVIEDALDKIKSNPDPTTEVNLNNIENITTQTL TSPSFFPKAATSSSSPSFTPREKAHYQKHCRSH
2179	A	1	456	SRFDPVRVQKQQEGYDGGPNFITKVVQRTGTPSSSPYVSPRHSPWSSP K/RPPPPSSSQRLLPPPPPPPPPLPEKKLITRNI AEVIKQQESAQRA LQNGQKKKKGKKVKKQPN SILKEIKNSLRVQEKKMEDSSRPSTPQR SAHENLMEAIR
2180	A	215	369	TLPPPPPPSSSQRLLAPPPPPPPPLPEKKLITRNI AEVIKQQESAQRA LQNG
2181	A	1	3405	MDTNDPDEDHLTSYDIQLS IQESIEASKTALCPEFVPLSAQNRKL VEAIKQGHIPELQEYVKYKAMDEADEKGFPLHEAVVQPIQQILEI VLDASYKTLWEFKTCDGETPLTLAVKAGLVENVRTLLEKGVWPNTKN DKGETPLLIGICVNILTVVFNHNFQAVKKGSYDMVSTLIKHNTSLDQ PCVKRWSAMHEAAKQGRKDIVALLLKHGGNVHLRDGFGVTPLGVA AE YGHCDVLEHLIHKGGDVLALADDGASVLF EAAGGPNDCISLLLEYG GSGNVPNRAGHLPIHRAAYEGHYLALKYLI PVTSKNAIRKSGLTPIH SAADGQNAQCLELLIENGFDVNTLLADHISQSYDDERKTALYFGVSN NDVHCTEVLLAAGADPNLDPLNCLLVAVRANNYEIVRLLLSHGANGVN CYFMHVNDTRFPSVIQYALNDEVMLRLLLLNNGYQVEMCFDCMGHDIF GNSFWWSEIQEEVLPGWTS CVIKDNPDLSSKVTVMVTLRREPYQGD RCLGCSPTSFFLILQRTTLSKLV RPTLGVSQQRKGLSSEDLFETAP SGSDKAGTMSTFGYRRGLSKYES IDEDELLASLSAEELKELERELED IEPDRNLPVGLRQKSLTEKTPTGTFSREALMAYWEKESQKLEKERL GECGKLSVVARHDEQELADGGCKSNSHNRENRAAVGWLGEQGSCVA EDKEESEELIFTESNSEVSEEVYTEEEEEESQEEEE/DRQ*RRGK NN*NCKRD*WNCKL**CQF*QL*AKDI*KSNREHK\LTNGSNGRNT SPA AIHPCGNPTVIEDALDKIKSNPDPTTEVNLNNIENITTQTLTRF AEALKDNTVVKTFS LANTHADDS AAMAI AEMLKVNEHITNVNVESNF ITGKG\ILAILRALQHNTVLT E LRFHNQRHIMGSQVEMEIVKLLKEN TTLLRLGYHFELPGPRMSMTSILTRNMDKQRQKRLQEQQEGYDGG PNLRTKVWQRTGTPSSSPYVSPRHSPWSSPKLPKKVQTVRSRPLSPVA TPPPPPPPPPPPSSSQRLLPPPPPPPPPLPEKKLITRNI AEVIKQ ESAQRAIPNGTNNEIREQQGETAKQYSGKNIKFSEVSAREENGRQFP TFYPT EISS
2182	A	3	140	GHFPCALKSVVPPDEKHWNDLAEFHYMRVWLASFISMRKIQRRI
2183	A	365	2078	NLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIA NRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVI VESGEPVGTRE IKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTLERCLQSLE KSQDVSVHITSNYLKQILNAAHYVEVTFHSGSSVTRMLWEQIKQIIQ RITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFTRLNSSH

				EAFASLRQLEAGHSGRL\ EKTEDLW\LRVR\ KDHAPRLARLSLESC SFTGCLCLHRKP\ KLGQELGRGQYGVVYLCDNWGGHFPKALKSVVPP DEKHWNDLALEFHYMRSLPKHERLVDLHGSVIDYNYGGSSIAVLLI MERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVHRDIKL KNVLLDKQNRAKITDLGFCKPEAMMSGIVGTPIHMAPELFTGKYDN SVDVYAFGILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERL PVFDEECWQLMEACWDGDLKRLPLGIVQPMQLGI/L*NRLCKS\NS EQPNRGLDDST
2184	A	2	468	GPEAVPHRACSLWLPTPSGPTCPATRHSEHEFTFQMWPGCASSSLLC VGTPGEARADHRCMRVTPVHLGLPGWVGAGARPHCCESATPGGPRG CPTP/DDWVAAHIPPSPFK*GNPGCIRGDPRLWPLCPMTCVASDK APALLGSACCSVWSVR
2185	A	170	1224	PVWRGPAGPTPGIPSTTEKHTRLPSANMMVLKV\ EELVTGKKNGN\G EAGEFLPEDFRDGEY*AAVTL\ERQEDLKTLLAHPVTLGEPQLRKRE THERAELKKKKLEQRSKLENLEDLEII IQL*EK/RKKSRETKVPVLK DPEP* IHYGTCWECPTFLKA/SLWENNLPVVEKFLSDKNNPDVCD KRTALHRACLEGHLAIVEKLMEAGAQIEFRDMLSTAIHWASRGGNL DVLK\LLLNKGAKISARDKLLSTALHVAVRTGHL*GCAEHLIACEAD LNAKDREGDTPLHDAVRLNRYKMIRLLIMYGADLNIKNACAGKTPMDL VLHWQNGTKAIFDSLRENSYKTSRIATF
2186	A	158	429	TSSGRENTVSWLTAGEENALFLWQASVGSVIKMMAGCGEIDHSINML PTNRKANESCSNTAPSLTVPECAICLQTCVHPVSLPCKHVFYCY
2187	A	1	192	EREKRKQQQEPLRKKAKMQTVRPGFDLTQGPNCCLTPHGKTSRSLPPK NHRRPYTSRPEGPRVKA
2188	B	1	819	MTKWSNPNQIHMELQRTLSNPNNLEKSNVKTYKAKIFDDNLIQLTF QQHRQDRDTEQEKKEEEREKRKQOPETLREKAKMQTVRPGFDLTQG PNCLTPHGKTSRSLPPKNHRRPYTSRPEAGAAPAQGRPSTYRPLTTP PPLSGPERKADPEYVAAGGDTASYASSPRVRILEWPAFTLLPREGLA PTPTSPATAAATSQSFLSGLGARSERARPSQCACFVLGPRGSERV QFQQKEIWGGGSKTCVGPAGGAAQKSSFAILRLKLWGA*
2189	A	694	1482	PVPECAICLQNM\ VHPVSLPCKHVFYCYLCVKASWAWESGCALCRQG NSRGISLIDKANLVVHQEGTQGGASRREVMNMHGYEGRNGWVAGRWS ALVGELEDAFSKG*K\ATEMLIAGFLYVADLENMVQYRRNEHGRRRK IKRDIIDIPKKGAVAGLKLDCDANTVNLARESSADGADSVSAQSGASV QPLVSSVRPLTSVDGQLTSPATSPDASTSLEDSFAHLQLRWRQHSL TGHRGEGEEDHGITIFQGRVPGTRHLH
2190	A	93	458	LLLWTMSVIFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLAL RLAQYPGRGSAEGCDFSI\HSIIQVKWHFNYVSSSQMECSLEKIQE ELKLQPPAVLTLEDTDVANGVMNGHTPM
2191	A	1077	1818	LLLWTMSVIFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLAL R\LAQYPGRGSAEGCDFSIHFS\SFGDVACMAICSCQCPAAMAF\CF L\ETLWWEF\TASYDTTCIGLASRPYAFLEFDSIIQVKWHFNYVSS SQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPN FRMEPV TALGILSLILNIMCAALNLQPQHVYLQGLDLGAH/HRKSF IGREKGNILVF*VDMIQ
2192	A	1	999	MRALRAGLTALGAGLGAVVEGWRRRRREDARAAPGLLGRLPVLPVAA AAELPPVPGGPRGPGLAKYGLPGLAQLKSRESYVLCYDPRTRGALW VVEQLRPERLRGDGDRRECDFREDDSVHAYHRATNADYRSGSGFDRGH LAAAANHRWSQKAMDDTFYLSNVAPQVAPAPRAGRGMGRRLASRGL GLFFCRTGQLPNAPPVPHLNQNAWNNLEKYSRSLTRSYQNVYVCTGP LFLPRTEADGKSYVKYQVIGKNHVAVPTHFFKVLILEAAGGQIELRT YVMPNAPVDEAIPLERFLVPIESIERASGLLFPVNILARAGSLKAIT AGSK
2193	A	1544	1928	QKVRGQIREGCLEEVALGSSRPPAHVCLGLPTGQTADGKSYVKYQVI GKNHVAVPTHFFKVLILEAAGGQI\ELRT\YVMPN\APVDEAIPLEA FL\VPISIERASG\LLFVQNILARAGSLKAITAGSK

2194	A	2	1068	ARGWVPRPKPLAVFVSGREVTLSAAPAALCPRWIPRRGSFKSLAGR PPLGRSPAMRALRAGLTASGAGLGAVVEGWRRRRREDARAALGLLGR LPVLPVAAAAELPPVPGGPRGPGELAKYGLPGLAQLKSRESYVLCYD PRTRGALWVVEQLRPERLRGDGDRRECDFREDDSVHAYHRATNADYR GSGFDRGHLAAAANHRWSQKAMDDTFYLSKVAPQVP\HSNQIAWNNL \EKYSR\SLTRSYQNVYCLH*GHFFLPRTAD\GKSYVKYQVIGKNH VAVPTHFFKVLILEAAGGQIELRTYVMPNAPV\DEAIPLERFL\VP ESIERASGLLFVFNILARAGSL\KAI\TAGSK
2195	A	204	507	GSPGTRSETREPGAMSQPPAPPPPLPPPPPPPEAPQTPSSLASAAAS GGL*SGETGESFPGAARIRSVRRVYFSRPPVLSASSVPSAASGTSS NSCWGLRR
2196	A	1	460	EFKQLIHIEHQPNGGASVIHAYSNELSHLSPMEMERFARKSLVGS* SSENENSGSFPT*WGIV\HGAATYLP\DFLDYFSFNFP\NSP\VKME ILGKKDIETTTMSNFHAQSLTVLQPGRQSETPSQKKRKKFMIMLSSR WEGETKNKYRRLTN
2197	A	199	769	APAQLRLRAMQPRVLGALPLCLLLPSPSSSRSSFSFSAGTAVPSSAS ASLSQPVPRKLLVPPTLLHAQPHHLLLPAAAAAASANAKSRRPKKEKR EKERRRHGLGGAREAGGASREENGEVKPLPRDKIKDKIKERDKER EKKKKVMNEIKKENGEVKILLKSGKEPKTNIEDLQIKKVKKKKKK KH
2198	A	182	2889	TEKGAAAGTAGSCSRQHASPOSYGSPASWSFAPLSAAPSPPSSSRSS FSFSAGTAVPSSASASLSQPEPRKLLVPPTLLHAQPHHLLLPAAAAA ASANAKSRRPKKEKERRRHGLGGAREAGGASREENGEVKPLPRAN DKTRSFDDFSPDQAAAECLSRKRRILKGCQTGYLRKALPSDTVTL GIKASTYGFWGGMIQSIKGLAETFNFWIHIWELNDLQYISALFACS EEMPDYHLEKQLADKIKDKIKERDKERKKKKVMNEIKKENGEV KILLKSGKEPKTNIEDLQIKKVKKKKKKKHENEKRRPKMYKSI QTICSGLLTDVEDQAAKGF\LNDNIKDYVGKNLDTKNYDSKIPENSE FPFVSLKEPRVQNNLRLDT\LEFKQLIHIEHQPNGGASVIH\AYSN ELSHLSPM/EGWERFAEEFVG/L*VFSENENSAAFYVMGIVHGAATY LPDFLDYFSFNFPNSPVKMEILGKKDIETTTMSNFHAQVKRTYSHGT YRAGPMRQISLVGAVDEEVGDYFPEFLDMLSESPFLKCTLPWGTLLS LKLQSRKDSDDGPIWVRPGEQMPVADMPKSPFKRRTTNEIKNLQ YLPRTSEPREMLFEDRTRAHADHIGQGFERQTTAAVGVLKAVHCGEW PDQPRITKDVICFHAEDFLEVVRMQDLHEPPLSQVCVQWVDDAKLN QLRREGIRYARIQLYDNDIYFIPRNVVHQFTVSAVCSLAWHIRLKL YHSEEDTSQNTATHETGTSSDSTSSVLGPHTDNMICAVSKASLDSVF SKLHSHKYELQIKHEPIASVRIKEEPPVNVNIPKTTALNNMDGKNV KAKLDHVQFAEFKIDMSKSFENSNDLKEELCPGNLSLVDTRQHSSA HSNQDKKDDILC
2199	A	2	122	LEYCLCWILFAGFMSFSGLCTPSFCWSIFSNSFPKKGTR
2200	A	1130	1437	LSRIMKAWFPLFFKIPFRDKVFFLSPPAWSAVAQSRLHCSLELVGSI NSSISAS*LGWEY\RCAPQCPG*FL\FFCRDGAALPCCPSWSQVICLP *PPKALGLQA
2201	C	279	449	MHPVSCWVIMSCRPLCTRLILSDSPPGPPSPDICVSRKNPSNYPAMVL PQCFTICII*
2202	A	1	1173	MSELRLCCDLLVQVQDKTKEVTTTGVSNSEEGIDVGTLKSTCNTFL KTLLEECMQIANAAFTSELLYHTPPGSPQLAMLKSSKMKHPIIPIHNS LERQTELSTCENGSLNMEINGEEIILMKNKNSLYLKSAEIDCSISSE ENTDDNITVQGEIMKEDRMENLKNHDNLSQSGSDSSCSPECLWEEG KEVIPTFFSTMTSFSDIELLEDSGIPTEAFLASCAVVPVLDKLG TVFAPVKMDLVENIKKVNQKYITNKEEFTTLQKIVLHEVEADVAQVR NSATEALLWLKRLKFLKGLTEVKNGEKDIQTALNNAYGKTLRQHH GWVVRGVFALALRATPSYEDFVAALTVKEGDHRKEAFSIGMQRDL SLYLPAMKKQMAILDAL
2203	A	1	2112	MGVELFTPASVMGVKRCCSIPGQLSGNGEPRFSEIDSSVSVRGGWQ

				PRWFLLCGGILSYDSDPEDAWKGCKGSIQMAVCEIQVHSDNTRMDL IIPGEQYFYLKARSVAERQRLVALGSAKCLTDSRTQKDKFAENT ENLKTMSSELRLCCDLLVQQVNKTKEVTTTGVSNSEEGIDVGTLKLS TCNTFLKTLLEECMQIANAAFTSELLYRTPPGSPQLAMLKSSKKNQK YITNKEEFTTLQKIVLHEVEADVAQVRNSATEALLWLKRGLKFLKGF LTEVNKGEKDQTALSFSSN/SCT/CIWRLGPGDVLTL*RKRR*RA NAAL*LQ*SQPVSAFSSLSPP/CGTIFNGKEKGCKFDIFVLMFRLI SKKTQTQQALKRFFFEKCLHNSYSEPVGSLMHISSGIMVPFHFVEP AFISRTDTLFEMREDNAYGKTLRQHHGWVVRGVFALALRAAPSYEDF VAALTVKEGDHQKEAFSIGMQRDLSLYLPAMEKQLAILDTLYEVHGL ESDEVLYPLGCLDCCPEGEQSWFQKKNVFGCLSQLPVGRGVQLPCGH EGPAKENRVWLCMLAITPESAEQNRDNHLWSSVVRVDGELMNDG LTSALRTQITFGMICCVNALSSSENKVVASLLTLVRFTAAPSLPTLHC VSRHLQVEDPHLVMSVCECGTTISLPEPRSQLQCSTAVSQLEDSRRM AEH
2204	A	1	348	GMAEKTVRDKEYKALQIKLERLEKLCRALQTERNELNEKVEVLKEQ VSIKAAIKAANRDLATPVMQPCTALDSHKELNTSSKRALGAHLEAEP KSQSAVHKPPSTGSAPANRVG
2205	A	62	398	KTVRDKEYKALRIKLERLEKLCRALQTERNELNEKVEVLKEQVSIKA AIKAANRDLATPVMQPCTALDSHKELNTSSKRALRAHLEAEPKSQRS AVQKARSTGSAPVIESVD
2206	A	595	712	NLNVLQYLSQMTKKIKKLEKETIIWRTKWENNKNKALSANG
2207	A	1	1621	ARGGAEATEAGRGRRRSPRQKFEIGTMEEAGICGLGVKADMLCNS QSNLILQHQSNGCGTSNKHSLBEDEGSDFITENRNLVSPAYCTQES REBIPGGEARTDPPDGQDSECNRNKEKTLGKEVLLLMQALNTLSTP EEKLAALCKKYADLLEESRSVQKQMKILQKKAQIVKEKVHLQSEHS KAILARSKLESRLCRELQRHNKTLKEENMQQAREEEERRIEATAHFQI TLNEIQAQLEQHDIHNAKLQENIELGEKLLKLEQYALREEHIDKV FKHKELOQQQLVDKQLQTTQLIKEADDKHHFLERVFIKRSDRIEAQI RT\KKQQEVQLKQQLSLYMDKFEEFQTTMAKSNEFTTFRQEMEKMT KKIKKLEKETIIWRTKWENNKNKALLQMAERENSP*RVQGPS\KKLE RLEKLCRALQTERNELNEKVEVLKEQVSIKAAIKAANRDLATPVMQP CTALDSHKELNTSSKRALGAHLEAEPKSQSAVQKPPVPRLCSGHRV RLTKMRCDHCIERYILCITFSVSS
2208	A	132	509	NMVQTTGPGMLSTPCTGPAQARR*K/WLVVECLSLTGMGPGEGRGQ GAAEAEPN*VLGTPAGGSGPCPPGIQQTTPPSPHQPHSQVLSLSPTP RICPGFLAYLLSLFTPREELQLTQNDTFLAPRV
2209	A	214	427	QLVQACDPGCI AHLQPRGLRHAGLPQRKEGQRWLLHARSRLKGAHP VEGRVQV*HHLQVEEVRI LPAVGWRRPLPVTEGLVEVRLSDSW/SQ ACDPGWIAH\YSHVCGMLGFPSEKRVNAGFYTPVAV*RAGLTL*RA VSKF*TASHLAQCGTPVGFI
2210	A	155	384	SPGPALFSQPLGSCSAKAFPAMRPVSVWQWSPWVLLLCLLCSSCLGS PSPSTAPEKKAGTQGLRFRLAGFPRKPYK
2211	A	177	445	SPGPALFSQPLGSCSAKAFPAMRPVSVWQWSPWGLLLCLLCSSCLGS PSPSTGPEKKAGSQGLRFRLAGFPRKPYEGRVEIQRAGNHSR
2212	A	157	417	SPGPALFSQPLGSCSAKAFPAMRPVSVWQWSPWGLLLCLLCSSCLGS PSPSTGHEKKAGSQGLRFRLAGFPRKPYEGRVEIQRAGNV
2213	B	301	488	MRPVRVWQSGSPWGLLLCLLCSSSLGSPSPSTGPEKKAGSQGLRFLA GFPRKPYEGRGRSASX*
2214	A	2	476	SFPGSTISSDSNVIEV\EHHLQVY*VRIRPAAGWGRPLPVTEGLVE VRLPDGWSQVCDKDWSAHNSHVCGMLGFPSEKRVNAAFYRLLAQRO QHSFGLHGVACVGTEAHLSCSLEFYRANDTARCPGGPALVNCPPG PVYAASSGQKKQQQSKP
2215	A	3	1018	PGRRFRERPQQPRGLRDAGLPQRKEGQRGLLQARVRIKGGALHGE\G RVVVPMASTWGA VCGREWDLHTASVVCREVFGFSARQPVIGARMGQG MGAHLSSEVRCSGQE\GSLWKCPHKNITAEDCSHSQDAGVRCNLPLYT

				GAETRVSSQLPWLRLSSYHRAWSPGLRGVNPQPIAPRPCPPAAPT *PITC*PIMCLSHASATSVRDSHYLAPKLSPALPFCVT\KIRLRGGR SQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGLGYANHG LQETWYWDGSGNITGVMSGVRCTGTELSLOQCAHHGTHITCKRTGTR FTAGVICSESE
2216	A	1	1389	MGQEPDRDLLALRPQEVGDGWMMAIHHVHPRTQADGLGIFPITVAESRE QHEFLKCSSMVFSRRWMRKIFIFPIMLPKGLSQKQKNNPVPFLRH ICNHLYQLPSPFCGPITKLKVKPKPRVVRGPHKRLLAQRRQHSFGL HGVACVGTEAHLSCSLEFYRANDTARCPGGGPAVVSCVPGPVYAA SGQKKQQQSKPQGEARVRLKGGAHPEGEG/RRVEVLKASTWGTVCDRK WDLHAASVVCRELGFSGSAREALSGARMGQMGAIHLSEVRCSSGQELS LWKCPHKNITAEDCSHSQDAGVRCNLPYTGAETRRFHSVSLQIRLSG GRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGLGYAN HGLQETWYWDGSGNITEVMSGVRCTGTELSLOQCAHHGTHITCKRTG TRFTAGVICSETASDLWLHSSLVQETAYIEDRPLHMLDWA
2217	A	154	2576	SPGPALFSQPLGSCSAKAFPMRPVRVWQSPWGLLLCLLRCRCLGS PSPSTGPEKKAGSQGLRFRLTGFPRKPYKGRVEIQRAGEWGTICDDD FTLQAAHILCRELGFTATGWTHSAKYGPGTGRIWLDNLSCSGTEQS VTECASRGWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEHHLQVE EVRIRPAVGWGRRLPVTEGLVEVRLPDGWSQVCDKGWSAHNSHVVC GMLGFPSEKRVNAAFYRKLKRAAKVSARHPKPLGRLLAQRRQHSFG LHGVACVGTEAHLSCSLEFYRANDTARCPGGGPAVVSCVPGPVYAA SSGQKKQQQSKPQGEARVRLKGGAHPEGGRVEVLKASTWGTVCDRKW DLHAASVVCRELGFSGSAREALSGARMGQMGAIHLSEVRCSSGQELS WKCPCPKNITAEDCSHSQDAGVRCNLPYTGAETRRFHSVSLQIRLSG EVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGLGYANHGLQETWY WDSGNITEVMSGVRCTGTELSLOQCAHHGTHITCKRTGTRFTAGVI CSETASDLLHLSALVQETAYIEDRD\LHMLYCAAEENCLASSARSAN WPYGHRRLLRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDF THYDILTPNGTKVAEGHKASFCLTECQEDVSKRYECANFGEQGIT VGCWDLYRHDIDCQWIDL\TDVKPGNYILQVVITPHFQVAESGFTSN AMKCNKYDGHRIWVHH\CHIGDAFPE*TRRRGGLILSLPQPDIFLS QRAFLEPRWHL
2218	A	491	813	VYNLYLAPTAGWFSEVEDRWVFGHEGGNLGAULTNLMGAWFLQPAEV GVLVGKDRSSFYVNGLTGGLQKCSVIRDSLLQDGEFSMDLRTKSTGG APTFTNVTVTKTDK
2219	A	2	948	IFKIAFAKFGVWAGEWGREGMGSRKWSARAAAQRAEPRSGRQVRPRA LRLPPARQPRQLEPSRPPAAAPESPSSSAMAGWN\AYIDNLMADG T\CVTGAIVRYQDSEPPFWHAVPGK/TRFVNITPAEVGCPWLAKTRS SFLR*MGLTLWGGQK\CSVNRLHCLQEWGIIACDLRYQEPGPGAPH LSIVTCHPRLNKDAKSWLMGQRKVSHGGLT\NKKCY\EMASHLSGFP STDRLRVFPPLSPFPTAFAPLSLPIHTQTNFYFLGPLPHTPYCCQNH MGLGGQGLMGQTPSPTHIPSRVWLEKLLFFGVFFFSE
2220	A	3	417	GRAGSRKWLTLTGSLASTSPSLLSGQGPWAPLQRAMKPPGGESSNLF \GFPEEATPSSRPNRMSSNIFGPTTEEPQNILKRTNPPGV*GSGIFDE STPVQTRQHLNPPG\GKTSDFGSPVTATSRLAHPNPKPDHVFLLM
2221	A	259	941	PVSWSLNSCRFFFF*QDQLSPVV/QAGSGQ*RNLDL\QPLASRFK *FSSSRLL\SSW\DYRHMATMARLIFIFLVMGFM\TMLARLVNLFLT SSDPPTSAPFKWLGQGVKPNTRAVGFN*LGYSIIILYHNSNPGTD LVFIFLFIYLFYFLRQEQNSAAQARVQ*WHNLGSLQSPPPGV\H*F LCLSLPSSWDYRCAPPHQANFCIF*\RDGVFPCWPWSRTPDLR
2222	A	343	600	MSPLSQFVDGTLTKIQCYGTFEFHSA\RLCIGMISAHCNLCLPG SSNSPASAS*IAGIAP/CHHAPLIFVFL*ROGFTRIYFFK
2223	A	142	583	ILTMREIVHIQAGQCGNQIGAKFWEVISDEHGIDEQMLNVQNKNSY FVEWIPNNVKTAVCDIPPRGLKMAVTFIGNSTAIQELFKRISEQFTA MFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQOYQDATAKEEE

				DFGEEA
2224	A	163	1603	IQAGQCGNQIGAKFWEVI\SDEHGIDPTGT\Y\HGDSDLQ\LDRIS\ VYYNEATG\GKYVP\RAIL\VDLEPGTMDSV\RSFPFGQIFRPDNFV FGQVWGQVTTWAK\GHYTEG\AELVDS\VLDVVRKEAE\SCDCLQGF QLTH\SLG\GGTSGMGTLTYQQGFEKEYPDRIMNT\FSVVP\SPKC LDTVVEPYNATLSVHQLVENTDETYCIDNEALYD\ICFRTLKLTTPT YGDLNHLVSATIE\CVVTTCLRFP\QQLN\ADLRK\LAVNMVFPFRL \HFFMPGFAPL\TSRG\SQQ\YRALT\PELTPARSFDAKN\MMAAC \DPRQGPINFNRGLLSSRGSGCPMKEGRMKQML*CKNK\NSSYFCG NESPNNVK\TAVCDIPTSWASKMAVTF\IGQ*HSPSQELFK\RI\SE QFTA\MF\RRKAF\LHW\YTGEGM\DEMEFTEA\ESNMNDLRL*SIK QLPRMPTQEEEEDFGEEARKRRPKGRAPNQLKASQFP
2225	A	234	1374	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAAMLLGSVGDALGYRNV CKENSTVGMKIQEELQPV\GGLGHLVLSPGEWVSDNTIMHIATAEA LTTDYWCLDDLYREMVRCEIVEKLPERRPDPATIEGCAQLKPNNY LLAWHTPFNEKSGSGFAATKAMCIGLRYWKPERLETIEVSVECGRM THNHPTGFLGSLCTALFVSFAAQGKPLVQWGRDMLRAVPLAEKYCRK TIRHTAEYQEHWFYFEAKWQFYLEERKISKDSKNKAIFFPDNYDAER E*TYRKWSSEGRGRRGHDAPIAYDALLAAGNSWTELCHRAMFHHG ESAATG\TIAACLFGLLYGLDLVPKGLSQDLEDKEKLEDLGAALYRL STEKK
2226	A	139	366	AMAYQLYRNTTLGNSLQESLDELIQGSNTYRFCDNVWTFVLNDVEF REVTELIKVDKVKIVACDGKNTG\SNTE
2227	A	160	588	AMAYQLFRILPLETSFQESL\D*LIQSQQITPPTCPFKFYQLQDRA\ INAALA\QVRNR\VNFRGSPKYGTRFC\DNVGDFWYRND\VEFORG *PEPIKRG*K*KLVA\CDG\KNTGLPIPTENRKKYDFFYTHLLFI AFEREA
2228	A	918	1085	QEKLF*VLCFNFFSFFFFFCFL\VD*F*FLFGKAV*TLFVFSSA SHRYRQKTR
2229	A	145	365	KDGFAPQPLEEATLSELKTVLKSFLSQGVLEKLEAKTDPSILGGMIV RIGEKYVDMSVKTKIQKLGAMREIV
2230	A	2	750	ILGFDLQPPGRRWAAPAV\SGLS\RKVRCFSTG*\VRPFA\KLVGPS \VQVYGIEGRYAT\ALYSAASKQNK\LE\QLEKELLRVAQNPRNP VACFLFLNPLCBSRSIKSEKALN\DITSKRRFSPSTTQ\LLNQFC LAGKMGPI*ANNPKGVV\SGLFLTMDGVFHSRERVPLHSGPLASSFR KESHTLLNLKTV\LKEFPKVKGVLELGAK\TDPSI\LGGMIV\RIG E\KYVDMSVKTK\IQKL\RAMREIV
2231	A	100	470	ATEPLAPSERREVSIPLLVPAPLPPPPRPPVPSRTRTRPWRRP*ACF PMTLAASCGPTRSPWPSQQPIQPAPVG\PGNIKTLGDAYEFAVDVR DFSPEDIIVTTSNNHIEVRAEKLAADGTVM
2232	A	228	721	LWQLHAAPLAGAPGLPRQVIRALRGGEVHREGTSAPGRHRRRCGCPVG LEQVLHSLQPCVATKTDVATGTDVAMKTGNIKTLGDAYEFAVDVRDF SPEDIIVTTSNNHIEVRA/REA/ERPDGTVMNTFAHKCQLPEDVDPT SVTSALREDGSLTIRAWRHPHTEHVQ
2233	A	3	605	KKLTVPVRSRVERDPRVRRGLRPHVLSLPPGQGPAPSVDEPQNL FHLPSGEKIPFLFLLLLLFTPPPRPPVLSRPRTRPWRRP*ACFPMTL AAICGPTRSPWPSQPAPV/VAGNIKTL*DAYEFVVDVRDFSPEDIIV TTSNNHIEVRPEKLAADGTVMNTFAHKCQLPEDVDPTSETSALGEDG RLTIARAGHPHTEH
2234	A	229	510	KGIWIYINMEEQFVI*IHFL*TRSQFYFVNITFKYIYTHIYVQLYIH VH/MICKIFIYINIFI*IDICRQVIDYRDPKQLNNCSKFSSLTAGV
2235	A	203	334	SRRDHSFIL*ILHLSIYIHTYMYNIYMCYMYQRKQYGKTNP
2236	A	1023	1470	TPKTKHNSNPFVSPHAHKFACSYFFFCCLCVFMGSKLNLAIYKNVNS KLYLLRNVIFF*FIPTQLFILIYFFYTVLNTQTYF\LFMIFLSCSHG ICFPILFSLISITGWDLTNNNVGRKYFATVDYTLKFYIMKIYNSL YASKKKKKA

2237	C	226	450	MSQNTGNIISIPYQDGLPVISMIVLKRYMKEQWPSFRLKLRNLXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX
2238	A	3	449	LLRRVSVTAVAALSGRPLGTRLGFGGFLTRGFP/KAAAPVRHSGDHG KRLFVIRPSRFYDRRFLKLLRFYIALTGIPVAIFITLVNVFIGQABL AEIPEGYVPEHWEYY\RVKELEVRKLMHVRGDGPWYYY\ETIDKELI DHSPKATPDN
2239	A	3	635	HASAHASAMSLRRVSVTAVAALSGRPLGTRLGFGGFLT\RGFPKAA APVRHSGDHGKRLFVIRPSRFYDRRF\LKLLRIH\LALTGLPVTIFI ALV\NVFIGQAEAEFPEG\YVP\EHWGILLRHPISKMGFAR*FLMI GPEKIMERNNGPSFQIGSLKXAGIYGVKGSWEVRKI*WHVEEGDG\ PWVLLWRPFDQGTLLDHSSRKPTPWTN
2240	A	811	1005	SNFTGKIHK*LTSFKIVNLFYIL/FFETGFHSLTRLECSGMILAHCN LRFPEsrklfffgaidSF
2241	C	256	540	MSPAKATEMLIFGKLTAGEACAQGLVTEVPDSTFQKEVWTRLKAF CKLSPNCLEIFKEVXRKRERXXLXAVNAEECNVQGRWLSDECTNAV *
2242	A	602	2067	SSSSGLALGMQRPLLARLGRTPGRALSAPAATGFAELRAAQGMAMAY LAWRLARRSCPSSLQVTSFPVVQLHMNRTAMRASQKDFENSMNQVKL \LKKDPGNEVKLKYALYKQATEGTCKMP\KPG\VFDLINKAK\WDA WNALGSLPQGSCPG*NYVDLVSS\LSPSIGNPPS\QVEPGTERDNQL GFETLVVTS\EDGITKIMFNRP\KKKNAINTEMYHEIMRALKAASKD DSIITVLGTNGDYSSGNDLTNFTDIPP/GVGVEEKANTNA\VLLR\ EFVG\CFI\DFPKPLDCSGSMGPSCGASPVTLGAYSMVLLHLDRG TF\HTTPF*SP*AQSPEG\CSSYTFPKIMSPA\KATEMPFI FGKEVNO REEACASRDLFTTEGFPWIALFRKKVWDQG*RAFCKSFPPQMALBEFS KEVIRKREREKLHAVK\AECCQCPFGKWLS\DEC\TNA\VVNFLSQ KIKNCDDHLQQHQSMSQGRMCCSLCLSSTGTK
2243	C	2163	2402	MSQAAASHKSKLTPKNQRAPFTLLRKSQCQDPSRGESEEGWWPIQRA CRSMETFLPQMFQSWHQIYKNVSRDQFFTLTK*
2244	B	125	304	EIPLPTGCLDELLKAAECPAAGSVDLGVCCLDTSSSSGLDLPKVVDMF RSCLPACAVNFK*
2245	A	3	181	DQACGTVGDDGRALGECDDRA/CPRAANSSGGPGWTPWPSGYPPALHT ARPKALCGQPRAF
2246	A	13	1188	LYGKADKTFIGLECLENVKFQIRNHKLRSNKTSI*ACGFPLSASSS GS*ENHHKSDMKILAPKIAFSLCK*KRVIYQV*CSPQRGHTRFLT PLQLPHLWTHSVPHKAKPAAAATS/DGHTRFLTKP/MPAAAATSLDT LGSSSQSAHCSCHIPGHTRFLT KPSPLQLPHRWTHSVLHKAKPAAAA TSVDTLDSSSQSAHCS/WPHPWTHSVLHKAKPAAAATSLDTLGSSSQ QARCSCHIPGHTRFLT KPSPLQLPHPWTHSVPHKAKPAAAATSLDTLGSSSQ QARCSCHIGGHTRFFTKPSPLQLPH/P/DGHTRFLT KPSPLQLPHRWTHSVPHKAKPAAAATSLDTLGSSSQ QARCSCHIGGHTRFFTKPSPLQLPHWAYGAAGAFFKTG IKMLGTRQKGDTRP NAG
2247	A	1088	1858	LRLAGTWGVKNRRRQEAFFPSLQRRNQGPQLPGSQNQFFYQAVPLPS FQLLATGRRCSKGFALRLPRRSCGKDSRGPVLIPLAPGVMCP*PKG AQSAOSSHPIRAAATPAGSSGNWFSLPAGSGKF*EKHLAKLLKGELT SLPVPTPIPRSPPG*PQVPGPNNPFPSP*LPHLDLRPFTTPLTWT* DPS/HRDSSRPSSA/RASHLTVMLSGNFPVCPTFSHTLVR/WEHLPA SNVLYVPL*APSSRPLANTVPPICG
2248	A	1100	2076	YASRGMGREEQKKRGKRFPSLPREBIKANQKLPGSQONQFFLPGSTTA VISASGHWEVLLERGLP*DSKKKLREGQQGSWGFASGPGVMCP*PK GAQSAPSSHPMGAAATPAGSSGTGLACPQDQESLRKASAVELPVPLS PQRPGGFLHVS/ASSCKHLEVHGTHRQTAPEHVHLSWGRARPTWRT CADRHGPPPTLEAGGSPPSSPGDADLDVLEMLLVDEAAVILPQRPF

				ACPA/WCC*PAGLAARGDASPARSQNPAP*RPTALCLGPQVLR*RSR KKPGP*MES\GAAQLHEEPVLQVQRCLFKERCRLVIDGHSPACSSSH
2249	A	761	1178	LSTPLTSWCWMRRTTPGSPTRCSCSSA\PGTQPLGGGHQ*RGCHQC VASSPR*AWPASGPAKLQ*LQQPKTQQRAPATGEHVPPVQPSAQ*PH SRFQSSSETSRPADGSEQQPARASGPGARRPPHQPRQVINCWLRRC
2250	A	135	408	PHSRFQSSSETSRPADGSEQQPARASGPGARRPPHQPRFHPPPSA/RA ISIECPA*AVMRSGSEPRARQEYSLGLWTPSQFLQGILYLARSPT
2251	A	123	578	TTNNIFKWAKYFKRHFSRDI*MANEHMKRCLTSLTIMEQMIIKTIRC HLT/PRMPIIKKIIC**GWRETGTLI/YAWWECKIVQ/PAFR/TVW QFLKRLSQHPTIPFP/GMCPRETCTHIHSKY/TQMFMAALFIEARK WKQFKCLSTNEWTVNVRP
2252	A	623	724	PYGTWMKLETIILSKLTQEOKTKHCMFLISGS
2253	A	1061	1156	GTWMKLEAIILIKLTQEOKTKHHMFSLISGS
2254	A	365	640	RPFSMLAYLILNSLVLMWKPHFREAACSNHIDGRW/VR*AWFS/YT VRSWAAIKKNEFMSFAGTWLKLEAIILSKLTQEOKTK\HHMFSLIRG S
2255	A	209	532	RVFLSYQLTLFSSQDDIIDDVESFVAAAEILKERGAYKIYVMATHGI LSAEAPRLIEESSVDEVVVTNTVPHEVQKLQCPKIKTVDISLILSEA IRRIHNGESMAYL
2256	A	1	308	AKRAQSYAERLRLGLAVIHGEAQCTELDMDDGRHSPPM\VKNATVHP GLELPLMMAKEKPPITVVGDDVGGRIAIIVVWLYVIHVQRWHSWLLVS RLSTLGLYF
2257	A	2	1161	VRKGTDLGALPVPPPAMNAARTGYRVFL\ANSTAV\CSELAKRITER LGABELGKSVVYQETNGETRVEIKESVRGQDIFIQTIPRDVNTAVME LLIMAYALKTACARNIIG\VIPYIP\YSKQSKMRKRSIVCKLLASM LATAGLTHIITM\DLHQKEIQGFFSFPV\DNLRSLHLFLAFSIIQGR KFPNLQEMQVIVG*VFLDAGKGAQSYA\ERL\RLGFVAVHSRGEFG SCTKL\DMDDGRHSPPMVKNATV\HPGLELPLMMAKE\KPPITVVG VG\GRIAIIVDDIID\DVESFVAAAEILKERGAYKIYVMATHGILSA EALRLIEESSVDEVVVTNTVP\HEVQKLQCPKIKTVDISLILSEAI\ RRIHNGESMAYLFRNITVDD
2258	B	80	402	XVPTVDTYDGRGDSVVYGLRSKSKKFRRPDIQYPDATDEDITSHMES EELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQDDQSAETHSHKQ SRLYKRKAYDESH*
2259	C	272	409	MXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXKXXXXKXXXXGPPF
2260	A	2	628	EHSIVGTRLVSGQLQPSQPNADQGLTTMRIAIVICFLLGITCAIPV KQADSGSSEEKQLYNKYPDVATWLNPDPSQKQNLAPQTLPSKSNE SH\DHM\DDM\DDDED\DDGPGDSQDSIDSNSDDVDDTDDSHQSDE SHHSDESDELVTDFPTDLPATEVFTPVVPTVDTYDGRGDSVVYGLRS KSKKFRRPDIQVNPLTDTDPGSD
2261	A	67	1276	SHASGRRQSTASSGPDVSGQLQPSQPNADQGLTTMRIAIVICFLL GITCAIPVKQADSGSSEEKHF\YNKYPDVATWLNPDPSHKQNLAP QN\AVSSEETNDFKQETLPSKSNESHDMDDMDEDDDDHVDSQDSI DS\NDSDDVDDT\DDSHQSDE\SHHS\DESDELVT\DFP\TALPATE VFTP\VVPTVDTYDGRGD\SVVYGLRSKSK\KFRRPDIKYPDATDED ITLHMESEELNGAYKAIP\VAQDLNAPSDWDSRG\KDSYETSQDD\ QSAETHR\HQQ\SRLYKRKANDESNEHSDCDW*ARTFPKVSREFHS\ HEFSSPWRFLFVAPKSREEDNTPLEFRYS\QELDSASSGGQLKGGK NTISPLCHLVQKKNGFIKMKENHEMLLSPVYWLKCVSI
2262	A	1	651	MTAFNSGKVDIVAINDPFIDLNYMVYMFYDSTHGKFGHTVKAENG LVINGNPIT\IFQDQDPSKIKWAP/LAKVIHDFNGIIEGFMTTVHTI TATQTINGPSG\NCHVMAAGLSRTSSLSLLA/LAKPVGKVIPELNGK LTGMAFHVPTANVSVADLTCRLEKPA/KYDDIKK\NTHSSTFDAGAA IVLKDHSVKLISWYDNEFGYSNRVHLMHNASKE
2263	A	2	5264	TRSAPRAASWLEDPREVRSVCLSATFFTLQKPRLLLFSPSVVHLG VPLSVGVQLQDVPRGQVVKGSVFLRNPSRNNVPCSPKVDFTLSSERD

				FALLSLQVPLKDAKSCGLHQLLRGPEVQLVAHSPWLKDSLSRTTNIQ GINLLFSSRRGHLFLQTDQPIYNPGQVRVYRVFALDQKMRPSTDTIT VMVENSHGLRVKKEVYMPSSIFQDDFVIPDISEPGTWKISARFSDG LESNSSTQFEVKYVLPNFVKITPGKPYILTVPGHLEMQLDIQAR YIYGKPVQGVAYVRFGLLDEDGKKTFFRGLESQTKLVNGQSHISLSK AEFQDALEKLNMGITDLQGLRLYVAAAIESPGGEMEEAELTSWYFV SSPFLDLKSKTKRHLVPGAPFLQALVREMSGSPASGIPVKVSATVS SPGSVPEAQDIQQNTDGGSGQVSIPIIIPQTISELQLSVSAGSPHPAI ARLTVAAPPSGGPGFLSIERPDSRPPRVGDTLNLNLRAVGSGATFSH YYMILSRGQIVFMNREPKRILTTSVSVFVDHHLAPSFYFVAFYHGD HPVANSRLRVDVQAGACEGKLELSVDGAKQVRNGESVKLHLETDLSAL VALGALDTALYAAGSKSHKPLNMKGKVFAMNSYDLGCGPGGGSALQ VFQAAGLAFSDGDQWTLRKRRLSCPKEKTRKRNVNFQKAINELG QYASPTAKRCCQDGVTRLPMRSCQRAARVQQPCREPFLLSCCQFA ESLRKKSRLDKGQAGLQRALEILQEEDLIDEDDIPVRSFFPENWLWRV ETVDRFQILTLWLPDSLTTWEIHGLSLSKTKGLCVATPVQLRVFREF HLHLRLPMSVRRFEQLELRPVLYNYLDKNLTVSVHVSPEGLCLAGG GGLAQQVLVPAGSARPVAFSVVPTAAAASVSLKVVARGSPFEPVGDV SKVLQIEKEGAHREELVYELNPLDHRGRTLEIPGNSDPNMIPDGD NSYVRVTASDPLDTLGSEGALSPGGVASLLRLPRGCGEQTMILYAPT LAASRYLDKTEQWSTLPPETKDHAVDLIQKGYMRIQQFRKADGSYAA WLSRDSSTWLTAFVLKVLSLAQEQVGGSPKQLQETSNWLLSQQQADG SFQDPCPVLDRLSMQGGVLGNDETVALTAFVTIALHHGLAVFQDEGAE PLKQORVEASISKANSFLGEKASAGLLGAHAAITAYALSITKAPVDL LGVAHNNLMAMAQETGDNLYWGSVTGSQSNASPTPAPRNPSPDMPQ APALWIETTAYALLHLLLHEGKAEMADQASAWLTRQGSFQGGFRSTQ DTVIALDALSAYWIASHTTEERGLNVTLSSTGRNGFKSHALQLNNRQ IRGLEEELQFSLGSKINVKVGGNSKGTCLKVLRTYNVLDMMKNTTCQDL QIEVTVKGHVEYTMEANEDYBYDELPAKODPDAPLQPVTPQLQFEGR RNRRRREAPKVVEEQESRVHYTVCIWRNGKVGLSGMAIADVTLISGF HALRADLEKLTSLSDRYVSHFETEGPHVLLYFDSVPTSRECVGFVAV QEVVPGLVQPASATLYDYNPERRCSVFYGAAPSKRLLATLCSAEVC QCAEGKCPRRRALERGLQDEDDGYRMKFACYYPRVEYGFQVKVLRD SRAAFRLFETKITQVLHFTKDVKAAANQMRNFLVRASCRLRLEPGKE YLIMGLDGATYDLEGHPQYLLDSNSWIEEMPSERLCRSTRQRAACAQ LNDFLQEYGTQGCQV
2264	A	56	1357	IRLSVCSSCSTVSRIFFCVASRATSLRTPMGKVKGVNGVGFGRIGRLV TRAAFNSGKVDIVAINDPFIDLNYMVYMFQYDSTHGKFHGTVKAENG KLIVINGNPITI\FQERDPSKIKWG\DAEYVVE\ST\GVFNQPK KAGAH\LOGGAKR\VIISAPSCLMPPMFVMG\VN\EKY\DNSLKII SNAFLQPPTCLA\PLAKG*FHDNFG*SWEGLIDHSSMAITGNPRKTV D\GPSRG\NCGRGWAAGL\SRTSSLGLYWALPKA\VGKGHP*G*TGK LTG\MAFPVVPNCQNV\VVDL\TCRSRKTLPQYD*HQGRVVKQA\S EGPPQGAIG\YTEAPRWSSDCNSGPPVFPFDDAGA\GIA\LND\H FVKLISWYDNEFGYSNRVVDLHGPHGLQGSKTPTGTEPQARGTRGRD ETLTAGESLPHSDPHHTESPLLTVM
2265	A	34	476	LSGGPRRAASCASSAGLLVLLPFMPM\FIV\NTKLHRASLPEG\FLS KL\TQQLAQANRQAPPN*FAFNVPDQV\YSFGGSSEPCAL\CSLHS IGKIGGAPDPAPYSKLL\CGPAGRSRLPIQARTRV\YINY\YDMNRG QMWAGNNFHLSP
2266	A	63	470	QQPPPERPAHQFARPPAPFTMQPASAKWYDRRDYVFIIEFCVEDSKDV NVNFEKSKLTF\SKLSFLSNDVK*SFTQLNNFDWLVSFLKLLIFVS LKRLNSFFIILYSLGGSNDNFKHLNEIDLHFCIDPNVSSLYA
2267	A	2	854	RAFCCVTSRRPASPLVCTHARSFVLAFLFLHFPLLPDRRSRSFRA VHFWGPRSSPPHAAVRLREARRGRDRREKAESPTGEKSTSPSSSRQ RGPPTKVRPPAPFTMQPASAKWY\DRRDYVLKWEFVFLNTRLRDV\N

				VNF\EKSKTYNFSCREGSDNF*GI*MEI\DLFH\CID\PNDFQGLK GTDRSIFMFVLRKRIWASSWPKGLTK\ERGKGLIWV\SVDFN\NW\ KDWEDDSDEDMNSFNDRFSE\MMNNMGGD\EVVDYPEVDG\ADDSQD SDDEKMPYLE
2268	A	117	390	RRYRPTPGVHRADGLLHVGRGHEVLQRRPEDLRCHSHCHPSHPTDRL LLLVIWTHLGGIWAGHSPWTVIQTAGRPPRDLSPSARPISSPP
2269	A	66	354	LPGLSGRDEASLWMGGGRGLLGRETLPGGGGCSGEGPLCYWPPPGSP PAPSLRASLPLEPPRCPLRSCSLPRSACLCSRCSWQPNRVSHFLLWT S
2270	A	148	398	RPAKGAAMDGRVQLIKALLALPIRPATRWRNPIPPFETFDGDTDR LPEFIVQTASYP\PWARTRSSARPISSPPPETSCVLA
2271	A	356	1241	KVTFLITRLTGPAQVGDPLHQEGEPPPQLITGAFWPEMKRVFGWGG GRGL\LGRETLP\PG\GGCSGEGPLCYWPPPGSPAPSF\RASPPLE PP\RCPLRSCSLPRSACLCSRNSAPGSCCRPWASLWSEPPSPSSQP APPMYIWTLSAPVAQS*APVTHWTDHPLPPLPSPLLPTRLPDDLHH FGPQTLRCQ\SHR\HPSHPRQDCWLL/M*IWT\HLGG\IWAG\HSP WT\VIQ\TAGR\PPRDLSPSARPISSPIPETFCAPATWLPGLSCAWQ AKFESLIFSLWTKLVFAHKRSIS
2272	A	2	178	EKLKFRFRKETDAAIIMKVDKDRQMVVLEEEFQVFEIRTTDDLTE AWLQEKLSFFR
2273	C	88	228	MKVDKDRQMXVLEEEFQNISPEELKMELPERQPRQLQRTTDDVCRE*
2274	A	3	382	VDRTIMSDSLVVCVDEPELTKLRKFRFRKETDAAIIMKVDKDRQM VVLEEEFQ\FVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMYA GSKTRLVQTAELTKVQTGMWLQSVRERWCGSW
2275	A	89	636	KTAELRKEEACQNNHALPGSLRQSDSLVVCVDEPELTKLRKFRFR KETDAAIIMKVDKDPARWWCLEGNFKNISPQREL\KMGFPRRDKP R\FVVYS\YKYVHD\DG\RVSY\LCFIFPPRPVGCKPE\QQMY\A GS\KNRLV\QTAELTKGVPKSRTT*LTSLRPWL\QEKLSFLSLISGA GD
2276	A	2	2453	EILLCPSLPFNCQYILVLLGSRIRAREPPMAVQAVTQGPCKYTKSVL KKGDKTNFPKKGDVHWCWYTGTLQDGTVFDNTIQTSAKKKKNAKPLS FKVGVGKVIIRGHVARKFLDDEAELESEDAEYVSSDENDESENEQDSS LLDFLNDDETQLSQAINAWFACKSPSIIICVDDDEVSSVCAFFSSGSSD LYKTSEWKLKLPQFLAEHLKLGNIKNVAKTANKDHLVTAYNHLEFET KRFGKTESISKVSEQVKNVKNEDKPKETKSEETLDEFIQLRRELAS VNGHSGDDGPPGDDLPDGIEDITDPAKVTSLILKFVSGQLITEIENM RHRIIIEIHQEMFNNEHEVSKRWTFEEGIKRPYFHVKPLEKAQLKNW KEYLEFEIENGTHERVVVLFERCVISCALYEEFWIKYAKYMNHSIE GVRHVFSRACTIHLPPKPMVHMLWAAFEEQQGNINEARNILKTFEEC VLGLAMVRLRRVSLERRHGNLEEAHLLQDAIKNAKSNNESSFYAVK LARHLFKIQKNLPKSRKVLLLEAIERDKENTKLYLNLEMEYSGDLKQ NEENILNCFDKAVHGSPLIKMRITFSQRKVEFLEDGSDVNAKAVTEV REVTRKSVPRNSLESAEYLKLITGLLNKADFRDRINGIKQLSDTEN NQDLVVGNIKIFDAFKSRLHDSNSKVNVALETMHKMIPLLRDHL PIINMLIPAIVDNNLSKNPGIYAAATNVVQALSQHVGDTSRMFRRT KSYDSLTLTIGAGIRILFSSCQEETADLLKELSLVEQRKNVGIHVP TVVNSNKTTHFKKSPCMHK
2277	A	1	1008	MVDKCRYHQSLHKVSNSESKISSGILLSRLQRRPRGRGDAELRRAG SVKRRQRGKMAAAVPQRAWTEQLRSEQLPKKDIIKFLQEHGSDSAV QQVITNLLIGQIELRSESDPDILTYSHERKVEKLIPLGEELAAIQK TYIQIPEQDETYLEDSCVDEEESCKGQSSEEEVCVDFNLITDDCFA NSKKYKTRRAVMLKEHMEQNCASKKKLSRIILPDDSSSEENNVDK RESNIAVNPSTVKKNKQQDHCLNSVPSGSSAQSKVRSTPRVNPLAKQ SKQTSNLKDTISEVSDFKPQNHNEVQSTTPPFTTVDSQKDCRKFPV PQKVLSE
2278	A	1	884	MVDKCRYHQSLHKVSNSESKISSGILLSRLQRRPRGRGDAELRRAG

				SVKRRQRGKMAAAVPQRAWTVQLRSEQLPKKDII\KFLQEHGSDSL LAEHKLLG\NIKNVGKTANKDHL\VT\YNHLFETKPF*GYLKV*SK VSEQVKKCERLMKINPKETKSERDPWNEG\PPK\YTKSCS*KRGDKT QLFPKRGDV\VH\CWY\TGNTTKMGTVF*YLIFQTSAKKKEKCPSL* GFKVRSRPKLSRGW\DEALLTMSKGEKAR\LEIEP\EWAF\GKKGLP DAKIP\PNAKLTF\EVE\LVDID
2279	A	3	510	AIRAVAYCADMAQSMNHTTLHQSRIWHRIGIKKPRSQTDQSLTGVD MFLKNMRFAKKHNNMGLKRMQANNAKAMSARAEAIKALVKPKEAYL* IPNGVSRKLDPLAYIAHPKLAKRALARIAKGLKLCRPEALAEARAKD QTKVQGVAPA*A\PAHAPKRTQAPTKASE
2280	A	9	674	IERLQVRIACSCRDAIPGSSHASAHASEALREPRLNGADMAKSKNHT TNNQ\SRKWP\RNGIKKP\RS\QRYEFS*RGWPPQVSLRN\MRFAQR STNKKGP*RRLOANKLPRAMSATCPRLIKAPPLKAPRRFKPQDPPKG \VSRKLDL\LA\YIAQPQGLGSVARCP*LPRGPRL\CPPKAKGQGGQ QAKAKDQTKGFKPRPRVQAPVSVSV\QAPKRTQAP\TKASE
2281	A	417	822	RENCILLSTRAQSVFNAQGTALWSFQDPATGEGGAGHGRLMRPSLL PSQGASAC*/PRFGESKLAPVGKFPKMCLLELPFLSHLSRGCSGAS EGQLCLLEVPATARVGVHKPSQSRGLEFSWVLMSDLCSGPPL
2282	A	1	239	HYQQRRQMMCLERHIKPPKELDTASSDEENKDGFTVFECPLAPT GEMEVRNPLLDHSPAPRPRGPRGGAGPGASH
2283	A	129	1471	RMATPLPPPSPRHLRLLRLLSGLVLGAALRGAAAGHPDVAACPGSL DCALKRRARCPGAHACGCPCLQPFQEDQQGLCVPRMRPPGGGRPQP RLEDEIDFLAELARKESVTLSNAPY/LKDRQRLPEPATLGFSSARGQ GLDLGLPSTPGTPTPTPHTSLGSPVSSDPVHMSPLEPRGGQGDGLAL \VLILAFCVAGATALSGALLC\WSGLQREIRLTQKADYATGEGPPGS PAAPRISPGDQRLAQSAEMYHYQHPTATKVCAG*RHKMPPKELDTGP PSDEENEDGDFTVYECPLAPTGGKWKVRQTLF\DH\ALSAPLPG PQAHPPATAMTWRQNRATCSPALEGPRGGAGPGASPLKTCFDAVCF WLGPRAPGPGTPCQGRPPNLCADTSWSPAPLLFGLDPQTGGGMENR RAQERVGNRSRDKSQLKSI SIDLKKKKST
2284	A	85	409	TCGLPMCQKQTVSWGGKTPSLRRFPQRPFRPPRGQPPSGARWEH/PP PGTTAPRRSRPPARLAGPEP*AKSPLHAANSRGQTKGHLWKTIV LVFKKPNFFFNFNH
2285	A	193	609	NQINFCLNGKYTYICIDTPLYMFIHTLKHINTSVIISLEFAI*HK GQVELHIKITYRSN*MWLGHNRN/LCPQEGEEIPNEA*IFSIIKR QSWPGTVAHACNLITLGG*DGRIS*DQVFKTSLINIVETPSLLKK
2286	A	117	435	NHPFKLRNPGGPGVVPVAMIPGMRGHKPFWLTPLGRAQLSLDTLIS LQSFLGSRGSYSSNRKSI SGRQPHVSDSLLNSRQNYKNYSMESRT HFRIQAATLQA
2287	A	2	1923	VETPPQGSVHSGHLGSLVGDPTGTGNAGERGPRGKGARVLALDSGG MDSSPSLPLIRTPESSLHEALDQCMTALDLFLTNOFSEALSYLKPR KESMYHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQLCQRHRRK SSVTDSFSSLVNRPTLGQFTEEEIHAECVYAECLLQRAALTFLQGSS HGGAVRPRALHDPHACSCPPGPRQHLFLLQDENMVSFIKGGIKVR NSYQTYKELDSLVSQSYCKGENHPHFEGGVKLGVAFNLTLSMLPT RILRLLEFVGFSGNKDYGLLQLEEGASGHSFRSVLCVMLLLCYHTFL TFVLGTGNVNIEEAELKLPYLNRYPKGAIFLFFAGRIEVIKGNIDA VSDGGPGRGWSLGSVQTSRKSGTCDILRDRIDWGRGGGPRENQPE RGRGPGSGRAAWEDKGGGICGAWDFDWEI*DCSIAVEGGGGRCLRE AEVRKAHLFRA*RLGWSLVPPLHYSSLLLFHVTKNQSPRRGLYLSP TSCKT*EVKPGLEARSPGSWGPT*A*HRAGPLCPGGVPVCCGVGRFG GCRGVGAGWAPVRLTRCLQAIRRFEECCAEQQHWKQFHHMCYWELM WCFTYKQGWKMSYFYADLLSKENCWSKVG
2288	A	1	1818	LGEAGGKGLWDLVAGLHPLGGQSPMGQKGHKDSLPCGGTPESSL HEALDQCMTALDLFLTNO\FSEALSYLKPRTKESMYHSLTYATILEM QAMMTFDPQDILLAGNMMKEAQLCQRHRRKSSVT\NSFSSLVNRPT

				LG\QFTEEEIHAE\VCYAKCLLQRAALTFLQDENMV\SFIKGGIKVR NSYQTYKELDSLVSQSSQYCKGENHPHFEGGVKLGVGAFNLTLMLPT RILRLLEFVGFSGNKDYGLLQLEEGASGHSFRSFLCVMLLLCYHTFL TFVLGTGNVNIIEAEKLLKPYLNRYPKGAIFFLAGRIEVIKGNIDA AIRRFEECCAAQQHWKQFHHMCYWELMWCFYKQGWKMSYFYADLLS KENCWSKATYIYMKAAYLSMFGKEDHKPFGDDEVELFRAVPGKLKI AGKSLPTEKFAIRKSRRYPSSNPISLPVPALEMMYIWNQYAVIGKQP KLTGILEIITKAEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRV QEAEENFRSISANEKKIKYDHYLIPNALLELALLMEQDRNEEAIKL LESAKQ\NYKNYSMESRTHF*IQAATLQAKSSSIENSSSRSMVSSVSL
2289	A	486	713	SKFYLFYIYLFYFFVYTYVINIVYIKI*QQIDLNFYIYLFYFWRQ SRAFLSKL*CSGANMTHLSLNLPGSRNTPAPALQAAGTTGM*HHTWL IFVVFVETEFHHVGLKFLSLD\IHPPWPSKVLG*QGGWIV
2290	A	1	4137	MDESTFAGGQYEGGWVPEHHKSNEPKSGHIEKGNTOCQERTPQPMI YPTGEIESTVNAWMLSHEKEQSQILLISNCLDALKHRSCDYGLKIAL DIKHLRLKIQPKIFIYTRTHKYAVTLHMLAHTITSERDDIEEWNNAV VDQCCPPEMSVMEMFYIYAVHYGRSLLSWSQEEKEKGGREEEEEE EE VNFHPVVLVSPWTWYRPAAILISLDRARAAAQGGSRKGWAEFQARGT ERREQCSAALVREMEQRLLCGLLHPRPGCTARIFDLVSARWLAARWG SACPGGAARAPRGALAPGLRQSEAVPAPLPPRVADAAGASGKRSRR ARSCPSPMARAARVAVAAVGPAGHRTRRLAGRGREGRAALAAGAQL PAIGDARRHLVSRKRPEMGFDPACGRRVFRRRGCGQAVPPLWFPGL LLAPSWPDGRPGRRRAHLKFALLYGEGKFESPEGKYFAKQARIRGWT QEDPEASGTSSNRARSEPSVLTVAGILQTESRKTAKICKIRCLCEE KENVLNINCENKGFTTVSLLQPPQYRIYQLFLNGNLLTRLYPNEFVN YSAVTLHLGNNGLQEBIRTGAFSGGLKTLKRLHLNNNKLILREDTFL GLESLEYLQADYNYISAIEAGAFSKLNKLVLIILNDNLLLSLPSNVF RFVLLTHLDLRGNRLKVMFPFAGVLEHIGGIMEIQLEENPWNCTCDLL PLKAWLDTITVFVGEIVCETPFRLHGKDVLTQLTRQDLCPKRSASDSS QRGSHADTHVQRLSPTMNPALNPTRAPKASRPPKMRNRPTPRVTVS DRQSFGPIMVYQTKSPVPLTCPSSCVCTSQSSDNGLNVNCQERKFTN ISDLQPKPTSPKKLYLTGNLQTVYKNDLLEYSSLDLLHLGNRIAV IQEGAFTNLTSLRRLYLNGNYLEVLYPSMFDGLQSLQYLYLEYNVIK EIKPLTFDALINLQLLFLNNLLRSLPDNIFGGTALTRLNLRNNHFS HLPVKGVLDQLPAFIQIDLQENPWDCTCDIMGLKDWTEHANSPIIN EVTCESPA KHAGEILKFLGREAI CPDSPNLS DGTVLSMNHNTDTPRS LSVSPSSYPELHTEVPLSVLILGLLVVFI LSVCFAGLFVFLKRRK GVPSVPRNTNNLDVSSFQ LQYGSYNTETHDKTDGHVYNYIPPPVGM CQNPIYM/SRKGRETQ*AYLPKPGKEFQLLGNLEEKKEEPATPAYTI SATELLEKQATPREPELLE* NIAE/PSQGTSSRRP*STITFVPYLG Q/CCFPFMEFSDGQNGQDSIKTVLYGTPRKCFVQSKPNHPLLQAK PQSEPDYLEVLEKQTAISQL
2291	A	1	774	MNRAFSRKKDKTWMHTPEALSKHFI PYNAKFLGSTEVEQPKGTEVVR DAVRKLKFARHIKKSEGQKIPKVELOQISIYGVKILEPKTKAEIITLT IGQAFDLAYTKFLESQKDVETRKQIAGLQKRIQDLETNMELKNKV QDLENQLRITQVSAPPAGSMTPKSPSTDIFDMIPFSPISHQSSMPTR NGTQPPPVPSRSTEIKRDLFGAEPFDPFNCGAADFPDPDIQSKLDEM EGFKMGLTLEGTVFCLDPLDSRC
2292	C	214	483	MTPKSPSTDIFDMIPFSPISHQSSMPTRNGTQPPPVPSRSTEIKRDL FGAEPFDPFNCGAADFPDPDIQSKLDEMGEFGFKMGLTLEAQYFV
2293	A	701	1034	TFIWLILIMNLAFSRKKDKTWMHTPEALSKHFI PYNAKTCLAPPAF CHDYKTWMHTPEALSKHFI PYNAKFLGSTEVEHPKGTEVVRDAVRKL KFARHIKKSEGQKIPKV
2294	A	440	1383	SSSWNRAFSRKKDKTWMHTPEALSKHFI PYNAKFLGSTEVEQPKGTE VVRDAVRKLKFARHIKKSGGQ\KIPKV\ELQISIYGSKN*DPKTKR

				EV\QHNCQLHRISFCADDKTDKR\IFTFICKDSESNKHLCYVFDSEK CAEEITLTIGQAFDLAYRKFLSEGGKDVETRKQIAGLQKRIQDLETE NMELKNKVQDLENQLRITQVSAPPAGSMTPKSPSTDIFDMIPFSPIS HQSSMPTRNGTQPPVPSPRSTEIKRDLFGAEPFDPFNCGAADFPPDI QSKLDEM/QAPEMEGFKMGLTLEGTVFCLDPLDSRC
2295	A	412	842	GKVSPPG*GP*GEQGPLG\PSGAATGLPHSLCPEAFASPRSVEYR* DQAQLALWAVPL*EGPL/PDLVRGVVPGSPVKVPGDEVRT/CHSCGR FPRALGQSKTLPPNLPLTTRRGVNSEDLPSPVYRAADRGNRFPGAVG GSCHR
2296	A	1036	1429	GRAWRTCPRAHQPRRSHLRPSSCSTLQRG*SPPPGRSSSPVQP*CA *ARGWGSPPG*HWTCLFLAWQSPQCTGPPQICQYPRPLRSPRAGPPG GTSGHSPPDARAPRRRPAAPCGRECSSSSGRNAAPLG
2297	A	44	397	VSWLPQESSHHYFKYCKISALALLKVMHARSGGNLEVMGLMLGKVD GETMIIMDSFALPVEGTETRVNAQAAAYEYMAAYIENAKQVGRLENA IGWYHSHPGYGCWLSGIDVSTQM
2298	A	298	409	HHVMCVFFSSCKTTIEAIHGLMSQVIKDKLFNQINIS
2299	A	123	1221	KRQLFPLSWAMAASGSRMAQKT\WE\LANNMQEAQSIDEIYKYDKKQ QQEILGGEALD*GVRSHHYFKYCKI\SALALL\KMV\MHARS/GEGN LEVMMGLMLGK/VWDGET\MIIMGKFFCLVEGT\ETRVN\SLQAAAY EYMAAYIENANQV\GSPENAIGWYHSHPG\YGCWLSG\IDVSTQML\ NQQFQ\EPFVAV\VIDPTRTISAG\KVNFGAFWAHPK\GGYNPPD\B GP\SGVPGFLPPLNKIEDLGVHCKQYYALE\VSFYKSLGSLQNCLELL WN\KIWGGIRWSS/SLAGLLNADYPTGQVL*FVLKLEQSRSPSLGR GEFPCWGLETHD\RKSEDKLAKA\TRSS\CKLPIEAI\HGLMS\QVI KDKLFNQINIS
2300	A	2	434	QRGGIRGNPDPPWVGLSVGLSVPTTGSERRLSGDLSSMPGPGTLSV RVSPQPILSRGRPDSNKTENRRITHISAEQKRRFNIKLGFDTLHGL VSTLSAQPSLKERAGLQBEAQQLRDEIEELNAAINLCQQQLPATGV PITH
2301	A	1	2423	MAGALAGLAAGLQVPRVAPSPDSDSDDTSEDPSLRRSAGGLLRSQVI HSGHFVSSPHSDSLPRRRDQEGSVGPSDFGPRSIDPTLTRFECLS LAYSGKLVSPKWNFKGLKLLCRDKIRLNNAIWRAYIQYVKRRKSP VCGFVTPLQGPDAHRKPEAVVLEGNWYKRRIEVVMREYHKWRIYY KKRVSGGGPGRPQSFPAAAGYRPPRKIPGKGILTPELAPLGPSIQS RADSATVWPQRLAASLPRGLRKPSSREDDLLAPKQAEGRWPPPEQW CKQLFSSVVPVLLGDPBEEFPGGRQLLDLNCFLSDISDTLFTMTQSGP SPLQLPPEDAYVGNADMIQPDLTPLQPSLDDFMDISDFTNSRLPQP PMPSNFPEPPSFSPVVDLSLSSGTLGPEVPPASSAMTHLSGHSRLQA RNSCPGLDSSAFLSSDFLLPEDPKPRLPPPPVPPPLLHYPPPAKQE TVPEFPCTFLPPTPAPTTPRPPPGPATLAPSRPLLVPKAERLSPPAP SGSERRLSGDLSSMPGPGTLSVRVSPQPILSRGRPDSNKALLGSFL GSPNSLLPETENRRITHISAEQ\KRRFNIKLGFDTLHGLVSTLSAQ SLKVSATTLQKTAEYILML\QGERAGLQEEAQQLR\DEIEEL\NAA INLCQQQLPATGVPI\THORFDQMRDMFD\DYVTRTLHNW\KFWVV SSLKPMAGGLQGLWQSSLTWAQFSILIRPLFESFNGMVSTASVHTL RQTSLAWLDQYCSLPALRPTVL\NSLRQLGTS\TSIL\TDPGRIP*/ EQATRAVTEGTLGKPL
2302	A	1	535	SVTVEWIENGDTKGKEIDLESIFSLNPDLPDEEIEPSPETPPPPAS SAKVNIKVNRRTVASIKNDPPSRDNRVVGSARARQSQFPEQSSSAQ QNARRKSNVCVKEVEKLQEKREKRLQOQELREKRAQDVDAATNPYIEI MCMIRDFRGSLDYRPLTTADPIDEHRIVCVVRKRPLN
2303	A	155	276	YNTYSLFLFFQDKVKSFRALQEEQASKQINPKRPRAL
2304	A	1	477	MRAFLAALVTDWYQYRLAANALFTFLYCDTFKLEILKAFKRYKESIR WLEDEKALLEMTEEVDYDVDSYATQLEAILEQKIDILTELRENETLV PKTTKTINKTHKDCGARGGANQKTEGKAHSEKRAPNKSATYTAKEE HNKTGQERREPEKYRESE

2305	A	221	2323	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\BIDLES IFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRRTV\ASI KNDPPS\RDNRVVG\SARARPSQFPEQSSSAQQNGSV\SDISPVQAA KKEFGPPSRRRSNCVKEVDKLQDKREMKRLQQQELREIRAQDVDATH PNYEIMCMIRGFTGSLDYRPLASADPIDEHRIYVCVRKRPLNKKETQ MKDLVDVITIPSKDVVMVHEPKQKVDLTRYLENQTFRFDYAFDDSA EMVYRFTARPLVVTIFERGMATCLAYGQTGSGKTHMTGGDFSGKNQD CSKGIYALAARDVFLMLKKPNYKKLELQVYATFFEIYSGKVFDLLNR KTKLRVLEDGKQQVQVVGVLQEREVKCEDVL\KLIDIGNSCRTSGQT SANAHSSSRSHAVFQIILRRKGKLGKFSIDLGNERNAGADTSSADRQ TRLEGAEINKSLLALKECIRALGRNKPHTPFRAKSLTQVLRDSFIGE NSRTC\MIATISPG/MWASCENTLNTLRYANRVKELTVDPATAAGDVR PIMHHPPNQI\DDLETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTF HEAVSQMVEMEEQVVEDHRAVFQESIRWLEDEKALLGD*LEEVDY\D VDSYATQLEAILEQKIDILTELRL\DKVKSFR\AAEQEEQASKQINP KRPRAL
2306	A	264	451	VLPNLTVHASPTTIKIWAG\KVTHAYNPSTLGGQGRGRIA*AQEFKTS LSNIMGLRLSKKKKK
2307	B	1	642	MLEEQLVRLMTREVMDLITVCCVSKKGADHSSAPPADGDDEEMMATE VTPSAMAELTDLGKCLMKHEVLSGTLADAVTWLFTSVLKGQMHGQ HDGCMASLVHLAFQIYEALRPRYLEIRAVMEQIPEIQKDSLQDFDCK LLNPSLQKVADKRRKDQFKRLIAGCIGKPLGEQFRKEVHIKNLPSLF KTKKPMLETEVLDNDGGGLATIFEP*
2308	A	3	101	STHASESNFISICILCFCLEAPISLMSLSASLEDQPWAWALCGGGR APSTT*PPLSL*HL
2309	A	360	485	SMCLTVSMLVTACPADPCVT*A*NRSSFVPPPPWTSDLRFF
2310	A	100	190	TLSTYFIPVIDSCPSLGIFSWQPPEHNKER
2311	A	2	193	WRRRRRRCFPQPSLIWSGMRSPKKLTPPR*NYLRQALRRNLSTLRR PFAQETAWYQWCFLGL
2312	A	103	237	FLCLGRYPHLPSSPGQRQVGISGPEVAVVVVYTHPSPSNPAFL
2313	A	3	1361	VETQEGKTTIIIEGRITATPKESPNNPNPSGQCPCIRWNLKHKNYDD VLLLSQFIRPHGGMLPRKITGLCQEEHRKIEECVMAHRAELQRELQ RLSPLPATQVYYQITGLGFLKELFRANPNSTGPLAKAQQGYLTRWA PGSVKPIYKKGPRWNRGEANRKAHFSTVQWPAPSAIAHAKDDVSPLO PTQCLLDNIKKKVPLSGRPGNTDSTCQESRSIYLKSQALAVTFTF LTATAEQAEPSQLSPPPGLGEKPPADLVLQ/SEAPRAKQHYCTSP SHPAQRVVSSSDS\EHPAASHPRRPPRPGTNGWSRRGSCRASWSD CSGVRSSRVALGMAMDQVNALCEQLVKAVTVMMDPNSTQRYRLEALK FCEEFEKCPICVPCGLRLAECTQVAIVRHFGQLILEHVVKFRWNGM SRLEKVFEEQWSWNLIAKGPFEHFGRGEPY
2314	A	138	397	SHCPLSMHVGGTRPSWWGGTGV*LWPRAC/RVGLLLPSTGAGGTLEA LLSVSDTASKVFLELARHCPSEGVNPTGHAHPVPSRGPFL
2315	A	16	548	QLNGRSIRHEVMSHRKFSA PRHGS LGFLPRKRSSRHRGKVKSF PKDD PSKPVHLTAFLGYKAGMTHIVREVDRPGSKVNKKEVVEAVTIVETPP MVVVGIVGYVETPRGLRTFKTVFAEHISDE/CRLPLRQKKAHLM EI HVNGGTVAEKLDWARERLEQQVVPVNPVFGQDEMIDVI
2316	A	2	451	PRAKAQKGS PVLWAQKSCPPKTTRALAKV\ACIGAWHPARVAFS VARVGQKGYHPRTEIT\KKIYKIGQGYLIK/DGKLIK\NASTDYDLS DKSINPLSLLVQTKRRALEKIDLKFDITTSKFGHGRFQTMEEKKAF MGPLKKDRIAKEEGA
2317	A	1	625	CKFIRVMAHTRLRLPLRRKKAHLM EIQVNEGTVAEKLDWARERLEQ QVPVNQVFGQDEMIDVIGVTGKGYKGVTSRWHTKKLPRKTHRGLRK VAC\KDGLIKNNASTDYDLSDKSINPLGGFVHYGEVTNDFVMLKGC VVGTKKRVLT LRKSLVQTKRRALEKIDLKFDITTSKFGHGRFQTM EEKAFMGPLKKDRIAKEEGA
2318	A	1	1251	MASKLRLSDMTGEKGLNLAPIKIILNSLFEDGSSIGLQGAQGA VDKP

				CGLEQPVVPTKCDCTASPKCSSGHCCKVKS LPKDDPSKPVCLTGF LGYKAGMTHIVQEVDPRGSKVNKKEVVEAVTIVETLPMVVGIVGYV ETPQGLRTFKTVFAEHISDECKRRFYKNWHKSKKKAFTKYRKKWQDE NGKKQLEKDFSSMKKYCQKKAHLMEIQVNGDTMAKKLDWARERFEQQ LPVNHVFGQDEMIDIIRMTKGKGYKGVTSWHAKKLPRKTHQGPRKV SCIGAWHLVHVAFSVARTWQKGYCHHTEINKKIHKIGQGYLIKDDKL IKNNASTDYDLSDKSINPLGVFGHYGEVTNDFVMLKGCVTQKRALQK TDLKFTDTSKFGHGRLQTMEEKKASMGRLKKDQIAKEERA
2319	A	1	903	KCSSGHCCKVKS LPKDDPSKPVCLTGF LGYKAGMTHIVQEVDPRGSK VNKKEVVEAVTIVETLPMVVGIVGYVETPQGLRTFKTVFAEHISDE CKRRFYKNWHKSKKKAFTKYRKKWQDENGKKQLEKDFSSMKKYCQK AHLMEIQVNGDTMAKKLDWARERFEQQLPVNHVFGQDEMIDIIRMTK GKGYKGVTSWHAKKLPRKTHQGPRKVSICIGAWHLVHVAFSVARTWQ KGYCHHTEINKKIHKIGQGYLIKDDKL IKNNASTDYDLSDKSINPLG VFGHYGEVTNDFVMLKGCV
2320	A	1	1341	MKAAGRGDVPCKARDAEIPKAMGAHLLHQHDL DVRHGVKEPFWVTPF LLQVCPGFCHLLPYHRYFQSLMVTYKIFIDVARKFSAPRHGSLGFLP QKRSSRHGKVKSPKDDPSKPVHLTAFLGYKAGMTHIMREVDSPAS KVNKKQTVFAEHISNECKRRFYKNWHKSKKKAFTKYCKKWQDEDVKK QLEKDFSSMKKYCHVIRVIAHTQMRLPLRQKKAHLMEIQVNGGTVA EKLDWVCERLEQQVNVNQVFGQDEMIDVIGVTGKGYKGVTSRWHTK KLPCCKTHRG LCKVACIGAWHPARVAFSVARAGEKGYRHRTEINKKIY KIGQGYLIKDGKLIKNNASTDS DLSDKSTNPLGGFVHYGEVTNDLVM LKGCVVGTKKRVLTLHESLLVQMKRQALEKIDLKFDITTSKFGHGCF QTMEQKKA FMGPLKKDGIKEEGA
2321	A	1	1131	MSHRKFSTPRHGS LGFLPWKRSSRHGCKVKS FPKDDPSKPVHLTAFL GYKAGMTHIVREVDPRGSKVNKKEVVEAVTIVERPPVGIVGCVETPQ GFRTCKTVFAEHISDECKRRFYKNWHKSKKKAFTKYCKKWQDEDGKK QLEKDFSSMKKYCQVICVIAHTQMQLLPLCQKKAHLMEIQVNGGTVA EKLDWAGERLKHQVPVNQVFGQDEMIDVIRVTGKGYKRVTSRWHTK KLPRKTHQGLCKVACIGAWHPARVGFVS GYLIKDGKLIKNNASTDYD LSDKSINPLGGFVHYGEVTNDFVMLKGCVVGTKKWVLT LRKSLLVQT KORALEKIDLKFDITPSKFGHGHFQTMEEEKAFMGPLKKDRIAKEEG A
2322	A	10	1304	ESDGVTS HRKFSAPRHGTLGFLPRKRSSRHGKAKSFPTDDPPKPGH LTGFLAYTAGMTHIVREVDPRGSKANTKEAGEAATIVETPPMVSVG\ IVGYVETPRGLRTFKTVFAEHISDECKRRFYKNWHKSKKKAFTKYCK K\WQDEDGKKQLEKDF\SSMK\KYCQVI\ RVI\AHTQ\MRLPL\ RQ K\KAHLMEIQV\NGGPCGPRSWDWAREKLE\QQVPVNQV\GQDE\M ID\VIGGDPGAKGYKRGSPVRWHTKKAAPARPHPRACAKVGLVLGAW \HPG\RVAFSV\ASRWGRKGLPFHRTEINQGRIFKDWPRATLIKD\G KLIKDQCLHLNYDLS*PRASNPLGGFV\HYW*SDRNDFVML\KG\CV VGTTK\RGAFPFRKSLLVQTK\RRALEKIDLKFDIT\TSKF\GHGRF QTMEEEKAFMG\PLKKDRIAKEEGA
2323	A	138	737	TTTMSKKAKTKTTKKRP\QRATSNVFAMFV\HSQIQGVQRGPFNMI DQ\NRDGFHSDK\EKVLHDM LAFSREESPLDAYLDAMNEAPGPHQV SPWFLTMFW*ESLNRTDPLKIVIQKPPFA\CFD*KKATRHPPFREDYL /REELLTNPWGDRVYQIEEVG*TCTGEAPI*QKKGNFQITSEFHHGI LTGRPPKHKKDDLKELLA
2324	A	2	307	KPSSNRMSLQWTAVATFLYAEV FVLLLCIPFISPKRWQKIFKSRL ELLVSYGNTFFVVLIVISALVHTLQAHYRGPD CYTFMRLLSSCCAC QACTALA
2325	A	2	215	KLEENRSLKADLQKLKDELASTKQKLEKAENQVLAMRKQSEGLTKE YDRLLEEHAQLQA AVDGPMDKKEE
2326	A	1	213	PSSNRMSLQWTAVATFLYAEV FVLLLCIPFISPKRWQKIFKSRLVE LLVSYGNTFFVVLIVILVLLVIGE

2327	A	2	935	FRPRYEGRGRGCCGRVRLRLRRGLHVDGKLGKLTSSCGKPSSNRMS LQWTAV\ATFLYAEVFWLLLCIPFISPKRWQKIFKSRLVGVVSVPM GNTFF/VLVLIVILVLL\VIECRAAKEREVWMDVDGKRVNLPGTIPG GHGEALSHMEAFSVAPGGNLLHWWLGFSLLL\SFLLRL\VTLSQQA \TLL\ASNEAFKKQAEKC*VKAARKYMEENDQLKKG\APFDEGKLN ENAELKLEEK\NRELK\ANLQKLKDELQQALESKLEK*KTSFWPMR KQFMRGLTQ/ERYDRLE\EQPKAAGLQVDGPM\KKEE
2328	A	2	1217	QARGASLRPSLLRIPSEYAFTMQLRLFRLLLAALLLVIWTLFGPS GLGEEELLTSLAFLLPAPALPGPPLALPRLLIPTQEACCGGAPPL LILGGTAPENLNQRNIRASRGGLREARGLRVQTLFLLGEPNAQHPV WG\SQGE*TGPSESAQQDILQAAFQDSYRNLTSLTSLNWAEEKHC PMARYVL\RTDEGIANVPELVSELVLRGGRWGQWERSTEQREAEQ EGGQVLHSEEVPLLYLGRVHWRVNPSTPGRHRVSEEQWPHTWGPF PPYASGTGYVLSASAVQLILKVAS\RAPLLPLEDVFGVSARRG\GL APTQCVKLA\GA\THYPLDRCCYKFLLTSHKLDPMQMEAWKLVG S\DGKDCAPFAPWFPKSLGILRCR\AIA\WLQS
2329	A	1	395	AINYNEKIYELRVMETKP\DKAVSIECDMNVDFDAP/LGYKEPERQ VQHEESTEGEADHSGYAGE/LGFRAPSGSGNRLDGKKKGVEPSPSP KPGDIKRGIPNYEFKLG\EAGGRFVAFSGEGQSLRKKGRKP
2330	A	1	1494	GTRKSGRRGFVALPERSGVCQVVSIMFSFNMFDHPIPRVFQNRST QYRCPSVSMALWPNDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFK LTNKNSDRMTHCGVLEFVADEGICYLPHWMMQNLLLEEDGLVQLET NLQVATYSKSKFCYLPWMMQNLLLEEGGLVQVESVNQVATYSKFQ QSADFLDITNPKAVLENALRNFACLTTGDVIAINYNKIYELRVME TKPDKAVSIECDMNVDFDAPLGKYEKEPERQVQHEESTEGEADHSG YAGE/LGFRAPSGSGNRLDGKKKGVEPSPSPKPGDIKRGIPNYEFK LGKITFIRNSRPLVKVEENRTTDIATPTPLTPATHRLHTFDRPMAV LG LHSQPPLQACVPWGGHSTLDPYVMPNQSQLLCEFTSILSGRSSK TGAADLGDMADGSGWQPPRPCEAYRAEWKLCRSARHFLHHYVHGER P ACEQWQRDLASCRDWEERRNAEAQEKDE
2331	A	2	1062	GRAVGGVSSSLHCPERSGVCQVVSIMFSFNMFDHPIPRVFQNRSTQ Y\RCFSLS\MLAGPNDR/SSIGEKEGKIIMPP\SALDQ\LSRL*HYRI PMLFKLTN\RNSDRMTALLQCLEFVADEGICYFPTL/WMMQNLLLE EGGLV\QVKS VNLSSATLLPNFQSP\DFL\DITNP\KAVFEN\AL RNFACL\TTGDVIAI\NYNEKILRNCVVMETQTPTRPVSHH*SVNH *TV\DFDCFLPLGPKNPGKTKSHHEESEQVKADPTVAYAWKSLGFPR FSRSG\NR\LDGKKKGVEPSP\SPIKP\GDIKRGIP\NYEFKLGKI TF/VSRNSRPLVKKVEEDEAGG\RFVAFSGEGQSLRKKGRKP
2332	A	1	214	APARSALCSGAPRTSGQPWGTAPAPPSFHQRNTPCPWSPSGAAP WGSTKGQRLDGPCCAPFPFRGLSM*SKVPWWPA*TAPAPPSFHQRN TPCPWSPSGAAPWGSTKGQRLDGPCCAPFPFRGLSM
2333	A	1	1516	MAPLQQHIAVLPTTADQVTTEDDGYTWTALQHVATAKEKRKSSQTM EESQDFPLHIPRPAQGTQRAVARPSGPKAWTEAGPAKDAARSEKPG GRKAPGGRGQLTCRRSLSPVRQPPVSVVSDSLRRSPCSPADWREA GATSLDRIRPILVLMVDKLLVVVFGSTGAQGGSVARILLEDGTFRK VVRNTRNPRKKAKEKRLQGAEVVQGDQDDQVIMELALE\WAYATFIG T NYWESCSQEQEVTPA/GSLDRIRPILVLMVDKLLGLHYVVSGL\GT SRS*RGQDWPPRTLTAAGRWRNISGTLAFP*PVWG\FLANLENLLQ LFFPRKTPEGKELLCGACQVTFPWWMACPCLTWGPVLSLFEDARKI RRPEHRG*ALAGTRPRSTLPCSPSTPARSCTMP*LPEDYEKLGFP GARDLGQHVFPFLCPETPTRDI/PSLTLRLNPKALTLDQWLGTAGRLQ PAVTLPASRPLVGIRGHQRGKAPTSEIKPICSPKKKK
2334	A	3	1037	ILRSVARAQRGRSLRFHWSGGHGGRRSEAGAAGP/VEMRRTAAPQ GRVPGL/PSKLGIPDALPTVAAPRPVCQRCGQPL\ALVVQVYCPLE GSPFHRLLHVAFACPCGCGSTGGARSWKVFRSQCLQVPERAQDAQKQ GNSLAAEDWCEGADD/CGK*Y*GGAFTTVYLGFE*CCQC/HKT*TG

				LLGSKTS/CLQDAVLGAHPVPPGLPLFLPYICVADEDDYRDFVNL DHAHSLRLDYQQREGIAMDQLLSQSLPNDGDEK/S*EDHN*KVGGSR PF*QIP*KRNWLLVREQILRVFPGVESHSHF*PAPTSEVTLPQLQPV WEAKRIFEFQLMPALQHASRVLI
2335	A	156	450	LQVEIYKTVKMHCIIWHKQMVSSYFFYQKKNELSNFEEVFLKTASGMF FSTVGCHPTRCGEPEKNNPDLYLKELLNLAENNKGVV\AIGECGLD FDRLQ
2336	A	349	1187	LHGGNLQDSKDALHLAQTNMGFFSTVG\IHPTRCG*/YFEKNNPDLY LKGVAKIFA/EKTLKGKLWQLGEC\GLDFD\RLQFCPKDTQLQYFEK QFE\LSEQTKLPMFF\HGRNSHGWNFLDIMKRNDRCVGGVVSFDG TKEAASCL\ITLDLYIGFNGWPHLKT*SLIWEGFGSQFPSEKLMIEA \DAP\WCGVKSTHA\GSKYIRTAFFS\KKKWESGHCLKDRNEPCHII QILEIMSAVRDEDPLELANTLYNNTIKVFFSWNIIGICLPLSIMYVK FHSKTS
2337	B	240	387	NGKERTGDVKLLKHKEKGAIIRLLMRRDKTLKICANHUITPMMELKP NAX*
2338	A	1	152	AAAKDTHEDHDTSTENTDESNDHPQFEPVSLPEQEIKTLEEDEEEL FKM
2339	A	1	830	MRRPRRRLCWLRLCLVECGPLQSRSAVGNSEEQRKAYVFFSSLSLVD T HEDHDTST\ENTDESNDHPQFEPVSLPEQEIKTLEEDEEELFKM RAKLFRFASENDLP\EWKERT\GD\VKLLKHKEKGAI\RLL\MRR\ DKDP*KIC\ANPLPSRPLMGAESPTAGRRSVPWVLETPHA\DFRPN CPPPELPGPPRF\LNA*RMPQKFQNSFEELQGRSEGEKEESRF QGKNDL/HRKKCAEKPGSSLR*REETKEDAEAEAINRLILLSFSSL SLS
2340	C	392	631	MRTAESCRRLSWAALLGSHWRCCSHPCAAGQGPYPRAAVNGPRTPLA YLRFKEMFSSGLINVEFPQFLYLSSHFSLLLR*
2341	A	3	121	FCLIGLFLFPQALSGFRQIHVIDMDTIDVSNLNRQFLFR
2342	A	1	2970	MRKKFHIIVCGLDSIIARRWINGMLISLLNYEDGVLDPPSSIVPLIDG GTEGFKGNARVILPGMTACIECTLELYPPQENCPACSQLPQNIQFSP SAKLQEVLDYLTNSASLPFIATSFSHEDIDNHTEDSVQYVGYEPRYL RLLAIRHIVLRFPGAHARQGGEERDWQSGEGRGWRSSEGRGQKHNR QGADRLPPPPPPDSGGEERKAENMDVNIAPLRAWDDFFPGSDRFARP DFRDISKWNRRVSNLLYYQTNYLVAAMMISIVGFGCCVGRSKRM RTWAPFVSAVRERPRLSFAKQALSQAQKSIDRVLDIQEEBPSIAE TIPYGEPAKXNLPEPEPRIASRLGHCWDPRSEVRKSSGKGRITANS GPTPVFFRISPPVSGWDTSTWGLKSNTPEQSPPIASPKAITKPVRR TVVDESENFFSAFLSPTDVQTIQKSPVSKPPAKSORPEEEVKSSLH ESLHIGQSRTPETTESQVKDSSLCVSGETLAAGTSSPKTEGKHEETV NKESDMKVPTVSLKVSESVIDVKTMTESISNTSTQSLTAETKDIALE PKEQKHEDRQSNTPSPPVSTFSSGTSTTSDIEVLHDHESVISESSASS RQETDSSKSSLHMQTSFQLLSASACPEYNRLDDFQKLTESCCSSDA FERIDSFSVQSLDSRSVSEINSDELSGGYALVPIIVNSSTPKSKT VESAEKXSEEVNETLVIPTEEAEMEESGRSATPVNCEQPDILVSTP INEGQTVLDKVAEQCEPAESQPEALSEKEDVCKVTLTVEFLNEKLEK REAQLLSLSKEKALLEEAFDNLKDEMFRVKESSSISLKDFTQRI AEAEKKVQLACKERDAAKKEIKNIKEELATRLNSSETADLLKEKDEQ IRGLMEEDWAAVFELYNCEDERCYLDLARLRGVHYITWRRQNKVFPQ DKGHHPTLGEHPKFTNYSFDVEEFMYLVLAADHVLQHPKWPFKKKH DEL
2343	A	48	1493	DGQYRIWWLIEWHVDGGCGDTETWKDR\WNHVKK\FLERSGPFTHPD FEP\STESLQFLLDTC\VLVIGAGG\LGCELLKNLALS\GFRQIHV ID\MDTI\DVNS*IRQFLFRPKDIGRPAEVAEFLNDRV\PNC\N VVPHF\NK\IQDFN\DTFY\RQFHI\IVCGTGTLSCARRWINGMLIS L\LNHYERMVS*DPSSIVPLID\GGTEGF\KENARVIL\PGMTACIEC TLELYPPQVNFPMCTIASMPRLPEHCI\EYVGMLQWPKEQPFEGG\V

				PLDGDDP\EHIQWIFQKSLERASQYNIRGVTYRLTQGVVKRIIPAVA STNAVIAAVCAT*/EVFKIATSAYIPL*IITWVFNDV\DGLYTYTFE GRKGK\ENCPAC\SQLPQNISVFLHQAKLQ\EVLGIIILTNASLQNE ILPAITATLGGEKIGTLYLQSVTSIEERTRPNLS\KTIGRIGGLLDG PKTGRLLDVTTTP\QTVLFQTSILLKKGKSP
2344	C	166	312	XXX CR
2345	B	355	487	MLGLRSGIPAPVRLQLAUVLGNLSGNFGTEGPGLKGRMTVTGDPX*
2346	A	754	1035	GKVRTVKIKYWMLARSSGSSL*SQHFGRRLQADHEVQEIKHHPG\KH SANP\SLKIQKVS*LVSQAWWWVPVPAIREVEAGEWCEPGRQSLQ
2347	B	80	432	MANGPRAXFCENFQAALALSRVGLHKNPEKEPYKSKYSARALLEEVK ALLGPAPEDEDERPEAEDGPGAGDHALGLPVAQRAVRLAVIEFHLGV NHIDTEELSAGEHLVKCLRLRLS*
2348	A	2	1060	HWLSTANVISDYD\KSSPTQDTAETV*DTEPLYHQKGGEIARCWIK YCLTLMQNAQLSMQDNI*ELDLKQSELIALRKELDEEESIRKKAV QFGTGELCDAISAIEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFF QIDGYVTDHIEVVQDHSALFKVLAFFETDMERRCKMHKRRIAMLEPL TVDLNPQYYLLVNRQIQFEIAHAYYDMMPLKVAIADRLRDPDSHIVK KINNLNKSALKYYQLFLDSLRLDPNKFVPEHIGEDVLRPAMLAKFRVA RLYGKIITADPKKELENLATSLEHYKFIVDYCEKHPEAAQ\BIEVEL ELSKEMVS\LFPTKM\ERFRTKMALS
2349	A	11	2571	VKCRKAEGRRRESRLQTFEESQAVEAAMANVPWAEVCEKFQAALALSR VELHKNPEKEPYKSKYSARANM\EEVKALLGPAP\EDEDERPEAEDG PGAG\DHAGLPAEVVEPEGPVAQANRLRL\AVI\EFHLGVNHIDTE ELSAGEEHLVKCLRLRLRRYRLSHDCISLCIQAQNNLGIVWSEREEIE TAQAYLESSEALYNQYMKEVGSPL\DPTEFLPEEEKLT\BQERST RF\SKVYTHILYYLAQVYQHLECFETAHY\CHSTLKRQLEHNAYHP IEWAINAATLSQFYINKLCFM\EARHCLSAANVIFGQTGKISATEDT PESEGEVPELYHQRKGEIARCI\KYL*LLMQNAQLSMQDNI LDKQSELRALRKELDEEESIR\KAVQF\GTGEL\CDASAV\EEK VSYLRPLGFEEARELFLLG\QHYVF\ERAKEFFQIDGYVTDHI\EVV QDHSALFKVLAFFETDMERRC\KMH\KRGLAMLEPLT\VDLNPQYYL LVNRQIQFEIAHAYYDMMPLKVAIADRLRDPDSHIVKINNLNKSAL KYYQLFLDSLRLDPNKFVPE\HIGE\DVLRPAML\AKFR\VARLYG\K IIT\ADPKERAGKIWATSL\EHYKFIVDYC\EKRHPE\AAQEIEVEL ELSKEMPGRRSETPSLKERNKDKIQTAKTTSAPPAQSLALATPQPV RMCRLTRVISLGSSKGKASFAGPDRPPYEDPHIVRLQLYHPQRERS CVTSSRRSCAKSPWTLRRWPHGSSWEKSYELSDGQVITSSNKRFC PEALFQPSFLGMESCGIYKTTFKSIVKCDVDIHKDLYANTVLSGSTT MYPGIALQDAEGDHCPGSQHEEDQDHCSF
2350	A	1	423	GTVMGLPKFYISLSTKFPPLSFSLSADELHIASFLWPRSKPFGVIQ RSCASQLNALPEVLKNPGDPDKMLRFAESPRNLPAGVL/GDIWTDGK GSVSLQEQVYHFPLIRPTPGS*ARASFLSCG*BEFRRHGLTFSSTRE
2351	B	211	1632	MSTELFSSSTREEGSSGSGPSFRSNQRKMLNLLERDTSFTVCPDVR TPVGKFLGDSANLSILSGGTPKCCLDLSNLSSGEITATQLTTSADLD ETGHLDSGLQEVHLAGMNHQHLMKCSPAQLLCSTPNGLDRGHRKR DAMCSSSANKENDNGNLVDSEM KYLGSPITTVPKLDKNPNLGEDQAE EISDELMEFSLKDQEAQVSRSGLYRSPSPENLNRPLKQVEKFKDN TIPDKVKKKYFSGQGKLRKGLCLKKTVSLCDITITQMLEEDSNQGH IGDFS KVCALPTVSGKHQDLKYVNPETVAALLSGKFQGLIEKFYVID CRYPYELGGHIQGALNLYSQEELFNFFLKKPIVPLDTQKRIIIVFH CEFSSERGPMMCRLREEDRSLNQYPALYYPELYILKGGYRDFPEY MELCEPQSYCPMHQDHKTELLRCRSQSKVQEGERQLREQIALLVKD MSP*
2352	A	200	1525	IMASAHLATSAFCTRSSSSGRSGSCKRGSWDSEQALIRAWTTLPSSL HAADGSFAGGRGIPSKRWSWRAGQSSSLCLIMQTSNCGNSFQLVSE

				GASWRGLPHCSCAELQDSLNFYSYHPSGLSLSVRPSSPGNSPKEQPF QVLRPEPPDPEKLPVPPAPPSKRHCRSLSPVVDLSRWQPVWRPAPSK LWTPIKHRGSGGGGGPQVPHQSPPKRVSSLRFLTSSQCLFSMCPSSQ TLQPSFLQPGPGP\SSSRPCAASPQSGSWESDAESLSPCPPQRRFSL SPSLGPQASRFLPSARSSPASSPELPLAT*G/LSATFPESRSQPCDL DARKTGKRRHEEDPRRLRPSLDLFDKMNQKPYSGGLCLQETAREGSS ISPPWFMACSPPLSASCSPGTGGSSQVLSESEKEEGAVRWGRQALS KRTLCQRDFGDLNLIEN
2353	A	2	280	RRRGFCFITYTDEEPVKLLLESRYHQIGSGKCEIKVAQPKEVYRQQ QQQKGGRGAAAGGRGGTRGRGRGNQSTYKASRGGGNHQNNYQPY
2354	A	2	971	RQRAQSAFFRSRLAAVLVGSSGRRSGSALANRGQKAGLTAFCSIQ RSAAAAAATRTARQHPPADSSVTMEDMNEYSNIEEFAEGSKINASKN QQDDGYRTLPLPLPQRAARALRSSKMFIGGLSWDTSKKDLTEYLS RFGEVVDCTIKTDPVTGRSRGFGFVLFKDAASVDKIENIELPMDTKT NERRGFCFITYTDEEPVKLLLESRYHQIGSGKQWNQGFNNYDQG YGNVNSAYGGDQNYSGYGGYDYTGYNYGNYGYGGYADYSAGTSLQA VCHPDHVYLWGS HVAGRAQGIHQKTLSCGMVSSNFMYQRKD
2355	A	604	878	SLHHKDFETGMLLLQFAHHLGEIGFSLISPKSQRPLFLPSVRQCGA AAA/RRCYRLAPRPVCSGKRRTAPGAGD*GGERARPPRARVFCPR
2356	A	1	1042	DLFRHFKSSSIQSSAAAAAATRTARQHPPADSSVTMEDMNEYSNIE EFAEGSKINASKNQDDGKMFIGGLSWDTSKKDLTEYLSRFGEVVD TIKTDPVTGRSRGFGFVLFKDAASVDKVLELKEHKLKGKLDIDPKRAK ALKGKEPPKKVFGGLSPDTSEEQIKEYFGAFGERENIEFSMDTKTN ERR\GFCFITYTDEEPVKLLLESTYHQIGSGKCEIK\VAQPKEVYRQ QQQQKGGRGAAAGGRGGTRGRGRGQGNWNQGFNN\YYDQGYGNYN SAYGGDQNYSG\YG\GYD\YTGYNYGNYGNYGYGGYADYSAGTSLQA LMGK\AS\RGGGQSTQNNYPAHT
2357	A	586	1970	PQEFTPLRFSLLILLFSQARVPSRVASLLAGRAAMEVPPRLSHVPP LFPSAPATLASRSLSHWRPRPPRQL\APLLPSLAPSSARQGARRAQR HVTAQQPSRLAGGAAIKGRRRRRDLFRRHFKSSSIQSSAAAAAATR TARQHPPADSSVTMEDMNEYSNIEEFAEGSKINASKNQDDGKMFIG GLSWDTSKKD\LTEYLSRFGEVVDCTIKTDPVTG\RSRGFGFVLFK AA\SVDKVLGT*KGKLDGKLDIDPKRAKALKGKEPPKRLWSGLSP DTS\EEQIKEYFGAFGEIENIELPMDTKTN\ERRGFCFIT\YTDEEP VKK\LESRYHQIGSG\KCEIKGCTTPKRYLGQQQQPPKGCK/RGAA AGGRVGTGRGRS\QGNWTQGFNNYDQGYGNYNAYGGDQNYSGY GGYDYTGYNYGNYGYGGYADYSAGTSLQA
2358	A	592	608	WLRWATYKAGQPQLEAQNYPYSFREGQPFRLDHLRTAGAEONCAA VWVRL*RNMGFVLLTGA\ASFI\MAVHLSHQCSQGPAAKVPKWEYP YPCATEPLNNGHHPSTCIQAKPHPRNTVGKV*PSPSLFFPSLLGGV YHPAV*ASWPWAWPWICWTEFLYA\YGLLHGENPSKRSRSPWGS\I ALLAFGWGTTVCSGFPSILVWVK\SLGQVEPKC\CHLKKL
2359	A	857	1343	SFRISSEFGIITFKIVSFGIMAQTHAMGQFFERNV*LTQGEIENLN RPIPVKL/ESITNNLL**KAPGLDGFTDD*SNIEINL*PRNISLKF FFLRKKSYPSTIASKKIEAKGTHPN*L*ETSITLILKSDKDMTRKG KLQSLINIDAKILNKILANQMQ
2360	A	84	326	DKAYQCSDCDK/ELHSVTLVSR*SVLSMHQSIHIWKKLICFLK/CH KAFSQ*SALI IKQRIHVAQII*ICCIWESLQPEVVL
2361	A	635	1170	RLFKCILGLLTFPPDSSHPQLPGESPGSFESRCPCGWPHPAQPHQS RWA\GPACSSYSGVLQG*EPQI*SLQHGRGGGGRTGGLEKETRTGSR ISDTALGG/EAGPCPCGQLPHLPGPPPAHDAGPYIP/PKGPGGSGY LHPHGSALGNSQAMKQAGRT\GSAGSQSAEFHKAALWT
2362	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERHFD LSHGSAQVKGHGKVADALTNVAHVDDMPNALSALSDLHAHKLKRV PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
2363	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERMFSPFTT

				KTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDDL HAHKL RVPVNFKLSSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
2364	A	3	522	PTLLVPTDSERTHPWLLSPADKDQRQGPAGWKVGAHAVRSMCAEAL RMFLSFPTTKTYFPHFDLSHG\SAQV*GPRARKVADALD/TNAVAV GRTLPNALVRPL\SDLHAHL\RVGPGSIFKLLKAIACL\LTARPP SPAEFQPLAVASLPWGQSFLGFLKHLRCLNLPNYR
2365	A	2	333	EPVCATWKNRTPEPTRQCRPAEKQRASATQHQEGRPQGWKPRRSSDP PHRPRGFSSTHDVSD*PK\TNCREAKGEEAGSGLPTGTGIGGSKPSN RLRSTTHTTTPTGTVFNT
2366	A	208	491	KQSQVWCVLWSEERGLLDPPNPSACGGDRLS/RTSAVPPVP*S*NS SAHGPGRPGKPGQGW*TVTSGRSVAGKPGVPSNRRCLPPHPWLLD N
2367	A	2	1010	PQPAQPCPGKELRTV\NGSQMLLVLL\VLWLPWLGAL\SLAE\ASR A\SFPGP\SELQLRRTSKI PKSLRKR\YEDLLNPGCGPNQSWEDSNT DL\VPAPAVRI\LTP\EVRLGSGGHLHLRISRAALPEGLPEASRLHR ALF\RLSPTASRSWDVTRPLRRQLSLARP\HGPALHLRLS\PPSSQ SD\QLLAESSARPOLEHLRLPQAARGRRRARA\SGDHCPLGPGRC CRLHTVRASLED\LGWA\DW\VLSP\REVQVT/LCAIGACP\SQFPG RQKMAQESKTNPAALKAPNTVPKRP\CLVPRQLQIPWVLHSKRPD TGVCQDL/SD*LVKPKTCHLHY
2368	A	68	430	HVLTAHPPPHRLGPGPQGRSGMGRELVGPTVCLSSLRLAASFPRPP /VGLGPQQVQVNGGCWPCRGYEGGTQAPQPPS*VGDPGEPPNPQAPG AQSSTPKPAHIPTTQEAGRRWEGKWF
2369	A	694	872	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDVGSS VSNSDDEISSSDSADSCDSLNPPTASFTPTSILKROKQLRRKNVRF DQVTVYYFARRQFTSVPSQGGSSLGMAQRHNSVRSYTLCEFAQEQE VNHREILREHLKEEKLHAKMKLTNGTVESVEADGLTDDVSDEDI DVENVEDDYFLLQPSA\PKRRRALLRASGVHRIDAEKQELRAIRL SREECGDCRLYCDPEACACSQAGIKQVS\DRMSFPCGCSRDCGN MAGRIEFNPIRVTHYLHAIMKLELESKRQ\GAAQQPQ*GALPDCQ LQPDRTGP*DPLTWHLIPAWLQAHASGSQYSRQSQPHSSRRDRMAR SSCFSSASIRCTPEALSRLRLVGRWLQEEVI IHLHIFHINIFT
2370	A	2	295	LVVMDALVEDDICILNHETAHKRDTVTPVSIYSGDESVAHFALVTA YEDIKKRLKDSEKENSLLKKRIRFLEEKVIFIFYLHVCVDIRNNSKY LKF
2371	A	2	345	ESLKVLEQLQSKEVELLQLRTEVETQQVMRNLNPPSSNWEVEKLSC DLKIHGLEQELELMRKECSDLKIELQKAKQTDOPYQEDNLKSRDLQKL SISRVSVAQPGVQWRNHGIA
2372	A	156	1437	GIETRRPWGRPYVAWLLVVMDALVEDDICILNHEKAHKRDTVTPVSI IL/PGESVA\SHFALVTPYEDIKKRLKDSRKRTSF\LKKRIRFLEE KLI/GSDLKKKQVT*GRE\QVNKAYHAYREVC\DRDNLKSKLDKMN KDENSE\LKVLNEQLQSKEVELLQLRTEVETQQVMRNLNLP\PSIQTG EVGKVGAGDL\KIHFGNQELELMRKECSDLKIELQKAKQTDOPYQED NLKSRDLQKLSISSDNMQHAYW\ELKERKCLN\HLVTSSYKLELLR KT*KT\STAIKK\ACAP\VGC\VEDLGRDSTKL\HLDGFLATYARH PPLLPNGKALCHTTSSPLPGDVKVLSEKAILQSW\TDNERSIPNDGY /DAFREHSSYGQNSLEDNSWGIFQSPPK/SQSETAFGETKTKTLPLP NLPLPHYLDQHNQONCLYKN
2373	A	28	405	FLYDPAPPFLSIYP\KELKVES*IDTCTLIFIAALF/LIGKRWK*PK YPLTDEWINK/VWYINTIEYY/SHLKRKDILTHYTTWVNREDLILSE ISQSQKINTVESTYMRYKYSIS*ISIGTSYKSHRV
2374	A	1414	1607	DRVSLWLPRLECSGAISAHCNLCFSGLSNPTSASRVAGTTGACHHT LLI*FLFVFFVVVFETES/HLWLPRLECSGAISAHCNLCFSGLSNSP TSASRVAGTTGACHHTLLIFVFLVEMGFHHVKG
2375	A	558	985	KKDPRWALYSLYVYKFLHFSYSSAKNPDGCFQKVLNGFTKFFCKEQ

				YCKLLKLYFYRLFALLWILCLSGFLKFFFYSEIMELVLAAGALLFC /GNFIIYDTHSLMHKLSPEEYVLA AISLYLDI INLFLHLLRFLEAVN KK
2376	A	664	937	VLLILFSNINIFL*SLPYSFFFIGEDNGSWVLAAG\ALLFCGDSS MDTHSLDGINWSPEEYVLA AISLYLDI INLFLHLLRFLEAVNKK
2377	A	1	739	DPTPVTPRSSLKNDSTNGSSVAS\ATVHIEWAFLRKVYSILSLQVLL TTVTSPVFL\YFESVRTFVHESPALILLFALGSLGLNFALTILNRH\K YPLNLYLLFGFTLLEALTAVVVTFYDVYIILQ\AFILTTT\VFVWF DCVYSYQSKKDFS\KFGAGLFALLVG*LCLS\GFLKVFFFYSEIMEL \ALA\AAGAPPPVDFII\YDTHS\LMHKL\SPEEYVLA AISLYL\D IINLFL\HLLRFPQSQNLKK
2378	A	272	1668	AMSQGSVT\FRDVAIDFSQEWEKWLQPAQRDVYRCV\MLENYGHVLS LAGLSISKP\DV\VSLLEQGKEPW/VWGKREVKRDLFSVSESSGENQ GLFHQKNVIYDGLHPSI*IMERNKVKAPVYSSFKGGWKCKDHTML QENQGCIRKVTVSHQEALAQHMNISTVERPYGCHECGKTFGRFSLV LHQRTHTGEKPYAC\RACGKTFSQISNLVKHQMIHTGKKPHECKDCN KTPSYLSFLIEHQRTHTGEKPYECTECGKAFSRASNLTRHQRIHIGK KQYICRCKGKAFSSGSELIRHQITHTGEKPYECIECGKAF\RRFSPL TRHQSIIHTKTPYECNECRKAFRCHSFLIKHQRHAGEKLYECDECG KVFTWHASLIQHTKSHTEKPYACAE*NKAFSRSPSLILHQRT\HTG EPPYVCKVCNKSFSWSSNLAKHQRTHTLDNPEYENSFPNYSFLTEH Q
2379	A	1322	1644	HLELFLGIRGIMFVGWNE*EEKAGLNGSRL*SQHFGKPRWVDH/L RSGVRDQSV\QGHGKTSSLQKNTKTSWAWWRAPVVPAT*EAEVGGWL EPRGGGCSEAVSGAF
2380	A	319	724	EASLDLAPNISPPKTSCLPTGSCCSFTQTWMPQSKVFIHGPEQGPWD WALGTDLTALPFKARNMPLD TAGLPSIALRLTVNHRRSPGSQELSC LPDSCLSQ/PPQPC*GSLLPLEYKCTPKEALRK*KRLSFLFV
2381	A	38	704	SSEEEQSRFSSWHQGDEPAVTWKWLPKVPWRFRSHFPLDSPWHFLL QTAVTFLPQISAAPPKPLLPPTSPLAFFSSLLTDLPYLHPQGFSAGA TA\NKAS\HNRTALQSHS\SPEGKEEP*TPYPPELEYIP\RKRGN PHGKLVGTGLGHSAPCGYSFLFHPSPKRGSGTRDRVEGRLKARQNI RVCSNN/AGEYEEARRFKGLSSQ\SGPVPPDV\GSGVQT
2382	A	107	449	LRRGRSRETNEEPPPTVQVQGGPGPQREEKQKTKMAKFVIRPATAAD CSDILRLIKVAESQSSRGVGVWRWLRFPGWGDSRLEVSAGVRAQVPV LSAPIPGSAATPPARPPIPP
2383	A	68	422	EEDAPGRRMRNHLFFFQVQGGPGPQREEKQKTKMAKFVIRPATAADC SDILRLIKELAKY EYMEEQVILTEKDILLEDGFGEHPFYHCLVAEVPK EHWTPEGNPSFPPEARETKLLCKK
2384	A	54	859	LRRGRSRETNEEPPPTVQVQGGPGPQREEKQKTKMAKFVIRPATAAD CSDILRLIKELAKY EYMEEQVILTEKDILLEDGFGEHPFYHCLVAEVP KEHWTPEGYSL*LRHVHGPSVYMDGRGKN*KILYTIK*MIMINEDTA LVGFAHVL IYPMNPWDWQSYLYLED FS\VMG Y\KGLGIGSEILRN\ LSPGCQ*RCR\CSSK\HFLVA\EWQ*THPITFY\KRRGASDLSQ*RR GWETCSKIGQGSTWLKIGQPEGVRECCLLGWTTSHSYF
2385	A	1	1110	MRDDFREAAALRPEKKSAREAEVLKMGKQEKERSKRNIIGYFEQKD SDNYRVFERVANILHDDCAFLSAFGDVSKPERYSGDNIIYKPPGHSA PDMVYLGAMTNFDVTYNWIQDKCVPLVREITFENGEEPSSETIRDKSL THSTEAPSGGSDFIMQELEQKEEAAGEEANDGGSGHSLGQEGRPRAQ RTQWTGAESPMGKEVLDDGRRAGPVPAASACPCHGPQRYHASCRPI LTRPQMLPSAPGAESPRPEKPVSGENGRISPEGLIRSHGVGASPSPR SPGVSVSASGPGGSLNRKRPSIDLAFPLTSLIWECEVDRCWGCVT LTGSRSLKRCPGWQIPLLWLDAIGWEPRTDGDFGFHWENRV
2386	A	3	1515	TEWGLSGSCPGCSPPEPGSRGRGAAAWRILRC\RLLPEPSPFLTQPN LAQSQPPAPVPVTDPSVTMHPAVFLSLPDLRCSLLLLVTWVFTPVTT BITSLDTENIDEIL\NNADVA\LVNFWLWDWCRFSVQMF A IQFFEEA

				SDVIKEEFPNENQVSVQCQELD/CVDQHPWT*AQ\RYRISKYPTLKLFRNGMMMKREYRGQRSVKALAD/YAVRQQKSDPIQEIIRDLAEITTLDRSKRNIIGYF\EQKSDNYRVFERNANILHDDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLG\AMTNFDVTYNWD/IQDKCVPLVREITF*KMEKELTEEGTALFSILFSHGKEGYRKV*GIFPDWR*APAFY*VEKGTI/NTFLHAD\CDKFRHP\LLHIEKTPQQDCP\VIAYWTAFR\HMYVFGRLSKVYLIPGKTSRQFRILD\LHSGENWHRGIPHHP*PPTDTAPQGEASPKDVGKAVPPGGGSFPGNLAPQ*ILGITLLRGSEDEAF
2387	A	112	861	NPGAAMPAYHSSLMDPDTKLIGNM/AHLLPIRSQFKGPAPKRDRIPDIVDEAIFLPSGPNVFF\KNYEIKNEADRTLIIYITLYISECLKKLQK\CQFPKAQGEK\EMYTGLIPLNFPPI\GEPGFSHFNANLCPNPANK\QEDE\VMRA\YLPTSLRPRTLGLKTL*EKFFGSPSRMDKPPQSGWTWLC*RDSFMNKSL\SGPWTIEREPGAHRLPRGPAAFFQODVTQSFCLYFSKVFIQKRRRACLYLKNS
2388	A	2	875	AQEIFFKSI FSPNISR\GSSAGFDRHITIFSPEGRLYQVE\YAFKA\I*PGGPLPSLAVRGK\DWAVIV\TQKKST*PNYLDSS\TVTSLFPR*LKNIW\CVMTGMT\ADSR\SRVQ\RARY\KASYWK\YTKYGYEIPVTMLCKGIARYCSGLHTRNAENEALLGCGMILIGYS*RSQGPSGYIRC\DPA\GY\CGFKSPTAAGS*NKPEVTPASLEKKK*RKEIWIWTF*TRPVETANYIACSTVLIQLISQPSEIEVGVTVENLK\FRILTEABIDAHLGCSRQRETKHCLLVYRDP
2389	A	1	397	AKAKMADVLDLHEAGGEDFAMDEDGDESIHKLKEKAKKRKGRGFG/SR*VWGKWGRVA**GRSYGFWSPPHRRNNGRKEEFSVISCMSLIEEGSRARMREDYDSVEHDGDEPGPQRSVEGWILFVTGVHEEA
2390	A	146	831	CLSGTDEISIEGEMADVLDLHEAGGEDFAMDEDGDESIHKLKEKAKKRKGRGFGSEEGSRARML*DYDSVEQDGDVPGPQRSVEGWILFVTGSP*RKPPEDIHDKFARIMGEIKNISSSTFDRRTG/YILKGYTLSLNIE TYKE\AQAMEGLNG\QDLMGQPI SVDWCFVRGPPK\GKRRGRRRSR\SPDRRPSLTGPLL SRCSLQDSIWTMAALGQIGLWELCCVYI
2391	A	2	442	FYVILISVRELYLCHHL PFLCAGVYMTNSAMKVFLIWLIVKITVLEFKKLSWPAGVWF*GLILYTHI*TL/NTHI*VQNVCYIILQRNK*FHRFCINIKSWLGAEPHACNPSTLGG*HS*\IT*AQKFETSLGNIVRPCLYKKYKN
2392	A	2	427	RRANPPSISPSAQDSRVTVPGEGPGSP/G*PSRPSV/GPA/PGSGGLRGSSAPATPLGEAPSPA\GPTPALQPCDPGAGP/GTARPGQTASAPAPLPPRRGAGAPP\QAGREGGPCGEEERPPSGREKVSC*KRQTGPQRRADK
2393	A	2	662	ACTAADLIAGTTISEAGPHMENQP/GEVAGPAGPPTPSWAPRIPLAPPWRAAAGRDPAT/GQEDSQ*PTPGCPSWPPWPTQLSPSAAGSPIHT\PPIQGFSQLLS*RSPTGTEEP*EANKLPPWTGHPHREPEHPGLPGHPC AAGSIGHWHL LLLCPLATLHGERQRHLHPGQRSGCGVQGRTPPGSAQIQDLPAAPSSILQNLSTQLCSAARPRSMPPASRMRM
2394	A	115	187	MESGHWGKPGHHLPIPAACLDPD
2395	A	93	584	KHSASAAQALPGTLGACTGSGGLRGSSAPATPLGEAPSPA\GPTPALQPCDPGAGPVLPGQVKLPQQ/PPAPLPPRRGAGAPPPPEIPSGSSFQGYWEGGAQTPGLLPAQRPLPPFPALGSGCSALEEG*ATGTRGHKGGSCS*GLWGEPRGAGKHPPHLLL
2396	A	46	440	LQKRVGDWLGEAPPWVGWVSHRCRARTARPGQTASAAPAPLPPRRGAGAPLARVPAPPCCAQRAPPSSSQPGRNQ**AASGPWRPPR/PGREV GTCGEEERPASGREKDSC*ERQTGPGQRRRAVKMTQIR
2397	A	455	1241	ARELRAGGFYVPHRGLEMPETALEAGVSGVGLQHLPH/HLGEAPSPSAWPDTRQCSRVI PVQGPVLPQGVKLPQQ/PPAPLPPRRGAGAPPLRLARVPAPPCCAQRAPPSSSQPGRNQ**AASGPWRPPRQAEKESNCGEEERPASGREKDSC*ERQNGARSAAGRQAKESPQTSRPPDGEPACEVAGPAGPPTPSWAPRSPLAPPWRAAAARDPATGRRTVSDPHRPAHHGLPGQHSYLLQLQDHL SIHSP IQGFHSQLLS

2398	A	2	330	PLFSDNGKKRGLALDGLKHEDTNLASSTIVKEGANKEVLGILVSyr VKVKLVVSRGG\APETDVPVDNLIEFDNTYATDDDDIVFEDFARLRL KGMKDDDDYDDQSTRP
2399	A	2	417	EIRAFCAKSL*ESHKNSVRLVIRKVQFAPEKPGPQPSAETTRHFL MSDRSLHLEASLDK/EVRQYADICLFSTAQYKCPVAQLEQDDQVSPS STFCVKYTTITPLLSDNREKRGLALDGLKHEDTNLAFSTIGKEGGH
2400	A	188	340	GGALLKDPLGGPNLPGGGKDKFFSFWGAF*NPPGDFWEGTFFLGGGI LGP
2401	A	117	459	SQPRPFPSAGDPPGLKEFRLFQNDTGS LGVYCFSGEHGGATPRGLEL WCGGGLCSIQSCLTPSHTVRQYADICLFSTAQYKCPVAQLEQDDQV SPSSTFCVKYTTITPLLSDN
2402	A	39	449	PVPAPRGFPQGAVLPWGAPOCKCPRRRPFQNLPCSVTLQPGPEDTG KACGVDFEIRAFCAKSL*ESHKNSVRLVIRKVQFAPEKPGPQPSA ETTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTP
2403	A	3	1359	FPGRFRGGAGILAAGEEAASEPRTERAAGARTMGEKPGTRVFKKSS PN\CKLTVYLGKRDVFDHLDKVD\VDGVVLVDPD/YTMKDRKVFVT /LSPCAFry\GREDLDV\LGLSFRKDLFIATYQ\AFPPVPNPPRPPT RLQDRLLRLKLGQHAHPFFFTIPQNLPCSVTLQPGPEDTGKACGVDF\ EIRAFCAKSL*ESHKNSVRLVIRKVQFAPEKPGPQPSAETTRHFL MSDRSLHLEAS\DKELYHGEPLNVKCSFTNNSTK\TVQGRFKVS C*GQ\YADIWPLSGTAQYKCPVAQLEQDDQVSPSSTFCVKYTTITPLL SDNREKP\CLAL\DGKLKHEDTNLV\SSTIVKEGANKEVLGILVSyr VKVKLVVSRGGDVSVLPFVLMHPKPHDHISLPRPQ\SAAPETDVPV DTN\LIEIDTNYAT\DDDDIVFEDFARLRLKGMKDDDDYDDQLC
2404	A	3	213	EPKPEITWWFEGEILQDGEDYQYIERGETYCLYLPETFPEDGGGYMC KAVNNKGSAASTCILTIEDDY
2405	A	3	1971	GGTRTVPPRGKKYLRRSPAPAGCKYIQSFIISPRPHRANMNDISQ\K AEIKEMLASDDEEDVSSKVEKAYVPKLTGTVKGRFAEMEKQQRQEEQR KRTEERKRRIEQDMLEKRKIQRBLAKRAEQIEDINNTGTESASEEG DDSLITVVPVKSyKTSgKMKKNFEDLEKEREKERIKYEEDKRIRY EEQRPSLKEAKCLS\LVMDDEIESEAKKESLSPGK\LKLT*RNLER QRQENRKKQAEERKRLEEEKRAF\EDARAQMVNEDEENQDTAKIF KGCRP\GNLKPSFEEMGRQRREDEKRAEERARRRIEEKK\AFAEA RRNMVDDDDSP\EMYKTISQEFLLTPGKLEINFEELLKQKMEEKRR EERKHKLEME\KQEFELRQEMGEEEEENETFGLSRBYEELIKLKR SGS\IQAKNLKSKFEKIGQLSEKEIQKKIEERARRRAIDLEIKERE AENFHEEDVDVRPARKSEAPFTHKVMKARFEQMAKA\R\QEEQR RIEEQKLLRMQ\FEQREIDA\ALQKKREEEEEEGSIMNGSTAEDDE QTRSGAPWFKKPLKNTSVVDSEPVRFVTVKVTGEPKPEITWWFEGEIL QDGEDYQYIERGETYWLILPETFPEDGGGYMCKAVNNKGSAAST\CI LTIESKN
2406	C	933	1070	MKRNKNILYYGTNKLNTNNLLNNFINILVSSLGLSERSFYRYIL*
2407	A	138	1166	VVAMAQVLRGTVDTFPGFDERADAETLRKAMKGLGTDEESI\LT\LL TSRSNAQ\QBEISCS/AFKTLFGRDL\LDD\LKSELT\GKFEK\LIV AL\MKPSRVL*MLIELKH\ALKG\AGTNEKVL\TEIIASRTP\BELR \AIKQVYEEYGSLL\ED*RWLGDPGSGYYPAGCWLVL\LLQANRDPDA G\IDEA\QVEQDAQALF\QAGEL\KWGTDEEKFITIFGT\RSWSSF* GKVFdkYMTISRISKLR*ETIDRE\TSGQFRSQQLLGCCGILFRRYTS PTLQETFIYAMKEAGTDDHTLIRVMVSRSEIDLVIIPGREF\RKNFC HPPYSMIKGRYIWGTIKKALL\LCGEDD
2408	A	1	498	MRKSQCKKAENSKNQKASSPPKDHNSSPAREQNWTENEFDDELTEVGF RRDMDEARNHHSQQTNTGTENQTPHVL*HKWELNNENTWTQVEVHHT PRPVRSAVFSVLSKQSWRVSETGFS*AEMLNGLPALLASYLIHAYL PFPGKPMYFSKRTSDTKAII*ISTALD
2409	C	14	394	MrgTFAXXXXXXXXXXXKTVEQTATTNNKPGQGT*PNSANTQGNSTP NPQVPDYPPNYILFLNNLPEETNEMMLSM*LFNQFP*GK*EVRLV*PGRH

2410	A	2	353	DIAFVEFENDGQAGAARDALQGFKITPSHAMKI DMDEARNHHSQQTNTGTENQTPHVLHKKWELNNENTWTQVEVHHTPR PVRSAVFSVLSKQSWRVSETGFSAEMLNGLPALLASYLIIHAYLPF PGKPMYFSKRTSDTKAIIISTALD
2411	A	1	349	LGSSTNALRQLQGFPFYGKPMRIQYAKTDSDIISKMRGTFADKEKKK EKKKAKTVEQTATTTNKKPGFKEVRLVPGRHDIAFVEFENDGQAGAA RDALQGFKITPSHAMKITIYAKK
2412	A	123	195	SWKPSFSAN*HSNRKPNTACSHS
2413	A	240	743	IHGKNFQLGKDRRQYWDNVSVVWHQVGAFEHSADHILHGSALREMRV LHSSPSQTLVLTARFHPLESSPWHAGSLGILLSRPLQPPPCSRSSVW QSRCLQSKSCPLAGVEPFHIESGSQGGNKLCSPPQSTAPHTSSFLHN ALAPELLGNPEPWHRVHVKVSSTFPLW
2414	A	284	672	GGWEGLTDTSYRRAPAGIRPVLQORKEQTVIFAVLQPLLVIPIR*TAGS VDLQQT/GRPAEERPVRRTKKQONATTSTKSTKGTPTQKPHSNVIRF KDERMDDEAGNHHSQQTNTGTENQTTTCSHSYVGVEQ
2415	A	579	1383	VGSCAFYLAVSVFLAPRPFLLHLLQLGADE\ARSWDFLRSPEE\FNTN MDIRPNHTIH\INNMNDKIKKEELKRSYALFSQFG\HVVDIVALKT MKMRGQAFVIFKELG\SSTNALRQLQGFPFYG\KPMR\IQY\AKTGS DII\SKMRG\TFADKEKKKEKKKART\VDQTATTTNKKP\QOGTPNS AIP\QGNSTQIPQ\VPDYPKLNFPYSLNKLQRETNNMMLSHAV*I SSTWPSSEVPSPGYPGRHD\IAF\VEFEN\DGQAGAA\RDALQGF
2416	A	1186	1451	DLKVLHEKPKLARRSGSHL*PR/HFGRLRWKDCIKPGVQDHSQYR ESPSLQNIKKKI IWAWWCMPIVPTTQAVKVGGSLELKRRLRLQ
2417	A	1	412	VLKQLQVYVAQSQQKVFVDVRLNGHVVKDLDFDRVGHSTARDEIIP MSIRKGLSVQGEVSTFTGKLYIEFVKGYDNPVKCALYIMAGTVDD VPKLHSNPLPLPVVRTNDYPEQGGGVWERNQPYWFWFLYFSQ
2418	A	298	532	MGSWSLPGRTLWKEKVRFLKSKERTNPGSNFFSFPGSQHTREERSQE CLSLPVLPSYLATRLSLPDSCPLKGRKAH*QRHSEI*LMGFEPGWPG KL*GWIELAFLGCLHLTLPLPCPTPLPPKSTKSGCFSLSIALCFNK QFAVTK
2419	A	5	977	VRGGLAAGRGRGSAGAAPVVVAAMLGAWAVEGTAVALRLLLLLLPP AIRGPGLVAGVAGAAGAGLPESVIWAVNAGGEAHVDVHGIHFRKCI PL*GRVGRASDYGMKLPILRSNPEDQSCYQTE\RSN\EETFGYESPI QREGGLTCWSLKFAE\VFYQSQKVFVDVRLNGHVVKDLDFDRVG HSTAHEIIPMSIRKGLSVQGEV\STLYTGNSNME\FVKGYL*PIPI KVCAL\YIMAG\TVDDVPKLQPHPG*ERKKGEEEEEE\YDEGSIPK KNRPIKNGGQSGP\RHNPPT*ASDNSSLMPFILV\AFGVFIPTLFLC CRL
2420	A	1	454	RNSEKEVEKRVKALQEAHLKAGLNPDPGTPALSTLGGFSPASKPSSP REVKAEEKSPISINAKTVKKEPEDRQQAS\KSPYNGYNNRRSRSGTY SSRSRSRSHSESPPRRHHNHSSPHLKAKHTRDDLQSSNRHGHKRRK SRSRSQSKSR
2421	A	19	434	QRGNYSFEIVAMACINLASKIEEAPRRIRDVINVFHHLRQLRGK\RT SYIYQSLGDVEWYIEMKLSSWQQTPSPILIDQNYINTKNQVIKAERR VLKELGFCVHVHHPHKIIVMYLQVLECEARNQTLVQTAWVVHDGIT
2422	A	171	437	TSNFYILSYNNRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKA KHTRDDLKSSNRHGHIRKKSRSRSQSKSRDHSAG*KHRL
2423	A	21	1855	FPGRRFRRLWACVRLAKTMASGPHSTATAAAAAASSAAPSAGGSSSGT TTTTTTTTGGILIGDRLYSEVSLTIDHSLIPEERLSPTPSMQDGLDL PSETDLRILGCELIQAAGILLRLPQVAMATGQVLFHRFFYSKSFVKH \SFE\IVAMACINLASKIEEAPRRIRDVINVFHHLRQLRGKRTSPIL ILDQNYINTKHQVIKAERRVLKELGFCVHVHHPHKIIVMYLQVLECE RNQTLVQTAWNYMNDSLRTNVFVRFPETIACACIYL\AARALQIPL PTRPHWFLFGTTEE\EIQEICIETLRLYTRKKPN\YEL\LEKEVEK RKVALQEAHLKAGLNPDPGTPALST/LGVGFSPASKPFIHQENVKAG RRKSPIFHLMWKDSKKEPGG*D/RQAFPKALYNGVKEKDS/RRRSR

				NSRSAS\RSRSTRSRSRSHTPRRHYNRRS\RSG\TYSSSPRSRSP \SHSESPRRHNNHG\SPHLKAKHTRDDLKSSNRHGHKRRKKSRSRSQS KSRDHSDAAKKHR\HERGHHR\DR\RERS\RSFEEVP*KARHGWVP RSGTWARAQGADLSSSLWSPAIOFLGFGPIYQCDGMGLNPKTIKRKT GLGDFLETPPRS
2424	A	1	1566	MLYEKFSFAGPILSIRVCRDMI TRRSLGYAYVNFQQPADAERALDTM NFDVIKGPVRIMWSQRDPSLRKSGVGNIFIKNLDKSIDNKALYDTF SAFGNILSCKVVCDENGSKGYGVHFETQEAARAIEKMNGMLLNDR KVFVGRFKSRKEREAEELGARAKEFTNVYIKNFGEDMDDERLKDLPFGK FGPALS VKVMTDESGKSKGFGFVS FERHEDAQKAVDEMNGKELNGKQ IYVGRAQKKVERQTELKRKFEQMKQDRITRYQGVNLYVKNLDDGIDD ERLRKEFSFGTITS AKVMMEGGRSKGFGFVCFSSPEEATKAVTEMN GRIVATKPLYVALAQRKEERQAHLTNQYMQRMASVRAPVNPVINPYQ PAPPSGYFIAAIPQTQNR AAYPPSQIAQLRPSRWTAQGARPHPAV HVQGGQEPLTASMLASAPPQEQKQMLGERLFPLIQAMHPTLAGKITGM LLEIDNSELHLMLESPELSRSKVDEAVAVLQAHQAKEAAQKAVNSAT GVPTV
2425	A	328	889	GLRTPAAYLYCGTVRTAGVAAASRYQGDNIYVKNLDDSIDDERLQKE FSPFGTI*SAKGMMEGGHKS\GFGFR/ICFSSPEEASKAGTELNGRT VATKPSYVALAQPKEECQAHLNQHMQRMASVRAPVNHVMNPYKPAP PSGYLMTGIPETQNRPPRPGAVGHPCNPSTLGGQEGKNTGSGDRDHP G
2426	A	1	2262	MKPKTSEEVCSPLVWQYSLFPSHTLGNPVHIIQALTMTFSKSLSPTS TIFRVLGQNSAKTAPVKGIHDHHA VKGNGLFSASSSGAGVQRAGRLG GPGAGGQDPRS QLV SASAAVGDSSSQAPLLRPTRVAAPVAGTRSA VRVAACGPAGSRAEMNPSAPSYPMASLYVGD LHPDVTEAMLYEKFSP AGPILSIRVCRDMI TRRSLGYAYVNFQQPADAERALDTMNFVDVIK GK PVRIMWSQRDPSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILS CKVVCDENGSKGYGVHFETQEAARAIEKMNGMLLNDRKVFVGRFK SRKEREAEELGARAKEFTNVYIKNFGEDMDDERLKDLPFGKFGPALS VK VMTDESGKSKGFGFVS FERHEDAQKAVDEMNGKELNGKQIYVGRAQK KVERQTELKRKFEQMKQDRITRYQGVNLYVKNLDDGIDDERLRKEFS PFGTITS AKVMMEGGRSKGFGFVCFSSPEEATKAVTEMNGRIVATKP LYVALAQRKEERQAHLTNQYMQRMASVRAPVNPVINPYQPAPPSGYF MAAIPQTQNR AAYPPSQIAQLRPSRWTAQGARPHNTSTQTMGPR PAAAAAATPAVRTVPQYKYAAGVRNPQQHLNAQPQVMTQQPAVHVQ GQEPLTASMLASAPPQEQKQMLGERLFPLIQAMHPTLAGKITGM LLE IDNSELHLMLESPELSRSKVDEAVAVLQAHQAKEAAQKAVNSATGVPTV
2427	A	365	2419	FSIPVDFCPSALAPRSPPPGSGPQPRHSLSSSHGKVAACGPAGSRAE MNPSAPSYPMASLYVGD LHPDVTEAMLYEKFSPAGPILSIRVCRDMI TRRSLGYAYVNFQQPADAERALDTMNFVDVIKGPVRIMWSQRDPSLR KSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYG FVHFETQEAARAIEKMNGMLLNDRKVFVGRFKSRKEREAEELGARAK EFTNVYIKNFGEDMDDERLKDLPFGKFGPALS VKVMTDESGKSKGFGF VS FERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRKFEQ MKQDRITRYQGVNLYVKNLDDGIDDERLRKEFSFGTITS AKVMMEG GRSKGFGFVCFSSPEEATKAVTEMNGRIVATKPLYVALAQRKEERQA HLTNQYMQRMASVRAPVNPVINPYQPAPPSGYFMAAIPQD*DR\AAY YPPSQIAQ\LRPSRWTAQGART\HPFQNMPGAIRPAAPRPPFSTM\ RPASSQVPRVMSTQRVANTSTQTMGPRPAAAAAATPAVRTVPQYKY AAGVRNPQQHLNAQPQVMTQQPAVHVQGGQEPLTASMLASAPPQEQKQ MLGERLFPLIQAMHPTLAGKITGM LLEIDNSELHLMLESPELSRSKV DEAVAVLQAHQAKEAAQKAVNSATGVPTV
2428	A	2	238	ATMATAPYNYSYIFKYIIIVMADCPHTIGVEFGTRIIEVSGQKIKLQ IWDTAGQERFRAVTRSYRGAAGALMVYDIT

2429	A	68	866	GSTGAVTAATATAATAAGASAPLGLPVYLPAPRSTAPAPSPAASALL FLVLTPPSPRPERLP SHQPPSATMATAPYNYSYIFKYIIIGDMG\VG KSC\LLHQFTEKKFMG*FVPHTIGCWNLGTRI\IESLVGQKIKL\QI WGLRQQQ\ERLRAVYT\RAYRGAAGALMVYDITRRSTYN\HLSSWL TRCQGISPNPKYW**FSIGN*SQIWRPQRDVITYEE\AKQFAEENGLL FLEASAKTGRRIVEDAFPLRACPRKIYQNIQDGKLS
2430	A	229	593	SLICFAVGVDCAEFVWTRLAPRAEKRR LAPAVPPHHQDERGGTSTP HFHNL SHGFVWTFPALLPQYDILPLNSFLHEIQEPSLG\SGLGPFSC NTYLISFSSTCHLAPVINLWALPGASIM
2431	A	594	829	PCALVLP LRPYATK*GMLPWLLLGHLSRAFAVALDHILF*VL/CHV *IPSILTKIFENGYFVISVLLMRNILSSALL
2432	A	1479	1734	LKVNISLGMVGHACNPSTLGSQE*ATVPLILYFLNKLAFTHSGITL NSFLHKIQEPSLG\SRGLPLSCNYHATALQPGQSKALS
2433	A	30	510	LWGLGNPETKEDTVFLKREYTFPRHLSNGVSSYLLNRNRERVSPNEK HLVLLRDGRTLIGFLRSIDQFANLV LHQTVERIHVGKKYGDIPRGIF VVRGENVVLLGEIDLEKESDTP LQQV SIEEILEEQRVEQQT KLEAEK LKVQALKDRGLSIPRADT
2434	A	338	853	EGRGFGRAGLPPLCIAALFQFKMNYMPGTA\TLIEDI\DKK\HLVLL RDGRTHIGFL\RSIDQFANLV LHQTVE\RIHVGQK/YTGDIPRGIFV VR\GENV\VLLG\EIDLEKESDTP LQQVSH*RKFL EEQKGWNQ\QT KL\EA EKLKVQ\ALKDRGLSIPRADTFDKDLFFCPEAVGS
2435	A	357	893	TVFQIWANHGPQRPARQLCPVHLLGGQSHQEP RH\TSNSEPSRASAS LRLRLPLKPTGIGPGSQILEDRDFRAFT*WGDYFWGKGAPACLIQDG VKGQWAGPHSGVGGVGPAPRACPPVFS PQGPQSSACGCQYYLSRP KAYPQGWGRGGDPPGQNVRSVCDLRCCMWT LNCTCSF
2436	A	233	567	RLLFLVRKRMISFSAPPLMLPFSFYFFVCPAARTARKRKPSPEPEGE VGPPKINGEAQ PWLSTSTGLKIPMTPTSSFVSPPPPTA*PHSNRTT PPEAAQNGQSPMAALIL
2437	A	219	702	ARKVRARAAGLESRTGSTGPRPCATRCWRCTSTATRGPSRASFKKEP ALTAVARTARKRKPSPEPEGEVRAPLRST EKAQP\GCPHSTGLKIP MTPTSSFVSPPPPTASPHSNPGPHRLESGPRMGQFPIGSPDLSSRQF RGQSCSKDANQVHSTTRNSN
2438	A	173	1136	ALEGAGKSRGFWRAGLGQQAQDRARHAAGRCTSTATSGPFESKFKE PALTAGRLFGVFEGQRGQPLKAVCKNSKKGKSPLEPRKVKSGPLK IQRRGPSRRL/SPHPQRGSRSP*LLHPLLCLRHPLPHLIPTGPHRL KRPRMASPPWQP*S**QTMQGASHASKDANPG\SLPTTRKE*PTVGP SSVLL*TKERLGPKRGGGPREQATQEDWEPVHPASLPDFLFGQPVAP LCCTLCHERLEDTHFVQ\CPSVPS\HKFCFP\CSSQGIKQQS\SGE VY\CPSG\DKCPSGLPMSPWA\FMQGEIATI\LAGDVKVKKERDS
2439	A	1	206	PTRPRTSYEKQGYLLLPVFSIVLEVLARAISET EIKSVQMGKEEV KLSL\FVCVYIYA*ENPVESTK
2440	A	611	1204	ERLLRVCLALGSAGTADDVKLHPVSCADTARSTPGTSAPSTSGTSAP FTPGTSAPSTPGTSAPSTPGTSAPSTPGTSAPSKPGTSAPSTPGTSA PSKPGTSASSTPGTSAPSKPGTSAPSTPGTSAPSKPGTSAPSTPGTS APSKPGTSAPSTPGTSAPSTPG\ PQHPPHRGPQHPPSRGPPQHPPHRG PQHPPSRGPPQHPPHLPQHPPSRGPPQHPPHQPQHPPSRGPPQHPP/P PGTSAPSKPGTSAPSTPGTSAPSKPGTSAPSTPGTSAPSKPGTSASS TPGTSA PSKPGTSAPSTPGTSAPSKPGTSAPSTPGTSAPSKPGTSAP STPGTSAPSKPGTSAPSKPGTSAPSKPGTSAPSKPGTSAPADPGVL
2441	A	447	920	GWHWFLASQKSLKPLSRNPCVLVSCHMAQSWARTQEFLCPMCPTT /CAQSGTGTESCFPNPN*VLGAGAPQPDQRCHKAGPFSS\PGFRLPS SRH\GGPVLPGTLGPPGPPGRPPHKPSNEQRDAGQQLQLPPPAC PQG KLPQLPFCLKFYSLPELPH
2442	A	1	376	LRKDDTQIREAFHIFVQSWRPALPSLPSLPLARALAE TLNQPFSGSL ITPSGILLNSQMLDFSWPNRTANHSAPS/TVVRPAEGLCGTYLALGA NGAARGLSGLTQVLLNVLN*NRNLSDSLARGR

2443	A	1	315	AAQVLMGPDFFIVAMVSSLNQPFSGSLITPSGILLNSQMLDFSWPN RTANHSAPELNSVQPGKRPLSFLLPVVRPAEGLCGTYLALGANGA ARGLSGLTQGC
2444	A	3	2027	NSRVDDFVARARMAAENEASQESALGAYSPPVDYMSITSFPRLPEDP APAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSEMGSQDG SPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATGVTVLVMQI YFGDPQIFQQGA VVTDAACTSLGIEVLSKQSSVDAVAAALCLGI VAPHSSGLGGGVMLVHDIRRNESHLDIFRESAPGALREETLQRSWE TKPGLLVGVPGMVKGLHEAHQLYGRLPWSQVLAFAAAVAQDGFNVTH DLARALAEQLPPNMSEFRETFLPFG\RPPLPGSLLHRPDLAEVLVDV LGTSGPAAFYAGGNLTLEMVAEAQHAGGVITEEDFSNYSALVEKPCV GVYRGHLVLSPPPPHTGPALISALNILEGFNLTSLSVSREQALHWVAE TLKIALALASRLGDPVYDSTITESMDDMLSKEAAAYLRGHINDSQAA P\APLRPVYELDGAPAAAQVLFMGPDDFIVPMVSSLNQPFSGSLITP SGILLNSQMLDFSWPNRTANLSAPSLNSVQPGKRPLSFLLPVVRP AEGLCGTYLALGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRC LS*QSNLLQVDSECAETS WGGHRDR*RKDSSQGC PWVHGSRRTNF IIAVKDPSPDAAGATIL
2445	A	83	310	IFQCTKFTWDSQITPRLFHPAPPTWCRPLPVSG*RRVRGW\TTRQGS GGGRGPAPLSSQAPPKGPVPFQWHLRAEG
2446	A	1	1833	MGLAMFAVPPGHTTPAGAPHSASSASLHSEPLSSAWAGPRPEGLH QRSCSVSSADQWSEATTS LPPGMQHPVLPADIKLREGQDSELEQKTA VCAAQASLAGEKGRGLGVSAPGASPLMLSVAANAALGWDGVGVPDVGW SGSPPSAVCVQTQARASTRRQASTVTRTHFEMRPPWSPPGAENQKRS CGESSWPAAPQQFALSNSAAIRAEIQRFESVHPNIYAIYDLIERIED LALQNQIREHVISIEWARRWCRLGGPGDLSRPGRGVGAAKWLSW GPSGIPSQQLAGGPPAVRALQLRGHPGEIQRFESVHPNIYSIYDLIE RIEDLALQNQIREHVNSIEGKRTGGCGNGPQWPLRRRPRAPQAVLAM LSLSGVLARLRTRPRGLPICVAEPAGSFAISRSGTLWGWSYADCV GREGGVAVWGRDQICPGLAGEEAESEFEFVVVSLTGTWHFEASTAE ERDSWVQSVQAQILASLQGACSAKDKVVISVGEDGFFLYGMHVPPTM EVPAGEGFPGRSDIIALWWSHIAQSSATPIALAIKESRKQDKES RKQDKESRMGTGRSSGEWKEKRCGEEDGQECRYLLLTARQFSEA
2447	A	3355	3951	RATRPPCDGSNSAAIRAEIQRFESVHPNIYAIYDLIERIEDLALQNQ IREHVISIEGERSRGLREPRGSLGAGRGLHRPCLAMLSLSGVLAR LRTRPRGLPICVAEPAGSFAISRSGTLWGWSFADCVPGREGGVAVW GRDQICPGLAGEGGRGRGLQGDPRLLGLEAAAGHAGADRPPTPHPE SGPETPGHCAA
2448	A	699	977	LPWLWRWAGMALGSLTAGAVGPRPQRCALRPRQGPAPEGRQAPRKGRS PHHPPLQSGSWRLPCPPRYRASRPPKPQARRSRPDARAPPAP
2449	A	3	132	GRFSSSESPRA\GPPAPHRGHVQRCVSPGTGLLIWKELERPFC
2450	A	2	1735	TDLKRCTYYETCATYGLNVERVFQDVGIIDSAPVCS\AQKVVALRKK QQLAIGPASHCPNSPK\HWA VSAASIPAVHI\TQAT\NGGGKAFSDY SSSVPTSPSISQREL\IETIAASSTPTPIRKQ\SKRRSNIFTSRKG ADLDREKKA AECKVDSIGSGRAIPIKQGILLKRSKSLNKEWKKKYV T\LCDNGLLTYPHPSLHDYMONIHGKEIDLRTTVKVPGRKLPATPA TAPGTSPRANGLSVERSNTQLGGGNRGRGVV*ICGWVSLTGADVGT EGFNRRERELLGFQSVQAQILASLQGC LQCQGD FDLGNQNAALAV QAVRTVRGNSFCIDCAPNPDWASLNLGALMCIECSGIHRHLGAHLS RVRSLDLDWPELLAVMTAMGNALANSVWEGALGGYSKPGPDACRE EKERWIRAKYEQKLFLAPLPSSDVPLRQQLLRAVVEDDLRLVMLLA HGSKEEVNETYGDGDRTALHLSSAMANVFTQLLI/WGESRASSLP *PRSS*PCSLKATSSFLPYNQSLSSHVLPTVNMCFLLQYGV D VRSR ARGLTPLAYARRAGSQECA
2451	A	329	3294	ESEEILWGEQLAGGPPQQFALSNSAAIRAEIQRFESVHPNIYAIYDL IERIEDLALQNQIREHVISIEDSFVNSQ\EWTLRSRVPK\VGIVG

				NLSS\GKSA\LVHRYLTGGPIVQGGSPKGGGLRSEIAADGHSYLLL IRDEGGP\GELQYAAW\VDAMVF/VWSPCEDGITFSKTVYNYFLRLC SFRNASEVPMVLVGTQDAISAA\NPRVIDDSRAR\KLSTDLKRCTYY ET\CATYGLQCGSVSFQ\DNAQKVVG/TLRKKQQL\AIGPCKSLPN\ SPSHFGRVRRLLHS/SAVYQSTSIQRE/LRIETIAASSTPTPIRKQS KRRSNIFTVPLPPAAAAAASSSSWSSSFSSSSLSFSSSSSFSSSSSS SSRCRRSPGAWVSALTGADRLSRKGADLDREKKAEECKVDSIGSGRA IPIKQGILLKRSKSLNKEWKKKYVTLCDNGLLTYHPSLHDYMQNIH GKEIDLLRTTVKVPVKRLPRATPATAPGTS PRANGLSVERSNTQLGG GTGPMFLFQGPSFHTFRPFQSPWLPPIAFPQDFS IPSVLDHWISCSL GPVTAALLVPFLCPVPAVSAWQHRSAAGAHTQELADGAHPARVPLPH ADADTDPRAPHASASSASLHSEPLSSSAWAGPRPEGLHQRSQSVSSA DQWSEATTSLPPGMQHPASGPAEVLSSSPKLDPPSPHNSNRKHKHRRK KSTGTPRPDGPSSATEEAESEFEFVVVSLTGQTHFEASTABERELW VQSVQAQILASLQGCRAKDKTRLGNQNAALAVQAVRTVRGNSFCID CDAPNPDWASLNLGALMCIECSGIHRHLGAHL SRAPHNNGPFLSVIS REEKERWIRAKYEQLFLAPLPSSDVPLGQQLLRAVV/DKNELRLLV ML\LAHGSKEEVNETYGDGDGR TALHLSAMANVFTQLVI\WTGWN *GTPDARGLTPLAYA\RRAGSQECADIL\IQHGCPGEGGLAPTNR EPANGTNPSAELHRSPSLL
2452	A	493	955	TLCTYILISEVISLPGTAFIQKGLGLRPSQNNAYSLSQTSPLGIIF LRVQGFDLNLALVLFSSGGTESRSIA\QLECSGMTSAHCNLRFLGS SYSPASAS*VAGTTGACHHAQLIFLVFLVEKGFHRVSRDGLHLL/NL VIRPPQPPKALGLQA
2453	A	158	720	PPPCRAKQHQTKKRKP\QRATSNVFAMFD\QSQIQEFKEAFNMIDP DQDGF\ID\REDLHMDLASLG\KNPT*WSILDAMMRAPGPPSNFTF WFPHHGFGEE/RLNGHQIPEDVHRKMPFACFE*KKPLGTIR\EDYL\ RELLTTHGGIGFTDEEVDELYREAPY*PKRGNFNY\SEFTRILK\HG A\KDKDD
2454	A	2332	3329	VAGATGTHHAWLILSFLRWSLTLSPRLECSGTFSAHCNFRLLGSSN SPASAS*VARITGAHHHTRLIFVFLVETRFHHGGQVGLKLLTSGDPP ASASQSTGITGVSHHAWPYKLFRCRDGVLLCCPG*SQTLGLKQ\SSC QSFPK*LDYRCEPPRPTNL*RCL\RDRVPYLTTSFVRSRGGTRM/EK EVPEQRLAGSRMGQELTQQPSTETSWSLGRRTKSPLF*IFFMFLRR SL/NSVTQAGVQ*HNLGSLQPPPHGFKRLSCLSSWDHRCSTPPCL DNF*IFGRDG/GFTMLARQVSNS*PQ\GPPTLASQSSGNTGLSHCNQ PVAPIFAPR
2455	A	566	1038	GSTLSPSLPGFCPENS NKCKFNTLLTAESLKL PQDLSFDP SQKPTQV RHL/ESPPGEGPP\SRAPQKNSHEIR\NCLM\KCIFL*LGRMKAQTP TLF\SPGLGMSPAARPRSFPGLGEVGAGTISVPSTLTPTSTSETTL PQPRYGMKLADADVGGKKKK
2456	A	349	679	ELGHWGNRVCLSEALGLAELHPCPGNEVGPPQROG*GLAVLILAIILL QGTLAQSIKGNHLVKVYDW\QEDGSVLLTCDABEQN/ISTWFKDGKM IGFLTEDKKKWESEGEVMPRDPRG\MYQC*RDHRNKSKTTSQVLFPTGM CSGTCI*/DLNAATISGFPLWLKTVSLF\VLAFGV\YFIA\GQGWSS ASPRADKQTLTP\NDPAPTQPLKDPKMTQYSHLQGN\QLRRN
2457	A	356	505	WTGGKKKAGWMPKKE/SVKLAQ*CMPVIPATQEAETGKLLLEPRSSRS AWET
2458	A	35	359	RRRRLPSVAIMIYGDLSHDEMFSDIYKIREIADGLCLEVEGKMVS RTEGNIDSLIGGNASAE GPEGEGTESTVITGV DIVMNHHLQETSFT KEAYKKYIKDYMKC
2459	B	102	431	MIYRDLISHDEMFSDIYKIREIADGLCLEVEGKMVS RTEGNIDDSL IGGNASAE GPEGEGTESTVITGV DIVMNHHLQETSFTKEAYKKYIKD YMKSIKGLLEEQRPD*
2460	A	1	581	AARAAGSECGGADARRSWNCCSCRRRRRNLDPRAPDTPGLAMADQLT EEQIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTAEALQDMI

				NEVDADDLPNGNTIDFPEFLTMMARKMKDSTDSEEEIREAFRVFDKDG NGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGVNYEEFVQ MMTAK
2461	A	88	779	STWAVRSGRWGVGVGGGGGSHDEMFLSDIYK\IRGDRGRGLCLEGG RGRWVSRT\GNIDSLIGGKCPPLKGPEGRRVPERHQLITGV\DIV MNHHLPGNKFSQKEASKKVHQRTMKSI\KGKL*RTRDPEKSKTFL* QGAAEQIAHPLPNFQKLTSFFI\GENMNPRAWVLLLDYRE\DGWC PP*YDFLLRDGLEMEKMLTNVGNFYGSITLSSITGLLPCHPTQPPGT
2462	A	12	159	WSHLRLMLQL*WS/HPPKNAAAYSSCRV**ERRGLIRTYGLDMCSQS FCQYAKDIGFIKLD
2463	A	46	371	FVILGKRCRGALGCLKSQVEEATGGTREHADWESLVPPLQACTVAWE SRDAGSSRLSAESCIFYDLQNRCLFSYSRVCSNRHGL\IRKYGLNMC RQCFR\QYAKYIGFI
2464	A	1	593	GLLQAEGPWRSSGEAAFREITMEIWLLOWAISPVALSESTDPETWQS RCEDRHFLFKFLVIGSAGTGKSCLLHQFIENKFKQDSNHTIGVEFGS RVVNVGGKTVKLQIWDTAGQERFRSVTRSYRGAAG/ALLVYDITSR ETYNLSLAAWLTDARTLASPNIVVILCGNKKDLDPEREVTFLEASRFA QENELMFLET
2465	A	3	496	GRDRVMAETYDFLKFVIGSAGTGKSCLLHQFIENKFKQDSNHTIG VEF\GSR\VANLGGEPPVKLQ\IW\DTAGQQTGFAGKTYTSLAAWLT \DARTLASPNIVVILCGNKKDLDPEREVTFLEASRFAQENELMFLET SALTGENVEEAFLKCARTILNKIDSG
2466	A	1	2022	MLLRLVQGDYDGLAARLGYPSSIVREDQTLKPGKVDVKTDEGAGA VAGVERLPAEEQARPRRHIAALSGRDRVMAETYDFLKFVIGSAGT GKSCLLHQFIENKCEFPVVLGTLSCVYAHVKQDSNHTIGVEFGSRV VNVGGKTVKLQIWDTAGQERFRSVTRSYRGAAGALLVYDITSRETY NSLAAWLTDARTLASPNIVVILCGNKKDLDPEREVTFLEASRFAQEN DGARDTVLETALGPTFMELTVQWVRVEGQTHFQTVTPQEAHVQEEIN LVVGHVRLPALKDRAAMPYTDMVIEHVQRFADIIPMNLPHRITRDTA FHGFLIPKGTDVITLLNTVHYDPSQFLTPQEFNPEHFLDANQSFKKS PAFMFPSAGHRLCLGESLARMELFLYLTAILOSFSLQPLGAPEDIDL TPLSSGVALANGERWRILRRFSLTILRDFGMGKQSIKERIQEEASYL LEEFQKTKTLCNVYNSMTLSKQHTHFEDDETSSEAKIHEEINQVIGP HRLPRVDDRVMKYPTDVVIEHIEIQLVDIVPMGVPHNIIQDTQFRGYL LPKGTDFVPLLGSVLKDPKYFRYPDAFYQHFLEDEQGRFKKNEAFVP FSSGKRICLGEAMARMELFLYFTSTLQNFSLCSLVPLVDIDITPKLS GFGNITPTYELCLVAR
2467	A	3	715	REQARPRRHIAALSGRDRVMAETYDFLKFVIGSAGTGKSCLLHQF IENKFKQDSNHTIGVEFGSRVNVGGKTVKLQIWDTA\GQERFRSVT RSYRGAAG/ALLVYDITSRETYNSLAAWLTDALTPVQPQKTGAFLC G\NKK*PGPLEREVTFLE/APSRFAQEN\ELMFLET\SALTGENVKK AFLKCARTILNKIDSGELDRERMG\SGIQYGIASLRKLQPRSAQAV APQPCGC
2468	A	3	953	VKMALVASVRVPARVLLRAGARLPGAAGFRTERAAGGGDGA\RP\FG SQRVLVEPDAGAGVAVMKFNPPVNSLSLEFTELVIS\LEKLENDK SFRDVILTSD\RPGVFSAGLDLTEMCG\RSPAHYAWVLERPVQELWL RLYQSNLVLVSAINGA\CPAGG\CLVALTCDYRILADNPRYCKGIQI RPKVGIICPFWG*KETLGKNLLGPGGGESA\LQVG\LLFPPAGRCK VG\IVDQVWSPEKQVQSIG\LSAIAQWMAIPKPMMAHK\LTKAIMRKG QGPPAWSRKGYADVQNF\VSFISKDSIQKSLQMYLERLKEEK
2469	C	1	774	MKEVVYVSPKKVADWLLLENAMPEYCEPLEHFTGQDLINLTQEDFKKP PLCRVSSDNGQRLLDMIETLKMEHHLEAHKNGHANGHLNIGVDIPTP DGSFSIKIKPNGMPNGYRKEMIKIPMEPELERSQYPMEWGKTFLAFLY ALSCFVLTTVMISVVHERVPPKEVQPLPDFTFFDHFNVRVQWAFSICE INGMILVGLWLIQWLLKYSIIISRRFFCIIGTLYLYRGITMYETTL TAPGMLCNCSPKLCGDCEAQLR*

2470	A	263	621	EVRLLSRPWPHEHEHGPWPLTI IKWDFPDY\QWKIEG\TPFRKTI\QKKLGCKKGLRD\PWG\RNEA\WRYMGGF\SVSFS*CILFKGFKWGDLLAFVAVRELEYLPGES*IKDKKH
2471	A	1	225	SSLSKIRESIIRRGSEKLSRLRGEAAAGAMKRAMSLNTLNVDAPRAPGTQFPSSHLDKAPRTLSASTQDLSPH
2472	A	99	494	TASPAPPQAFRRSSSLKIRESIIRRGSEKLSRLRGEAA/RRTSRVSVDQVGKEP*HQQRQPTPPPPFCRSTFHGSHLPCDTHRSNPVLERSLVEGGHSHIHSFPPCCPLCRMKRDMSLNTLNVDAPRAPG
2473	A	70	299	AVGSVHAGVQQWVSGGVGPP\GSAGPPGRKPR*RGPSDPARRNAPAIERLSRRRGRCARSGLRGRDQEEGQPGRT
2474	C	129	602	MFERIVXADEHVIDQDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFGEALALMYNTPRAATIVATSEGLWGLDRVTFRRIVKNNAKKRKMFESFIESVPLLKALKDQGRFNPHLHFAFEGPFIRPLVKITPTQFLYLWFKTACLSNNLSA*
2475	A	38	1523	RRVARPGNAEPAKERRDVSRGRARRDLAGAERKAGVSERGDSGRRRPNPSIPSAAGMSHIQIPPLTELLQGYTVEVLROQPPDLVEFAVEYFTRLREARAPASVLPAAATPRQSLGHPPPEPGPDRVADAKGDSESEEDDLEVPVPSRFNRVSVCAETYNPDEEEDTDPRVIHPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKADEHVI*PKGD\DGRQFYCHRTGGTYDIL\VTLDNQTRSVGQYDNR\GSFWRLALMYNTPR\AATIVATS\EGSLWGLDRVTFRRIVKNNAKKRKMFESFIESVPLLKSLEVSERMKIVDVIGEKIIR\DGER*ITQGEK\ADSFYIIESGEVSILIRSRTKSNKGGNQVEIARCHKGQYFGELALVTNKPRASAYAVGDVKCLVMDVQAFERLLGPCMDIMKRNISHYEEQLVKMFGSSVDLGNLRVAVGPHPTSLLSVTPKPSGQPQNTYRKQT
2476	A	1	912	SLLTRLLGDIRQWVGKEGEVQDILRQHILQQGPGGTAQVVMQAFGAGWPVPGLASWKSVDWRWCPYPLQHLICISLQPLIGAHKVIHVHGTSLAQVHGHPLIHALRVLHQVSQELGECDIVACRAGPRSSPVPHYLSPIALLVLSDLAKLVAVGREEFQGLPHKQELKVVLQAVANLLRPQVGQEHQVTAVHLEADVHAVQDACQHLHPLPVRAGHLGDVAVEEAVTVTYEDVAQQGARLPHRQVPVPGHAWLSAHRPQVLFRTSCRTCKSASPALPVPNLLVNSLRDCSCLGKHHP
2477	A	3	806	EEFAAVSERIHEQVRDRQLENEYVCRVEGEFPTEEVTCKEPILVVSYKVGVCVRDPRGKPCETVFQRLSYNGQSSVVRCPRTGRTHQIRVHLQFLGHPILNDPIYNSVAVG\PSRGRGGYIPKTNE\ELLFVPG*AEHQAQSLDVLDLCEGLSPGT/LTDSTAPSSSELGKDDL\EBLATA\AQKMGK*AEAAPQELDTIALAS\EKAVETDV\MNQETDPTLCMPAGATGSLAPRPCDVPTCPNAIKGQALSTFHPMPAWAQDDWQKD
2478	A	184	793	DFLLLVLTGLYIYRKSIIHKVLE*IIEFINVTSYKVNIQKDIAILRTSQKH*KTN*KYKAKY\LEIN*TNQDFYNENYKTLRLKVKDNLGKWTIIPYSSTGKLDIVKMSIILRLFYKTNATGIVPK/HSFVKINPEIPKLI/YGNMGNREGKTILKNKKVGRSLSLPDFQKYKAT*IKIVWY*CKKRQMNQEABITSARKKPWSL
2479	A	69	403	SALRRGAGAKAGRPLAPATALGGQTQPEKGPAPP*NGWTGLGAGPPAWRARPRSPPEFSQFSLSYNMS*AKVGG*EHGSTAPGEGG/P*RKGGGPPPPNPQRQGSPTSP
2480	A	502	834	RRLPTGILAGRVSAAVKPTHRTQNSLLQQRITPRPWRGGSHL*SQHFGKPRQADHLSPGV/PRVSPG*RGETPSLQRIQTLAQVLCAPVVPATREVEVGGSPEPGRSRLQ
2481	A	456	869	KCKKYQENISESSQVCFNIYLLIICKLPNWSYVFSW*LIYIYIFEMEHSSHRLCSGTISAQCALHLLGSSDSPASTSRVVGTTGVCHHAWTVLGFF\VLVETGFCSDQANLEPLT*VIRQWPPKVLGLFEVRS
2482	A	1	220	VNMRRFQGQIMENLRRRQCELAGVETCKSLES\RIESLEFLDEM*/LLEQLM/RHYCLCWATKGGNELGLKEITY
2483	A	98	394	GPTLFCCFLPVARAVPRRPSTPLPCPWRTQLPGTSTPMATRQRESSITSCCSTSSCADDEGVRGTCEASLCKRCLSGAGFGAGIWGAGLGGR

				WACI
2484	A	1	381	MTAGLRQRPWAVTGKNVEHRVWAEKSKGRGEELQVRVDVDVITYTDG HILDSKRYAVIGADLRDLSELEEKLLKCNMNTQLPTLLIAECVLVYM TPEQSANLLKWAANSFERAMFINYEQNVKSQIF
2485	A	1	645	MESFGVLPLFLGADAGYVGVIAVRCLLSGVVPVDLEEFITGDVLFSA CGPRSFESGSKKTVVQLLFRVMPSPRVRLATTCRWDPKPSLDLCHFG GNEACQTPLECEVGVRRAGDNLLICRRLMPSQKPKPLALLEETCK LPERQVVNAKEKFLEEMKKCYSEHMNDKKAALYYRYGESLSGLYR RSNQPPPSLKPKNREQGPNSLQLCDG
2486	A	10	1228	AAPAEPRALPSSVAFSLWLAPSPAARRPRFHVPGGAQLPGTVHARW PARQR\ESSI\TSCCSTSSCDADDEGVRGTCEASLCKRFAVSIG\Y W\HDPYIQDL\VRLSKQR\KAPEINRGYFARVHGCSVQLIK\AFRL\ KTECHCSNCSNLGGQGMGSPFW\RLKDEDLSSQVNI FEVD FPMIVT \RKLHSIKWLAFLPLSSPILELHSED TLQMASDCIC\DGHILDSKRYA VIGADLRDLSELEEKLLKCNMNTQL\PTP*IAECVLVMTPE\QSAN LLKWAA\NSFERAMFI\YYQQVNMGD LFGQIM IENLRGPV/CDLAG VET\CKSLESQKERLLS\NGWENKHRPVRT*LEFVPPGLPSKLK*SR IESLEI\LDENWELLEQL\MR\HYCL\CWATQRRK*SLGLKEITY
2487	A	3	247	FEDGSVLKQFLSETEKMSPEDRAKCFEKNEAIQAADAVAQEQGQCRV DDKVNFFHIFLNNVDGHLIYENIYPPMQSKMLQYL
2488	A	1	922	MQLKPMIEINPEVSARCTATRRARGRGRSVADRFGFAFFFAFAFQM LNKVLS\RLGVAGQWRFDVGLLEESLGSVPAPACALLLFLPLTAQ HENF\RKKQIEELKGQEVSPKVYFMKQTIGNSLGPLGNSTQGPNIK DQLGFEDGSVL\KQF\LSETKKNVPLKDRAKCF\EKNEAIQAAP*MP VGTGKAQCRVDD\RVNFHFYSG*PTVDGPPSMNLDPNAFSPWTHGP QLQEDTLK\KAS\KVCRRNSPEREQRRSPASSARGFSCKGSNLALW GGICWIFPSFPFKHGKYITPPCQSKMLQYL
2489	A	18	255	NWISFLPWHYSHFEVYERYDSVL*IPFSLQ*PIENVYPKI*KKKST SSNKIALVLSGTIYKNSLEPRSGASSVLWFTPNL
2490	A	2	568	ERGRKMAVESRVTQEEIKKEPEKPIDREKTCPLVLRVFTTNNGR\HH EMDEFSG\NVPSTELQIFPL/WMDATLKELTSLVKRV\YPEARKKG THF\NFAIVFTDVKRPGYR*FSFLQS*GGLAST\MSGRKGT\DDSHE PLQSQ\KF\QIGDYL\DIANYPLPNRGTHPPS\GRMRPI LN FYLLFV EFIFPSVM
2491	A	3	506	FFFFFLKTSTLSFITHCLQIQREGPGAEGA AVAGGAPRGAEGPAAT STETGGSAGD/AAPSPP/RGLPSK*QEGPGPFWDPNARQWPGGRR REAWRGLRAGSGESHQVGPWPASRSTGGGSGQVGGAGERLGEDSGLG QVKATRWGLSPPPAALAEAVANTGPSPPC
2492	A	3	639	APEFPGRHLLLTQLCSLASLIQTRMVHLTPEEKSAVTALWGKVNVD \VGGKALG\RL\VVLPWDPKRSFEVLWGNLSQLPECC*WGKPLKVK GSMKEKVLGCPLSDGLAHLGQPSKGTFAHTEVSLHCDK\LHRGSLK NFRLLG\NVLGLCCLAHF\GKRISTPPVQA\A*SRKLVGLVLAKCP WPHKYHLKLAFLAVQFLFKGFLWSLKTNY
2493	C	217	396	MSEETAKEVMRAYLQQLRQETGLRLCEKVFPDQNDKPSKWWTFCVVR QFMNKSLSXPGQ*
2494	A	79	778	NPGAAMPAYHSSLMDDPTKLIGNM/AHLLPIRSQFKGPAPKRDTRI PDIVDEAIFLPSGPNVFF\KNYEIKNE\ADRTL\IYITLYIS\ECL\ KKLQK\CQFPKAQGGGKEMFYAGESTNFSHLGEPGFFPL*PPFYAQ TWPTTQDEDEVMRALFTTQLR\QETGL\RLCGESFSDP\QNG*TPAKW \WTCFV\KRQF\MNKSLSGPGTVEGSPGQPTVFPEALGQHFSSKMLH NLFAFIS
2495	A	1	471	PAGRGMALDLALEGMAVFGFVLFLVLWLMHFMAL IYTRHLNLKAT DKQPYSKLPVSLKPLKGVDPNLINNLETFFELDYPKYEVLLCVQD HDDPAIDVCKKLLGKYPRYISANVTGFKCVTGMSCMLMRKDVHLQAG GLIALAQYIAEDYFMA
2496	A	1	1524	MIDKIDAYHKTVMRMEIVQTFPSEVYQDLVLELFIYSFQVIVYDHI

				KFISVVRKQTAACDIFSTVRDKGVGLSKTEIAPDPESTHMTLMPRKQ FKKGSSQEASSSEWKKQKSDALGLAACEKDMKAMGTDIWKLQQRCS TQVIPDTLTDMVNQMTEKVLVHGLPYVADRQGFATLEQVYFGTSH PRYYISANVTGFKCVTGMSCLMRKDVLDQAGGLIAFAQYIAEDYFMA KAIADRGWRFAMSTQVAMQNSGSGSYSISQFQSRMIRKTIITRMVTQINC EFEEVVPSSNPDSQIEVEEVSLYTHMDYNEVFTPVSCLEKCSALQNO NQEKVKS VGESYELSGGLIKKASISSRDEVRFVSAFIDSTGQMVLS VTGRDAGSRGLQAGLAANLILRFQPLAAKRYNHDFPEQESPNSLSLP IKTVEPREIYRLIQEQWSTLICKLPDLPIRELQSENTGLLPRTNST SVEIRKRSIVRQCFSGRAWHLRDTNTSFNNMLSVHDA
2497	A	2	719	RPQRAGPVRRAGVMALLDLALEGMAVFGFVLFLVLWLMHFMAYTR LHLNKKATDKQPYSKLPGVSLKPLKGVDPNLINLETFFELDYKPK LFFSVAPMKRIEKTQM**P* CSTY*YEVLLCVQDHDPAIDVCKKLL GKYPNV DARLFIGGKKVGINPKINNLMPGYEVAKYDLIWI CD SGIRG TMEMPMSLEQSYDPNVRDPIYRNNGDADGQHLVLHDFYQQSGPKCS LINA
2498	A	200	370	GGTLCFSKLDYAVAWFIRESMTIYIFLSALWDPTISWRTGRYRLRCG GTAEEILDV
2499	A	295	1546	CVLLDLALEGNVPVFGFV\LFLVL\WLMHFMAYTR LHLNKRATDR QP\YSKLPVGSLLKPL\KGVDPNLINNL\ETFFELDYP/KKFNLHTM LFD*YEVLLCVQDHDPAIDVCKKLLGK\YPN\VDA\RLFIGGKKVG \INPKINNLM\PGYEVAKYDPIW\ICDSGIR\IFPDTLTDMVNQMTE KVGL\ VHGLPYVADRQGFATLEQVYFGTSHPRYYISANVTGFKCVT GMSCLMRK\DVLDQAGDFIAFA\QYIAQYFMAKAIADRGWRFAMST QVAMQNSGSGSYSISQFKSR\MIRWTKLRINMLPATIICEPI SRMPLLP SLINWDGQAH\HVFRWDIMVFFYG\CHCL\AWFIFDYIPTPGVSQGG \TLCFSKLGMLQSPWFIRESM TIYIFLSALWDPTISWRTGRYRLRCG GTAEEILDV
2500	A	3	331	GAILAHCNRLRP/GFKQFSCSLPRHS*TSQ*PLTSRLPMVRHG*VK KSEGILCSLPPCTT*VPTSSAPMPWPSRQWERSRRTMTVISSSQLMA LGPSCPQRDGSPTSSP
2501	A	15	310	DRVSL/LSPRLECSGAILAHCNRLRP/GFKQFSCSL\SLPSSWDYRRA PPHLANFLYF**RRFFRH/GCPGWSLLSSGN/PATLAF*KC*NYGHE PPHPARKIHI
2502	A	3	467	PAPQSLLSARHVSALPTPAS/R/RCSGLPPMTPKTM PRA/VGSPLCV PARRRSSEPRKNSAM/RALLVDIKLEPLAVTPDAA/SQPLIDLPLID FCDTPEAHVAVGSESRLIDLMTNTPDMNKNVAKPSPVVGQLIDLSS PLIQLSPEADKENVDSPLLK
2503	A	2	275	FASIPANSSRPLSNISKSGRMGHAMLRPALPAGPVGASSWQAKR\SE SSQLNKTIRSIRRRHSCLSNKTVMPTPTNQFKIPKFSIGDSPKA
2504	A	1	473	VGRVTVHSTPVRRSSGPGPQSLLSARRVSALPTPASRRCSGLPPMTP KTM PRAVGSPLCV PARRRSSEPRKNSAMRTEPTRESNRKTDSTLVDV SPDRGSPPSRVPQALNFSPEESDSTFSKST\PLIDFCDTPEAHVAVG SESKPLIDLMTNTPDMN
2505	A	759	1664	TAGCGLGCASGPQAGHPATAGPQTLLPSAGGRAWSSCPPRPALHRWP AGWEGCGYRRWS/RAASYPWKKNVLLIKPFSIRYKAQ\SNSYDKPT YQSPSRRSLSAA*IPTHP*SLLSSRG CERRCAPTM RQPGAADTEPMC YHSWPHHSLFLPSSCLWGAGVEDKELVPLWRVFLPGRRSWFPSSQK SRCLSHSCLGGCQVSRRGKFEQQNLSSVPDSPGKNKHGKISGPTCL SGGPGESVPIVHRLSESSHQMSLLQTRAAAPALSAAGFLKSPPLSS QPGPALCPASRSFQCQSAQGO
2506	A	1	377	ASRRC\SGLPPMTPKRCPCGRGSPLCVPARRRSSEPRKNSAMRTEPTR ESNRKTD SRLVDVSPDRGSPPSRVPQALNFSPEESDSTFSKSTATEV AREEAKPGGDAAPSEVGGLLEPRSSGPAWEMM
2507	A	3	2112	ILLLADEKFDLSSSSSANEDDEVFFGPFHGKERCIAASLELNNP VPEQPPLPTSESPFAWSPLAGEKFVEVYKEAHLALHIESSRNQAA

				QAAKPEDPRSOGVERFIQESKLKINLFEKEKEMKKSPTSLKRETYYL SDSPLLGPP/VGESCTAHAASQAATQRPKPTKLLLPRAASVRGRSIP GAAEKRTARMPKGRKRK*QVLF*G*GCCGG*GEG*GCGEAGSSRIA \PKKEIPASPSRTKI PAEKESH RDVLPDKPAPGAVNVPAAGSHLGQG KRAIPVFNKVNNEIFADSVFHFAP\LGLKKTLLKAPGSTNLARKS SSGPVWSGASSACTSPAVGKGLCCTPVCPARPARPLHSCCKMTPSR PWLWQCREGLECP*GSGGTWV\RHSCDRRAGRSGSQSPRPHFGSSE VLG*TWRPGETGDSPTSSTPKLSRAQR PQSCTSVGSSRH*CCVC\R VTVHSTPVRSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTM PRAVGSP LCVPARRRSSEPRKNSAMRTEPTRESNRKTD SRLVDVSPD RGSPPSRVPQAL\NFSPEESDSTFSKSTATEVAREEAKPGGDAAPSE ALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSESRL IDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADKENVDSPL LKF
2508	A	68	2331	LLTALSMEEGGRDEPSASRAGDVNMDDPKKEDILILADENISTFDL SLSSSSANEDDEVFF*PFGHKERCIAASLELNNPVPEQPPLPTSESP FAWSP LAGEKFVEVYKEAHLALHIESSRNQAAQAAKPEDPRSOGV ERFIQESKF\KINLFEKEKEMKKSPTSLKR\ETYYLSDSPLLGPPVG \EPRL LASSPALPSSGAQARLTRAPGPPHSAHALPRESCTAHAASQA ATQRPKPTKLLLPRAASVRGRGIPGAAEKPKKEIPASPSRTKI PAEK ESH RDVLPDKPAPGAVNVPAAGSHLGQGKRAIPV\NKLGLKKTLLK APGSYSN\LQRKSSSGA\VWSGASSACTPQPVAKAKSSEFASIPAN* LPGLCPNISK\GRMGP\AMLRPAL\PAGPVG\ASSWQAKRVDVSEL AAEQLTAPP\SASPTQPQTPEGGG\QWLNSSCAWSESSQLNKTRISIR RRDSC LNSKTKVMPTPTNQFKIPKFSIGDS\PDSSTPKLSRAQR PQS CTSVGRVTVHSTPVRSSGPAPQSLLSARRVSALPTPASRRCSGLPP MTPKTM PRAVGSP L\CVPARRRSSEPRKNSAMRTEPTRESSRKTD SR \LV\DVSPDRGSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKP GGDAAPSEALLVDIKLEPL\AVTSDAASQPLIDLPLIDFCDTPEAHV AVGSESRLIDLMTNTPDMNKNVAKP\SPVVGQLIDLSSPLI\QLSP EADKENVDSPL LKF
2509	A	1	355	DVQLEGAKIGSTEITFTPEKIKGGIHT\AYTKTAGSVCLLMQVSMPS VLFAASPSQLHLKGGT\FKVAQDMATAAVRCIKKEIRDLYVNIQPVQ EPKQDAFGNGNGIIIIAETSTGCLF
2510	A	29	1262	TKVSELLCGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGSIME GGGQILRVSTALSCLLGLPLRVQKIRAGRSTPGLS IMT*RPQHLSGL EMIRDLCDGQLEGAIEGSTEITFTPEKIKGGIHTADTKTAGSVCLLM QVSMPCVLFAASPSSELHLKGGTNAEMAPQIDYTMVFKPIVEKFGFI FNCDIKTRGYYPKGGGEVIVRMSPVKQLNPINLTERGCVTKIYGRAF VAGVLPFKVAKDMAAAA\VRCIRKEIRDLYVNIQPVQEPKQDAFGNG NGIIIIAETST\GCLFAGSSLGKPGFNSDKVVEA\AEWLLANLRHG GT\VDEYPARPSLIVFHGH*PNGVS\RIKTG\PV\TLHTQT\APIHF AEQIAKG*ILL*RNPEDEEDA\AKDTYII ECQIGIMTNP NL
2511	A	109	743	RLFHSNQTVDHSQKNVDITLKGTPQ*SCKGPRGNLCGRDFIHI\NVE PQPFLEK*KKRLPGLTKWNGNRKGNWPTRSGLFGSHVQDHDPRGVTT GASVTMRVLCPHLPP IQPLVYPQENGSSLLKSRNFLG*KWYIGRV RMETRVLLCSVSQGG\KDELI\LKGNDI\ELVSN\SAALIQQAPP\V KNKDIRK\FLDGI*VS\EKGTVPGLIE
2512	A	900	1189	SQHFRPRRADHLSSGVQDQPGQRGKTPSLLKIQLLAGRGGSL*SQ LPRRLRQRENRLNPGGGCSELRSRDCTPAWATEGNSVS\KNK*KK KKK
2513	A	1710	2221	SPLLDVYFKTRLLSRGRREPACTLR LNTIGTLLSHCPLGIQGPHPGP SGKTCGPFKPRGPGHSCPPDPKQVPTVLP LPAPLRWAQAGLPGYA GISGSPGRPLGAQAG*GSGVIGESNYFVHCMHPRGPGSPHL/PGG*G LQPKPPRPLPSSSGSTTGLGDRKPCSYSQ
2514	A	205	295	GCNGNKDSCGPIAPSSGDILLTVKRS LPR*NFSP\CA\PCSSSSKR

2515	A	1	927	AMCSRVCSWPGL*CGPIAPSSGDILLITVKRSLPR MAYLQDRTLRSRYSNYSRPKSTGLERLFPPQIKTRIPTYDEDDNTIL YAYETKPEFVNKVIYDALQNLDDKIDVIRRKVSKIQRFHARSLWTH KRYGYKKHSYRLVKKLKLQMKKNEVYETFSYPESYSPTLPVSRREN NSPSNLPRPSFCMEEYQRAELEEDPILSRTPSPVHPSDFSEHNCQPY YASDGATYGSSSGCLGNPRADSIHNTYSTDHASAAPPSGMLAQGEP NLVHAPEMMSYSALMENRYTGSSLCFPGSGLEIDGKALLLTSDVLLK HLGVKLGTAVKLCYIIDRLKQKGCFEN
2516	A	932	1688	KGFKNPTFPCEIPAGQTHKPHHNKHSSPPVQKLKLQMKKNEVY\ E TFSYPESYSPTLPVSRRENNSP\SNLPRPSF\CMEEYQRAEL\ EEDP I\LSARTPSP\VHPSDFSE\HNCQPYAS\DG\ATYGSSSG\LCLGN PRADSIHNTYSTDHASAAPPSVTRSPVENDGYIEGSIKHPSTWSV EAVVLFLKQTDPLALCPLVDLFRSHEIDGKALLLTHGVTVLPEATWG VKLGTL*SLC\YLH*PDLKQKCL
2517	A	3	179	ARIPGICGSGSSSCLTRSSKAQLCWWNMGLGIFRICITRVSEEAQT TSSRRCSQSTQ
2518	C	140	490	MAWFHDMNPQSIALIPPATTEISADSQLPICKGSEGVKDVELVLPE XSMFEDASVSEGRGTQIEENPLEENILAGEXASQTGDSGNEXANRGD GSDVSSQTPQTSSDWLEXXXLX*
2519	A	194	405	KKILWKKIFWRGKQHLKLVTVTTAANRGDGSVDSSQTPQTSSDWLE QVHLV*TAHIWGSKWIYRVSVC
2520	A	1	2046	MRQNSGGNVHLPAHLVLCGLVNPWPWGKKNKRHHLCGICPQPPTL AKIAKAAGSAGNFRYPLILGSFPANWVFMFFQSKATLDFNLICSL NVKDVAEVFQKWLKIEGKKCHLSEKTKQNMGNNTTKFRKALINGDE NLACQIYENNPQLKESLDPNTSYGEPYQHNTPLHYAARHGMMKILGT FLGRDGNPNKRVHNETSMHLLCMGPQIMISEGALHPRLARPTEDDF RRADCLQMILKWKGAKLDQGEYERAAIDAVIDNKKNTPLHYAAASGMK ACVELLVKHGDLFAENENKOTPCDCAEQHHKDLALNLESQMVFSR DPEABEIEABYAALDKREPYEGLRPQDLRRLKMDLIVETADMLQAPL FTAEALLRAHDWDREKLLAEAWMSNPENCCQSGVQMPTPPPSGYNW DTLPSRTPRTTRSSVTSPDEISLSPGDLDTSLCDICMCSISVFEDP VDMPCGHDFCKGCWESFLNLKIQEGEAHNIFCPAYDCFQLVPVDIIE SVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAVRLTKQGSNT SGSDTSLFPLLRAPAVDCGKGLFCWECLGEAHEPCDCQTWKN\WLQ KITEMKPEEL\GVSEAYEDDRQ/CVC*VMN*TAKPCANCKSPIQKN EGCNHMQCAKCYDFCWICLEEWEKT
2521	A	2	1431	GSAHIRSPGSPARHRASLPAPRRQPASKDQCGMSAPGAYTGVNFEG ALFSGYAPDGGFLMPEELPQLDRETLQWSTLSYPGLVKELCALFIG SELLPKDELNDLIDRAFSRFRHREVHLSRLRNLNLELLHGVTYA FKDLSLSCTTQFLQYFLEKREKHVTVVVGTSGETGSAIESVQGAKN MDIIVLLPKGHCTKIQLQMTTVLE\ENV\QCLGVEGNSD*ASIEPI KTVFADVAFVKKHNLMSLNSINWSRVLVQMAHFFAYFQCTPSLDTH PLPLVEVVVPTGAAGNLAAGYIAQKIGLPIRLVAVNRNDI IHRTVQ QGDFSLSEAVKSTLASAMDIQVPYNMERVFWLLSGSDSQVTRSLMEQ FERTQSVNLPKELHSLSEAVTSVSVSDEAITQTMGRCDENQYLLC PHSAVAVNYHYQQIDRQQPRYRQW/VAWATEGPFQGPSSSPSSGR DRTTKKWL
2522	A	2	119	ESTVSCCEKPTGAMP*MHTACGRPCPSIWRLTKLSMRLR
2523	A	159	627	LGRMQDPQGGQMRWAYSITFAKDVQQLGLSHYFAGAASGGCAQARCG PGPRR*GPPAPVSPSPPLALPPMGTRKLHPGMWTALH/VRIP/VPKG EGCVQLIGEISCVLLQKASWSEASTLCPAKGAIPNGAAFHQRCGRPE AHLGHRLSLAPPREPVE
2524	A	3	307	ISSAPQLAGHKRQFGSVCHQDPRVCDEPSSSEDPHWEPEDITKWVWSC SGGVVREPSVSCGRECHTPPTGDRSHHGTTSRFQRLCTCPLYLSL INQRLPL
2525	A	1053	2813	RTWEKAPEQADLTGGALDRSELSHMLPLERGWKQKEGAAAPQP

				KVRLRQEVVSTAGPRRGQRIAPVVRKLFAREKRPYGLGMVGRLTNR YRKRIDSFVKRQIEDMDDHRPFFTYWLTFFVHSLVTILAVCIYGIAPV GFSQHETVDSVLRNRGVYENVKYVQENFWIGPSSE\DLIHLGA*IS PCMRQDPQGLSFIRSAREREKHSACCVNRDRSGCVQTSEECSSTLA VWVKWPIHPSAPELAGHKRQFGSVCHQDPRVCDEPSSSDPHEWPEDI TKWPICTKNSAGNHTNHPHMDCVITGRPCCIGTKGRYVCVPASAAGL WAQSIAGCEITSREYCDFMRGYFHEEATLCSQVHCMDDVCGLLPFL NPEVPDQFYRLWLSLFLHAGQVTLILHCLVSI CFQMTVLRDLEKLAG WHRIAIYLLSGVTGNLA\SAIFLPYRAEVPAG\SQFGILACLFGR SSSRAGQILGAALACLLQACWLWVLFHLWGLLPWDLTTFAHIFGG SSVALFLSFAFLPYISFGKVRFPETLPDHHLSGGLPRASWLAWSS STSILSAVSRVSSSPASPFTDKLL
2526	A	1	936	MAALYACTKCHQRFPFREALSQGQQLCKECRIAPVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPGSSDSPASSSRVAGITGIKTNTICKKCAQ NVQLYGTTPKPCQYCNIIAAFIGNKCQRCCTNSEKKYGPYSCEQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSRAGH QEKEQYSRLSGGGHYNSFSPLALDSPGTDHHEVATLKK MLHQKQDMIJ.RKKEVTEQ LQAKNREL
2527	A	1	1023	MAALYACT ERLECNGT NVQLYGTTP CAFDRKDDR QEKEQYSRL SPDLALDSP LKADFQYQE KKSEKSGAI
2528	A	157	512	LG*LQPPPP SASRVAGIT LGPPKSAGIT SYDKEIFPIL
2529	C	11	133	MFCSLQPTDL
2530	A	367	678	KVVTLIILIL ADGRLGLAWG VIPATAYDNG
2531	C	156	683	MKLRQRWRHPAHFSGTGKMI GEGTQVSVGTGVTVDTGVGCLSTSSHY ANRNADTFRCLCRKRCQRLLSQRRGVKKSCISVPHRQLSQALQAMR DSSEPWALS IKS LFREDEALASKHYRRNAPRAALRQFLSDFHRDCLN VFKT KYHTLMYMGRTIMRCEPCACGGEGKKNVLF*
2532	A	427	458	KNSQYTPLTLIQMMGF*FFVF/ERQSHSVVEAGVQSCSHGSLQPLPP GSSNPPTSASRVAGTTGAHHDDLIFLFL*RRGFALLHRLVSNWSRS RDSAWPSAFP KWGLWDVEATTPRPGLFSHLVAG
2533	A	57	463	ARTPLQGAGGLVLSRLLSLPLPGLSPLPTVSCARWPLCPRPWSSLPQ FWD SWHCNHR TGHTGPGGLDTQSA*VNKLIWGKGNHL*POATAQLW P\QLGGWQGWTRPS/RWWPLSSPHC*PGYRSLKDSFANTFLLF
2534	A	3	469	RKTTTATMTSLCRKVNGGHAG*ETLRLLLVVYPWTQRFDDSPGNLSS ASAIMGNPKVKAHGKVLTS LGDAIKHLDDLKGTFAQLSELHCDKLH VDPENFKLLGNVLETVLA IHFGKEITPEVQASW/QEDGDWSGQSPVL QIPLSSLAMMQSCQ
2535	A	41	676	APSPRRPWGHFTEEDQGLLSTSLWCKV\NVEKCWKEKTPGKGLSVVY P\WT\QRFFD\SFGN\LSSAF\AHGQTPKVKAHGK\KVLTFGLRCQ QSTLDDLKGTFAQL\SELHCDKLHVDPENFKLLG\NVLVTV\LA IHF GKEFTP/ERLQASW\QKMGD*SGQCPVLQ\IPLSSL\PMMQSFRI RLFLQAITNNKSISAKRSHMIFSSFFYIFLNI
2536	A	107	332	SRMATLIYVDKENGEPTGRVVAKDGLKLGSGPSIKALDGRSQVSTPR FGKTFDAPPALPKATRKALGTVN RATEK

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2537	A	386	1074	NNPEWRTLIIYVDKENGEPPGTRVVAKDGLKLG\SGPSIKALDG\RSQV S\TPRFGKTFD/APHPALPKAT*KGFGELSTGATEKSVKDPGDPKQ KNGPAFSGPKMDLKKDCLKQKS\SVSWPSGLMPNPRNKTFFPLQI LLDF*GVFD/LCPEEHPDLRHLPPLS\GV\PLMIPLTREREL*KSWF QLGPPFHLWKDGLPPWGIPICLQFSFQGISVRTWGV\DLPPVCCDI DI
2538	A	1	359	GTRVIKRISSSREGLAVPGLNATPAPSAFVLSALQSPSTHSSSNTQR LPHRVTTGGFSLNGQLIGNKARSPGQHDGTYFGRGLIANAATDFQLEV TPENITLNPFGGAPAFSWRDQAVLR
2539	A	1	483	FQLEVTPOINITLNPFGGPPVFSWRDQAVLRQDGVVVTINKKRNLVVS VDDGGTFEVVLHRVWKGSSVHQDFLGFYVLDShRMSARTHGLLGQFF HPIGFEVSDIHPGSDPTKPDATMVG\LQKDYSKDPWHGAEVSCWFIH NNGAGLIDGAYTDYIYVPDIF
2540	A	3	310	EVRLANLSSQALRMWLDYGFVTPLTSMISIRGMADQDGLKPTIDKPSD SPPLEMLGPRRTFVLSALQSPSTHSSSNTQRLPDRVTGVDTP*VVT*P YVLCWNL
2541	A	1	1482	TKEALLRIEDMKEEDYLNFIILFSGDVSTWKEHLVQATPENLQEART FVKSMEDKGMDFLMRKGKTKAKLEERGANQDSRNGSKVRYRRAASH EESSEAAACIRDAMAYSVHHNLRCLVSVDSSVGEFIDNWEQELPV SAASDYKGLTGPLQQTQRGATTGSQVEKVRWCWQKINCDDSAVAQI QQPVQGVMSQKARHTYLVAKPSSGKPLGASGRTEQFTIHLTVNPQ SKVTFQLTYEEVLKRNHMQYEIVIKVKKQLVHHFETKEALLKILGD MQPGDYFDLVLFGTRVQSWKGSVQASEANLQAAQDFVRGFSLEAT NLNGGLLRGIEILNQVQESLPELSNHASILIMLTDGDPTEPPVFI DKLMERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAADGVTFV PVTPTFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEVTYKVFALD VAARHRVQFAMPESDAVAMLKQLS
2542	A	37	2885	SMDGAMGPRGLLLCMYLVSLILQAMPALGSATGRSKSSEKQAVDT AVDGVFIRSLKVNCKVTSRFAHYVVTQVNTANEAREVAFDLEIPK TAFISDFAVTADGNAFIGDIKDKVTAWKQYRKAAS*EKA\GLVRAS GRTMEQFTIHLTVNPQSKVTFQLTYEEVLKRNHMQYEIVIKVKKQL VHHFEIDVDIPEPQGISKLDAQASFLPKELAAQTIKKSFSGKKTSG SHSRFQGHVLFRTVSQQQSCPTCSTSLNGHFVKTVDVSRDKICD LLVANNHFAHFFAPQNLTMNKNVVFVIDI\SGS\MRGQVKVQKTEA LLKILGDMQPGDYFDLVLFGTRVQSWKGSVQASEANLQAAQDFVRG PSLDEATNLNGGLLRGIEILNQVQESLPELSNHA\SILIML\TDGDP TEGVTDRSQILKNVRNAIRGRFPLYNLGFGHNVDNFLEVMSENN RAQRIYEDHDATQQQLQGFYSQVAKPLLVDVLDQYPQDAVLALTQNH KQYYEGSEIVVAGRIADNKQSSFKADVQAHGEGQEFISITCLVDEEEM KKLLRERGHMLENHVERLWAYLTIQELLAKRMKVDREERANLSSQAL QMSLDYGFVTPLTSMISIRGMADQDGLKPTIDKPSDSSPPLEMLGPR RTFVLSALQSPSTHSSSNTQR\LPDRV\TGVRHPPFNFIHSTCPKR DTLCF\NINEEPG\VILEPGYRDPNTGFFSGMQLIGQQGPGSLGEG IDGH\YFGAAGEFANPATELFSWEVTPSEHLR*NPGF\GGPVFSW/R RDQVFLSGRDGVVVTINKKRNT\VVSVDGGTF\EVV\LHRVW\KGS S\VHQDFLGLLMCWDKSIGMSSPGRKGCWQIFPTPIGFE\VS\DI PQGSDPHKSPNA\TMVVRNPPGLTVT\RGLQKD\YSKDPWHGAEVSC WFI\HNNAGLIDGAYTDYI\VPDIF
2543	A	159	1222	NNSGVMPPEMPEDMEQEEVNIP**GGFWVTGCHWGFLGRAVHKBF\QQ NNL\WHAVGCGF\RRARPKF*TG*ICWDSNAV\HHII\HDF\QPHVI VHCAAERRPDVV\ENQPRCLPLQLNV\ASGEF*AKGKAAACLGSI PFYI*AQVVFV*WEPNPPY\REEDIPAPLN\LYGQTK\LDGRKGCPW RNHLGAAVLRIPILYGEVEK\LEKKCELLMFE*KCQFSQQSPAKQW IHWQARGSPPHMSKDVAPLCARQ\LAEKRLDP\SIGKTF\HWSGNE QM\TKYEKGMCQLPDA\FNLPSHL\RDPIITDSPV\LGAQRPRNAQL DCSKLETGLIGQRTPPFRIGIKESLWPFLLIDKRWRQT\VFH

2544	A	211	463	STISAHAYALELLFDQLHEGAKALDVGSGSGILTACFARMGGCTGKV IGIDHIKELVDDSVNNVRKDDPTLLSSGRIQLVVG DG
2545	A	188	366	SCQSACQKNGKIILRLQLLGP*DRLED TLLNTHGLLQSQILCQCFCL CTCQOKVLRISK
2546	A	1257	1441	VHFCRIFFMAFLFTWRSSSELSVDMYKESRTGKV FVTATARACSGVC LPICPKAQAAAALI
2547	B	74	733	MAWKSGGASHSELIHNLRKNGIIKTDKVFVEMLATDRSHYAKCNPYM DSPQSIGRVQLVVG DGRMGYAEAPYDAIHVGAAAPVVPQALIDQLK PGGRLILPVG PAGGNPNVGASIPGSRMASIQNEALWMGGDIRAL*
2548	A	45	972	TVQPHVSGSGGDGNSGSGSYSGDASGAVTVWEVVSLLGKLLGTVVALK VVLYLLRVCLAMAWKSGGASTS\ELIHNLRKNGIIKTDK\VFEVMLA TD\RSHY/SQKCNPYMDSPQIK*GFQ\ATISCSTHCNAYALRNFLFW IQL\H\EGSLKLFVVGSGKWESLLACF\ARMVG\CTGK\VIG\IDAH *RS**DDSVKLMFREGTIP TLLSFRGGVQLVCGGMGRMG\YA\EEAP YDAIHVGAAAP\VVPQ\ALIDQLKPGGRLILPVG PAGGNQMLEQYDK LQDGS IKMKPLMGVIY\VPLTDKEKQWSGGMIVKATSA
2549	A	2	479	RPPRVPSWRGWPAGALRGAPARGIRSCGSRAGRSMAAAAAAGEARR VLVYGGRGALGSRCVQAFRARNWVVASVDVVENEEASASIIVKMTDS FTEQADQVTAEVGKLLGEEKVDAILCVAGGWAGGNAKSKSLFKNC DL MWYKQNYMDSVLVSFSCV
2550	A	392	1245	CTFTKVFLLLRIWYRNMLLKNSVTPLPSCHPSAQCLGTLMRALSQVF RDAW/WWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGKLLG EEKVDA\ILCVAGGWAGGNAKSKSLF\KN\CDLMWEAEHYWTS D HLP SHL\ALTKHLKEGGL\TLAG\AKAALDGTGPMIGYGMAGAVHQLC QSLAGKNSGMPP\GAAAIAALP\VTLDTPMNRKS\MPE\AD FSSWTP L*FLVETFDWITGKNRPSS\GSLIQ\VVTTEG\RTELTPAIFGLI SVP MRWPAQKSH
2551	C	60	266	MSWLSCLSNITVWNISPVLSSFFGGNSLISHLXKIPEEPPFLTPLLS SSPSGFXPHVPRVLRQSATV*
2552	A	1	513	MDLEPVQTEQSGAGVKENRGRNTAWRTPGDLHRRRIHTGEKPYKNEC GKVFNQISHLAQHQR IHTGEKPYKNECGKVFHQISHLAQHRTIHTG EKPYECNKCGKVF SRNSYLVQH LI IHTGEKPYRCNKRKGTEIKGRER LKGAIEIERRKMMRSDSKVGEDSKKTTYPI
2553	A	345	2343	LLGHEEQTRKGKRKAKAAGMVLSQGLLTFRD\EAIEFSQE EWKCLDP AQRTLYRDVMLENYRNVLVSLGIFSKCEIKELPPKESN\KEKYSRQ* CWKDMKSHRHTKIFCFRETQKNVHDSQCLWKHD*RHYKRVRVTYKGK SH/CVEETMPG*KG*CHKSQPC*KSSLGLNPAVT\CLPRTCQPI SKP EGKIYKYDHMEKSVNSSLVSPQRISSTVKTHISHTYECNFVDSL TQKEKANIGTEHYKCSERGKAFHQGLHFTIHQIIHTKETQFKCDICG KIFNKKSNLASHQRIHTGEKPYKNECGKVFHNMSHLAQHRR IHTGE KPYKNECGKVFNQISHLAQHQR IHTGEKPYKNECGKVFHQISHLA QHRTIHTGEKPYECNKCG\KVFSRNSYLVQH LI IHTGE\KPYRCNVC GKVFHHISHLAQHQR IHTGEKPYKNECGKVFSHKSSLVNHWR IHTG EKPYKNECGKVF SHKSSLVNHWR IHTGEKPYKNECGKVF SRNSYL AQHLIIHAGEKPYKDECDKAFSRNSH\LVQHRIHTGEKPYKDECD GKVFSONSYLAYHWR IHTG\EKAYRCNECGKVFGLHSFLAHPKIH\ TGEKPFKNECGKAFSMRSSLTNH\QRLHTGEKHF KNECGKLF RDN SYLVRHQRFHAGKKS
2554	A	3	517	STRTONVLGEKGRRIRELTAVVQKRF GFF\AESLRYKLLGGLAVRRA CYGVLRFIMESGAK/GCEVVVSGKLRGQRAKSMKFVDGLMIHSGDPV NYYVD TAVRHVLLRQGV LGIKVKIMLPWDPTGKIGPKKPLPDHVSIV EPKDEILPTTPISEQKGNAEPPAMPQPVPTA
2555	A	3	495	ERGGKMAVQISKRK FVADGIFKAELNEFLTRELAEDGYSGVEVRVT PTRTEIIILATRTONVLGEKGRRIRELTAVVQKRF GFFPEGSVELYAE KVATRGLG IGVKIMLPWDPTGKIGPKKPLPDHVSIVEPKDEILPTT PISEQKGKPEPPAMPQPVPTA

2556	A	24	861	INPPPPRLSFQRSAAARWPVQISKRRK\FVA\NGILSKLNLNEFL\TREL\AEDG\YSG\VEVRVTPTRNRKSFIFSHQKHRMVLGEKG\RRIR\ELP\AVVQKSF\GFPRGAAVELYA*KRWPT*/RGLCAICPGQSLCVYKPS*GG\LAARRAL\CYGLV/RGSFIGEVGPKGCEVCGCLGKLRGQRA*NP*SFVDG\LMI\HSGDPV\NYVDT*\VRHVLLRQG\VLGIKV KIMLAWDP\TGKIGPKKP\LPDHVSIVEP\RRDEILPTTPISEQKGG KPEPPAMPQPVPTA
2557	A	116	718	IFLQAGCLKLVRISKAGDISHVDTHCQTVHPKAVSISTMTENTPFLT LSPALSPIFNNLPFQCIEK*YLILTLIFLIAEYESLCL*SVFLIYK IFL*PLSNFCCCL*V/LLYIILNLLFYMYFPTPLFMKSNFIKVL*KV KGFTF*KCSQIYLFHGYWVLCGLWECLSYTFTITIFFQYFLLVIFNF HV*FILIFFIHDMK
2558	A	88	811	GSGGNHVSCCDTMEGGGGSGDKTTGVLAGFFGAGGAG\YSHADLAGV PLTRMNPLCPY\LVN\DPYRLVQGYKMKFIFTLPELIKTRGQDLKLA FFTIGGCCMTGAAGFAMNGL\RLGLKETQNMMAW\SKPRNVQILNNG* LGKGAL\WA\NTLGLWALLY\SAFGV\IIEKTRGAEDDLNTVA\AGT PAG\LLYTCTG\GLRGIA\RGGLTGLTSL\SLCTIYNTWGAHGKGS LASNSSLWKVFAQPP
2559	A	1	210	VIIRLPIGKKLFRCKPG*TWAPPGIL*SGRPRSSSSSPF*N*MHFLP ERESSFHRCKWKAGITCVKSWYP
2560	A	128	687	THVLWAFPGARVHLQTGWSRAGVAAAAALALGGQASLSYARGKES*GH SPPPTHTHKAASGGREKAVSPSAVAVSHGPSPLLESTSSQVKGHSG PGDPDVVTHL/WAPFPDQLPPSPCPPLSRKEPEPSPLSHPPQGVTPG QAQIGQLRTSGLWGHKRGGWARAEGAPVSLLLRGPFDGPATVSEAQR
2561	A	246	412	RLGDLPRDRQLAGRERHGGHRRPGERRVCRAAGLEAHYVAGDLPRC RHGRRTRG
2562	A	1	414	AWHEETHKVDLGLPEKKKKNKKVVKEPETRYSVLNNDYFADVSPRA TSPSKSVAHGQAPEMPLVKKKKKKKK\VSAALGKEVKRSQSKLRLRN TSP*VMTLRPPQQRK*SPKRR*SSQSSRSQ*KGKRRRGKRG
2563	A	198	531	RNNPLLSLLALCLVHSSHLICWALPDEGGGQGKERALNSRKIATFFL SSQGTQFGQWDTAGFENEDQKLKFLRLMGGFKNLSPSFSRPASTIAR P\HMALGKKAADSLQONL
2564	A	190	510	KSISSTGATVITGSCLTLYPSGKGGCSASYSLQICSHRFLLDGSVTC HDETGKLAGRERHGGHRRPGERRVCRAAGLEAHYVAGDLPRCRHGRG FHGNRVRKKAANS
2565	A	1	1977	MEVDFKIRKVGQWTITLQEHVSVLLFIEETHPENKPTSTAVEESHI SRDVTVMVNFQCQLDWSKGYLEAYLTKINSICSHRFLLDGSVTCHDET GSSRDARDTVGTGVRVNDSEVEQLGLRRTMWLGICRGAAMAAVSTVT AFAGRPRPGRSRNPRGWAGDSKWTSGSRRSWLSRGGEISPTGMITK THF\VYLGLPEKKKKKRVVKEPETRYSVLNNDYFADVSPRATSPS *\DVAHQAPEMPLVKKKKKKKGVSTLCEEHVEPETTLPARTEKS PSLRKQVFGHLEFL\RGKRKNKKSPLAMSHASGVKTSQ\DPQGEET TRVGKK\SKKHKEKKGGPGPHSL\PVQDPWFCEAREARDVGDTCVS GKQDEEQAALGQKRKRKSPREHNGKVKKKKKIHQEGDALPGHSPSR SMESSPRKGSKKKPVKVEAPEYIPISDDPKASAKKMKSKKVEQPV IIEPALKRKKKKKRKESGVAGDPWKEVVPSEMDFAVGELRETDTDL EVVLEKKGNMDEAHIDQVRRKALQEEIDRESGKTEASETRKWTGTQF GQWDTAGFENEDQKLKFLRLMGGFKNLSPSFSRPASTIARPNMALGK KAADSLQONLQORDYDRAMSWKYSRGAGLGFTAPNKFYIDRNASKS VKLED
2566	A	1781	2150	VRRFAAAVATLPPGAAPSG/PAPGT/PGPQTRIPGFPPWPLCPLMSG SLGP*TRLLLVPPAPQGPAGSPGPIQAGRGLAAPPPQPLSPSRGPCA GSSWELRLEGLSDWGTCPVPCPCHYIHPKKN
2567	A	1	345	GRGWSLLGATAMDALEGESFALSFSASDAEFDAVVGYLEDIIMDDE FQLLQRNFMKYYLEFEDTEENKLIYTPIFNEYISLVEKYIEEQLLQ RIPEFNMAAFTTTLQPNRLSS

2568	A	1	582	SGRALHASWAAGGVGAYSGRLRSDALEGESFA\LSFSSASDAEFDAV VGYLEDIIMDDEFQLLQRNFMDKYLL\EFEDTEENKLIYTP\IFNEY ISLVEKYIEEQLLQR\IPEFNMAAF\TTTLQH/HIRDEVAVVTIFGN AGSTFHKIFLGF*RKCFLDYRAEKES\RGL\DLSSGLV\VTSLCKSS SL\PASQNNLRH
2569	A	2	705	GSVGAATVRPQPNALRCRLRSRAGRSPVLVFGVGIKQPPCPSKKA KTTKKRP\QRATSN\VFAMFDQ\SOIQGVQRGPFNMIDQ\NRDGFHS DK/EKVLHDMLAS\LGKNPH*WHYLDA\M\MNEGPKGPFKFHQCSLT MFWLRKLNG\TRSPEDCHPETAFCAFD*KKAT\GTHFRKDYLRSC *PTHGGIRFPD/EREVDLYRGGTLDDQKKGNFQITFEFHTASWKHG SORPKMT
2570	A	1006	1022	TRNSFLFFIYIYLFLRMGSCSVAQGWKCSGTILG\HCSLCLRLPG\S SNSPTSASHVAGD/SHGMCRHARLIFAFLVEMG\FHPCWPGLGLELL TLRVIHPTLGLPKCWGL*AGGSAKIGRRAQIG
2571	A	668	863	TFCFFSDLKYSLASCENHLVCFVCFVAFVLT*NYFCL*TVNLI\F SVRVTELCPPFIFIVLIIT
2572	A	1	1282	MRAVSLVLVLVLTMSYVMPWPQTENYTIYFPGSEAFKLGRAISSLP SIQYPGSSAYRWPVMELLSLYNYARRALMGNLANVIPWGWSEKMTIE YLNPGTGELLNNSRGDAPHSEHVHRRVPRAGNAAASDCCVGAAAPP GQDRRGASGVGKTGSRCPGLVGLAVVYATRLLPQTGETRIKNGQAA FWGHRHRRHQNFVFEPLQCLAQKGLVKLAPLGGLVVRFLTKR FIGDYERNAGNLYTRQVQIEGETLALQVQDTPG\FRSMRTA*AAVNS LI*CIGCAHAGMGYSITDYKSYELISQLHQHVQKLHLGTRLPVVVA ANKADLLHIKQVDPQLGLQLASMLGCSFYESVSENYNDVYSAPHVL CKEVSHKQPPSSTPEKRRTSLIPRPSNMQDLKRRFKQALS AKVRT VTSV
2573	A	258	579	FKQICLFLLLFFEMESCSVT\RLECSGTISAHCNLHLP\GSSDSPAS ASPVTGITGTCHHAQLIFLYFYMTGFRHVAQVGVVELL**AIHLPW LPKVLGLQAPAPDL
2574	A	157	371	GGPGNGLHRLGFSPYNVSKTALLGLNKTALAIELAPRNIRVNCLAPGL IKTSFSRMLWMDKEKEESMKETLR
2575	A	1	1431	MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFA IARRLAQDGAHVVSRRKQONVDQAVATLQGEGLSVTGTVCHVGKAE DRERLVATAVKLHGGIDILVSNAAVNPFFGSIMDVTEEVWDKTLDIN VKAPALMTKAVVPEMEKRGGSVIVSSIAAFSPSPGSPYNVSKTA LLGLNNTLAIELAPRNIRVNC/LAPGLIKTSFSRM/LGEPEDCAGIV SFLCEDASYITGETVVNLSVMFTGGGVCRAASWKEGGTGTPTPRE SPRQREPGETSSTDTQENKVWNL PANPQRPAAEGPVRRKTNKQKGI ASTSAKDSINIRTKDHTKTPSIGHQHQRPKVDKTTKMERNQSKKA ETSRNQNVSSLPKEYKSSPAREQNW MENKFDDLTDSVFRRSVITNYT QLKEHVLTHCKEAKNLDKMLNEWLTRMKNLEKSLNDLMELITTVQEL HEGYTSFNS
2576	A	201	398	SLRLSSHQTYSPSSFVPLLVRTCIPLEEKRRSDFWKFPFCSGFSPS LWFYLPVFDVGDLMWGF
2577	A	195	434	TSVPSCVRCRYIILRSSSALTNILGTHSNSSFFHASSSALHSCFPF FSWLQTL DINVKAPALMTKAVVPEMEKRGYRE
2578	A	150	284	SMHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDG
2579	A	1	625	MHKARLRGH CARAGKSVRLASSGMTRRDPLTNKVALVTASTDWIGFA VAQRLAQDGAHVVSRRKQONVDQAVATLQGEGLSMTGTVCHVGKMK DWERLVATGFSPYNVSKTALLGLAQTLPIEL\APRNIRV\NCLAPG \LIKTSFSRMLWMDKEKEESMKE\TLRIKKV*ASPEDCAG\IVSFLC SEDASLHSLGKTVVVDG\GTPSRL
2580	A	84	1413	ARKSVRMASRMTRRDPLTNKVALETASTDGIGFAIARRLAQDRAHV FVISRKQONVDQ\AVATL\QGEGLSVTGTVCHVGKAEDRGAAWPPA VKLHGGIDILVSNAAVNPFFGSIMDVTEEV\WDKTLDI\NVKGPKP* MTKAVVPEMEKRGGSVIVSSIAAFSPSPGSPYNVSKTALLGLTK

				TLAIK\ LAPRNIRVNCLAPGLIKTSF\ SRMLW\ MDKEKEESMKETLR \ IRRLEPEDCAGIVSFLCEDASYITGETVNNLSVMFTGGGVCRAA SWKEGGTGTPTPTPRESQREPGENQARSSPRMALRPEFPPEASTS WMGPEPVGNRRERPCPKPARKVGASPRALRRLGSATRMLSRAALRAGVG ARAPRPGGGRGAHATATVWSGLASAAALTARALLKRSLACAAAPQRC GWRRLLCSSLGIRSGWPCPPWSSI
2581	A	1	560	MVYRQNQLPSSCAPEMGREDGLRALHPAQQPPPPRAQQSPPPPPLSA/P EEPPPPRAQQSPPPPPLLTPHRRHPQSFPAPSAPSALSQRPGLYSAV TFSGSLSGPRTSTCTPSPASSPSAHGLGHIHTDAGVCSLEAQEEAKA PGGRGPPSCSAHGALGPTCTSGVAGDSGPVVGSQLERALDPRRQGLQH
2582	A	775	1408	TIPVAYVWADPPLPPKHSCPHPPGSD/DGTRTTGTA/PPCLGFGD PDPVHPAPAPPDW**FPNMGQPGPPPPFPTWRAQLQLLKSSVNMRGH RWRNVPSGPHLPEQISLSELGHSHKPLFLRQNPNTVPWDVMLPFPL LNLLYGKMNWVSLDLWGCHRNEWRPTNIILLAPWRHGRLQLKGAG ARGRQLPQLLLPALLLILVGYEMSF
2583	A	3	560	GVPPKSASKFLCTRNGKGRWAQSPPPSTA\PPPPRAQQSPPPPPLSAQK /KPPPPRAQQSPPPPPLLTPHRRHPQSFPAPSAPSALSQRPGLYSAV TFSGSLSGPRTSTCTPSPASSPSAHGLGHIHTDAGVCSLEAQEEAKA PGGRGPPSCSAHGALGPTCTSGVAGDSGPVVGSQLERALDPRRQGLQH
2584	A	189	608	AFLT FNKLHRTDTCRGNKPHPPPPPGSKVRKRTWGFAPPGGSPWAS LPHGLPPTAGRQGR/EGGGPRGGPGKGSAPSSGTRAWRKPMGGC LTEDGPYGGPKGLWP*TTNG*K/PPGARPWPLPLGCPLEPRHPVLG P
2585	A	2	847	LKMAAEEPHQQQEPLGSDSEGVNCLAYDEAIMAQDRIQQEIAVQN PLVSEERLELSVLYKEYAEDDNIYQKIKDLHKKYSYIRKTRA\DGNC FYSGFRILPLGRHCWDDSKELQRFKAVS/WPRARVDLGCSQ/WGFT* ISQF*GIFHNKFHGT*LSRWRKQTSVADLLASFNDQSTD\YLVVYL RLL\TSGYLQRESKFFEHFIEGGRTVKEFCQQEV\ EPMW\KESDHIH I\MALAQGLNGAIQGEDMDRGEGETTNPHIFPEGSEPKGYLLYRPGH YDILYK
2586	A	468	1191	DVSRVGCPLPPSRAMGWTLLALLRRGSVAVALASGLVEEPMGLGPPFHPT PRFKAVSAKSKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADL LASFNDQSTSDYLVGYLRLLTSGLL*GPRASSSTSSKGGRCDFKEF CQ\QELEPM*KESDHHSHHCAGPGPSACPSRVGVHGTAAEGGNEQS AHLRLASEPKVYLLYRPGHYDILYKIGLGSSPLLPCCPPLPGARHV TEVFLWL
2587	A	1	326	HSVNRKRLNRNARRKAAPRIE/CVRGLGFRVAVGLGRDGRDDGSAM SLFAGSSHIRHAWDHAKSVRQNLAEMLAVDPNRAVPLRKRKVLTWQ GLGPCLLYSSPAILT
2588	A	879	1528	AAGAVVSAMPKAG\KTR*\QKFGYSTLRKR\MSRNARRKAA/RAGL ECSHIRHAWDHAKSVRQNLA*MGLA\VDPNRA\VPSRKRKVKAME\V DIEEEE*KNLYRKPYVLNDLEAEPSPLEKKGNL\SRDLHLTMYRYM V\ENHGE\DYKAIA\RD\EKNYY\QDTPKQISELRSNVY\KRFYPAE WQDF\LDSLQ\KRKMEVKVPLHHCPSAEASPGPSEAG
2589	A	1	310	EKKPKRPPERSRPLWVPEPQLEIRRRRPTPAMLFRLSEHSSPEEE ASPHQRASGEGHHLKSKRPNPCAYTPPSLKVIQRIAESHLQSI SNLN ENQASEED
2590	A	1	716	SALQRLEKKPKRPPERSRPRWVPEPQLEVGGACSAQAQSPSEKLD PACLKPLS*S*IRRRRPTPAMLFRLSEHSSPEEEASPHQRASGEGHH LKSRRPNPCAYTPPSLKAVQRI\AES\HLQSYSAILNENQGFREGED ELGEFV\ELGYPREEDDEEEEDDEEEEDSQAENVLKVIQSAQK TTCGQGLEGPWERPPPLDESERDGGSEDQVEDPALSEPGEEPQRPS SEPGT
2591	A	39	370	RGWSLVQTPNPRFKNVPGPPTPQVIAECEESQCGGLGTLGGL*LSPG P\G*TDSRGPPMMPSEAQGGGAASKGPLGPPQAAGIHQGTPLRMGEA LEGQAGQTAGPRVQDGL

2592	A	229	358	RSIMWFLQMAQLSTTISQAQRATAFHFFTSKRFLPAPLLVPLG
2593	A	257	387	RSIMWFLQMAQLSTTISQAQRATAFHFFTSKRFLPAPLLVPLG
2594	A	217	398	KAWWNLLRKSEPKSCGS*GGLSTSRRERLVECCSSPLGLGYCG**LCHL QEPHYGSLHRMSS
2595	A	1	3386	MAILPNVIYRFNAIPIKLPMTFFTELEKTTLKFIWNQKRARIKXIL SQKNKAGGITLPDFKLYYKATVTKTAWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPFLLTP YTKINSRWIKDLNVRPKTIKTLEENLGITIQDIGVGD FMSKTPKAM ATKAKIDKWDLIKLSFCTAKETTIRVNRQPTTWEKIFATYSSDKGL ISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMKCS SSLAIREMQIKTTMRYHLTPVRMAI IKKSGNNRCWRGCGEIGTLLHC WWDCKLVQPLWKS VWRFLRDLLELEIPFDPAIPLGLGIYKDYKSCCYK DTCTRSHPGYHIAF SHQVFLGFANIFLILDDLESSEYWSGLCMLCDE FVATVQCLGEKTYAQCGLAADGAHQNALNSNPSPHEAIISKAFPTDG VGPAHGGVGPVAVMIWVFGEPERWQESQTSPTLRDGLADRP SLKGS SQQPQAEGEKKEAAQTPVEIALI WPDNLNSGANLWQSCCEQAQGLRSC LWPHSQGRHASDGRTPQPTPAVEPTLEVKGSLRAGTYCMVDPEQPV LQGRRECSTWLLSKSFTCWLFDRDFLSAYSRETEPIEGVCVDRKRE REREREIVLKEADAVIAAGKSNICRVPLLGPPAGPSHSIVNIPSGS YLGKENLVGKCALNVSVNVNVQFIADVVDGTEAKGPGGEWKRTSDKN HDFSIDAKKAFGKIQQRFMLKALNKL GIDGYLKI IRDSGTPGDAAG PLLQERNVATTLP SAHIPMAPSTLNQGNDEKAGDQRRARACVKSNNL YTEGCESWKSEGVVWPTLHSSAWSVSCGACTDKELRN LASRLKDW F GALHEDANRVIKPTSSNTAQGRFDTSILPICKDSL GWMFNKLD MNYD LLDPSEINAIYLDKYEPCKPLFN SCDSFKDGKLSNNEWCYCFQKP GELIAPGPKLVKGPVILTNSQSPSSAADPAADILTWAFIPRCNEEG YYKATQCHGSTGQCWCVDKYGNELAGSRKQGA VSCEEEQETSGDFGS GGSVLLDDLEYERELGPKDKEGKLRVHTRAVTEDDEDDEDDKDEDEV
2596	A	442	2093	CGFLQMGTVINHNI PGPEGYWHFHFNFKALLARA AVGAARGIHIHR CGLTKRPDARRRRVAGA QGREPAISLPGDRAAGARATRTRGPGPAPK MPAIAVLAAAAAAWCF LQVESRHL DALAGGAGPNHG\NFL\DNDQ\W LSTVSQYDRDKY\WNRFRDEVEDDYFRNW\NPNKPFQDAL\DP SKDP CLKVKCSPHKV\CVTQDYQTAL\CVSRKHLLPRQKEWGTW AQKHGWL DL*ILVK\CKPC\PV\AQSAMV\CGSRWATPNSIPSC\LEFHACST GQK/SFATLCDG\PCPCSSQSLEPPKHKGRKGV PCTDKELRN LASRL KDWFGALHEDANRVIKPTSSNTAQGRFDTSILPICKDSL GWMFNKLD MNYDLLLDPSEINAIYLDKYEPCKPLFN SCDSFKDGKPLNNEWCL LPSQNPGLP/CAQNEMNRIQ\KLSKGKSL LGAFIPRCNEEGYYKAT QCHGSTGQCWCVDKYGNELAGSRKQGA VSCEEEQETSGDFGSGGSV LLDDLEYERELGPKDKEGKLRVHTRAVTEDDEDDEDDEDDKEDEVGYIW
2597	A	1	844	LHQAAVAWLPTSFLPSQEHCSTEWRA PQPAASGVHGICFA/RPFA SSTVSTEVSGSFCYLPAP\WVYGFL*TERPLAWWCLGKYWLQELLG CHPVPLAML*DC LALLKSSLVPMGSPTHCKAIVTEEPLHLP EAAAA AHTSSPSSSCRC KGCLGWVWP GGSAPGPLGPLS FDPWTVSHQSGPSP AAPGPTTSSS*RPSAPSHGMQGLADSQGHLCRHSRKLRSFLLSHTH HSTCPHLLQTGMPSPLISIDADSSPPRIHRLRGQGHFSGLAKGGQ R
2598	C	145	342	MQLXXVVPPLLPGLPQLIQR SRGHHAPPAXASSRPGQDDXXXTC GAXLLRPRGHFLRAAXVPN
2599	A	4	213	AGKFLHRCPPCWSHEFTIP*KCLPQGGRTGR ISEACL/HRP SHSLCP PQCRLEHLASCDPSTLASQSMIC
2600	A	2	589	RPREPEQELQRRREQRRRHDAQQLQLKHLESFYEKPPPG\ LIRE DELPEDCIPDVPGNEHAREFLAHAPTGLWMP LGKEVKVMQCWRCK RYG\HRTGDKECPFFIKGNQKLEQFRVAHEDPMYDI IRDNKRHEKDV RIQQLKQLLEDSTSD EDRSSSSSSSEGKEKHKKKKKKKEKHKRKEKK KKKKRKHKS

2601	A	3	1105	IWRPRPGLQGSPSRASRWAAAGRGAAARRKCPLGRSQSRASAGAAMSSCP GREDARAGGAWWPPEPLDQELQRRAREQKRRRHDAQQLQQLKRLESIV QGGHSGSQLPFGTTRNSGPDGLGLALPWLQFKEGPDDPGECGVKKIQ SYEKPPGLIKPYLAQSLSPSCVGFSLISSSESSQLRGDPTAHVPQL PGGGILPAAPGYGTREDEAKPEDSIPDIPGNEYAREFLAHAPTKGLW LPLGKEVRVMQCECWRCKR*GHRTGGKEWPFFQSNPSLKQVRRQAQ* NSPWYHSIQGNKQHERDVR\IQQLKQ\LLED\STSGEDRSSSSSSEG KEKHKKKKKKKEKHKKRKKKEKKKKKKRKHKSSKSNESGSDSE
2602	A	144	522	IGKEEIKLLLPDNLMEYTVNF*MYKPLELIS*FSKVTEYQVNTK/ SNCIYT*QLQIENETAKTI*FMIASKSIKYLEISLTKCN\KWRDILC ICIGRLSIIKVLVLPKLMCGGEKIFNPNTGFW
2603	A	105	440	RSTPDPVCLGIRSSGCRADTFREP*MLLSDRSSGSFVSEEPYPAV*SV SLPLLGECLPVRLLRDGHSW*HDSOSS*VFKMADNFPAGFHLGRSG DGRAEHRRCCLASQRCC
2604	A	1	1047	MVSISWPRDLPASASQSAGITGLIGALVLSVGIYAEVERQKYKTLES AFLAPAIILILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLI MELIGGVVALTFRNQQLLLRQQVLSHTLGCADLSDGPGSGPVKMFMG VPVIPAQPPELLASLRSLRGYGLVLSWLEPRYEKMISGMYLGEIVRN ILIDFTKKGFIFRGQISETLKTGRGIFETKFLSQIESDRLALLQVRAI LQQLGLNSTCDDSIIVKTVCGVVSRAAQLCGAGMAAVVDKIRENRG LDRLNVTVGVDGTLKLPHPFSRIMHQTVKELSPKCNVSPLLSEDS GKGAALITAVGVRLRTEASS
2605	A	1	690	MVLISGPRDLPASASQSAGITALPSASSIMPSLQFLKYIKLILANPV LGKSYTVRSFCMFTSQFSPPLPLCRYFAAAVDDMNLGLSRAPANPFD PSVPLDCLEATHVLDKQANCWSMQLAVLGTAAAGSQFHVRCAYFPFT FHDCITGLVPDWHQNPRLGSPLEADALKGFLADRCIPQTHFCSP TIPDSAATSSKCLSMKPGESNRYRADYRSGNLNRGNVKGRERL
2606	A	210	426	RGAPSSAARGFSAMPKSKRDKVSLTKTAKKGLELKQNLIEELRKC DTYKYLFI FSVANMRNSKLDIRN
2607	A	651	835	PRWSRFPDLVICPPRPPKVLGLQA*ATVCASISITKMWLNRNAGLTSS MNWPRRSARVLSVS
2608	A	198	757	RPVSGGERRLVLPFRCSCKANWVGRQLLNTAPGYACCRFGPLFPTS ALSHLPALPPWLPFPFSFTVSLTKTAKKGLELKQNLIEELRKCVD TYKYLFI FSVANMRNSKLDIRNAWKHSRMFFGKKNVMMVALGRSP SD EYKONLHQVSLWPSRGGAkakppslpllpCDslpQPLAGQRLRES
2609	A	1	1305	MMRAHAPPTAVPACTAPRAPPPRDRHAGIAREALGRTGRSGFRDCLG TREVALQAREKAQAAAWQGEAGCSAHWVRHTRGAAPGRPRVPRAG VLTGCTVFRRTWIQRDAQIQARQERWAKGESGPWGELRGLATQPAVR ASGRRGRRLERQDILEVFRCLAASWNGGFGAVKPPEVADARSGLGSG DSFCLVSVSLTKTAKKGLELKQNLIEELRKCVDTYKYLFI FSVANMR NSKLDIRNAWKHSRMFFGKKNVMMVALGRSP\ SDEYKONLHQVSKR L\RGEVGLLFTNRTKEEVNEWFTKYTEM DYARAGNKEGFHC*AWDPG \PLEQ\FPH\SMEPQLRQLGLPT\ALKRGV\VTLLSD\YEVCKEGDV ADPRARASRS*KLFGVMRWLNFKVTIPNYMWDSSQSGRFQQIGKTD\L PESA\SEFPEESDSEDD
2610	A	319	632	GEPNISMGLPWGPGSGSTGMPAPAMPLPAMTPQC/C*GQGPV\GPC AS/CASA/CFRCGL*AGRFC/G/PCPGHC*CFYFSNSVFPNVECMGL REPAVLPAFHLGEEAGRISGQGRSQNLPA
2611	A	156	621	LHVPMEQLQSHSKDEVSPTYLGMSLPGVAPLGSTGDASPCAPPWPWT PQCSKGQGPCCAP/WCP/CCP/CPPCPWSHGCL*LLCDPCPPPAPLPA AEGQQPLCKLASAVSQVVSRLGNFATCPWPLLMRPASSPRWKAGRTA GSLRPIHSTLGNTFEK
2612	A	1	585	MAELLQPLLQDCDGSCSIPVGPRMQPAEASLTNLVQMKATRPDPG TERNISRLNKRILYKRWSLLCLSDAKLVQTPKGEHYGISHERFPVP PSRQSDREPPFDGEDEDELQFSIMEHNVSYPKSLSKEAVSVCKGLMT KHPAKRLGCGPEGERDVREHAFFRIDWEKLENREIQPPFKPKVLDS

				CRAPPHD
2613	A	1	1047	MAALRAMGVSSLWTAQSLWSEWNPQVFAGVQDRKLRCLQVCRTES SGVRRACAGQKAQVFAGVQDRKRRCSSQKAKLGPAGNKVISPSSEDRKQP SNNLDRVKLTDNFNLMVLGKGSFGKVMLADRKGTEELYAIKILKKDV VIQDDDDVECTMVEKRVLALLDKPPFLTQLHSCFQTVDRLYFVMEYVN GGDLMYHIQQVGKFKEPQAVDLKLDNVMLDSEGHIAIDFGMCKEHM MDGVTTTRTFCGTPDYIAPEGLLPRSILPVNTALLAYALLWPVEESVD GCFQGWDAVRHAGAIGLTTNVIDVFVFTQIIAYQPYGKSVDDWWAYG VLLYEMLAGQPSTDQLHRIS
2614	A	1	1674	MRSQGEVRRYLKRQSCRFGGLSREKDMVTPSASSVCLIDEQIPAAGE SYDIIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMKCDTCDMN VHKQCVINVPISLCGMDHTEKRGRIYLKAEVADEKLHVTGKACSSRSS IVGRHLDEGYTDIKAGPQLDAFLCISSQPPFGKNAIIITSSSSSIIT LLKHGPRRFYSFASCSCMSSTVSVTNPKILGKGFIDSVVWVTPCHPGPM DCDWRADMGWGPVRLCIWFSTRNHQEQEKFMGPVREPKGPSHNTWGL GELQDEIWWQTQGGTTSRNHIQKPPTQGGVNMMAKARTKIVSSLIFFP YSLQIDCNFQKRAVVVRDAKNLIPMDPNGLSDPYVKLKLIPDPK NESKQKTKTIRSTLNPQWNESTFKLKPSDKDRRLSVEIWDWDRTR NDFMGSLSFGVSELMKMPASGWYKLLNQEEGEYYNVPIPEGDEEGNM ELRQKFE/RDDL*VP*TPSASSVCLIDEQIPAAGESYDIIIDPRSKH KFKIHTYGSPTFCDHCGSLLYGLIHQGMKCDTCDMNVHKQCVINVP LCGMDHTEKRGRIYLKAEVADEKLHVTGKACSSRSSIVGRHLDEGYT DIKAGPQLDAFLCISSQPPFGKNAIIITSSSSSIITLLKHGPRRFYS FASCSCMSSTVSVTNPKILGKGFIDSVVWVTPCHPGPMDCDWRADMGW PVRLCIWFSTRNHQEQEKFMGPVREPKGPSHNTWGLGELQDEIWWQT QGGTTSRNHIQKPPTQGGVNMMAKARTKIVSSLIFFPYSLQIDCNFQ KRAVVVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTIR STLNPQWNESTFKLKPSDKDRRLSVEIWDWDRTRNDFMGSLSFGV SELMKMPASGWYKLLNQEEGEYYNVPIPEGDEEGNMELRQKPFELMIL DKFLKLSLCLFCLRSGDDNRDCRIGLLGGFTQFTYVRIIHMAVPHL CILSHWKVFRGNTGAVITPDNNAFWNTS
2615	A	3	2089	RPQLPGGKRWLGGMADVPFGNDSTASQDVANRFARKGALRQKNVH EVKDKHFIARFFKQPTFCSHCTDFIWGFGKQGFQCCVVCVVKH\RC HEFVTFSCPGCG*GDPTLDDPRRQATRF\KIHT\YGSPTF\CDH\CV GSLLYGLIHQGMKCDTCDMNVHKQCV\LNVPISLCGMVHTEKRGRIYL KAEVADEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPK\NESKQ KTKTIRSTLNPQWNESTFKLKPSDKDRRLSVEIWDWDRTRNDFMG SLSFGVSELMKMPASGWYKLLNQEEGEYYNVPIPEGDEEGNMELRQK FEKAKLGPAGNKVISPSSEDRKQPSNNLDRVKLTDNFNLMVLGKGSFG KVMLADRKGTEELYAIKILKKDVVIQDDDDVECTMVEKRVLALLDKPP FLTQLHSCFQTVDRLYFVMEYVNGGD\LMYHIQQVGKFKEPQAVFYA AEISIGLFFLHKRGIYRDLKLDTVML\DSEG\HIKIA\DFGDVQGN T*WDGSHGPGTFCGTPDYIAPEIIAYQPYGKSVDDWWAYGVLLYEMLA GQPPFDGEDEDELQFSIMEHNVSYPKSLSKEAVSICKGLMTKHPAKR MCGPEGERDVREHAFFRRIDWEKLENREIQPPFKPKVCCKGAENFD KFFTRGQPVLTTPPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV
2616	A	1	1136	MTQISNIKQPFAMQHRFFISLLHWTQIVYPALFLGLCERGRNGRCD QVPEGSVLSLLVWVVPGLAFPEVAPGTCGTSYVVPDAGLHGPEVESKL GLDPGSMGTGTQPTRTPAQPAAEPPALTGPGRVHQEQAVLACGFLGI YHLGAASALCRHGKLVKDVKAFAAGASAGSLVASVLLTAPEKIEECN QFTYKFAEEIRRQSFGAVTPGYDFMARLRSGMESILPPSAHELAQNR LHVSITNAKTRENHLVSTFSSREDLIKVLLASSFVPIYAGLKLVEYK GQKWVDGGLTNALPI\LPVGRVTVTISPFSGRLDISPQDKGQLDLYVN IAQDIMLSLANLVRLNQALFPPSKRKMESLYQCGFDDTVKFLLEN WFE
2617	A	118	1018	VTARPRASRLKGLVQHGSVPGLHCATARMKHINLSFAACGFLGIYHL

				GAASALCRHGKLVKDVKAFAGASAGSLVASVLLTAP/EKKLEECNQ F\TYKFS\EEIRRSFGAVTPGYDFMA\RLRSGMES\ILPPSAHELA \QNRHLVSI\TNAKTRENHLVSHFFSS\REDPQLRSLLSPASFVP\I YART*SLVEYK\GQKWVDGGLTNALPHPCPVGRVTISP\FSGRLDI SPQDKGQLRSVCLISAKQDI\MLSLANLVRL\NQALFPPSKRKMESL YQCGF\DDT\VKFLL\KENWFGIKCIKVL
2618	A	60	388	GLDSFSATETRRTHNTTEPHSQSQEPSNGEPQKEEPAAESRDPTPGQ QTEEDQDTAEIPVRDMEGDLQELASVKHRG*ILDLS\SVKVKIIPK EEHCKMPEAGEEQPV
2619	A	1	4123	MEEVEEDRFKENLEGALAGQLLGDEATQALQVLAVELDVVPGALHP QRLHRLGAALVERQPVREVDHLVLPVAVDDEHGRDLGHLDDVREGVE AVGLLGVAEGDAHARGERRVQHHRGTLVARGQVHGHRADALPVQDD AVRADAVPGGAGAGSAAASNARAPFPAGVPGPSSGCDPPPSPLSQV SAHWELCGPHILNASYLPARVRKPFLVHWPGQRTFLPLAALAHPLGH EEFRQLCPQMSPPNFGLSSESPRPVRCQCNPGQHRGWLLRRWHPLPPA PSLGSGQVLGHLSTTSSHPGAPSPPGHWCAAPDPADPAPVTRPPRAQ SQARGTHLPPCPCRDPTTLLPHALGSDPRQTSPCKAGAWAGRSQPLP PGCHHSNERDTSPEALGTLWPPPHGSGPRFLQDKGAAGQMAEQTEL RAGHGRMAKLRSRASWASPPDLAAASPHLAPSAASADGLPATRAQ TPRPPPTPSRQAEPLPGSPSPGAQGLPGVDVGIEVPLGRPARAGTV AGGVVGEDVAEAGAQAQNEAAHLAQVHGIAREEDRVPGRHAANI HAGDTVAAGALGGEDLDGVQLALAVLEVGTLRQGFNWTLRGTDVETY PFSAPRAASHGVGRHEELPDPTGPCGRLLSLTIHGVTRIYHALLWA RGPIMSKSQVLGEWEPVQCGKSSSENDKWTMSDPGAAPTCSRAASGV DKEQQGRWQGLWNSHIKPLKIRMVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGGHETDGHRIVSVLHIFPLISILSY ATWGLSLECI PGSPVCTLLVRF SNVGTWRSLEVRGSPCGFGSNKVC GVMTP EIKMVCVCEGKAGKAVGSGGVEGTKEVSTGNAEGPVRHEAVD GGVHLAFALLQGLLWSLLGPPGLAGWGGGELDAVPDSTSSATNVSM VVSAGPWSSEKAEMNILEINEKLRPQLAENKQFRLKERCFLTQLA GFLANRQKKYKYECKDLIKFMLRNERQFKEEKLAEQLKQAEELROY KVLVHSQERELTQLREKLREGRDASRSLNEHLQALLTPDEPDKSQGG DLQEQLAEGCRLAQHLVQKLSPENDEDEDEDVQVEDEKVLLESSAPR EVQKAEEKVPEDSLECAITCSNSHGPCDSIQPHKNIKITFEEDKV NSSLVVDRESSHDGCQDALNILPVPGPTSSATNVSMVVSAGPLSSEK AEMNILEINEKLRPQLAELKKQFRLKEKCFVTQVACFLAKQONKYK YBECKDLIKSLRNERQFKEEKLAEQLKQAEELROYKVLVHSQEREL TQLREKLREGRDASRSLNEHLQALLTPDEPDKSQGGDLQEQLAEGCR LAQHLVQKLSP
2620	A	71	547	KQIPSLPISRPSVLAVMVTMTLKVGAAPPMLFIQRSVVNSPSCSSSR TTVYFWPPSVSPFMTKLDQSLPTRTPTSAGVMLRKVFPPPTSREKPTC FSSNA*KELP*GWQESGCSRQCPLSSRETCSRASCINESANARGEAVC VLGARVVFLFTSETGNS
2621	A	241	452	ENVMLCIIRAKEKNHMITLSYTVKAFG\KLKTTFFMIYKNKPQKTL IRREGNTFNPIKGRFEKNS/AGNIILNGIGLNAF/PIKSEKKVEYLL LFFQFSIILEI*INAIK*EK*IKGRFEKNSEVTLY
2622	A	1014	1432	SARLSLPKCWDYRREPPCPASFLYLKNIILYIIRAKEKNRMITLSYT VKAFGKIENFF\MIYNNKPQKMLYMRTEGNTSNPIKGRFEEPTGNI ILNRHKIGCFSIKSEKKVEYLLLLF*FSIILEL*VNAIK*EKLIKYP
2623	A	55	316	NFWGGGAPKAPPKKGFFPKIPRGVLNRPPQKEKKLFFPPPVKLGP KDFLKRAPP*TPKKGFFPKP/YKFLGGGGPKSPPKRVFSQNP GFKSPPKRKKIIFPPPRKIGPPQGFFKKGPPPLFIFFCLPFAFMET TCPFSKSLSKFTKTK
2624	A	1	3669	MGCTPSHSDLVNSVAKSGIQFLKKPKAIRPGCQGGSERGSIPLLVKN STCYDAGEGLAEQPSPRRNQTTAKGLCQLMGDPASGKRKOMEGLIP GTKTSSSQLNKSQSHMAKDIPFKTQGSHGSGQADFGDESEESSTQD

				TSKWKRTAKCHTSSTQSHCYQTIHPAHEPEGKVDPFPEPLVKAHQQAY TYLHSSLSKYBAILCIIHQATQTRELLQPMVSFLLLCFEEISQLLGE ISKDGEVLLQEVREDLAWPLKKREPQEQPNLLQQLLQYTVSKLQVLN GTVASLTGSFLEGSSSYLHSTATHLENKLSTKRNVDRLRLALRQLE SLASGCGDPGVQGLPLCSEDSGIGADNESVQSVDKLGKQTSWDLAPE PEEWKSVTSPHTEARQSGHTWQQSPFCLGSGRPQDCLLGGAPMAKVQ PRAQDEARSPCLSTSPENITSPPLKLTSTPCDSFGIGVSVEPHLS KTSRPMDDASSLSDSEDSSPEEEEEEDKMSSMSLCAWQEKTPHSRPQSS PADRESPPFQARTRRLRSLQAQEMILKMKESISERIKFVPVPCGHQDW SEEEEGRTVVPPRPSTVSGSRRAPERQTRSQSESLQSHVEDPTFQE LRRVQRDLQKLEAFYALGAKGQGSQEQILQPRAAAVWPNGTCRVS PSNTTSRLKASLTKNFSILPSQDKSILQKCNPHPEDEQKGAKLPNA IPSGEVSEAAKATDWNVRGCETRTSVKKLIETFSPTESLRMLGDSKD AGASPCLRNCIMPPRFKYTGLAPLYPKPQISPASGRES/PQNGHRL EALSTYLSPSA*SRSSQE*GAQL*NGGEPRAPPS\PPMEVLMDKSFA S\RSPQKAASPQRTPPRKPRSQGRERLAPPGEHGLPQS*GPL*APWT CCPARAPPA*PSLTAQGGVAGAAASPGSQPWT*AAHQPPAKAPR*R VGLGVQRRRPPASTGSPGRPSPGTTPA\PIWTKQDLRVQPGQTKAEP \KRSPPVGRKASPTRTHWVPQADKRRRSLPSSRYAQPSPSAVQTPP SPPVSPRVLSPPTTKRRTSPPHQPKLPNPPPEAPQCKVPSPTQH PEASPPFSIPSPSPMSPSQEHKETRDESDSQAIAKVSNGTHSIFC PATSSLFKAPPLSTAHPLTPPSLPPEAGGPLGNPAECWKNSSGPWL RADSQRRAALCALNPLPFLRRTASDRQPGGRPQPPTLDPTSTSYESQ LGQNR
2625	A	1	963	PTRPPNFHSPHTSPAAVGSAALRCSGRRRSLEVATSLPHPSGPRP AADVKMSSSEEVSWIS\WFCGLRGNEFFCEVD\EDYHPGTNFNLT\D LNKQVP\HYRTSSKP*SLDPEPD\EEL\EDNPN\QSDL\IEQAAEML LWDLIH\ARYIPLPTRRRHRPRCLGKVPSKGDGFG\YC\PRVYCENPAN CFPIGLSDIP\GEAHGESSYCPQ\CAMDV*HTPSQSRQPSTRMGA*L RATGFPSHGSFMVAIPELPGPKRPAQPSFVA/RGFLRGFKIH\PMAY PAGSFQGRPATFKKPQFKTDSLIPSTCPAVFCLFLSFLPTLSGTLY GF
2626	B	44	403	MKALILVGGYGTRRLRPLTLSTPKPLVDFCNKPILLHQVEALAAAGVD HVILAVSYMSQVLEKEMKAQEQLGIRISMSHEEEPLGTAGPLALAR DLLSETADPFFVLNSDVICFPFQAM*
2627	A	159	311	IGPSLALGSKVFLQKQSLLFIRCWLIALQDLWPQGWNTAEMGWA* QMG
2628	A	545	2302	AACAPSPRTESSTVSSLPLLQECLLGAMKALILVGGYGTRRLRS/LTL STPKPLVDFCNKPILLHQVEALAAAGVDHVILAVSYMSQVLEKEMKA QEQLGIRISMSHEEEPLGTAGPLALARDLLSETADPFFVLNSDVIC DFPFQAMVQFHRHHGQEGSILVTKVEEPSKYGVVVEADTGRIHRFV EKPQVFVSNKINAGMYILSPAVLQRIQLQPTSIEKEVFPIMAKEGQL YAMELQGFWM DIGQPKDFLTGMCLFLQSLRQKQPERLCSGPGIVGNV LVDPSARIGQNC SIGPNVSLGPGVVVEDGVCIRRCTVLRDARIRSHS WQESCIGSGGSWKLTLTDQDLMAQFSTPSLPPTLKVGFLPSAGKE QSVLWVSLEEAEPIDIIHWGIRVLQPPPRARECAEVRMENVTVLGED VIVNDELYLNGASVLPKHSIGESVPEPRIIIHDGGFAEEAVLVVHVQV LVDTGSTTGEMRTALHVPTALPTTKLWGPLLADLWAQGWDTAEMGG GSCCLGRCRQVRQDLFQLGQLIGTDIIIRIWGVVGSVKSEVAEDVMP LEYSQPTTLLFLRLLTRPSRFP
2629	A	124	1315	RARGRARRWECAAGTGQAGCRHLRARDTPSTSAGAMKALILVGGYGT RLRPLTLSTPKPLVDFCNKPILLHQVEALAAAGVDHVILAVSYMSQV LEKEMKAQEQL*IRISMSHEEE\PLGTVGPLPLARDLLSETADPFF VLNSDVICDFPFQAMVQFHRHHGQEGSILVTKVEEPSKYGVVVEAD TGRIHRFVEKPQVFVSNKINAGMYILSPAVLRRRIQLQPTSIEKEDLP IMGKEQLYAMELQGFWM DIGQPKDFLTGMCLFLQSLRQKQPERLCS

				GPGIVGNVLVDPSARIGQNC\ IGPNVSLGPGVVVEDGVCIRRCTVL RDARIRSHSW\LESCIVGWRCRVGQVVRMENVTVLGEDV\ IVNDEL\ YLN GASVLP HKSIGESVPEPRIIM
2630	B	162	276	MGRRANESLNVLIVYHFLFQKGVQCRLQLVQVVLQHLLX*
2631	A	2	292	HVFIDLPTLQERREIFEQHLKSLKLTQSSTFYSQLAELTPGFSGAD IANMCNEAALHAAREGHTSVHTLNFYAVERVLAGTGGAPWVKALLS RA
2632	A	3	2111	SSCGLGGQHGLGAARVRSLFKEARARAPCIVYIDEIDAAGKKRSTTM FGFSNTEEEQTLNQLLVEMDVFYAKIEELKLVNRRRAETGVSLSRCST QK*KS*NWCILITVFYAAIEELKLMYPYHGVLCSSRRKLSSCSNKEM TQSEKSQA*YRMTPLGMGTTDHIIVLASTNRADILDGALMRPGRLLDR HVFIDLPTLQKGVALSRLCSAAITTHCGNLQGS*GARTTMGV RRRAG*FLTESRCVAKAGVQAAI SAHCNHHLPGEA/RKIFEQHLKSL KLTQSSTFYSQLAELTPGFSGADIANICNEAALHAAREGHTSVHTL NFYAVERVLAGPHGFQLWESSGFLPEEWGQLLQTLQNTPGFSPTA LRGREDWRCLCLTENLFSCNHL LLLCGNRKAFYNSSKAGRTEWEPQAS *KKIHDVLECSGPRADSSCTEWTLTDVWKI*DRK*SLTRTAKKSKIL SKBEEQKVAFHESGHALEGWMLH/TEAVMKVSIPT\RT\NAALGFG Q\MLPKDQHLFTQ/ESSFERRFIALGGRAS\EHFSLNEVTS\GAQDD LRKVTP IAYSMVKQVGMAPGIGPISFPEAQEGLMIGRRPFNGQLQ MMDHEARLLVA\KAYRHTKVLQDNLDKLQALANALLEKEVINEDI EALIGPPPHGPKMIAPQRWIDAQEEKQDLGEEETEETQQPPLGGEE PTWPK
2633	A	2	2416	FQANMAVLLLLLLRALRRGPGPGPRPLWGPGPAWSPGFPARPGRGRPY MASRPPGDLAEAGGRALQSLQLRLLTPTFEGINGLLLKQHLVQNPVR LWQLLGGTFYFNTSRLKQKNKEKDKSKGAPEEDEEERRRRERDDQM YRERLRTLIV\ IAVVMSLLNAL\STSGGISWNDFVHEMLAKGEVQR VQVVPESDVVEVYLHPGAVVFGPRPALMYRMQVANIDKFEELRAA EDELNIEAKDRIPVSYKRTGFFGNALYSVGMTAVGLAILWYVFRLAG MTGREGGFSAFNQLKMARFTIVDGKMGKGVSFKD VAGMHEAKLEVRE FVDYLKSPERFLQLGAKVPGALLGPPGCGKTL LAKAVATEAQVVF LAMAGPEFVEVIGGLGAARVRSLFKEARARAPCIVYIDEIDAVGKKR STTMSGFSNTEEEQTLNQLLVEMDGMGTTHVIVLASTNRADILDGA LMRPGRLDRHVFIDLPTLQERREIFEQHLKSLKLTQSSTFY\SQLA ELTPRFSVADIANI\CNEAALHAAREGHTS\VHTLNFYAVERVLAG TAKKSK\ILSKEEQ\KVAFHESG\HPLVGWMLHTEAVMKVSIPT TNAALGFAQMLPRDQHLFTKEQLFERMCMALGGRASEALS FNEVTS AQDDLKRVTRIAYSMVKQFGMAPGIGPISFPEAQEGLMIGRRPFSQ GLQQMMDHEARLLVAKAYRHTKVLQDNLDKLQALANALLEKEVIN Y*/EDIEALIGPPPHGPK\KMI\APQRW/VSDAQREKQYLG\EEETE ETQPSLGGEEPTWPK
2634	A	1	395	CEGNSTCSENEVCVRPGECRCRHGYFGANCDTKCPRQFWGPDCKELC SCHPHGQCEDVTGQCTCHARRWGARCEHACQCQHGTC HPRSGACRCE PGWWGAQCASACYCSATSRCDPQTGACLCHAGWWGRS
2635	A	1	3040	MEGAGPRGAGPARRRGAGGPPSPLLPSLLLLLLWMLPDTVAPQELN PRGRNVCRAPGSQVPTCCAGWRQQGDECGIACEGNSTCSENEVCVR PGECRCRHGYFGANCDT SERGVGPVLVGGAESWRD GAGSKVGRGRIR LRGGSPEVAAGVRDAGRFRLAGGTYSSTGA FHPLRSSPAECPRQFWG PDCKELCSCHPHGQCEDVTGQCTCHARRWGARCEHACQCQHGTC HPR SGACRCESGWWGAQCASACYCSATSRCDPQTGACLCHAGWWGRSCNN QCACNSSPCEQQSGRCQCRERTFGARCDRYCQCFRGRCHPVDGTCAC EPGYRGKYCREPCAGFYGLGCRRCGQCKGQPCPTVAEGRCLTCEP GWNGTKCDQPCATGFYGECSHRCPPCRDGHACNHVTGKCTRCNAGW IGDRCE TKCSNGTYGEDCAFCADCGSGHCD FQSGRCLCS PGVHGP CNVTCPPGLHGADCAQACSCHEDTCDPVTGACHLETNQRKGVMGAGA LLVLLVCLLLSLLGCCAC\PARTLRADPAPQGVSLGRKKAPHRCLG

				RFSRISMKLPRIPLRQKLPKVVAHDLNTLNCSFLEPPSGLEQP SPSWSSRASFSFDDTDEGPVYCVPHHEAPAESRDPEVPTVPAEAPA PSPVPLTTTPASAEAIPLPASSDSERSASSVEGPGGALYARVARREA RPARARGEIGGLSLSPSPERRKPPPPDP/GHQA*GVLDPRQAQRRC WPCALTTAARLRGRAQPQEQETDAQRQIGAYGRTRQ/SPGPATQRR PRGCPRRRQPSLRPRRPGPER\GRAPASWSRTPAVPREARRGCLHV GR*RARQDSQPGPRRGPGRAGPQKGAGAPTESQALRAASLARPRAP SDRNPGA*EGGDLARA*DPPEEDPHPEAAAQEEPGLVRAGQGGRT HPVAGCGSSARSPSASQRRPPHTSHATGHGGLLAGHRAASGGCVS LAQVLQPLLDWSSVLSAGRAHPVGRGLTGA
2636	A	350	1256	LCLFPLPARKMATNFLAHEKNLVDKFKYDDAERRFYEQMNGPVAGC/ ASRQENGA\TVILRDIARARENIHKS LAGSSGPGASSGTSGDHGELV VRIASLEVENQSLRG\VVQELQQAISSEAR\LNPLEK\TWPG\HRA TGPQ\TQHVSPMRQ\VEPPSPRSPPTPAEG/DARDDIALF\GSDNE \EEDKGGGTS LREE/RGFREFPGEKRPKPRLV\AQLSFLLG*NPW\ DR*KDMAQLEACVRSIQ/LGTGRSWGASKLGAPWATGIRK\LQIQCV VEDDKVGTDLLEEEITKFEHVQSVDIAAFNKI
2637	A	1	304	GKTFDTFCPLGPALVTKDSVADPHTLKICCRVNGKVVSQSGNTNQMF KTEDLIAVWSQ\DVILTGTTPPGVG VFRKPPVFLKKGDEVQCEIEELG VIINKVV
2638	A	1	927	MALGSSVSWILHFS LQALMVVSGRRLLTALLQAQKWFPQPSRDMRLV QFWAPHLVGPLHGLGLETGNRGIIINLNAFDPTLPKMTQFLEQGEATL SVARRALAAQLPVLPRSEVTFLAPVTWPKVVCVMNYVDHCKEQNV PVPKEPIIFSKFASSIVGPYDEVVLPQSQEVDWEVELAVVIGKKGK HIKATDAMAHVAGFTVAHDVSARDWLTRCNGKQWLLGKTFDTFCPLG PALVTKDSVADPHNLKICCRVNGEVVQSSNTNQMFVKTEDLIAVWSQ KPPVFLKKGDEVQCEIEELGVIINKVV
2639	A	3	849	PSGSDFAAAVVPRLDAVTGASAPAAALDLPREP*LSAGGPVAAAA AARALAAQLPVLPRSEVTFLAPVTWPKVVCVMNYVDHCKEQNV PKEPIIFSKFASSIVGPYDEVVLPQSQEVDWEVELAVVIWKRKAST SR*SGKGLPVQSAEAPAPASPSDDLTHQHTVPAVPDTRKQSASLL PDATFPFTHLWLALATNMG*QLRDPLP*VLVSPMI*PPVWPNPLPP* ATDAMAHVAGFTVAHDVSARDWQMRRNGKQWLL*KTFTDFCPLGPA
2640	A	2	562	ITPRFHLCISDPHNLKICCRVNGEVVQSSNTNQMFVKTEDLIAVWSQ *VTRAVLSAPLHPLHMRWL*ALHLWLWPLSQPLVSLGPFALLQ\FV TFYPGDVILTGTTPPGVG VFRKPPVFPQGRFSEKREQGPPKPLAGLP SDLRSTGLCMCV*RKGLTLSWPALLQKGDEVQCEIEELGVIINKVV
2641	A	867	1476	LVPVLRRLPLPLTSRASPNSAQEDRLPPP\RRQEVNWEGLAGVIGK KGKPIKATDAM\AHVGG\FTVAHDVSARDWQMRRNGKQWLLGKTFDT FCPLGPALCDQVTGVADPHNLK\ICC\R\INGEMVPERQTPNQMVIS RQRT*IALGLPSLVTLPPGDVIPNLGPPHLHPGVGVFRKPPVFL\K KGDEVQCEIEELGVIINKVV
2642	A	3	846	LNLSCADVVWHQMDENLLAT/AATNGVVVTWNLGRPSRNKQDQLFTE HKRTVNKVCFHPTAHVLLSGSQDGFMKCFDLRRKDSVSTFFG\QSE SVRDVQFSIRDYFTFASTF*ERAMLQLWDIRRPDCERMFTA HNGPV FCCDWHPEDRGWLATGGRDKMVKVWDMTTHRAKEMHCVQTIASVARV EW/RPECRHHLATCSMMVD/YNIYV/WDVRRP/YVPAACLRHRTSHG I/AWRTPRPSSVFGQTVVASLFGAAAGRAGPCTPWDCSRKNPGRWG SYLDGPPF
2643	A	1	2693	SPAALRADSVDDGSLAPLLGLTDRAFSDCPDADGAMEKMSRVTTA LGGSVLTGRTMHCHLDAPANASVCRDAAQVG\LAG\RSIFKIYAIE EEQFVEKLNLRVGRKPSLNLSCADVVWHQMDENLLATAATNGVVVTW NLGRPSRNKQDQLFTEHKRTVNKVCFHPTAHVLLSGSQDGFMKCFD LRRKDSVSTFSGEATEAGPREWAMAGCVPILPVLSCRILRLHHSFAH GPMQDAESTANDARESWGCPYPLGLCSGPQAGQSESVRDVQFSIRD YFTFASTFENGVLWDIRRPDCERMFTA HNGPVFCCDWHPEDRGW

				LATGGRDKMVKVWDMTTHRAKEMHCVQTIASVARVKWRPKCRHHLAT CSMMGDHNIYVWDVRRPFAPAAMFEEHRYVTTGIAWRHPHDPSEFLLA GSKDSFLFQHLFRDARQAVKRANPEGLCYGLFGDLAFAAKESLVAAE SGRKPYTGDRRHPIFFKRKLDPAEPFAGLASSALSVFETEPGGGGMR WFDVTAERYALAGRPLAELCDHNAKVARELGRNQVAQTWTMLRIYC SPGLVPTAN/H/RTTVWARVAPVASRS*TVST*RIWPQGWAVRRGWT AAKEMHGATQFCS/HSSATLITNEDNEETEGSDVPADYLLGDVEGEE DELYLLDPEHAHPEDPECVLPQEAFLRHEIVDTPPGPEHLQDKADS PHVSGSEADVASLAPEDSSFSLLSVSHALYDSRLPPDFFGVLVDRML HFYAEQGTQMAVSVLIVLGERVRKIDIDEQTQEHWYTSYIDLLQFRFR LWNVSNEVVKLSTSRVSCNLQASTTLHVNCSSHCKRPMSSRGW\FCD R\CHTCASMCVACHHVVKGLFVWCQGCSSHGHLQHIMKWLEGSFPLF PQAAAHLCSEYS
2644	A	33	222	NGPM\CFVKQLEIPQYGYRNNVPTTTTPRSNLAKELEKYSKTSFEYTI NDNHTYGGGLGCMRPLV
2645	A	1	1377	MRTAVLGQAPTQVQPAAVREDQNEIFYLLNVEYSESFPVAISLRPAP MSLSHFPPQLPVGIEENDEEIKQLDEEIKELNESNSQMEADMIKLRTQR LRLGKVEGLSHSQPGVVNGSAQQVVSTHWTQFSQGWHRPLGLGPHQA TERDFQAPRRGPDNLNIKNSKRRKKETPSKPLNFTPVDPGEDRHAC AGWRETAAPVPDGGRRPRLCRRRGRPPRLCRMGGDRACAGWRETA PVPEKRETAAPVPDGGRRPRLCRRRGRPPRLCRMGGDRACAGWRETA AAPVPEKGETAAPVPEKGETAAPVPEKGETAAPVPEKGETAAPVPEKGET ERPLLPLSAEGVACYLSSPGVFLKLKGIITMESNLKTIEBENKVIE QQNESLLHELANLSQSLIHSANIQLPHMFLRIFVEQAFWIVTRDSD QDSCTSDLQIAGGHPGLLLAGDTRSSCGLQQESCVL
2646	A	1	2232	MQDTEKDDNNDEYDNYDELVAKSLLNLGKIAEDAAAYRARTSEMN NTSNSLEDDSDKNENLGRKSELSLDLSDVRETVDLSKLLAQGHGV VLSNMNDNRNYADSMSQQDSRNMNYVMLGKPMNGLMEKMEVESDEE VCLSSLECLRNCFDLARKLSETNPQERNPQNMNIRQHVRPEEDFP GRTPDRNYSMDLNLMLREEQLSPRSRVFASCAKEDGCHERDDDTTSV NSDRSEEVFDMTKGNLTLLKAIATERAKAMREKAMEAGRRDNM RSYEDQSPRQLPGEDRKPKSSDSHVKKPYYGKDPSTREKKESKCPTP GCDGTGHVTGLYPHRSLSGCPHKDRVPPEILAMHESVLKCPTPGCT GRGHVNSNRNSHRRDIQVFNLQKQEMIDRLESLSGCPAAAAEKLA QEKHQSCDVSKSSQASDRVLRPMCFVKQLEIPQYGYRNNVPTTTTPRS NLAKELEKYSKTSFEYNSYDNHTYKRAIAPKVQTRDISPKGYDDAN GYCKDPSPPSSSTSSYAPSSSSNLSCGGSSASSTCSKSSFDYTHDM EAAHMAATAILNLSTRCREMPQNLSTKPQDLCAIRNPDMEDVENGTL DLSMNKQRPRDSCCPILTPLEPMSPQQQAVMNNRCFQLGEGDCWDL VDYTKMKPR\RIDEDESKDITPEDLPFQEALEERRYPGVETIPSPK PKYPQCKESKKDLITLSGCPPLADKSIRSMLATSS\QELK
2647	A	623	4268	LWACVLPVLTLPFPLGEKTSCKMEVDTEEKRRHTRSKGVRVPVEPAI QELFSCPTPGCDGSGHVSCKYARHRSVYGCPLAKKRKTQDKQPQEP PKRKPFVADSSSVDECDDSDGTEMDKEEEDGEEYSEDNDEPGD EDEEDEEGDREEEEEIEEEDDDDEDGEDVEDEEEEEEEEEEEEEEE ENEDHQMNCHNTRIMQDTD\LDDNNDEYDNYDELVAKSLLNLGKIA EDAAAYRARTSEMNNTSNSLEDDSDKNENLGRKGELSLLDSDVVR ETVDSLKLLAQGHGVVLSNMNDNRNYADSMSQQDSRNMNYVMLGKPM NNGLMFMV*ESDEEVCSSLECLRNHCFYLARKLSETNPQERNPQQ NMNIRQHVRPEEDFPGRTPDRNYSMDLNLMLREEQLSPRSRVFASCA KEDGCHERDDDTTSVNSDRSEEVFDMTKGNLTLLKAIATERAKA MREKAMEAGRRDNMRSYEDQSPRQLPGEDRKPKSSDSHVKKPYYGK DPSRTEKKESKCPTPGCDGTGHVTGLYPHRSLSGCPHAKDRVPPEIL AMHESVLKCPTPGCTGRGHVNSNRNSHRSLSGCPAAAAEKLAQEK HQSCDVSKSSQASDRVLRPMCFVKQLEIPQYGYRNNVPTTTTPRSNL AKELEKYSKTSFEYNSYDNHTYKRAIAPKVQTRDISPKGYDDAKRYC

10112

				KDPSPSSSTSSYAPSSSSNLSCGGSSASSTCSKSSFDYTHDMEAA HMAATAILNLSTRCREMPQNLSTKPDLCATRNPDMEVDENGLDLS MNKQRPDSCCPILTPLEPMSPQQQAVMNNRCFQLGEGDCWDLVPDY TKMKPRRIDEDESKDITPEDLDPFQEALEERRYPPGEVTIPSPKPKYP QCKESKKDLITLSS\CPLADKSIRSMLATSSQELKCTPGEDGSGHI TGNYASHRSLSGCPRAKKSGIRIAQSKEDKEDQEPIRCPVPGCDGQG HITGKYASHRSASGCPLAAKQKDGYNLSQFSWKS VKTEGMSCTP GCDGSGHVSGSFLTHRSLSGCPRATSAMKAKLSGEQMLTIKQRASN GIENDEEIKQLDEEIKELNESNSQMEADMILRTQITTMESNLKTIE EENKVIEQQNESLLHELANLSQSLIHLANIQLPHMDPINEQNFDAY VTTLTEMYTNQDRYQSPENKALLENIKQAVRGIOFRSEQLL
2648	A	1	568	MPQQVQNHGNNRNSLSDHSAIKLELRKIKLTQNHITITWKLNNLLNDY WINNEIKVEINKFFDTNKNKDTTYQNLWDTGFPISKPDGLSQLEQDL QVFDLETKTREVLRDDFSEFRQITISKEAFTSEKNNECNKPEKSFSL DSTIDADQKVLRIQNTDDNDKNDMSFSQNSASGKHEHINLTQDFQSS I
2649	A	157	700	WSLSSRAVMEEIPAQEAAGSPRVQFQSLETQSECLSPPEQFVQDTDM EQGLTGAPPVPQVPALPREGSPGDQAAALLTARYQEFVTFEDVAVHL TREEWGYLDPVQRDLYREVMLENYGNVVS LGILLRLPTTRIHSVNSC PALSHTOASAFSGETLAVLTAGISKRWPKYRLPHRYCSSL
2650	A	1	2674	MEGSGTGKRRGKAAKTSLRIMDARAQLLLRVPHPGPSLTSGALTHIR DHPHGLSPTSGTLMPPRRRGPHSGPCTPSPEVPPRSAGLGAVYSGP GEAVVAPSASVAVMEEIPAQEAAGSPRVQFQSLETQSECLSPPEQFV QDTDMEQGLTGAPPVPQVPALPREGSPGDQAAALLTARYQSSQDVLF QEFVTFEDVAVHLTREEWGYLDPVQRDLYREVMLENYGNVVS LGFPI SKPDGISQLEQDLQVFDLETKTREVLRDPCSDGETREENKLLIPKQK ISEEVHSYKVRVGRGLKHDITQVPETREVIKSEDRLERLQ/ANSKEIS VPGERV*ANNNQQGNL\TSEKNNECHEPEKSFSLDSTIDADQVLR QNTDDNDKYDMSFNQNSASGKHEHLNLTEDFQSSECKESLMDLSHLN KWESIPNTEKSYKCDVCGKIFHQSSALTRHQRHTREKPYKCKEKEK SFSQSSSLSRHKRIHTREKPYKCEASDKSCEASDKSCSPSSGIIQHK KIHTRAKSYKCSSCERVFSRSVHLTQHQKIKHEMPCCKCTVCGSDFCH TSYLLEHQRVHHEEKAYEYDEYGLAYIKQQGIHFREKPYTCSECGKD FRLNSHLIQHQRHTTGEKAHECNECGKAFSQTSLIQHHKMHRKEKS YECNEYEGSFHSSDLILQQEVLTRQAFDCDVWEKNSSQRAHLVQH QSIHTKENS*M**R/CGRYLSNSGFIQHLRVHT\GRNHVC*TACGKAF SHSSAIAQHQIHTREKPSCEDE/CKKRY*C*TLNRLQIYTSEKSY KCIIECGKFFMLLVFSYLSHIWRIHMGIKFHCCNECBKAISQRNYLG* HQIHAMHKDYKC/N*ACMCVRRFSHNPTLIQHQRITY*ENLFGCSKW QIFQ
2651	A	28	352	VRVWVGNAGCRLCFRADGVASGVGCAWDGDRMCLPES\FIRAPVLSV STAGPQSSQSSGRSATPGEGAQGINRTLPSALPSPPMAPPSYLV GTSPAPHSSDDGCWP
2652	A	1198	1889	LKLPIFRDLKVQCGWVELENRLTKMLLSTSVLSCFSSRPNMSEVSCN KRYDYLEWPEYFMAVAFLSAQRSKDPYSQVGACIVNSENKIVGIGYN GKPNGVHN\SLFP*RRTPK\NKLDTKYPYVCHAEINA\ILNKKFRPD VKRPEVCMFALVPPGK*NGGLSLII/LQAGIKRKLIFHVLINYPG*L TGATA\ARLLF*YGPVTF\RKFIPI\KCSKIVIDFDSINSRPSRKLQ
2653	A	159	572	ILVLES LAFKEAWNGGKVRIDSDRILRWAE LTSGRGHSVLIYLTVCV QDQQAMLWDLNEGKHLTYLTDGGDIINALCFSPNRYWLCAATGPSIKI WDLEGKIIIVDELKQEVSVQQQADHPRHLLPVCDAKLCCATRHL
2654	A	45	1111	AIQCHPRRCSDTALAAAMTEQMTLRGTLKGHNQWVTOIAT\PRSSRK IISPPPGEKAIILRKPARGWSQPMNFQRRSRRIHSHLLRMVVIS*DG QF\ALSG\SW\DGTLR\LGDLTNGH/STRGRFCGPDKDVLVSFAFSS DNRQRLSLGSRRLNHQSLWKYPVCANTTVPG*EPTQSWVLCVPLPR PNNQOTPINRSPCGLGQSWSKLWK/LWAKLOS*RTKPTLGHTGLSEP

				R*LFSP\DGSLCASGG\KDGQA\LLWDLQRRPTPTTLEWWGHQSTP LCFSPN\RY\WLCGCHR/HPGIKIWDLEGKDPL*MN*SKKLSVPAK QNQPQCTSLAWSADGQTLFAGYTDNLVRVWQVTIGTR
2655	A	1099	1712	CALGEGNSGHRAFSKDRARLRPGWWSGRAKDELGKPKPLGPS*RRAD RR*GQSACDSSPPSGPGP/TGDGARGRC*AARPGPRARRRRRLGPSGE DRSCQMGTGEEHHGRLWGLSVGPAPKPESAPSSLTCPREETPGRGRP PAPQFQSLARSHGIRGAGDKPTEESLLPQQRHRGGASSVGRGPLGF FPLEEAPLPYPWPPNLQ
2656	A	1	900	MDKFLDITYTLPRLNQEEVESLNRPTTGSEIEAIINSLTTKKSPGPDG FTAKFYQRTNDKNTIISIDVEKAFDKIQQPFMLKTLNKGTDGYL KIIRAIYDKPTPNIILNGQKLEEFPLKTGTRKGCPLSPLLFNIVLEV LARVIRQEKEIKAPAPDATAAEMLMPPKKNRIAIYELLFKEGAMVAKK DVYTPKQPELADKNVPLHVMKAMQSLKSRGYMKEQFAWRHFYWYLT NEGIHHLRDYLHLPPEIVPATLCHSRPETGRPRPKGLEGSEEHLCAA AHLRCGEHLCPALSGM
2657	A	465	1269	TSSSCSCHPPPNACCRGTSSVLSQKAGQAPHLPGPTGKPLRSSGSLR AVRAPGPIGGGQAPWSDPPVLQAPPRPPQAPRGSWRGAGPRQPGRDA APRMLLPFQPRYRTLQQRLLMPKKNRIAIYE\LLFK\EGVMVPKK\ DVPIPKHPELAD\KNAPNLVRVMKPMQVSQGRGGYVKGQF\AW\RHF\ YWYLTG\GSKCQLHTEAARLGQP/DIIPTR*TRAL*PATGHLSMRAR SLEVQRPTAAPSGPSWLSLLQKGMWTGKNEDLHFRRCR
2658	A	1	433	LNLLMSPQGGVLSAHVSGRVVMKSYLSGMPECKFGMNDKIVIEKQK GTADETSKSGKQSIADDDCTFHQCVRLSKFDSERSISFIPDGEFEL MRYRTTKDIILSFRVPLVREVGRTKLEVKKVVIKSNFKPSLLAQSSP KGQ
2659	B	140	480	MVFEFLYKMCVMAAYFGKISEENIKNNFVLIYELLDEILDFGYPON SETGALKTFITQQGIKSQHQTKKEEQSQITSQVTGQIGWRREGIKYRR NELFLDVLEKVNLLMSPQGS*
2660	A	100	1674	SAAMIGGLFIYNHKGVELISRVRDDIGRNAVDAFRVNVIHARQQ\V RSPVTNIARTSFFHVKRANIWLAAVTKQNVNAAMVFEFLYKMSDEMA AYFGKIS\EENI\KNFVHYMELLDEILEFGYPQEFRD/SGALKTF ITPAGHSRSSGFRQKEGSSQFTSQVTGQIGWRREGIKYRRNELFLDV LESVNLLMSPQGGVLSAHVSGP/VWVMKNYLSGMPECKFGMNDKIVI EKQKGTADETKQEPGSNQLLIDDDCTF/HTQCVRLS\KFDERSISF IPDGEFELMRYRTTKDIILPFRVPLVREVGRTKLEVKKVVIKSNFK PSL\LG\QKIEVRIQPP\NT\SGVQVICMKGKAKYK\AGENSFVWKI K\RMAGMKESQIQRRGFELLLTNDKKKWC/RPPFPMNFEVVF\APS GLKVG\YLK\VLNPKLNYSDHDVIKWR*\IGR\SGIYENSACKATR QLAQLPQPPFLQQVQVPLLPQTTHQVSPSLPALLPSPLHQARSLRSG PKQHYKVGPEPALGLPGQGEF
2661	A	1	356	HPNRDGFRAPRECLCLVTRISTMFLSLQAENSSYFVSRELCAHSIRK LQESPGGGPGMRLQVLCVSTTSLRLKIFFGKPPWQQGHGRRKVRGGE GSGSRGWAGAVPCLSTGVSGGMPR
2662	A	303	774	DPKSCGRWRRGRNGELADLQAESHARAAGRGLPGALARVQPEAA AAEVGARCGRGA\AENSIDFVSRELCAHSIRKLQAHVLLIKAVHGYF DPRENYSDKESLSFMIDTMKSTLKERFQFVEVPGNHCVHMSEPQHVA SISSFLQCTHTLPAQL
2663	A	572	902	GALARA*PPQQRWVSCPR/GVP/GAL*REFTMFLSLQAENSIDFISR ELCAHSIRKLQAHVLLIK*VAQAGAQRSQLTGYGSLTWCAPPLTTVK SHGTAPPHPLLHEPSPTSDDLPPSMTLLPGGLPKKDLES
2664	A	1	400	PNPLSTQMGTSGGKGHQLLEYSPPGGGPPGPRKQFHCSPPPPNPAS GKKGH/SPPL/SPHSFSKVFNQFAPPPP\TPTPKQERKS*LKMLF NFSAPVDPTPAQMAPPGFLFVPSPPPLHRLPPQAWGQRHSQQ
2665	A	119	496	TGAVSFQMPEETQTQDQPMEEEEVETFAFQAEIAQLMSLIINTFYSN KEIFLRELISNSSD/GEPMGRGTKVILHLKEDQTEYLEERRIKEIVK KHSQFIGYPITLFVEKERDKEVSDDEAEKEDN

2666	A	1	235	VDSEDLPLNISREMLQOSTILKVIRKNLVKKCLELFTELAEDKBNYK KFYEQFSKNIKLGIHEDSQNRKKLSELYLDV
2667	A	1	2424	RKVREASGKSAARWAGPSLYKAGAGVARQLLQRPVAVPLVLCGHLA KMPEETQTDQPMEEEEVETFAFQAEIAQWISLIINTF*LETKRSFL RELISNSSDALDKIPVLNA*HDPHSIRPLGKEL\HITLLPDQTKIRT \LTIVDTWNLE*PKAD\LINN\LGTIA\RLSGTKAFMEALQAG\ADI SMIG\QFGVGF\YPA\YLVAEKVTVITKHNDDEQYAW\ESSAGG\SF TVRTDTG*TYGSGVGTKVILHLKEDQTEYLEERRIKEIVKKHSQFIGY PITLF\VEKER\DKEVTDDAPQEKEDKEEEK\EKEEKESDKPEIED VGSDEEEKKDGDKKKKKKIKEKYIDQEELNKT\PI\WTRNPDDL N\EEYGEFYKSLTNDWEDHLAVK/HFFQFEGQLEFRALLFVPPTVLP FD\LFENKKKN\NIKLYVRRVFI\MDNCEELIPEYLN\IRGVGDS EDLPL\NISREMLQOKPF*KFSRKNFGPKKCLELFT\ELAEDKENY \KKFY\EQFSKNIKLGIH\EDSQNRKKLSELLRYTS\ASGDEMVS KDFCPR\MKENQKHIIYITGETKDQVANSFAVERLRKHGLEVIYMIE PIDEYCVPL\KEF\EGKTLV\SVTKEGLELPEDEEEK\KQEEKT KFENLCKIMKDIK\EKKVEKVVSNNRLV\TSPCCI\VTSTYGTANM ERIMKAQALRDNSTMGYMAAK\KHLEINPDHSIIIEPLGPKA\EADKN DKSVEGILVIWLKETAPPS\SAFSL\ENPRTHATR\IYRMIKP\GLG \IDEDDPTADDYQWLLVTEENPP\LE\GDDDTSRMEEVD
2668	A	524	797	AVSPSEGEQERGERAGA\CGSRL*SQHFVRPRWADHLRSGV*DQPG QHGETPVSTKNTKISWAW*ASVIPATREAEAGEWLEPRRRRLQ
2669	C	102	323	MTGRSREGKWSTVPSAGCVHVCVNREKATLSHVFPVSLVFLGKPEG LPEVAPSCPGSVGLGPHPPPLVRSRVP
2670	A	146	804	TETRFSDSVAQAGPGTFGLLLLLLALPRLTFSPLLSFPTVGTKGNP LWAPKPCPALAAPSGCRMTWKEQGRKMVNC/PRPVAACMCV*TGKR PPSPMFLPSPRFSSETRRAARGSELFWAGAWSASSSDSPLPRSTA PRRSVCTHCGLTQPTRHACQKGAGVCVRGPRSEAKGGWRGRALLLA ATPCPLSCP NLGLPAKVTPEQGLVRRGGRPAGP
2671	A	1	787	LNSRVEPRVRSRTMETKPVITCLKTLIIYSFVFWITGAILLAVGVW GKLTGLTYISLIAENSTNAPYVLIGTGTIVVFLGFCFATCRGSPW MLKLYAMFLSLVFLAELVAGISGVVLRHEIKDTFLRTYTDAMQT\YN GNDE\RSRAVDHVQRSLE/SCCGVQD\YT\NWSTSPYFLEHGIPPS CMNE\T\DCNPQDLHNLTVAAATK\NQKGCYDLVT*FSWETNMG\II AGSGRLGI\AFSQLIGHAGWACC\LSRFHHGPIQY
2672	A	1	670	YKVLIFT/SPCS/VDQLCSALCSCFRPKDTER/LRG/APEGFSRTDL HLA/VVPVLTALISYHNYLDKTKQREMVYRLEQGLIHRCP/RQCVVA LSICSVEMPDIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLP HLYRNFAAEQYASVFAISLPYTNP SKFNQYIVCLAHVIAKPLHRLQ PSPHLAMRWASGSASSPRWRTSPSLCEAGALPPALALDGIACQ
2673	A	1	154	LSHIPEDKDHQVRKLATQLLVDLAEGCHTHFNSLLDIIIEKVRVAVP GAGC
2674	A	237	410	VGDVDSASSQTAAASPPADFVLQWMDVGLSSEFLLVLVNLVKFN SCYLDEYIAKMVQ
2675	A	1	414	NYLDKTKQREMVYCLEQGLIHRCASQCVVALSICSVEMPDIIKALP VLVVKLTHISATASMAVPLLEFLSSESPPCLRMHPRGSGCVTCAGFS GALSQDSLGNLGVSPSAASRPGRCLCPAAMSALLPGFEGRLLSPL
2676	A	1	6371	MPDSCGLHIPAAHAAPSRDARIAGLSARGHRHTTTPSKLPRRPSAQC RYRKCGSRFRRRPGARGVRLSPRRGGPERGGAAREGFSGASWSTMAK PTSKDSSLKEKFKILLGLGTPRPNPRSAEGKQTEFIIITAEILRELSM ECGLNNRIRMIGQICEVAKTKKFEHAEALWKAADLLQPERPLEA RHAVALALLKAIVQGQGERLGVLRALFFKVIKDYPSNEDLHERLEVF KALTDNGRHITYLEELADFLVQWMDVGLSSEFLLVLVNLVKFN SCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPL FIVTLCRTINVKELCEPCWKLNRNLLGTHLGHSIYNMCHLMEDRAY MEDAPLLRGAVFFVGMALWGAHRLYSLRNSPTSVLPSFYQGRWGDVV

				<p>FVHSLQPNSGQLSVAAGLAHRVPRIQLLAMACPNEVVSYEIVLSITR LIKKYRKELQVVAWDILLNIIERLLQQLQTLDSPELRTIVHDLLTTV EELCDQNEFHGSQERYFELVERCADQRPESLLNLISYRAQS IHPAK DGWIQNLQALMERFFRSESRGAVRIKVLVDVLSFVLLINRQFYEEELI NSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLDIIIE KVMARSLSPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLP ASHATRVYEMLVSHIQLHYKHSYTLPIASSIRLQAFDFLLLRADSL HRLGLPNKDGVRFSFYCVCDYMYAGPRPRPMRLRASEALGLWEPER GSEKKTSGPLSPPTGPPGPAPAGPAVRLGSPYSLFRVLLQCLKQE SDWKVLKLVGLRPLPSLRYKVLIFTSPCSVDQLCSALCSMGLPSPSG YPVTWPLGRGFMPGFHQLSGPKTLERLRGAPEGFSRTDLHLAVVPV LTALISYHNYLDKTKQREMYCYCLEQGLIHRCAQCVALSICSVEMP DIIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLPHLYRNFAAE QYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFI RCRLPFRKDFVP FITK\GLRSNVLLSFDDTPEKDSFRARSTSLNERPKRYGLRGWEYGI FQRDLNSEAVVSSPWGPGAKLGHYQORLLSGVLVSFPSDLQGLATEA SVPPRLRIARPPKQGLNNSPPVKEFKESSAAEAFRCRSISVSEHVVR SRIQTSLTSSASLGSADENSVAQADDLSKNLHLELTETCLDMMARYVF SNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTTVTSVGTGRSLLG LD SGELQSGPSSSSPGVHVROTKAPAKLESQAGQVSRGARDVR SMSGGHGLRVGALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVP VQECTNLAAYVPLLTQGWAEILVRRPTGNTSWLMSLENPLSPFSSDI NNMPLQELSNALMAAERFKEHRDTALYKSLSPAASTAKPPPLPRSN TVASFSSLYQSSCQQLHRSVSWADS AVVMEEGSPGEVPVLVEPPGL EDVEAALGMDRRTDAYSRCGAQLVAVLLRQRAGAVAWCSGWSVALGW RTDRASPPPGQPQSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGG PSVDLSFQPSQPLSKSSSPQLQTLQDILGDPGDKADVRLSPEVKA RSQSGTLDGESAAWSASGEDSRGQPEGPLPSSSPRSPSGLRPRGYTI SDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFVFLQLYHSPFF GDESINKPILLPNESQS FERSVQLDQIPSYDTHKIAVLYVGEQSNS ELAILSNEHGSYRYTEFLTGLGRLLIELKDCQPDKVYLGGLDVCGEDG QFTYCWDDIMQAVFHIAITLMPKDVVDKHRCDKKRHLGNDFVSIVYN DSGEDFKLGTIKAATSVTLFLEVGVWGQCHSTVRGQFNFVHVIVTPL DYEENLVSLQCRKDMEGLVDTSVAKIVSDRNLFPVARQMALHANMAS QVHHSRNPDTIYPSKWIARLRHIKRLRQVRGNMGLPQRGVLAQAQV GRICEEAAYSNPSPPLVHPPSHSKAPAQTPAEP TPGYEVGQRKRLIS SVEDFTEFV</p>
2677	A	1	5405	<p>MAKPTSKDSGLKEFKILLGLGTTPRPNPSAEGKQTEFIITABILRE LSMECGLNNRIRMIGQICEVAKTKKFEHAEALWKAVADLLQPRT LEARHAVLALLKAI VQGQGERLGVLRALFFKVIQG/DYPSNE\DLHE \RLEVFKALTDNGRHITYLEEELADFLQWMDVGLSSEFLVLVN\L VKFNKLVTLDEVQSQRNGFKMICLL\CVRTASS\VDIE\VSLARLLD AVGLANNCL\PAESLPLFIVTLCRTINVKELCEPCWKLMRNLLGTHL GHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVGMALWGAHRLYSLRKS PTSVFP SFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDILL NIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFE LVERCADQRPESLLNLISYRAQS IHPAKDGWIQNLQALMERFFRSE SRGAVRIKVLVDVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQ VRKLATQLLVDLAEGCHTHHFNSLDIIIEKVMARSLSPPELEERDV AAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLH YKHSYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVRFSFYCV CDYMEPERGSEKKTSGPLSPPTGPPGPAPAGPAVRLGSPYSLFR VLLQCLKQESDWKVLKLVGLRPLPSLRYKVLIFTSPCSVDQLCSALC SMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYLDKTKQ REMVYCLEQGLIHRCAQCVALSICSVEMPDI I I KALPVLVVKLTH ISATASMAVPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPS KFNQYIVCLAHHVIAMWFI RCRLPFRKDFVPFITKGLRSNVLLSFDD</p>

				<p>TPEKDSFRARSTSLNERPKSLRIARPPKQGLNNSPPVKEFKESSAAE AFRCRSISVSEHVVRISRIQTSLTSASLGSADENSAQADDSLKNLHL ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLV TVTTSVGTGTRSLGLDSEGLQSGPESSSSPGVHVRQTKEAPAKLES QAGQQVSRGARDVRMSGGHGLRVGALDVPASQFLGSATSPGPRTA PAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVRRPTGNTSW LMSLENPLSPFSSDINNMPLOELSNALMAAERFKEHRDTALYKSLSV PAASTAKPPPLPRSNNTDSAVVMEEGSPGEVPVLVEPPGLEDVEAALG MDRRTDAYSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGRPVS DLSFQPSQPLSKSSSSP\ELQTLQDILG\DPGDKADVGRLSPEVKAR SQSGTLDGESAAWSASGEDSRGQPEGPLPSSSPRSPGLRPRGYTIS DSAPSRRGKRVERDALKSRATASNAEKVPGINPSFVFLQLYHSPFFG DESNKPILLPNESQSFSERSVQLLDQIPSY\DTHKIAVLYVGEQSNS E\LAILSNEHGSYRYTEFLTGLGRL\IELK\DCQDPKV\YLG\GLGR VVGEDGPVSPYLLGHD*HSWQAVFHIAITLMPKDVDKHRCDDK\RHL GNDFVSIYVNDSEDFKLGITKGQFNFV\HVIRHPAGITECNLGVWP QCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRNP TDIYPSKWIARLRHILKRLRQICEEAAYSNPSLPLVHPPSHSKAPAQ TPAEPTPGYEVGQRKRLISSVEDFTEFV</p>
2678	A	1	5469	<p>GASWSTMAKPTSKDSGLKEFKILLGLGTTPRPNPSRAEGKQTEFIIT AEILRELSMECGLNNRIRMIGQICEVAKTKKFEEHAVEALWKAVADL LQPERTLEARHAVLALLKAI VQGQGERLGLVRLALFFKVIKDYP SNED LHERLEVFKALTDNGRHITYLEEELADFLQWMDVGLSSEFLVLVN LVKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYN CLPAESLPLFIVTLCRTINVKELCEPCWKLNRNLLGTHLGHSAIYNM CHLMEDRAYMEDAPLLRGAVFFVGMALWGAHRLYSLRNSVTFPSF YQAMACPNVSVSYEIVLSITRLIKKYRKELQVVAWDILLNIIERLLO QLQTLDSPELRTIVHDLITVEELCDQNEFHGSQERYFELVERCADQ RPESLLNLISYRAQSIHPAKDGIQNLQALMERFFRSESRGAVRIK VLDVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQVRKLATQL LVDLAEGCHTHFNSLLDIEKVMARSLSPPELEERDVAAYSASLE DVKTAVLGGLLVILQTKLYTLPASHATRVYEMLVSHIQHYKHSYTL IASSIRLQAFDFLFLRADSLHRLGLPNKDGVRVFPSPVCTDYPEPE RGSEKKTSGPLSPPTGPPGAPAGPAVRLGSVPYSLFRVLLQCLKQ ESDWKVLKLVGLRPESLRYKVLIFTSPCSVDQLCSALCSMLSGPKT LERLRGAPEGFSRTDLHLAVVPVLTALISYHNYLDKTKQREMYCLE QGLIHRCARQCVALSICSVEMPDIIKALPVLVVKLTHISATASMA VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVC LAHHVIAMWFIRCLRPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFR ARSTSLNERPKSLRIARPPKQGLNNSPPVKEFKESSAAEAFRCRSIS VSEHVVRISRIQTSLTSASLGSADENSAQADDSLKNLHLTETCLD MMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGT GTRSLGLDSEGLQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSR GARDVRMSGGHGLRVGALDVPASQFLGSATSPGPRTAPAAKPEKA SAGTRVPVQEKTNLAAYVPLLTQGWAEILVRRPTGNTSWLMSLENPL SPFSSDINNMPLOELSNALMAAERFKEHRDTALYKSLSVPAASTAKP PPLPRSNNTVASFSSLYQSSCQQLHRSVSWADS AVVMEEGSPGEVPV LVEPPGLEDVEAALGMDRRTDAYSRSSSVSSQEEKSLHAEELVGRGI PIERVVSSEGGRPVLDLSFQPSQPLSKSSSPPELQTLQDILGDPGDK ADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQPEGPLPSSSPR SPSGLRPRGYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPS FVFLQLYHSPFFGDESNKPILLPNESQSFSERSVQLLDQIPSYDTHKI AVLYVGEQSNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQDPKV YLGGLDVCGEDGQFTYCWDDIMQAVFHIAITLMP\TKDVKHRCDDK RHLGNDLWSIVYN\NSGEDF\KLG TNQGPVNLWST*SSTPL\DYEC\ NLVPL\QCRK\DMEGLVENQAWPKNRV*PATLPFVA\ROMP\LANM ASQVHH*PLQTPTDIYP\SKWIARLRPI\KRLRQRII/CEEALLPT</p>

				PALPFV\HPPSHSKAPAQTPAEPTPGYEVGQORNAL\ISSVEDFTEFV
2679	A	35	239	SPSSQPP\VPVIPH*PVCKQPTSCRSPRKRVLNLVGGGEGAASY
2680	A	118	359	AVCKQPTSCRSPCCPSPGQASPC*AFRRLEI/CRAGF*A*ALGPGK SQGQNCPRSSPPSP/CPLLKYQONCG*KCPQRLH
2681	A	229	455	TMQGSLNKPLPSP*PRAATKIPNP/SPSPPPQAPQTTPHSILSTKA MTPVTIQALFSRIVRYLCDRRDSLTSQSF
2682	A	1	373	EKFRHNIAYFPQIVSVAARMLKDPRSYPLGALTSLYPQNTTDLDDR GLQVHVVDACSSRSQVDRVALARMRQSGAFLSTSEGLILQLVGDA VHPQFKEIQKLIKEPAPDSGLLGLFQGQNS
2683	A	72	1031	GCPRILILLRGRSGLEPGTFRKMAAARPSLGRVLP\DSSVLFLCDMQE KFRHNIAYFPQIVSVG\SRMLKVARLLEVPVMLTEQ\YPQGLGPTVP EAGD*GPSAAWQKTCFSM/CCLPLQQLDSRPLRSVLLCGIEAQAC ILDPRSYPGLALTSLYPQNTT\WDLDRGLQVHVVDACSSRSQVDR LVALARMRQSGAFLSTSEGLILKLVGDAVHP/QFKEI\QKLIKEPAP DSGLLGLFQGQNSLPLNSNPALREDHPPVHPPGQWEARFPPSLGFP RVGAIPPGSCRPLVGGGQWCCLPIGQLPEMQMRLLETGWEMG
2684	B	1	792	MGVLPSPYFWDDEEAQEGICLSLKQRMVGRAGHSGHFLADATSRAL ARRREEWGKQEERGKESSESTNTTSRMKTPKEDVRPGMTAFEPEAL GNLVEGRSIDSILKTVSNSFSLGACCLLSFHVLLDGTAGRGS DRDE QNAHSVPEQQARAHHPESHILMGDESACIAYIRTRSTWTLAASH APPSRRDPCLAPPGWQADRLHRS GAPSVLPHSQD TDTEMNQERYM NASISFPKPPHSTSQQVLFIQPGEEREI*
2685	C	10	126	MTAFRGGTPLPDLRPSLYPADPGGCAALPPEGVVRDLK
2686	A	2	372	HCIQQILEAVLHCHQ/MGVVHRDLK\PGKKNQTLGRAVLLSFT*RR LQSLGLHQLHSLAPSAGTSWISLLILMVS VAGFAGT/PGYLSPEVLR KDPYKGP/VDLWACGG*RFSGPLPGVILYILLV
2687	A	1	1593	MATITCTRFTEEYQLFEELGKGAFSVVRRCKVVLQAGQEYAAKIINTK KLSARDHQLEREARICRLKHPNIVRLHDSISEEGHHYLI FDLVTG GELFEDIVAREYYSEADASHCIQQILEAVLHCHQMGMVVRDLKPENL LLASKLKGAAVKLADFGLAIEVEGEQQAWFGFAGTPGYLSPEVLRKD PYGKPVLDWACGVILYILLVGYPFWDEDQHRLYQQIKAGAYDFPSP EWDTVTPEAKDLINKMLTINPSKRITAAEALKHPWISHRSTVASC MH RQETVDCLKKFNARRKLKGAILTMTLATRNFGSGKSGGNKKS DGVKK RKSSSSVQLMESSESTNTTIEDEDTKVRKQEI IKVTEQLIEAISNGG FESYTKMCDPGMTAFEPEALGNLVEGLDFHRFYFENLWSRNSKPVHT TILNPHIHLMGDESACIAYIRITQYLDAGGIPRTAQSEETR VWHRRD GKWQIVHFHRS GAPSVLPHSQD TDTEMNQERYMNASISFPKPPHSTS QQVLFIQPGEEREI
2688	A	3	1607	IPGSTISCSSVKPVLCLHSAARACKWSLGSAGAEQQRLSPGPPVPSLT CLPSARMATITCTRFTEEYQLFEELGKGAFSVVRRCKVVLQAGQEYAA KIINTKKLSARDHQLEREARI\CRLKHPNIVRLHDSISEEGHHYL IFDLVTGGELVEDIVAREYYSEADASHCIQHILEAVLHCHQMGMVVR DLKPENLLASKLKGAAVKLADFGLAIEVEGEQQACVGFAGTPGYLS PEVLRKDPYGKPVLDWACGVILYILLVGYPFWDEDQHRLYQQIKAG AYDFPSPEWDTVTPEAKDLINKMLTINPSKRITAAEALKHPWISHRS TVASC MHRQEARGPA*KKFN\ARRK\LKGAILST\MLA\TRNFSGGK SGGNKKS DGVKESSESANTTIEDEATKVRNQEI IKVTEQLIEAISNG DFESYTKMCDPGMTAFEPEALGNLVEGLDFHRFYFENLWYRNSKPVH TTILNPHIHLMGDESACIAYIRIT\QYLDAGGIPRTAQSEETR VWHR RDGKWQIVHFHRS GAPSVLP
2689	C	6	167	MXXX XXISKH*
2690	A	310	593	LQVISEYLFWRINFFLFLF*TVSLSVAQARVQWRDPG\SLQPLLP GF KRFLASASRVARVTGAHHLHAQL/ILYF*VETGFHHVQAGLELLTS GK
2691	A	58	481	LQVISEYLFWRINFFLFLF*TVSLSVAQARVQWRDPGSLQPLPPG\ S

				RDS*ASASRVARVTGAHHLHAQLFCIFK*ROGFHPGWSGWSSNLPDL QANPAASALPKVPGITGTSPHPPWSINFKNIKIWNQETSILVFFRL
2692	A	1	398	DSIDARVFDLIRSINDPEHPLTLEELNVVEQVRVQVSDPESTVAVA FTPTIPHCSMATLIGLSIKVKLLRSLPQRFKMDVHITPGTHASEHAV NKQLAERPLTPQPAYWYGPSSCQGCYRCFLESITMRN
2693	A	3	267	AMVGGGGVGGGLENANPLIYQSRGERPVTAGEEDEQVPDSIDAREI FDLIRS*AWPLTPQPAYWYGPSSCQGCYRCFLESITMRN
2694	A	1	942	MVIYPLDKHFTSPCRSKLWGRRTPGPMCPLRPGSGLYVSARYWLARP SAAVVPSQRLLLQRPSCSRVRAARAASATSLAPQAENPQRGVSLARL RRHATPPSRSPVRLERKRTPARISGGGSAMVGGGGVGGGLENAN PLIYQSRGERPVTAGEEDEQVPDSIDAREIFDIRRCWARAEELNVVE QVRVQVSHFRGERVVPESQKGFCAAGAGVLYAHEHRRVSDPESTVAV AFTPTIPHCSMATLIGLSIKVKLLRSLPQRFKMDVHITPGTHASEHA VNKQLADKERVAAALENTHLLEVVNQCLSARS
2695	A	3	707	AMVGGGGVGGGLENANPLIYQSRGERPVTAGEEDEQVPDSIDAREI FDIRRCWARAGSGGLRWGEQ*YRAAGGAASQGVPGRGF*VGKGAES LFLHFPQ\LIRFLNDP\EHSLTLEELNVVEQVRVQVSDPESTVAVAF TPTIPHCSMATLIGLSIKVKLLRSLPQRFKMDVHITPGTHASEHAGK CGLVVRVLARAPPKQSEASPLHRSWARLEMGNCVSEIARDSSVWVI A
2696	A	2	604	ARSHRISGGGSAMVGGGGVGGGLENANPLIYQRFGE\RPVTAGEED EQVPDSIDAREVF\DLIRSHQMTPEHP\LTLEELNVV\EQVR\VQVS DP\ESTVAVGFPPKPTHSGTCRHGPPLIGLS\IKVK\LLRSLPSAFSR WDVAHLLPGDPLPQEHAVEQATLQIKEAGWATALGRTPHLLVVN\Q CLSSPAPGTWAFVPLSLA
2697	A	79	690	KVSKAIAGCLRNYGVCLAHRLTWAIPPEPKMNPVVEPLSWMLGTWLS DPPGAG\TYPTLQPFQYL\EEVHIS\HVGQAMLNFSFNSFHPDTRKS MH\RECGFHFASKPDT\NKVGLCQAPQNTGLGWNWKEGEVKRARS LCIRIPLPFARISFRQGKPHVEQIT/RGKFRL\NSEGKL*ADGSPMGNP RHSPMT\QHHDITYQEGEHRKP
2698	A	1	405	RYHLLAHTTLTAAVQDGFRTDHLTLASHEENPAWLPLYGVSVCRLA AQPLCMTQPTASGTLRVQETRVVRAGELDQALGRPFTLSISNQYGDDE VTHTLQTESREALQSWMEALWQLFFDMSQWKQCCDEIMKIE
2699	A	1	1437	MFSRNHRSRVTVARGSALEMEFKRGRFRLSLFSDLPEDTELQRLDH EIRMREGACKLLAACSQREQALEATKSLVNSRLSYMGELQRRKE AQVLGKTSRRPSDSGPPAERSPCRGVRCISDLRIPLMWKDTYFKNK GDLHRWAVFLLQLGHEIQDTEMILVDRTLTDISFQSNVLFAGAGPD FELRLELYGACVEEGALTGGPKRLATKLSSSLGRSSGRRVRASLDS AGGSGSSPILLPTPVVGGPRYHLLAHTTLTAAVQDGFRTDHLTLAS HENVESFVQQAGEMQNWAVHGVKGTNLFCYRQPEDADTGEEPLLT IAVNKVMGPLVETRVVRAGELDQALGRPFTLSISNQYGDDEVHTLQ ESREALQSWMEALWQLFFDMSQWKQCCDEIMKIETPAPRKPPQALAK QGSLYHEMVLSEPVAPGGPAIPTDQRPLQQRPTSHLAPVTSVREKGA GIGSAQKRK
2700	A	78	399	FIHRPSDSGPPAERSPCRGVRCISGKKHSYPSCWYPLPKHTASCPIS TSILTPLPL\DLRIPLMWKDTYFKNKGDHLRWAVFLLQLGHEIQD TEMIIVDRTLTYCI
2701	A	2	368	VVAGALGCSWLIGAGFLSGREGACRRERGQQQTGTPLPSSPLLLPS LEKRAGRTAATKARLDTLCLEPPLQLAFPPGDPTYP\TSLSFSSLP LPA/WPPEQQWGEENLSQQPEGV*QELQRDKGSFCPLPKSWPPL*RG GGARLQLARNRGWFPVWKGRLQKGAGTAADRHTPAFLSPSPFFSGK ASWENSCHQSETGHSVPRAPSAAGLSSWGPLSSLRFLPLCLGSRQ APGAAVGRGKFVTAARGGLTGVAEG
2702	A	1	588	VRAGELDQALGRPFTLSISNQYGDDEVHTLQTESREALQSWMEALW QLFFDMSKREGGWVEPLGRTGVCHFY*RPLFQDYVEGNVAGERAAWL SLLISALLPGQWKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIE

				PLDDIAAETDILTQREGARLETPPPWLAMFTDQPALPNPCSPASVAP APDWITHPL
2703	A	46	1825	AAAGSETGLGSCLEGKGAEGSGDSSRQAHPCLPLSLSSLLWKSEDT ELQRKLDHEIR\LRKGPC\KLLANLLPSEKQALEA\TKSLLVC\NSR IL\SYMGE\LQR\RKÉA\QLLGKTSRRPSDSGPPAER\SPCRGRVCI SDLRIPLMWKDEYFKNKGDLHR\WAVF\LLLQLG\EHI\QDTEMIL VD\RTLTDISF\QSNVLFABAGPDF*TCGLELYGACVEEEGALTGGP KRLATKL\SSSLGRSSGRRVRASLNSAGGSR/GAIPFMLPTPEVGGP RYHLLAHTTTLTAAVQDGFRTDHLTLASHEENPAWLPLYGSVCCRLA AQPLCMTQPTASGTLRVQQAGEMQNWAVHGVKGTNLFYRQPEDA DTGEEPLLTIAVNKVMGPLVETRVRAGELDQALGRPFTLSISNQYGD DEVTHTLQTESRGSTCRAW\MEAL\WQLFFDMSQWKQCCDEIMKIET PA\PRKPPQAL\AKQGS\YHEM\ALFEPLDDI\AAVTDILT\QREG ARLETPPPW\LAMFTDQPALPNPCSPASVAPAPDWITHPLPWGRPTF SL\DAVPPDH\SPRASLRFAPLPTFSESPTRTGRLLOAKGQPTWLQS PV
2704	A	1	370	LVTRRAVLACLRLVQREAAEVSEHAVMLAKDSREELTPDANIREVG LEGALILLDKETDERLCHDIKETLNYMLTSMAVEKLSLWLKCKDV LAASAGKYWTLSVKIILKLPFETLHKIVYP
2705	A	1	363	TMESITACILHALQALLDVPWPRSKIGSDQDLGILLNLVLRVILTRE SPSIQLASLEVVRQIICAAQEHVKEKRRSAEGSISILPTILYLTIGV LRETAVKLPGGQLSSTVAASLQALKGI
2706	A	158	301	IIMTLAEDLLCSAAQNSRLSAQRTQAGWLLISALMTLGNLS*KVYIP
2707	A	182	396	CCCNVFNCSLSLQTWALHSLSLIIDSAGPLYVHVHVEPTLSLIIIVV VNVPPTHAEVHQSLGRCLNALITT
2708	A	1	436	SSYIPSFISIQLFPTHTFTL*HPVSWKNCRK*TRENK/ITAELEI FQEGIKVLETLVTVAEEHHRAQLVACLLPILISFLLDENSLGSATSI MRNLHDFALQNLMOIGPQYSSVFKSLVASSPALKARLEAAIKGNQES VKVKI
2709	A	112	501	PKFNEKNCDQLGGLLQGMELAHSLLLNEEAYNQLGEVQKAEIFEWL RYLEKLLLATSRNDVREKQKTLVEQLLSLNNSSPGPPTRKLLAKNLA ILYSIGDTFSVHEAIDKCNDLIRSKDDSPSYLPTKL
2710	A	1298	8400	FPTNTTFPLLKVCYRFHYAEPVPGHCRAVGVRREGADWGTGSADKQR GPFLLDYGKVL\PCAQONDVREKQKTLVEQLLSLNNSSPGPPTRK LLAKNLAILYSIGDTFSVHEAIDKCNDLIRSKDDSPSYLPTKLAADV CLGSLYKILGRILGNFTDTVGNILKAMKSAESQGRYBIMLSLQNIL NGLGAAAAPCHRDVYKAARSCLTDRSMAVRCAAACLLELQNEAIFM WSTDLDVSATLCFKSFEGSNYDVRISVSKLLGIIAKAVISKHPGTA SRQSIIRVSLVEVLELLGTGFLRGSSGFLRASGDMKGTSSVSRDVR VGVTQAYVVFVSTLGGAWLEKNFAAFFSHILSLASPSHPKATQTQID AVCCRRCVSFIILRTTIGGLLGEKAQLAAVKDICAIAWKLKKVMDAVM SDGNLETRLGSTDVAASQHMLVLCALQELGNLIHNLGTTAAPLLQDSS TGLLDSILSVILHPSISVRLAAAWCLHCIAVALPSYLTPLLDRCLEL LTGHKSSPEAVTGFSFAVAALLGAVKHCPGIPHGKGIIMTLAEDL LCSAAQNSRLSAQRTQAGWLLISALMTLASPKDLETEKSRGDSFTWQ VTLEGRAGALCAIKSFVSHCGDLLTEEVTRQLLPPLCAVDLLTQEL AADLTAPDIQVAASTFLLPPLCHQDDLLILSPFLOQETHRHFIEEQLL LGNGVACGSLEYDPYSIYEKDVEGDSVPKPLPPALSVISSASKLFGV VCAHVGETQRLILEQLLDSIKHTKGARQQVQLHVSVSSVFLKYV AGSKGCLGPEEMKRFALTLVMGALESNPPLRCAAESWARLAQVVD DGAFTAGLAQVSFDKLSARDVVTRTGHSIALGSLHRYLGGISSSQH LNSCIGILYTLAQDSTSPDVQTWALHSLSLIIDSAGPLYVHVHVEPTL SLIIMLLNVPPTHAEVHQSLGRCLNALITTLGPELOGNSTSISTR TSCLLGCAVMQDNPDCLVQAQAI SCLQ\QLHMFAPRHVNLSSVSL CVNPCSPYM*LRRRAVLACLRLVQVQRAAEVSEHAVMLAKDSREELTP VNWYQEWGTAIKIPKNLEAAELGNRQWLEWFGGLRRRQEDVAKSGT

				SRDLLNGFDQONADNNVDNEAQAVPAMAKRDQGTQAIASESASPKPW QLLHGVGPAGAQNSTRTEVWELPPRFLRMHGNAQMSRQKSAAGVKPSW RTSARAVQRENEGSEPPHRVPTEALPSGASETPSQKNKKRRGSLDPR VVDPLTAYTVRLKKPHILNASCENANIREVGLLEGALLILLDKETDER LCHDIKETLNYMLTSMAVEKLSLWLKCKDVLASADFTAVTCVDTM QEEEGDKGDDASVLTTRDEKSHPFNTNPRWATRVFAAECVCRIINQC ENANSAHFDIALAQEMKKRDSRNDFLVLHLADLIRMAFMAATDHSDQ LRLSGLEMLLVVIRRFATVPEPEFPGHVILEQYQANVARREFQTSVV SRDTDTAAKFIGAGSATVGVADSGAGIGAVFGSLIIVYARKLSLKQK LLFYAILGFALSEAMGLFCLMISFFILFAIAWIASGVVSDNLDRRV HQLLVSSLTQKIQAGKEALSHLYNESASTMEILAVLKAWAEVYIIAVQ RHKNHRQPLKTTTTCLEDGIRNGSCSSDGLLDLVYADLGTLSRLWLAA LQDFALLTLPSEFASQLPAEGGAFYTAETSENAKLHYNSWALILHA TALWLTSTGFFVADPDEGASNLSRPVTPSMCQSSSGATIKSPEDV YTDRFHLILGISVEFLCSLRS DATMESITACLHALQALLDVPWPRSK IGSDQDLGIELLNVLHRVILTRESPSIQLASLEVVRQIICAAQEHVK EKRRSAEVDGAAKETLPEFGEKDTGGLVPGKSLVAFATLELCVCI LVRQLPELNPCLTGPVGKATKPQILLEDGSRVLSAALVILSELPAV CSPEGSISILPTILYLTIGVLRETAVKLPGGQLSSTVAASLQALKGI LSSPMARAEKSRTAWTDLLRSALTITLDCWDPEHFSLVDETHQELDE VSLLTAITVFILSTSPEVTTIPCLQKRCIDKFKATLEIKDPVVQIKT YQLLHSIFQYPNPAVSYPYIYSLASCIMEKLQEI DKKRPENTAELEI FQEGIKVLETLVTVAEEHHLVSSTRNTSSRS LFKHKSSLKIDFLNYG NAFVSVVNRSILSSAISHARVKSSHSTRSSLVTCKAKEVSSCNTGKQ SFRPKKNLPRTLPTPQKQNTPKGMSDDFVLNSLKGFKLLEAFSRFS DTTGGKEGRRFYSRHAVYALGECGLSHREGVWLYAKKLEASCLLTC DSHGMLQDLIPNISQEEIS
2711	A	2107	2424	TTRYLKKTSTTGQRKKRGRNGSFPTENLVPSGTVTGSQQLGPPFR* N/HTEECWGPPTADGRAGKGPQQPQGRAQRIYRWDPDGTGTTWHHRP CGSRGTDQPETK
2712	A	1	368	FRREGRPAGAGAFADSGGAPSSCCGPTVRPVAATAENVLHVRGAFO EFPVCQAGVQWRNHGSLRPPPP\GSSHPPISAS*VVETGTMCHHVWL IF**NFFVETGSPYVAQALILLMLGIKTL
2713	A	1	278	LWSRSHPFCCSRGPLAMAGILFEDIFDVKDIDPEGKKFDRGDKFRLV IASTLYEDGTLDGGEYNPTDDRPSRADQFEYVMYGVYRIEGRG
2714	A	188	406	HNSRKMPLLFLRLRLRAEWQCSRITGWGLLFQLCVTCPMGGLLMRL QGDANNLHGFEVDSRVYLLMKKLAF
2715	A	123	914	PRAGGCGSGRVTACLACATLVWPPRFQEVLLVLSGLVHARGCTYS QLWSRSHPFCCSRGPLAMAGILFEDIFDVEGY*PEGQEVWTECSRLH CESESFRMDLILDVNIQIYPVDLGDKFR\LVIASTLYEDGTLDGGEY NPTDDRPSRADQFEYVMYGK\YVRIEGD\ETSTEAAATRL\SAYVS\Y GGLL\MRLQGDA\NNL\HGFEVGLPRVYLLMKKLSLLNLALNQPSLP SHSGRGHCSSLSGQPLFAHLRLKGWLTVHRWRHL
2716	A	1	2415	MGFHHVQGADLKLLTSDNAYDPDVNAKQIWI DKTVIN DHI CLTFTDN NGMTSDKLHKMLSFGFSDKVTMNGHVPVGLYNGFKSGSMRLGKDA IVFTKNGESMSMINLAESKASLAAILEHSLFSTEQKLLAELDAIIGK KGTRIIWNLSYKNATEFDFEKDYDIRIPEDLDEITGKKGYKKQE RMDQIAPESDYSLSRKTVRITFGFNCRNKDHYGIMMYHRNRLIKAYE KVG CQLRANNMGVGVVGIIECNFLKPTHNKQDFDYTNEYRLTITAGL EKLNDYWNEMKVKNTEYPLNLPVEDIQKRPDQTVWQCDACLKWRKL PDGMDQLPEKWYCSNNPDQFRNCEVPEEPEDEDLVHPTYEKTYKKT GIISEYPPIEAYREGVTEEVIEHFEYQFTCCLKRRLLSTRSSILNAKNR RLSSQFENS VYKGDDDDDEDVILEENSTPKPAVDHIDMKSEQSHVE QGGVQVEFGDSEPCGTGSTSTSSSRCDQGNATATQTEVPSLVVKK EETVEDEIDVRNDAVILPSCV EAEAKIHETQETTDKSDADGCLQOE LRNQLLLVT EKENYKRQCHMFTDQIKVLQQRILEMNDKYVKKETCH

				QSTETDAVFLLESINGKSESPDHMVSQYQQALEEIERLKKQCSALQH VKAECSCSNNEKSEMDEMAVQLDDVFRQLDKCSIERDQYKSEVEL LEMEKSQIRSQCEELKTEVEQLKSTNQQTATDVSTSSNIEESVNHMD GESLKLRLSLRVNVGQLLAMIVPDLDLQQVNYDVVDVDEILGQVVEQM SEISST
2717	A	2	965	NCEVPEEPEDEDLVHPTYEKTYKKTLKRLSTRSSILNAKNRRLSSQ FENSVMKGGDDDEDVILEENSTPKPAVDHIDMKSEQSHVEQGGVQ VEFVGDSGPCGTGSTSTSSSRCDQGNTAATQTEVPSLVVKEETVE DEIDVRNDAVILPSCVEAEAKIHETQETTDKSADDAGCQLQELRNQL LLVTEEEKENYKRQCHMFTDQIKVLQQRILEMNDKYVKKETCHQSTET DAVFLLESINGKSESPDHMVSQYQQALEEIERLKKQCSALQHVKAEC SQCSNNEKSEMDEMAVQLDDVFRQLDKCSIERDQYKSE
2718	A	276	482	GDDFSLQQINAELLFRPTALSTPSFSSPKESVPRRHLSEGTNSYATR LLNNHQVPPQSGTWGANRVSG
2719	A	329	3354	PVRQFIFPKLPIRHCLEAEVGGRGQTCAPPRKWAVPIGLHSRSATSQ SGCGGGRSWLCCSSLKMAAQPPRGIRLSALCPKFLHTNSTSHTWGHVS QLLELIG*CLWIPDVNAKQIWGLTKQWI\NDHICLTFTDNGNGMTSD KLHKMLSFGFSDKVTMNGHVPVGLYGNFGKSGSM\RLGKDAIVFTKN GESMSVGLLSQTYL\EVIKAEHVVPVIVAFNKHQRMINLAESKASLA AILEHSLFSTEQKLLAELDAIIGKKGTRIIWNLSYKNATEFDFEK DKYDIRIPEDLDEITGKKGYKKQERMDQIAPESDYSLAYCSILYLK PRMQIILRGQVKVTQLVSKSLAYIERDVYRPKFLSKTVRITFGFNCR NKDHYGIMMYHRNRLIKAYEKVGCQLRANMVGQVVGIIIECNFLKPT HNKQDFDYTNERYLTITALGEKLDYWNEMKVKNTEYPLNLPVEDI QKRPDQTVWQCDACLKWRKLPDGMQDQPEKWYCSNNP\DPQFRNCEV PEEPEDEDLVHPTYEKTYKKTNKEKFRIRQPEMIPRINAELLFRPT\ ALSTPS\FSSPKESVSKR/RHLSEGTNSYATRLNNHQVPPQSEPE NSLKRRLSTRSSILNAKNRRL\SSQF\ENSVYKG\DDDDDEDVILEE NSTPKPAVDHIDMKSEQSHVEQGGVQVEFVGDSGPCGTGSTSTSS SRCDQGNTAATQTEVPSLVVKEETVEDEIDVRNDAVILPSCVEAEA KIHETQETTDKSADDAGCQLQELRNQLLLVTEEEKENYKRQCHMFTDQ IKVLQQRILEMNDKYVKKETCHQSTETDAVFLLESINGKSESPDHMV SQYQQALEEIERLKKQCSALQHVKAECSCSNNEKSEMDEMAVQLD DVFRQLDKCSIERDQ\YKSEVEL\LEMEKSQIRSQCEGLKTEV\DL KSTNQQTAPDVSTSSNIEESVNHMDGERLKLRSFRVNVGNLLAMIVP DLDLQQVNYDVVDVDEILGQVVEQMSEISST
2720	A	1135	1476	HGVSLLLPRLECTGH/VISAHCDPRLPGFE\RFSCSLP\SSW\DY\ RHAPTHAQAKCIFKWRRGFSHVQAG*HFYFPSQVLGTNMEFFLT GLILHGLFQEDSNAPYSFKWGLR
2721	A	670	1253	ACYALNLFPKHTDIFYFFFIYFFCRDRGPRYITQAGLKVFDFK*ILP PWPYQSVGIIISVSH\PPGPH*CILNAINKNYRYRN*LLY/IQYPMFL GVFLRQGFVAVT/SAAVQWYDHGSMQPLPGLRWFSHLSLLSGWEHRR TPPRLG*FCIFSRESFVMLPRLVLNSWGSNDTPALASQSVVITGMSH HAPAFPMFL
2722	A	25	479	RAGQEFQAHKAILAARSPVFSAMFEHEMEESKKNRVEINDVEPEVFK EMMCFIYTGKAPNLDMADDLLAAADKYALERLKMVEDALCSNLSV ENAAEILILADLHSDQLKTQAVDFINYLGAGPRISQRWYFGDTCLH LTEQNKSSGA
2723	A	354	426	LWKSRLTFKLAMSRVPSPPPPAE
2724	A	201	1432	LWKSRLTFKLAMSRVPSPPPPAEMSSGP\VAESWCYTQIKVVKF\SY MWD/TINNFSFCREEMG\EV\IKSSTFSSGANDKLKWC\LRVNPKG\ LDEESKDYLVTFTCYLVSC\PKSEVRANFKFSILNAKGEETKAMESQ R\AYRFVQKDWGFKKFIIRDFFLDEANGL\LP\DDKLTLCFCEVSVV QDSVNISGQNTMNMVQVPECRLADELRGLWENS\RFTDCCCLVAGQE FOAHKAILAARSPVFSAMFEHEMEESKKN\RV\EINDVEPEVFKEM MCFIYTGKAPNLTKMA\NDLLAAADKYALERLKMVEDALCSNPV/S

				VENAABILILADLHSADQLKTQAVDFINYHASDVL/EKTS GWKS\MV VSTPPNLVA*/AQYRLSGFQAQCPFFWGPPTQNALKAIKDPALLR IPF
2725	C	95	310	MREYNLVVLGSGGVGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVD CQQCMLEILDTAGTLSPLRTTYRT*
2726	A	1	1101	MREYKLVVLGSGGVGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVD CQQCMLEILDTAGTEQFTAMRDLYMKNQGQFALVYSITAQSTFNDLQ DLREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQGNLARQWCNC AFLESSAKSKINVNEGPIIRPLVGETKGTGHTSLAAVILALSITNV SCTGWGVQRSHQDQGNKHAASSVWKVGFGIVRLGTGTCLSSLERGY MCMEKEMFDPYTPSRVLKPRVKLGPDVVAKEDKEMNPARKTSGKGS KKGKNVEDRTVQFVQGIFVEKYDPTIEDSYRKIVLHTVTIIIPFKWR SPMHWTAQPSPTGAWSLMNLVGGSHGGKDKDSKEPH
2727	A	53	772	IPRSGITGSEGDYPVYKSMCLTAPSMALSRSSVFKQITSLEKYKLVV LGS*GVGKSALTVQFVHGIFVEKYDP\SIEDSYRKQVEVDCQQCMLE IL\DTAGTEQFTAMRDLYMKNQGQFALSIFYLQLQSTF\NGLYRDLE GNQILRV*GTRE/VMFPMILVGNKCDLEDERVVGKEQGNLARQWCT LALLESSA/RRSEIQVNEVL\YDPVRQINREY/TPVEKKK*KNMS TLLGPIVRRQL
2728	A	377	615	VPAQCSF*DTASCLLVKRMRLDAVAHAYNPSTLGGRGGWI/TRGQE FKTSLANMVKPVSTKNKKISRVVWHNRNPSYSGG
2729	B	1	1224	MPTVGKAQARRRTRDTLLDITQVLIDQSPRKDTGLAQQTGVIVPSK GIVKYWRAQLKGDMMKYASPAFELFYFSVRAQSTDGIVTLLDPTTRED CDISSAPNPEVRTQQAQEVAGVGLLAVKVPDEEGVLGGAPGPQKRS RVCGEPTLQRRSGPLPVARPGSRCPPPTSVSSPVPEDEYGRVTVMIR LDNPGISGRTIENNPPELEKQLPGEPSSENSPYLGPPQVLFLLRDPRE DVMILLNQTPTTAEKQAVLQAABIFRNEQQISYNTSKGKKGDRECEE IAETPFQIGSEAVPLDNPWNSSSSAGEWKRRHFLICILEGLERTKA KFLNCSKLSMVDQKPDENPAAFMERLREALIEQTSLSPPDSVEKQLIL KDKFVTQSASNIRRLQKQAIGPISTLKNLLK*
2730	A	877	1536	TNFLFALSPSCLAGLLPPKFKQFSCSLSSWDYRNFIW*RWGFT MLARLVNS*PQ/CDPHTSASHSAGITGMSHCAS*TLNFFSYELFF SFTSALS*KDHCKGGHMGQFT*MHQ*L*EKPP*LLF/ETESRVA /QAGVQWRNLGSLQPPSPGFKRFSCLSLPSSWDYLRTPPRANCCCI FSRDGVSPCWPGWSQSLDLVICPPWPPKVLGLQA
2731	A	3	643	RLEEDLGRRQSLAPVGVVETVYFTVVLWTITMGIQG\GSVLFGLLL VLAVLC\HS\GH*PCQC/YNGFLPQTADCQKQPFNCSSGFWMRVFI TKLGYQVYNK\CWKFEHCNFNDNRHNP*RMGLTILLCKKG/LRCNF TE\RENGGTSL\SEKTVLLLGELHFWAAWEPSPKSNTRCFLTK LPRSLRSSVFPLGWPHSKGLDIFQMGSWLGKE
2732	A	11	431	RHLAAPPAPPAAPAAAAALSHCLRSSGRLAPHTSRRLPRVVKRRVN ALKNLQVKCAQIEAKFYEEVHDLERKYAVLYQPLFDKRFEIINAIYE PTEEECEWKPDDEDEISEELKEKAKIVDEKK\DEEKEDPKGIPEFW
2733	C	257	358	MILLVFLPXHQVFLERXQSEILHHLNLTADVL*
2734	A	2	387	SRSSWSLPAEPLVTWVKTFGPFGSGTQDNLTMYMDLVDGIFLNQIML QIDPRPTNQRINKHVNNVDNLRIQNLTILVRNIKTYQYQWGGDYDEE GEEADEPGEEGGDEEHDPDYDPKKDQNPTECKQ
2735	A	64	468	PAAWLPILVAARQLTVQMMQNPQILAALQERLDGLVETPTGYIESLP RVVKRRVNALKNLQVKCAQIEAKFY\EEVHDLQRKYAVLYQPLFDKR FEIINAIYEPTEECEWKPDDEDEISEELKEKAKIEDEKCD
2736	A	1	795	MDVTVSELLELFLQSPLVTWVKTFGPFGSGSQDNLTMYMDLVDGIFL NQIMLQIDPRPTNQRINKHVNNVDNLRIQNLTILVRNIKTYQDMGY GQTQAWGAGILESFLGGNVCLRLVGLTGREGVSSGEERHLSFGDIK QPEGWGVSCGYRFRKGELEPLEVAVFVGTGSVGAAMVAMGAATLEA PEALESINQESSCGCIKPCGNSLEWRQLARALLVRWGGDYDEEGEEA DEEGEEGGDEENDPDYDPKKDQNPTECKQ

2737	A	1	982	MDVTVSELLELFLQSPLVTVWVKTFGPPFGSGSQDNLTMMDLVGDIFL NQIMLQIDPRPTNQRIKXHVNDVNLRIQNLTLVRNIKTYYQDMGY GQTQAWGAGILESPFGNVCLRLVGLTGREGVSSGQERHLQSGDQIK QPEEAQGRMVGSFERTPQICGLGYRFRKGELEPLEVAVFVGTGSGVGA AVMVAMGAATLEAPEALESINQESSCGCIKPCGNSLEWRQLARALLV RWGDDYDEEGEEADEEGEEEGDEENDPDYDPKKDQNPACCKQQLKQG CMWPLRDNLHWSTFCFPGKGLNLHHLTSLFSLKLFVVCLLCFCFCS
2738	A	2	138	SARGAASCSSRCCRCRPESLPAQLRAAWLPILVADIWSSYNMADID NKEQSELDQDLDDVEEVEEETGEETKLKARSA*LFRMM\QNPQILA \ALQERLDG/LWVETPT\GYIESLP\RUVKRR\VNALKNLQVKCAQK ETQ\FYE\EVHDLERKYAVLYQPLFDKRFELINAIYEPT/EKECEW ETR*RKDEDFGGNWKEKGQIEDEKKDE\EKEDPKG/IFPEFWLTVFK \NVDLLSDMVQEHDEPILKHLKDIKVKFSDAGQPMFVLEFHFEPNE YFTNE\VLTKTYMRSEPD\SDPFPSFDGPEIMGCTRVPR*DWKKGK NVTLKTIK\KKQKHKGRTVPYCDLKPVSNDSFNFPGPLPESSLSRS GDLDDDAEA\ILAADF\EIGHFYRERIIPRSVVNFT\GEAIEDDDDD YDEEGR*RS*GRLAPHTSRRYLEFLQHGRH
2739	A	1	435	PRARAERPAPASCSSPTSTRTPDTEVCIVERLFSSSLVAIVSLKA PRKLKVCHFKKGTICNYSYSNTILAVKLNQRQLIVCLEESLYIHNI RDMKVLHTIRETPPNPAGLCALSINNDNCYLAYPGS*SGEAGAGQLL FANFNQDNT\DTEDVCIVERLFSSSLVAIVSLKAPRKLKVCHFKKGT EICNYSYSNTILAVKLNQRQLIVCLEESLYIHNI RDMKVLHTIRETP PNPAGLCALSINNDNCYLAYPGSATIGEVQVFDITNLR
2740	A	3	438	LLFANFNQDNTSLAVGSKSGYKFFSLSSVDKLEQIYECTDTEDVCIV ERLFSSSLVAIVSLKAPRKLKVCHFKKGTICNYSYSNTILAVKLN RQLIVCLEESLYIHNI RDMKVLHTIRETPPNPAGLCALSINNGFGEG DRD
2741	A	1	1336	MLLRLQRIKTLRPPGCPHPMTTCSAGTLSAVPCVSPRQVVFERRFC LWHSHEMFTHVLPFVISADTEDVCIVERLFSSSLVAIVSLKAPRKL KV\CHFKKGT\EI\CNYSYSNTILAVKFNQRQLIVCLEESLYIHNI RDMKVLHTIRETPPNPAGLCALSINNDNCYLAYPGSATIGEVQVFDIT NLRAANMIPAHDSPLAALAFDASGKTLATASEKGTIVRVFSIPEGQK LFEFRRGVKRC\VSICPLAFSMDG\MFLSASSNTED/TVHIFKLET KEKPPEE\PTWTGYFGKVLMASTSYL\PSQVT\EMFNQGRAFATV\ RLPFCG\HKNILLG*PTIQKIPRLLVGAA\DGYYLYMY\NLDPQEG\G ECALMKQHRLDG\SLETTNEILDSASHDCPLVT\QTYGAAAGKAYTD DLGAVGGACLEDEASALRLDEDESEHPPMI RTD
2742	A	152	1616	VQPDPPSRARPPRPGPLAARPAAMNLASQSGEAGAGQLLFANFNQDNT EVKGASRAAGLGRRAVWVSLAVGSKS\GYKFFSLSSVDKLEQIYECT DTEDVCIVERLFSSSLVAIVSLK\AP\RKLKVC\HFK\KGTEICNYS YS\NTILAVKLNQRQLI\VCLEE\SLYI\HNIRDMKVLHTIRETPPN PAGLCALSINNDNCYL\AYPGSATIGE\VCQVFDITNLR\ANMIPA HDSPL\AALAFDASGT*L\ATASEKGTIVRVFSIPEGQK\LFEFRRG VKRCVSI CSLAFSMDGMFLSASSNTETVHIFKLETVKEKPPEEPTW TGYFGKVLMASTSYLPSQVTEMFNQGRAFATVRLPFCGHKNICSLAT IQKIPRLLVGAAADGYLYMYNLDPQ\EGGECALMK\QHRL\DGSLGKR PNE\ILDSA\SHDCPLVTSDITAQLAGKGTYPSSPTETCPTRDD\L GAVGGAC\LED\EGPALR\LDEDESEHPPMILRTD
2743	A	122	1162	LGLEGDGGASQWVGGRQRLQDCRNRSQGSPETLIPP/SLQITVPSR TCFP/SLQVGLT/FPPRAVPSAAAALGRNLRL*RGWHRRIPWVAS ISRAASSWG/TKPPLFKVPSQPETLGETWVIAMAGTYGGSRNTLPR SPGGNFRSTVPR*VQTTPRQPGAGLPKPVVATSSD*QASRSSPGRS RKDGPDSFPALPVS/RGEPESPSLQPPPPSTR*PSRLGRPR\PSAL SGPLRAPEHAQSSTSPSRWTTSPRMLRAPARAPCPSPTLVPVSTPS PPFP*RWSQ*SGHTPGRFFPCSPPRIRASACASLGGTTDGTAYQIA HAPHHVFLTSLRAFLRLAGSCTNHG

2744	A	53	394	RETGLPALGTCAVPLARAAPILQRLQQSPRTSLKARPKTRITGALPM DHTEGSPAEEPPAHAPSPGKFGERPPPKRLTREAMRNYLKERGDQTV LILHAKVAQKSYGNEKRFF
2745	A	2	358	ALPRLIIRKVDKQTALLDADDPVSQLHKCAFYLKDTMYLCLSQER IIQFQLNGRWGRRQCLNLQGNFTSKFTECGFGGCRKAGNYVTGVGG GVWLLCSPDISGISEEGWEMGSR
2746	A	3	452	ILMDKTVKLVCPVTGMALPRLIIGKVDKQTPLWDADDPVSQLHKCAF YLKDTMYLCLSQERIIQFQATPCPKENPKEMINDGASWTIISTDK AEYTFYEGMGPVLAPVTPVPVVESLQVVRTPSSNWPSSSLQLLSAVTW HHFISWEF
2747	A	1	1814	MRSAAARGPRQSCSAFNRFRANSSSPGFGAPCGRQCWIWESLGKERA KEGKDGGLOSPRTSLKARPKTRITGALPMDHTEGSPAEEPPAHAPSP GKFGERPPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFF FCPPPCVYLMGSGW\RKKKEQMERDGCSEQ\GLNQCAFIGIGNSDQE MQQLKLW\NGKNYCTAKTLYISDSKRNFTMLSVKMFYGPST\YDIG VFL\SKRINVISKP/SPKRKQSLKNADLCIASGKERWALFNRLLSQT V\STRYLHV/EKEGNFHASSQOWGAFFIHLDDDESEGEFTVRDGY IHYGQTVKLVCSVTGMALPRLIIRKVDKQTALLDADDPVSQLHKCAF YLKDTMYLCLSQERIIQFQATPCPIAPS\REMINDGASWTIISTD K/AQKKTFFYEGMGP/VSLPPVNPCLV*ESLQLKGGADGSQCLNLPQG NFTPKFTECGLGKVEAETMYRCGESM\LCVVPDI\SAFRER\WRWVR QPSRFPVTLVPKLIIGIPFISHQPLPFT\YTPEP\GPRATIAPVAGA ILRAQFKPGCPLTESNTNSEGSLHKRQHKFNQCHIIYSHSGILTTVF LLGLKLT
2748	A	54	188	NMTKLQVVSKNLLLLKMLIKERETQRKGGSS*KSTQGAQGGAPR
2749	A	572	857	GQKGFSGMGG*GEKGS LGNPSWGTAGGQAPVPPQGLTGTRFTQGGSSG \TAGPPASTFCLGGHGAUVGTYGRQMYMEFVFCSVGVAQKQDLCPR E
2750	A	3	127	EICQFLKGAKITRLQDQQVPYAVKGNQWVGYYDDVKSMETKD
2751	A	1	359	LILVKAALDTHLSPWFGVRCAFQNPGRGCS/PEGKQLQSRVI* G*EFQSTAACEEHYMASIRRSVSPSLSVCTSPPLSVLDILPPTDLYF EQHSPIL*LKVKGSLH*RSSPLRKES
2752	A	1	1270	MGATTMDQKSLWAGVVVLLLLQGEMGFCYVARAGLELLGSRSPASA SQSAGITGSAYKLVCYFTNWSQDRQEPGKFTPENIDPFLCSHLIYSF ASIENNKVIIKDKSEVMYQTIINSLKTKNPKLKILLSIGGYLFGSKG FHPMVDSSTSRLEFINSIILFLRNHNFGLDVSWIYPDQKENTHFTV LIHELAEAFQKDFTKSTKERLLLLTAGVSAGRQ MIDNSYQVEKLAKDL DFINLLSFDHGSWEKPLITGHNSPLSKGWQDRGPSSYYNVEYAVGY WIHKMPSEKVVMIPTYGHSFTLASAETTVGAPASGPGAAGPITES SGFLAYYEICQFLKGAK\TRGSRDQQVPYAVKGNQWVG\YDDVKSMG DQGSVL*RFKTWGGAMIWSIDMDDFTGKSCNQGPYPLVQAVKRSLS L
2753	A	385	570	KLGTEDQKGGRIILLVWAKLHQLSY*HIRVLSIGGN*GPGE*MGMP GVHLLFFRTKIRIQI
2754	A	1	1022	MTLAPSDQDLFVFRSGPPAAAGMPCLFFPEVPFCTRVHQPTGRDGSK NLLNELFIACPGGLMAQGPLDPTESSVPNTKALCGIFSDVAATAENR QTFMQSAIQFLRKYNFDGLDIDWEYPGNRGS PADTQQLFTILLKEMY EAFEQESTRSKKPRLMSAAVSAGKGTIETACQIPEMSSSTPSRKEP PRVWNAPWEVPYVYKGNQWIRYDNSKSFTLK/AVLPHSKDKV*TTEF FALLCLSPA HGKFTQAEPKSGGDRASGLLQSTHLYPGHQL\APIITA APGGGSTGGSGFCTGKSKGLYP\PHSKHAFYNCVDEHTYEEACQEG LVFDT\SC\SCCNWA
2755	B	143	867	XVVVLLLLQGSAYKLVCYFTNWSQDRQEPGKFTPENIDPFLCSHLI YSFASIENNKVIIKDKSEVMYQTIINSLKTKNPKLKILLSIGGYLFG SKGFHPMVDSSTSRLEFINSIILFLRNHNFGLDVSWIYPDQKENTH FTVLIHELAEAFQKDFTKSTKERLLLLTAGVSAGRQ MIDNSYQVEKLA

				KDLDFINLLSFDFHGSWEKPLITGDN\$PLSKGWQDRGPSSYYNCEIC CGVLD*
2756	A	2	394	CSAHSTALRVVRNHFYFTITATQVHKGSSSHPCSTRGNEMMASSQP SAFGIPGWGAR*PAPAPLPHRRGLPGSVTG*WRPIVGQ*/PSPHHC KASTKAQPEGPGTPPP\GKPSWKELPESHKKSLAPSPF
2757	A	499	1592	QPSQPFLSAGLNQTVPWGTCLHRAELSPST\ENSSQLDF\EDVWNSS YGVNDSFPDGDYDANL\EAAPCHSCNLLDDSAFFILNQCSWGIL ASRTGLFMPFR\PFWRQLCPG\WPVLGTAGCGAVAFQHLWVPVFG PQGYGS\TRSSALL*LGATGVWYGSAPQAALL\GC\HASLGHRLGA GQVQG\LTLGLTVGIWVAALLTLPVTLA\SGASGGLCTLIYSTELK ALQATHTVACLAIFVL\LP\LGLFGA\KGLKEGIGLMGPGPLDEISL WA\WFIFWPHGVVLGLDF\LVR\SKRLLSTCLAQALDLLLLNLAE ALAILHCVGTPLLALFCHQATRLLPSLPLPEGWFFHLDTLGSKS
2758	A	1541	1830	KRFLHLHQHTSGKSGRGRHLCGCGFSSKSP/GS*PGAGGASSSSQS KSPGPRPARVRRRLWVRAPPATSQEEASAGRRVRPPSSVHVNIPPPS VRPA
2759	B	4	1698	MGDFNTPLSTLDRSMRQKVNKDIOELNSALHMDLIDYRTLHPKST EYTFFSAPQRTYSKIDHIVGSKALLSKCKRTEIITNCLSDHSAIKLE LRIKLTQNHSTWKLNNWLLNDYWVHNEMKAEIKMFFETNEIKDTT YQNLWDTFKATLNQEEVESLNRPIITGSEIQAMINSLGTTKLQDQDTS QPSSTRDDMIVYLENPIVSAQNLLKLI\$NFSKVS\$GYKINVQKSQAFL YTNNRQTESQIMSKLPFTIASKIIKYLGVQLTRDVKDPFKENYKPLL NEIKEDTNKWKNI\$PCSWIGRINIMKMAILPKVIYRFNAIPIKLPMTF FTELEKSTLKF\$IWNQKRACIARSILSQRNKAGGITLPDFKLYYKATV TKTAWYQNRDIDQWNITEPSETMPHIYHYLIFEKPDKNKKW\$KDS L\$FNKWCWENWLATCRKLKLDPFLTPYTKINSRWIKDLNVRPKTINTL EENLGNTIQDIGMKDFMSKTPKAMATKAKIDKWDLIKLSFCTAKE TTTRVNRQPTWEKIFAIYSSDKGLISRIYKELKQIYKKKTTTPSTSG *
2760	B	1	1044	MGRNRSRKDENS\$KNQ\$ASS\$PPKDRSS\$SPATEQ\$WMEN\$FDELTEVGF RRLNQEEVESLNRPIRGSEIEAIINSLPTKKSPGPDGFTA\$FYRRYK EELVPFLLKLFQ\$YEKEVILPNSFYEASIIILIPKGRD\$TTKKENFRP ISLMNINAKILNKILANQIPQHIKLNHEDQVGFIPGMQALFHIQES INVIHHINRTKDKNHHIIISIDA\$KAFDKIQ\$R\$F\$MLKTLNKLDDMIVY LENPIVSAQNLLKLI\$NFSKVS\$GYKINVQKSQAFLYTNNRQTESQIM SEL\$PFTIATKRIKYLGIELTRDVKDLFKENYKPLLQIKEDTNKWKNI IPCSWIGRINIVKRATLPK*
2761	A	1331	2176	TEPKTKTT*LSQ*MQKRPLTKFNNPSC*KLSIN/IVLEVLARAIQ\$E KEIKGIQLGKEEVKLSLFADDMIVYLENPIISAQNLLKLI\$NFSKVS GYKINVQKSQAFLYTNNRQTESQIMSEL\$PFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNKWKNI\$PCSWIGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLKF\$IWNQKRARITKSILSQRNKAGGI TL\$PDLKLYYKAI\$VT\KTAWYCYQNRDIDQWNRTEP*EIMLHIYNYLI F
2762	B	1	2898	MRQKVNKDTQELNSALHQEDLIDYRTLHPKSTEYTFFSAPHHTYSK TDHIVGSKALLSKCKRTEIITNCLSDHSAIKLELTIKLTQNHSTTW KLNNLLNDYWVNNEMKAEIKMFFETNKNKDTTYQNLWDTFKAVCKG KFIALNAH\$K\$KQERSKIDTLTAQLKELEKQEQTH\$KASRRQEITKIR AELKETETQKTLQKINESRSWFFERINKIDRPLARL\$TEKKRKNQID AIKNDKGDIITDPTEIQT\$TIREY\$K\$HLYANKLENLEEMDKFLDTYVL PRLNREEAEPLNTP\$IAGSEIEAIINSLPTKKSPGPDGFTA\$FYQRYK EELVPFLLKLFQ\$IEKEGILPNSFYEASIIILIPKGRD\$TTKKENFRP ISLMNINAKILNKVLANRIQQHNKKLIHHDQVGFIPGMQGW\$FNIRKS INGIQHINRTKDKNHTIISTDA\$KAFDKIQ\$KPFMLKTLNKL\$GIDGY LKIIRAIYDKPTANII\$LNQ\$KLEAFPLKTGT\$RQGCPL\$P\$LLFIVLE VLARAIQ\$EKEIKDDMIAYLENPIISVQNLLKLI\$NFSKVS\$GYKINV

				QKSQAFLYTSNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIS IKLPMTFFTELDKTTLKFIWNQKRACIAKSILSQENKAGGIMLPDFK LYYKATVIKTAWHWYQNRDIDQWNRTEPSEIMPHIYNLIFDKPDKN KKWGKDSL FNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVR PKTIKTLEENLGNTIQDIGMGKDFMSKTPKAMATKDKIDKWDLIK SFCTAKGTAIRVNRQPTWEKTFATYSSDKRLISRIYNELRHIYKKK TNNPIKKWAKDMNRHCSKEDIYAAKKHMKKCSSSLAIREMQIKTTVR YHLTPVRMAIISQETTGADEVEK*
2763	A	3	670	IQTTIREYYKLLYANKLENLEEMDKFLDITYLPRLNQEEVESLKTP TGTEPRFGPTKNVQDQMSQLNSTRVLEVLARAIRQEKEIKGIQLGK EEVKLSLFADDTIVYLENPIVSAQNLLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFRITTKRIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCSWIGIINITKMVILPK
2764	B	64	1242	MINS LGTKKLQDQDTSQPSSTRDDMIVYLENPIVSAQNLLKLISNFS KVSQYKINVQKSQAFLYTNNRQTESQIMSKLPFTIASKRIKYLGVQL TRDVKDPFKENYKPLLNEIKEDTNKWKNIPCSWIGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKSTLKFIWNQKRACIARSILSQRNKA GGITLPDFKLYYKATVTKTAWYQNRDIDQWNITEPSETMPHIYHY LIFEKPDKNKKWGKDSL FNKWCWENWLATCRKLKLDPFLTPYTKINS RWIKDLNVRPKTINTLEENLGNTIQDIGMGKDFMSKTPKAMATKAKI DKWDLIKLSFCTAKETTRVNRQPTWEKIFAIYSSDKGLISRIYK ELKQIYKKKTPSTSG*
2765	B	287	898	MNINAKILNKILANQIPQHIKKLNHEDQVGFIPGMQALFHIQESINV IHHINRTKDKNHIIISIDAFAFDKIQQRFMLKTLNKLDDMIVYLEN PIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPC SWIGRINIVKRATLPK*
2766	B	1	1443	MKLPEEASGSNICCYAIFAVLQPLLVIPKETVSGVDLQQTPTDLQLS DLTPGRKTNKQKGIASPSTKRTSTPKPHLQANAQRFCCHQACVTRVP KGSTKHGKEQLVPATAKTCQIVKNINAMKXLHQLQITIREYHKH LYANKLKNLEEMDKFLDITYLPRLKQEEVESLNRPIMGSEIEAIINS LPTKKSPGPDGFTAKFYERYKEELVSFLLKLFQSIEKEGILPNSFYB ASIIILIPKGRDTTKKNFRPISLKNIDAKILNKILANRIRQPIEKL IHHDQVGFIPEMKGWFKKCKSINV IHHINQTNKDNHMIISIDAFAF DKTQPPFMLKTLNKLGTIRQKKEIKGIQLGKEEVKLSLFADDMIVYL ENSIVSAQNLLKLISNFSKVSRYKINLQKSQAFLYTNNRHMESQITS ELPFTIDTKRIKYLGIQFTRDVKDLFKENYKLLLNEIKEDTNKWKNIP CSWIEESIS*
2767	A	1	966	MGRNQCKKAENSKNQNTSSPPKDNFLPAREQNMENEFDELTEVRF RRWVITNSSEQEHDLTQCNEAKNLEKRSWFLEKINKIDRPLARLVK KKREKNQINTIKNDKGDIIITDPTEIQTTIREYYKHLIYANKLENLEEM DKFLDITYLPTLNKEEVESLNKPITSSEIEAVIISLPTKKVQDQKDS QPNSTRVLEVLATAIRQEKEIKDTQTGNBEEVKLSLFADDMIVYLEN IVSVQNLFKLISNFSKVSQYKINVQKSQALLYTNNRQTESQIMSKLP FTIATKRIKYLGIQLTRDVKDLFKGNYKPLLKEIREDTNK
2768	A	1	216	LFVRCPVGSISLPTLSSPVKRYRFPHMAYPSLTRCIHSGLPQYCMSI NCFPMHPGYRVPSRCFPVSPIFFPT
2769	A	3	2074	CKLLDGGQFYLVPCISGENNIDWYMRDRSTRQKVNKDTQELNSALH QADLIDIYRTLHPKSTEYTFFSAPHHTYSKIDHIVGSKALLSKCKRT ENVRNCLSDHSAIKLELRIKTLTQNC SATWKLNNLLNDYVWNNEMK AEIKMFFETNENKYTTYQNLWDTFKAVCRGKFIALNAHKRQERSKI DTLTSQLEKEQEQTHSKASRRQEITKIRAELEIBIEIQTLOKINE SRSWFFEKINEIDRPLARLIKKREKNQIDTIKNDKGDITTNPTIEIQ TTIREYYKHLIYANKLENLEEMDKFLDITYLPRLNQEEVESRNRPI TG AEIEAIINSLPTKKSPGPDGFTAIFYQRYKEELVPILLKRFQSIEKV

				GILPNSFYEASTILIPKAGRDTTKKNFRPISLMNIDAKILNKILAN RIQQHIKKLIHHDVRGFIIPGMQGWFNHKSINVIQHINRTKDKNMI ISIDAFAFDKIQQPFMLKTLNKLDDMIVYLENPIDSAQNLLKLKSN FRKVSGQKINVQKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELEKTTLKFIRNQKRACITKSILSQKN KAGGITLPDFTLYYKATVTKTAWYLYQNRDID
2770	A	1	1632	MHCILPTPSGSGSFPVYTSQSQPKTPGAFSGTSLVREPLSPEPDVLL PGSAKCAALCWFVSVLDAASPVTRWPVSRSPWECRCVSPPVREAPV SPPFQCAPPYTDCLSPYLYEYTVCPSPCARVPIPSSTHPWEYKVPP PHAERLCPVSEDPCLCNWKTRAAGARESSLVPCPYAARYPPSPPRV AWSSHFSYRGLSPSLGPNKPGNPRGPSESAAAAASRPAAAAASAPP GAARLPASPTPRLARDRGVSHPARPCPAWPLRALTVAAASHGSATPA SGPPPGREGVRSASLSPACRPAHLVALNRPHRPPSTLTGAGPKSLE FCSWDGTSERLNQEDVESLNRPIITGSEIEAIINSLPTKNVQDQKDSQ PNSTRVLKVLARAVRQKKAIQIGIGKEEVKLSLFADDMIVYLENPI VPAQNLLKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSELLF TIATKRIKYLGIQLTRDVKDLFKENYKPLLKEIREDTNKWKNIPCSW IGRINIMKALLPKVIYRF/NAIPIKL*LPTPSGSGSFPVYTSQSQP KTPGAFSGTSLVREPLSPEPDVLLPGSAKCAALCWFVSVLDAASPV RWPVSRSPWECRCVSPPVREAPVSPPFQCAPPYTDCLSPYLYEY VCPSPCARVPIPSSTHPWEYKVPPPHAERLCPVSEDPCLCNWKTRA AGARESSLVPCPYAARYPPSPPRVAWSSHFSYRGLSPSLGPNKPGN RGPSSESAAAAASRPAAAAASAPPGAARLPASPTPRLARDRGVSHPA RPCPAWPLRALTVAAASHGSATPASGPPPGREGVRSASLSPACRPA HLVALNRPHRPPSTLTGAGPKSLEFCSWDGTSERLNQEDVESLNRPI TGSEIEAIINSLPTKNVQDQKDSQPNSTRVLKVLARAVRQKKAIQIG QIGKEEVKLSLFADDMIVYLENPIVPAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSELLFTIATKRIKYLGIQLTRDVKDLFK ENYKPLLKEIREDTNKCKNIPCSWIGRINIMKALLPKVIYRFMLSP SSYD
2771	A	842	2353	TEPKTKTT*LSQ*MQKRPLTKFNNPSC*KLSIN/IVLEVLARAIQBE KEIKGIQLGKEEVKLSLFADDMIVYLENPIISAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIMSELP\FTIASKRIKYLGIQL\T RDVKDLFKENYKL\PLIKEIREDTNKWKNIPCSWIGRMNIMKMAILP KVIYRFNAILIKLPLTSFTKLEKTTLKFIRNQKRARIASILSQKNK AGGITLPDFKLYYKAIT\KTAWYCYQNRDIDQWNRTEP*EIMLHIY NYLIFDKPEKNKQWGKDSLFNKWCWENWLTICRKLKLDPLTSYTKI NSRWIKDLNVRPKTIKTPEENLGNTIQDIGMGKDFMTKTPKAMATKA KIDKWDLIKLSFCTAQETTIRVNRQPTWEKISAIYSSDKGLISRI YKELKQIYKTKTNNPIKKWAKDMNRHFSKEDIYAAKRHMKKCSSSLA IREMQIKTTMRYHLTPVRMAII/RIKSGNNRCWRGCGEI
2772	A	1	299	KHFMRKIDLCLSSEGSEVILATSSDEKHPPENIIDGNPETFWTTTG MFPQEFII CFHKHVRIERLVIQSYFDLVHTEGQLQNEEIVAPIPNYG STGHL
2773	A	2	294	HERESQVKHFMKIDLCLSSEGSEVILATSSDEKHPPENIID\DLV HTEGQLQNEEIVAHDG SATYLRFIIVSAFDHFASVHSVSAEGTVVSN LSS
2774	A	247	411	QLTSTAKSIYIDFFPIQAHDG SATYLRFIIVSAFDHFASVHSVSAEG TVVSNLSS
2775	A	136	714	RESQDKHFMMRKIDLCLSSEGSEVILRYQSSDEKHPP\ENIIDGNPE TF\WTTTG\MFPQEFII GF\HKHVRIERLVI\QSYFVQ\TLKIEKTH RLNEP\VDF*RNWIEKDFGTHQRGFSFKNEEIV/AHIDGSATYLRFI VSAFDHFASVHSV\AEGTVVSNLLIMITKWLHDLFTIYLNKLS LIYFIKRIKFIK
2776	A	3	2077	PAEEVVTYIPLDFCHYHSEDGKQFLLPLTPTLLTHPLCLVTGTSSL

				LVCVGKPEIFVAIHYYTPNTKLVLARPRNSHVPHPPERTTTVTQYST CALLTALCLLLPVLQETAQSRMVTSHPEDRPALARKHGASQPAGLG FPRTQTVTPAFTFQTPATAEPALLTAWLGRAPETETITDMAGAAGTH RRKRRLEPEKRPASQKTTTLKERPPETGPWDLPPPPTERTTTVTQYST CALLTALCLLLPVLQETAQSRMVTSHPEDRPALARKHGASQPAGLG FPRTQTVTPAFTFQTPATAEPALLSAWLGRAPDTENITDMARATSRS ITWGRMVSAKARGAAVTEERETPERNLVQRNPDSNSSDISPESFLN SDLCWSQWASMPAEKSWNLCPHSLSALASSQLNLRLLGSGNDGSTSA ALRLLGLRDGSTSPTLRLLGSGDDGSTSAALRLLGLRDGSTSPTLR LGSGDDGSTSAALRLLGLRDGSTSPTLRLLGSGGAHAVVQCSSIAD WEREEVFKPHEDRGS LICTEL VHTYYDLQEVMDGNVITAKRTAAVS AIATKCDNLKTCHTSHGVSMAETAVINHKKRKNSPRIVQSNDLTEAA YLSRDQKRMLYLFVDQIRKSDGTLQEHGDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFYRPEKDPAMKKL
2777	A	3	1038	TAEGTWIAVRRLLEGTTGEMSRVPAFLSAAVEEHLRSSSLIPPL ETALANFSSGPEGG\VMQPVRTVVPVTKHRYLG\VMPAYSAEDAL TTKLVTLLRGPRHHLRSSLPTRVIVVTLLSPAMGTL LAVM\DGKCS* IAKRTAAVSCHLPPSFLKPPSSEVLCILGAGVQAYSHYEIFTEQFSF KEVRIWNRTKENAEKFADTVQGEVRVCSSVQEAAGADVITVTLAT \EPILFGEWV\KPGAHINAVGAS\RPDWRELDDELMEAVLYVDSQE AALKESGDVLLSGAEIFA*AGEK*FKGVKPS/YCEKTPRCSKSLGM AV\EDTVAAQTHPMIPWSSGK
2778	A	2	2037	LPFRSVGAYFAASWSVAMNPDLRREDSASFNPPELLTHILDGSPEKT RRRREIENMILNDPDFQHEDLNFLTRSQRYEAVVRKSAIMVKMREF GIADPDEIMWFKKLHLVNFVEPVGLNYSMFIPTLLNQGTAEKEKWL LSSKGLQIIGTYAQTEMGHGTHLRGLETTATYDPETQEFILNSPTVT SIKWWPGGLGKTSNHAIVLAQLITKGKCYGLHAFIVPIREIGTHKPL PGITVGDIGPKFGYDEIDNGYLYKMDNHRIPRENMLMKYAQVKPDGTY VKPLSNKLTGYTMVFVRSFLVGEAARALS KACTIAIRYSAVRHQSEM KPEGEPEPQILDFTQYKLFPLLATAYAFQFVGAYMKETYHRINEGI GQGDLSSELPELHALTAGLKAFTSWTANTGIEACRMACGGHGYSHCSG LPNIYVNFTPSCTFEAGENTVMMLQTARFLMKSYDQVHSGKLVCGMVS YLNDLPSQRIQPPQVAVWPTMVDINSPELSTEAYKLRAARLVEIAAK NLQKEVIHRKSKEVAWNLTSDVLVRASEAHCHYVVVKLFSEKLLKIQ DKAIQAVLRSCLLISLYGISQAGDFLQGSIMTEPQITQVNQRVKE LLTLIRSDAVALVDAFDFQDVTLGSVLGRYDGNVYENLFWEAKNSPL NKAEVHESYHKHLKSLQSKL
2779	A	3	194	TFFFQVKPDG\TYVKPL\SNKLTYG\TMVFVRSFLVGEAARALS\KA CTIAIRYSAVRHQSEIKPG
2780	A	1	903	MTGGGFGGCTVTLLLEASAAPHRMRHIQEHYGGGLPPSTSLKQPMERPC CACEAPPGQHTLHALTAGLKAFTSWTANTGIEACRMACGGHGYSHCS GLPNIYVNFTPSCTFEAGENTVMMLQTARVGDNSIDCWKDARRLFQDG DKSRAPHPDILTDTQTEWGSATFTSDGGIRLFYTDYSGKHGKQSL TTAQVNVSKSDDTLKINGVEDHKTFLFDGAGNTYQHVQQFIDEGNYTS GDNHTLRDPHYVEDKGQKLVFEANTGTENGYQGEESLFNKAYSGGG TNFFRKESQKLQOSEERQK
2781	A	133	402	IADSVTPDDSSLKCPSLIFPRS FVHRGRPEPLDLHLGMFLPTLLHQA TAEQQRFFMPAWNLEIIGTYAQTEMGHGMEYSVYLKEMGGPL
2782	A	2	242	MTEPQITQVNQRVKELLTLIRSDAVALVDAFDFQDVTLGSVLGRYDG NVYENLFWEAKNSPLNKAEVKIQCLCTFLKVFT
2783	A	26	2229	RFRAGAADLDCHCHLGRCLLRCLLVAMNPDLRREDSASFNPPELLT HTLDGSPEKTRRRREIENMIL\NDPDFQHEDLNFLTRSQRYEAVR KSAIMVKMREFGIADPDEIMWFKNFVHRGRPEPLDLHLGMFLPTLL HQ\ATAEQQRFFMPAW\NL\EIIGHFIAQTEMG\HG\THLSRLSET TATYDPETQEFILNSPTVTSIKWWPGGLGKTSNHAIVLAQLITKGK CYGLHAFIVPIREIGTHKPLPGITVGDIGPKFGYDEIDNGYLYKMDNHR

				IPRENMLMYAQVKPDGTYVKPLSNKLTGYTMVFVRSFLVGEAARAL SKACTIGILYS AVRHHSEIKPGEPEPLILDFQTOQYKLPPLATAYA FQFVGAYMKETYHRINEGIGQDLSELPELHALTAGLKFTSWTANT GIEACRMACGGHGYSHCSGLPNIVNFTPSCTFEAGENTVMMLQTARF LMKSYDQVHSGKLVCGMVSYLNDLPSQRIQPQQVAVWPTMVDIN\SP ESLTEAYKLRAARLVEIAAK\NLQKEVIHRKSKEVAVNLTSDVLVR\ ASEAHCHYVVVKLFSEKLLKIQ\DKAIQAVLKE/SLCLLYSLYG\IS Q\NAGDFLQGSIMTGP\QITPSNPAV*RELLTLIRSDAVALVDAFDF QDVTLGSVLGRYDG\NVY\ENLFEWAK\NSPLEPKAEVHGIFTRHLE VHCQSQALEVFTDRDKFKSGFQKAPVWQLQILWESFSNSNRL
2784	A	61	241	ANLGPTAPPRSGPVLGAGEKGRGEMRRAPFFLSAGGLETPPPSAALL WAPGRRADEISGL
2785	A	60	341	ANLGPTAPPRSGPVLGAGEKGRGEMRRAPFFLSAGGLETPPPSAALL WAPGRRADEISGLWLLHTTAPQVGELRDERRGQRQEKMLIKKDEN
2786	A	70	428	IGGPQGFSPTPSLKPRPRIFKTPPIRGNWGPRPPPGVSPQFQFGGD TKFNLIIEILFVVLTFVS*AQSGDPAAPPRSGP/RPGGRGEREG*NEK SPVLPQCWGGWRHPPSAALLWALIW
2787	A	38	243	TPSTIDKSLTSLIKKK\KA*INNFRDKKGNIAKDIPEM*KIIREYYE NIHANTFENLGDIDKNKIDQN
2788	A	2	114	KNGMNMFSFSFNYAQSSSQFRTWQDSSVSYAAGALTVH
2789	C	50	214	MSIIEQLDSVSFSNYLKKYHNTICGRHPIGVLLNAITELQKNGMNM FSXLNYAQ
2790	A	1	624	MAEKCTSQQKRTQNKHGSTGIKMSNRVVRWEASHSGNWTASGPQLN AQLEDKDEHGIEMHLPCTAKAMEIHKDEFTIIPVLVGALSESKEQEF GKLFISKYLADPSNFFVSSDFCHWGQRFYRSYDESQGETYRSIEHL DKMARASPTSAAPCSTAPSPIDRPRAEERCERMAQDWQAAPPAALVRD PLGEASWAPESGGDVENLYV
2791	A	2	851	ARGTIGGTGTMKMSNRVCREASHAGSWYTASGPQLNAQLEGWLSQVQ STKRPARAIAPRRIFILGPSHHVPLSRCALSSVDIYRTPLYDLRID QKIYGELWKTGMFERMSLQTDDEHSIEMHLPYTAKAMERCPVDVVM QILPKKPLHCRGTGDLDFISQLTGHKDEFTIIPVLVGALSESKEQ EFGKLFISKYLADPSNLFVSSDFCHWGQRFYRSYDESQGEIYRSIE HLDKMAITELQKNGMNMFSFSLNYAQSSQCRNWQDSSVSYAAGALTV H
2792	A	1	1116	MQVPCDHHWDCAGSDLKPMHWTLKALSLRVTRIRDALGVGTQKG CHTDSSLSCSALKPSVDGKAKRALFVTHAFWGSRGGRGQLLDAVWGL VFKFLELYTGMSADEMICYSGKSTELSGKLVNLVLTVMEGERSRG VRPQQGNDCCDGLSLRLGPPQLNAQLEGWLSQVQSTKRPARAIAPV GWTSATHIQRTEYGRKIATLQQTNLANTYYLNQTIKMQILPKKPLH CRGTGDLDFISQLTGHKDEFTIIPVLVGALSESKEQEFGLFSKY LADPSNLFVSSDFCHWVYGEWKTGMFERMSLQTDDEHSIEMHLP YTAKAMERCPVDVVSRRGPQLVRGLLGTGLCNRMRTVGQALPT
2793	A	53	1408	HRCCLWTFQCLSLISGITFLIKEGKEGLEPAREGPYLVLLTTETAV LLISITIPPTSNSNPTLERFCGLGAEVTGKDPMGFFKVLQRSLDADE GTAVDIQSFRPQKDFGRRRTLEECHVTGKGGTGTMKMSNRVCREASH AGSWYTASGPQLNAQLEGWLSQVQSTKRPARAIAPHAGYTYCGSCA AHAYKQVDPSITRRIFILGPSHHVPLSRCALSSVDIYRTPLYDLRID QKIYGELWKTGMFERMSLQTDDEHSIEMHLPYTAKAMESHKDEFTI IPLLVGALSESKEQEFGLFSKYADPSNLFVSSDFCHWGQRFYR\ SYDESQGEIY*SIHLDKMGMSIIEQLDPVSFSNYLKKYHNTICGR HPIG\VLLNAITELQKNG\MNMSFSFL\NYAQSSQC\RNW\QDSSVS YAAWEHSRATEALNPQGCHLPHSSYSVRGSPA
2794	A	53	699	SLPSLTPPGSRQPPAGRLNTEHHINEHILMYSLDLNSSSQMPSI\K AQTSDEGEIFEVDGEMPNHLLPIKAHVE\DLG\MDDEGDDDPV\LPN VNAAILKKV\IQ\WCT/HPHKDDPP\PPEDDEEQRKSVPDDIPVW\D QGIPGKFDQGTLF*NSFLGLQTYFRTSKGLLDVTCKTVCQYDQKGL

				P*BIRKFPKSKMTFTEEEEAQVRK\EN\QWCEEK
2795	A	162	522	WVRRGTISPARQRQDGVGAAPANYAKVLEWQLAPSPRHKCCQORPGTH LGCDSIGPLSPVGLPGLKG*PDNSSEGPCSS/QALPVSPSPGHPGSG GPKGQARSLLNCRGCPINWQHRCCKI
2796	A	2	1214	QPFQSGSCVIAILGRKMFSVAH\LARANPFNTPH\LQLVHDGLGDL RSSSPGPTGKPRRP\RN\LA AAAVEEQYSCDYGSGRFFILCGLGGII SCGTTHT\ALVPLD\LVKCRMV\DPQKYKG\IFNGFSVTLKEDGV\ RGLAKGLAPTF\LGYSMOGLCKFGFYEVFK\VLYSNMLGEENTYLWR TSLYLAASASAEFFADIALAPMEAAKVRIQTQP\GYANT*EGISFPK CIKEKGL\KAFYKGV\ALLWMRQITYTMN*SSPCLERTV*SHCTSLG VPKP\RSE\CS\KPEQTGCNHLVAGY\IARVFCA\IVSHPC*FVWYL VLNKE*SVAVS\LLVFSVTLDFKGV\WKGLFARII\MIGT\LT\ALQ WFIYYSVKGYFRT/LPRPPPPRDQSLLNNKFGLTpvvrskQIVD
2797	A	276	728	CFGFVFPSPWPYGPLSTGDVPKLGPPN*AMGGFRPG\KPQVSLPGFA GGHACSPASLPSGPGPAPPRACLPSPRGGRKSLGAPGGFPPGDSHGA PCSRVVTVSPGNDLKPGHSPRTLQRGGSPLGRRVWWSGCVVCPVWWP VLSASISGWI
2798	A	451	1030	VPEALSPFMEGEPQFPTMCCCSAPPAMPFPTT*QPSEAAAGQGVPG PHRL*GGLAPAGRS*APAGAFWGQGPAPQGEPAVSSKGGAAASTQRV L*HRRGHRGDASRGCPGDQNLQ*KLCSSRAEGGAVSQPGWPALPHA AGEPLASALPGLHAAQAPAPAVVSGPTTIRSCSGNSGKIFPSSCLDS CFPPS
2799	A	1	933	MLGAILSKLTGTENQIPHVVIHKWQLNDESTWTQSGEQQTGPVVG EIDLQILSKVQAQYPGVCINNEVEPSAEQIAKYKELVAKTSNLENV KFAWHKETSSEYQSRMLEKKELQKWDFIHMIQMLYYVKDI PATLKFP HSLLGTA NMLII VVSAHWSVGPTPTYPG DYSSLLAVLPTSALMRQ YSLPIGSSGWDKLWKYGS RFPQDDLCQYITSDDLTQMLDNLGLKYE CYDLLSTMDISDCFIDGNENGDLWDFLTETCNFNATAPPDLRAELG KDLQEPEFSAKKEGKVLFNNTLSFIVIEA
2800	A	1	1563	MRREGFKFSRSKV FVQDEM TKKWHKSDLHWVSRIQCTVLGVLTNATE MRSLLPIESLFLIQCFVVGASRNEATDCSGECYSSMRETRGSKECA AARFIKVGKVLQKVESYKLYHPYFLANWFSASFSGVKLVEMRGQE EETLGTFAHVLMFQAASSRALVLPPTMQLEQNGTCSYRKPNMAS SMRSLFSDHGKYVESFRRFLNHSTEHQCMQEFMDKKLPGI IGRIGDT KSEIKIL\SIGG\GAGEIDLQILSKVQ\AQYPG\VCIQH*SCLRPSA GTNWPNYKELVA\KTSNLENVKFAWHKETSSEYQSRMLGEKGAFKSW DFYSI*FKMLYYVKDIPAT\LKFFHSL\LGTA NMLII VCVQSSGW \DKLW\KKYGSRF\PQ\DDLQYITSDDLTQMLDNLGLKYECYDLLS TMDISDCFIDG\NENGDLWDF\LTETCNFNA\TAPPDLR\AELGKD L\QEPEFS\ALRKEGKVLFNNTLSF\IVIEGITIQSQKYIQKLYFEQ LES LIYFHIKITNSSH
2801	A	1	6750	MPTSESEGGSGTQACRKTQPNIHDIYWNIGVEDWIAAERWIKFRFQ TMDGDWENSVSWADDENEASIGSWSGADKAGIIRSWAVACDETSVK SWAGARAENVVGIGTWARAGEQASGGLWAGGQTSEGTWAGDKASGGA WTGAENQASGGSWALAGNQAIGELWAAGQASDGSWPGGQASGVSWVG EEAIGGSWTGAENQASEGSWAGAGAGNMSSVS YWAGVVDQAGGGSWA GTNDPFGVRLHRTNRNKEVMKAVALFTIAPVNLLKKHRLANWIKSQDP SVRCIQETHLTCRDTHRLKIKGWRKIYQANGKQKAGVAILVSDKTD FKPTKIKRDKEGHYLMVKGSIQEEELTILNIYAPNSGAPRFIKQVLS DLQRDLDSHTLIMGDFNTLLSTLDRSTROKVNKDTQELNSALHKVDL IDNYRTLHPKSTEYTFFSAPHHTYSKIDHILGSKALLSKCKRTEIIT NYLSDSHSAIKLELRKLNLTQNRSTTWKLNLLDDYVWHNEMKAEIK MFFETSENKGTTYQNLWDTYKAVCRGKFIALNAHKRKQERSKIDTLT SQLKELEKQE QTHSKASRRQEITKIRAELEIETQKTLQKINESRSW FFERINKIDRPLARLIKKEKNQIDA IKNDKGDIITDPTIEIQTTR EYYKHLYANKLENLEEMDKFLDTYTLPRLNQEEVESLNRPIITGAEIV

				<p>AIINSLPTKKSPGPDGFTAEFSSQRYKEELVPFLLKLFQSIEKEGILP NSFYEASIIILIPKPGRDTTKKENFRPISLMNIDAKILSKILAKRIQQ HIKKLIHHDQVGFI PGMQGWFNHKS INVIQHINRAKDKNHMIISID AEKAFDKIQPPFMLKTLNKL GIDGTYFKI IGAIYDEPTANIILNGQK LEAFPLKTGTRQGCP LSP LLLNIVLEV LARAI RQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPL LKEIKEDTNKWKNI PCSWVGRINIVKMAILPKGVLGRASSAVTRGP HVTRSCRATQPSLQSSLASGYQLPAALRSAGWHRARGKRSRSACMSA AGLKITGSKETKRRLLLISIDWSRDL MNLCIYFRVYCQEKQEERREL PRIITGPPPEAAVVAFEWLKTS TLTLGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVTAGLVIWAGTCYIIYKFTKGRAQSVRTLAR NGSTVKMETVVGVSQTLAINEAEIKTKPQVEIGAETGARS GPRAEV ETKATAIAIHRANSQAKAMVGAEPETQSESKVVAGTLMTEAVTLTE VKAKAREVAMKEAVTQTD AEAGKIVKKEAVTQTKAKAWALVAKTEAK REAMTQTKAETHILA EKETEINRVMVTQSETLAVPREVAKMGATNKT GIVDET KTRALEETVSVAKTQSEARPGATVDARGNPNGMSREVAGVD MKSCAQSQAVTKIQGDDMPGTGVEDMGNC KTMSRAESGADTRASAQ QIFAKTQTEAIPGAKIDAGGNTNAMWKIPMSYLKAITGADMRAAAQ QAVASTHAEAMSDAKVKNRGNPNAMTKAGAKANLRANSQVEALPDAR DKSRGNPNVMKAVG DGT DMLSCTQPQLVASVQADTLSDGKIKVRGNV NSMPKEGAGVDMKAQDDNRRVSQVASVKSTDGKTEDRTL RKPSTCGA LAENSAELKPRLELPSTIKACEVTTLTHKLWDNSVKAGTLITKLFLS SAQSMKIFCCLWNFVYKQLEDAAQGLTMGGDVEEHESRLGAGEEAGV ESWTLARNVGEDELSRESSPDIEEISLRS LFWAESSENSNTFRSKSGK DASFESGAGDNTS IKDKFEAAGGVDIGSWFCAGNENTS EDKSAPKAK AKKSSES RGIYPYMPVPGAGMGSDGAMIWSETKFAHQSEASFPVEDE SRKQTRTG EKTRPWS CRCKHEANMDPRDLEKLCIEMIEMTEDPSVHEI ANNALYNSADYSYSHEVVRNVGGISVIESLLNNPYP SVRQKALNALN NISVAAENHRKVKTYLNQVCEDTVTYPLNSNVQLAGLRLIRHLTITS EYQHMVTNYISEFLRLLTVGSGETKDHVLGMLLNFSKNPSMTKDLLI ANAPTSLINIFSKKETKENILNALS L FENINYHFKRRAKRAFTQDKFS KNSLYFLFQRPKACAKKL RALAAECNDPEVKERVELLISKL</p>
2802	A	3	91	<p>KKNIN*EILN*KQMEETLYVGNFP IQLT</p>
2803	A	3	7501	<p>GAGEEGELGGDARSSRDP ELQSYAAFVAVVTRIWL PAPRC PALGGLA SGPGKAEQFSRSLYLPDHLGEGNGGLLGKSLEPYRSACMSAAGLKIT GSKETKRRLLLISIDWSRDL MNLCIYFRVYCQEKQEERREL PRIITG PPPEAAVVAFEWLKTS TLTLGLHPQLPLSLPQPECALPYLVRAF SRGD YMGRIQEVGWVTAGLVIWAGTCYIIYKFTKGRAQSVRTLARNGSTVK METVVGVSQTLAINEAEIKTKPQVEIGAETGARS GPRAEVETKATA IAIHRANSQAKAMVGAEPETQSESKVVAGTLMTEAVTLTEVKAKAR EVAMKEAVTQTD AEAGKIVKKEAVTQTKAKAWALVAKTEAKREAMTQ TKAETHILA EKETEINRVMVTQSETLAVPREVAKMGATNKTGIVDET KTRALEETVSVAKTQSEARPGATVDARGNPNGMSREVAGVDMKSCAQ SQAVTKIQGDDMPGTGVEDMGNC KTMSRAESGADTRASAQ PQIFAKT QTEAIPGAKIDAGGNTNAMCKVGAGADVRACIQPQTVAKKQAEVTS ARVDGRGNTNVI SKAITGADMRAAAQPQAVASTHAEAMSDAKVKNRG NPNAMTKAGAKANLRANSQVEALPDARDKSRGNPNVMKAVG DGT DML SCTQPQLVASVQADTLSDGKIKVRGNVNTMPKEGAGVDMKAQGMAQS QGEALPNTRGKARGKAKAKCKTGPGMDMKTCTQPQAGVKTPAEALLD SRVDGRGNPNATSKAGTKADQRVCGQPLVVANPQGEALPGAKNVKVG NPHTVLKVGAGEGTTDS AQPEAVVSFQGEALLGTKNKVKGNPNVVLK AEVGE GAGMTAQLQIMASSKGEALLDSKNKVKGNSNAVS KAGAGTDT TGSVQPQIVANSQGEVLP GAKNKIRGNPTTVPNSGVGPYTTDSARLQ AVANSQGEVLP GAKNKVKANLNAVSKAEAGMGATG SVQPQAVANS HC ETLPGAKNKVRGNWNAVS KAGAGMDTRGSAQPQAVANSQGEVLP GAK</p>

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				<p>NKVKGNPNVSKAGAREDTVGSTQPQVLASSQRETLPGARNKVKGNS NVVSKAGAREDTMGSAQPQVVANSQRETLPGARNKVKGNSNAISKAE AGAGIMGSVQVQVVASFQGEVLPQAKNKVRGNSNAVPKAEAGADTVG SAQPQAVANSQSETLLGARNKVKGNTIAVPKAGTGAGTRHSAQPQIV AGSQGETLPGARDKSMSTSEAEATAEDEAYAKPEAEAMPTSESEGGGS GTQACRKTQPNIHDIYWNIGVEDWIAAERWIKFRFQTMGDWENS SWADDENEASIGSWGASDKAGIIRSWAVACDETSVKSWAGARAENV VGIGTWARAGEQASGGLWAGGQTSEGTWAGDKASGGAWTGAENQASG GSWALAGNQAIQELWAAQASDGSWPGGQASGVSWVGEAIGDSWTG AENQASEGSWAGAGAGNMSSVSYWAGVVDQACGGSWAGTSDQSGGGGS KPRFEDQASGEGSWAGAGGQASGGSMGLPEDQSSGRSWADTADQASG GSRLGHVDQSSGGAWAGTLDQSGGGSKPRFENQTEEGSWAGAGGQA GGGSKVGPEDQSSGRSWANSQDQISGGFLVGIQVQANGGSGWTGAGHP ASVGPKPFIQEDQVSGRGSWADAREQVVGDSRLGLRDQSSGSDSWADTG DQASGWFCVCPGSQTNGGSGWGGASGQDVGGSRPGPTNQSSAGSWDSP GSQVSGSCWTGAGAVDQAGGCSKPGFEDQAIQGGFWPAGDQDTGGGS RPGSEDQSSGIGSWGAVAGGQVLGGARPGPADQSSGGSWAGTGNQSSG RSWIGPGDQAVDCSKPEFEDQACGGGSGWAGAGSASGESWAGSRPGN EAIGGSRMGSEDQATGGSWARSEDQASGRFQVSFEVEANEGFWFGPG AEAVIGSWCWTEEKADIVSRPDDKDEATTASRSGAGEEAMICSRIEA ENKASSGSWIRSEEVAYMGSCVGAEGAGAGAEAGAGAEAGAGAGAEAG AEAGAGAGAGPGTESGAGIWSWDGDATTVESRLGAGEAGVESWTALA RNVGEDELSRESSPDIEEISLRSFWAESENSNTFRSKSGKDASFES GAGDNTSIKDKFEAAGGVDIGSWFCAGNENTSSEKSAKAKAKKSSE SRGIYPYMPGAGMGSWDGAMIWSETKFAHQSEASFPVEDESQRKQTR TGEKTRPWSRCRKHEANMDPRDLEKLCMIEMTEDPSVHEIANNALY NSADYSYSHEVVRNVGGISVIESLLNNPYPYPSVRQKALNALNNISVAA ENHRKVKTYLNQVCEDTVTYPLNSNVQLAGLRLIRHLTITSEYQHMV TNYISEFLRLTLVGSGETKDHVLGMLLNFSKNPSMTKDLLIANAPTS LINIFSKKETKENILNALSLEFENINYHFKRRAKAFQDKFSKNSLYF LFQRPKACAKKLALAAECNDPECLEAAETAAGNSAQGKFYKGGGPL GVDPKSIIP</p>
2804	A	3	3223	<p>PPPEAAVVAFEWLKTSTLTGLHPQLPLSLPQPECALPYLVRAFSGD YMGRIQEVGWVTAGLVIWAGTCYIIYKFTKGRAQSVRTLARNGSTVK METVVGVSQTLAINEAEIKTKPQVEIGAETGARSQGPRAEVETKATA IAIHRANSQAKAMVGAEPETQSESKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTDAGAGKIVKKEAVTQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSETLAVPREVAKMGATNKTGIVDET KTRALEETVSVAKTQSEARPGATVDARGNPNGMSREVAGVDMKSCAQ SQAVTKIQGDDMPGTGVEDMGNCMTMSRAESGADTRASAPQPIFAKT QTEAIPGAKIDAGGNTNAMWKIPMSYLKAITGADMRAAAQPAVAST HAEAMSDAKVKNRGNPNAMTKAGAKANLRANSQVEALPDARDKSRGN PNVMAKVGDGTDMLSCTQPQLVASVQADTLSDGKIKVRGNVNSMPKE GAGVDMKAQDDNRRVSQVASVKSTDGKTEDRTLKRPSTCGALAENSA ELKPRLELPSTIKACEVTTLTHKLWDNSVKAGTLITKLFLSSAQSMK IFCCLWNFVYKQLEDAAGLTMGGDVEEHESRLGAGEEAGVESWTALA RNVGEDELSRESSPDIEEISLRSFWAESENSNTFRSKSGKDASFES GAGDNTSIKDKFEAAGGVDIGSWFCAGNENTSSEKSAKAKAKKSSE SRGIYPYMPGAGMGSWDGAMIWSETKFAHQSEASFPVEDESQRKQTR TGEKTRPWSRCRKHEANMDPRDLEKLCMIEMTEDPSVHEIANNALY NSADYSYSHEVVRNVGGISVIESLLNNPYPYPSVRQKALNALNNISVG \SENHRKVKTYLNQVCEDTVTYPLNSNVQLAGLRLIRHLTITS\EYQH MGYKLLFQDFFVC*RWGSGRNLKDPV\LGMLLNFSKNPSMTKE\LLI ANAPT\YLGNIFFSKKETKENILNALSLEFENINYHFKRRAKAF\NPRD KFSKNSLYFLFQRPKACAKKLALAAECNDPEVKRVELLISKL</p>
2805	A	1	374	<p>NYFLSLRFDWHSSKS*GHPTCVHCF*/TKNE/CASCHCGAGLLGFLG</p>

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				GSSEGASHPCPSCLPLEVRS LHCS LGHC GECMPGASGWGPWTGPGHC PNLCQDKGSKRISWRVGRNGWGRPSFDNAPVAL
2806	A	162	789	AGQNGVSGSAERCLSCLLIPLALWSIENILLYIPNGHTFYASSNKL TNYVWYSERI*LSGIM\MLIVTTVLLVLENNNNYKC\CQSENCSKKY VTLLSIIFFSSLGIAFSGYCL\VISALGSCP*AIC/LAPLMGWGVCF* RALLGRFLTDS\SIWDSVPGNLAHVVEWNIILFSILITLSG\VQVII CLIRVVMQLSKILCGSYSVIFQPGII
2807	A	1	3282	MVWRVPPFLLPILFLASHVGAADVLTLLANLRLTDPQRFFLTCTVSGE AGAGRGSDAWGPPLLEKDDRIVRTPPGPPLRLARNGSHQVTLRGFS KPSDLVGVFSCVGGAGARRTRVIYVHNSPGAHLDPKVTHTVNKGDT AVLSARVHKEKQTDVIWKSNGSYFYTLDWHEAQDGRFLLQLPNVQPP SSGIYSATYLEASPLGSAFFRLIVRACREGRFGQSCQECPGISGCR GLTFCLPDPYGCSCGSGWRGSCQCEACAPGHFGADCRLLQCQCQNGGT CDRFSGCVCPSGWHGVHCEKSDRIPQILNMASELEFNLETMPRINCA AAGNPPFVRGSIELRKPDGTVLLSTKAIVEPEKTTAEFEVPRVLAD SGFWEICRVSTSGGQDSRRFKVNVKVPVPLAAPRLLTQKSRQLVVS LVSFSGDGP ISTVRLHYRPQDSTMDWSTIVVDPSENVTLMLNLRPKTG YSVRVQLSRPGE GEGAWGPPTLMTTDCPEPLLQPWLEGWHVEGTDR LRVSWSLPLVPGPLVGDGFLRLWDGTRGQERRENVSSPQARTALLT GLTPGTHYQLDVQLYHCTLLGPASPPAHVLLPSPGPPAPRHLHAQAL SDSEIQLTWKHPEALPGPISKYVVEVQVAGGADPLWIDVDRPEETS TIIRGLNASTRYLFRMRASIQGLGDWSNTVEESTLGNGLQAEQPVQE SRAAEGLDQQLILAVVGSVSATCLTILAALLTLVCIRRSCLHRRRT FTYQSGSGEETILQFSSGTLTLTRRPKLQPEPLSYPVLEWEDITFED LIGEGNFGQVIRAMIKKDGKMNAAIKMLKEYASENDRDFAGELEV LCKLGHPNIINLLGACKNRGYLYIAIEYAPYGNLLDFLRKSRVLET DPAFAREHGTA TLSSRQLLRFASDAANGMQYLSKQFIHRDLAARN VLVGENLASKIADFGLSRGEEVYVKKTMGRPLPVRWMAIESLNYSVYT TKSDVWSFGVLLWEIVSLGGTPYCGMTCAELYEKLQADRMEQPRNC DDEVYELMRQCWRDRPYERPPFAQIALQLGRMLEARKAYVNMSLFEN FTYAGIDATAEEA
2808	A	136	447	PRCPHNLPLSLCPGLQAEQPVQESRAAEGLDQQLILAVVGSVSATC L TILAALLTLVCIRRSCLHRRRTFTYQSGSAFLGSGASLCLHTSLAD VLSPAVATCQ
2809	A	3	3593	SSDRPSSFWLVWVGLWSMVWRVPPFLLPILFLASHVGAADVLTLLA NLRLTDPQRFFLTCTVSGEAGAGRGSDAWGPPLLEKDDRIVRTPPGP PLRLARNGSHQVTLRGFSKPSDLVGVFSCVGGAGARRTRVIYVHNSP GAHLDPKVTHTVNKGDTAVLSARVHKEKQTDVIWKSNGSYFYTLDW HEAQDGRFLLQLPNVQPPSSGIYSATYLEASPLGSAFFRLIVRGCGA GRWPGCTKECPGCLHGGVCHDHGECVCPPGFTGTRCEQACREGRF GQSCQECPGISGCRGLTFCLPDPYGCSCGSGWRGSCQCEACAPGHF GADCRLLQCQCQNGGTCDRFSGCVCPSGWHGVHCEKSDRIPQILNMA ELEFNLETMPRINCAAAGNPPFVRGSIELRKPDGTVLLSTKAIVEPE KTAEFEVPRVLADSGFWEICRVSTSGGQDSRRFKVNVKVPVPLAA PRLLTQKSRQLVVSPLVSFSGDGP ISTVRLHYRPQDSTMDWSTIVVD PSENVTLMLNLRPKTGYSVRVQLSRPGE GEGAWGPPTLMTTDCPEPL LQPWLEGWHVEGTDRLRVSWSLPLVPGPLVGDGFLRLWDGTRGQER RENVSSPQARTALLTGLTPGTHYQLDVQLYHCTLLGPASPPAHVLLP PSGPPAPRHLHAQALSDSEIQLTWKHPEALPGPISKYVVEVQVAGGA GDPLWIDVDRPEETSTIIRGLNASTRYLFRMRASIQGLGDWSNTVEE STLGNGLQAEQPVQESRAAEGLDQQLILAVVGSVSATCLTILAALL TLVCIRRSCLHRRRTFTYQSG\SGEETILQFSSGTLTLTRRPKLQPE PLSYPVLEWEDITFE\DLIGEGNFGQVIRAMIKKDGKMNAAIKMLK EYASENDRDFAGEL\EVL\CKLGHPNIINLLGACKNRGYLYIAIE YAPYGNLLDILRKSRVLETDPAFAREHGTA TL/SAPRQLLR/ASD A\ANGM\QLPGVRKAVHSTGDLGLARECCWSGENLGLQDLQTFGLFS

				/RGEEVYVKKTMRPLV\RWMAIE\SL\NYSVYTKSDVWSFGVLLW E\IVSLEGTP\YCGMTCAEALMKSPLQG\YPHGSKPRN\CDDEVYEL \MRQCW\RDRPYERPPF\AQIAL\QLG\RML\EAREGPM*NHVAV*K TFTYAGN*MPATAEAGPEAAHPSPEPWVLLAGSKTLLS
2810	B	85	283	MEKTELIRRSARWVSISSIEQKTDTSDDKLQLIKDYREKVESELRSIC TTVLELLDKYLIANATNPEX*
2811	A	1	932	KAKSRSKEVGLASRPRRRGSSRGSSRCGSALALALLALRPGPGGPA PAMEKTELIQKAKLAQAES/RYDDMATCMKAVTEQGA/QSLSNNEER NLLS\VAYKNVVGRRSA\WRVSKHPSRKTDTSK\KLQLIKDYRE KVD\SE\LRSI\CTTVLGICLDKYF/ILANGNLIPESK\VFYL\KMK G*FTFR\YLCLEVACC\DDRK\QTIDN\SGQAYQEA\FDISKK\EMQ PT\HPIRLGALLLTFSVFYIEI\LNNPEACLHAWLKTA*WRAIA*L DTLNE\DSYKDS\TIMQLLRDN\LPLWTSDSAGEECDAEGAEN
2812	A	199	214	PPSPLNSSTCCLAKTDEK*CKEKGSLLH
2813	A	1	2176	QGFLKFMADAGIE\FSQDEWKCLDPAQRTLYRDVMLENYRNLVSLGIC LPDLSTVSMIEQKRDPTLQSEEKIANDPDGREGICKGVNTERSSKLG SNAGNKPCKNQLGFTFQLHLSDLQLFQAERKISGCKHFEKPVSDNLS VSPLEKISSSVKSHLLNKYRNNDHAPLLPQEQKAHIREKAYKCNH GQVFRASASLTNQVIHNADNPYKCECGKVFSCSSKLVHRRMHTGE KPYKCHECGKLFSSNSNLSQHQRHTGEPYKCHECDKVFRSSSKLA QHQRHTGEPYKCHECDKVFNQIAHLVRHQIHTGEPYSCNCKGK VFSRHSYLAHQTVHTGEPYKCEECGKAFSVRSSLITHQLIHTGRK PYKKECDKVFGKRCFLTSHQRIHTREPRYGCSCGKIFSQKSDL/* RHRKTHTDKPYNGNKGTAFAREFSDLTAFHLSGKPYECKEKGK VFRYKSSLTSHHRIHTG\EKPYQM/CNRCGKVFSSNLVCHQKIHT GEPYKCNQCGKVFNQASYLTRHQIHTGERPYRCSKCGKAFRGCSG LTAHLAIHTEKKSHECKEKGKIFTQKSSLTNNHRIHIGEPYKCTLC S*GLSVTILTLHSFRGFHHEGPKLC/DGKTIIMSSSINHQQ*VHTK WKSYS*NVCDTGFIKACQITGHHITVEDESTQMNCVYLGYYSRTIA IEHDRIYTRSNSVSGSLILIYDIA
2814	A	3	276	VFSCGGSVTVKMLRNLLALRQIGQRTISTASRRHFKNKVPEKQKL F/QGTAYAIYELAVASFP/NEAGVTSVIPAIWFSFIQLSMDQ*SDK
2815	A	1	566	MDECRKKERKPLFGPERFKFVNAYARLGGSSGSGVAIFVGGVQLWRL LVSNSQDAAESAGRYWVDVRSAGEVTRDSWALRPDLGQRTD*ATA SPQGIKKNKVPGEAKNCSPEDEIP\LYLKGGV\ADALLYRATH\MI LTVG\GTSICPYELAVASF\PKKAGS*LQVIPSNSLWFQFSFQLFY GTK
2816	A	26	736	EPIPVTPDHLVMTTHIVANLLSCQQRPRLPNYEMLKEEQEVAK\LG APQKPCLPCEPPVIH\IRNE\TSWPDHVRVLPVQ\HPLHEHLLRLGF IRFA\YSVKSRLDRK\MVGEVNRGPKA*CLHRQSA*KIWGPDPFG\HL HEPILAHQSSPPKFWVVPGPAT\DREASL\RGALPVT\IPRTL\S SIPRPAPRGQEVLP\LTCTPLTPPSIPRPVPTAESCSPLSSHAFLQW HSIKCICFW
2817	A	748	1637	DIMESGFTSKDYLHFNPRDYLEKYKFGSR\HSAESQILKHL\K NLFK\IFCL\DGVEGETCLI\DIGFWAPLILSSSSSCFVESF*GRIV RSLDYFRTPQEPRELGRKW\LEGKEARGLFDWVPPMVTMCLNLERE TEVKGPRRRRKLK\QAVKARCLM*M*TQKPSHLGAVPL\PPG*TA VPQAHLCGLGCPPCPRPPQPTCKGASGTGQPYLKPRGPSLVIMDAAQ EQPTYMIGEQQFS\SLP\LGREAVKA\AVKEAGYTIWFVVISQSYS STMANN\EGFLSLVARKLSRPL
2818	A	1	1538	MENPIVKSIAKAREERLEDSKLEAVSDNNLELVNEILEDITPLINVDE NVAELVIGILKEPHFQSLLEAHDIVASKCYDSSPSSPEMNNSSINNQL LPVDAIRILGIHKRAGEPLGVTFRVENNDLVARIHGGMIDRQGLL HVGDIIEKVNHEVGNNPKELQELLKNISGSVTLKILPSYRDTITPQ QVFVKCHFDYNPNNDNLIPCKEAGLKFSKGEILQIVNREDPNWWQAS HVKEGGSAGLIPSQFLEEKRAKAFVRRDWDNSGPFCTISSKKKKMM

				YLTRNAEFDRHEIQIYEEVAKMPFFQRKTLVLIGAQQVGRRSLKNR FIVLNPTRFGTTVPFTSRKPREDEKDGQAYKFVSRSEMEADIKAGKY LEHGEYEGNLYGTKIDSILEVVQTGRTCILVDNPPQALKVLRSEFMP YVVFIAAPELETLRAMHKAVVDAGITTKLLTDSDLK\KTVDESARIO RAYNHYFDLIIINDNLDKAFEKLQTAIEKLMEPQWVPISWVY
2819	A	1	1749	EFVLNYPEPRVCRWGCSAAPVAEGEQRRRGATGSGGSGGAEEAAEVRAA MQQVLENLTLPSSGTAEEDLIFLKGIMENPIVKSIAKAHERLEDS KLEAVSDNNLELVNEILEDITPLINVDENVAELVGILKEPHFQSLLE AHDIVASKCYDSPSSPEMNSSINNQLLPVDAIRILGIHKRAGEPL GVTFRVENNDLVIAIRILHGGMIDRQGLLHVGDIIKEVNGHEVGNNPK ELQELLKNISGSVTLKILPSYRDTITPQQVFVKCHFDPYNDNLIP CKEAGLKFSKGEILQIVNREDPNWWQASHVKEGGSAGLIPSQFLEEK RKAFVRRDWDNSGDELDTIKFDRHEIQIYEEVAKMPFFQRKTLVLIG AQQVGRRSLKNRFIVLNPTRFGTTVPFTSRKPREDEKDGQAYKFVSR SEMKADIRAGKYLE\HGEYEGNLYGTKIDSILEVVQTGRTCILVDNPP QALKVLRSEFMPYVVFIAAPELETLRA\MH\KAVVDAGIHHPRL*P NSDLKKTVDDESARIQRAYNHYFDLDPNINDNPRPKPFKE\QTA\IE KPENGPPQWVPQSAWVYLMIQ
2820	A	14	230	FATLYPLKIFIFPKAFNPWREVGPLCPPPK/CKGPSKSPGW/CLNR PPIGKKLIPCKPRLTWAPPRIL*NGPP
2821	A	170	303	RPLRGTPC*CAAWASSWWGCCSACCSHCCLLGPCWHSGPCSA*WAFW CSGG
2822	A	208	547	AAPGAMGPWPDRLCGSALPSCRLPCYSSASVSLRCAEAENTFTQAGPC CWAHPHRAHQDFPLQIPFRHLEAPRCSPPLSAWPPRHLLPAGDPDLQ QEPPIRGAP*RPLRGTPCCGS\CGVAAGVRGCGPVL*HPEPADSH TATAEPRI*AAPGAMGPWPDRLCGSALPSCRLPCYSSASVSLRCAAE NTFTQAGPCCWAHPHRAHQDFPLQIPFRHLEAPRCSPPLSAWPPRHLL LPAGDPDLQEPPIRGAPLSLRRLLL
2823	C	48	173	MVRKRMEMKMRKLSQLRASGQLKMMRMXMSIPSRRRPRGIX*
2824	A	183	423	HGLFSVEENEENGEQADNEVEDEEEEGGEEEEEEEEEGDGEEDGDDE DEEAESATGKRAAEDDEDDVDTKKQKTDEDD
2825	A	147	588	TLAFLIPICIGSPACPTMSDAA\VDTSSEITTKD\LKEKKEVV\EEA ENG/REDRPLCTGNAENE\ENG\EQEA*QLR*DEE/EREGRLGREGG REGRKEG*LVEEEDGRLKIEEAESATGKRATE\DEDDDDCRYQSRRR PDEDDLDSKKAKS
2826	A	1	77	SGRPFFFFFFF*CKGFLIGYM
2827	C	175	351	MKLIQLSCQPFNSRHVLKKKPLTFMILSHFQASLSSIFGFCSSLFR QSSFFSNILFF*
2828	A	56	380	KYLVLDQHAGSPPVKNILAEAVQNIVQILH*EIQKSVNHYML*KLDT DSL**FIIQLQ\EPTILGIKVDVYKHEYKDKDGHSDFSNYSSHQVFF LFLILFNKDNMAIN
2829	A	3	129	GDCRLDPLHLAWNQPLWLSILPSINCLRYHNIPSYMYQNSY
2830	A	472	756	SSADSKCTLTIGKPAKSRVQLCHKEETFPNQTNAYRTCVD*CLMSPT LLGTSIF*SQMIIIRVVPICMPNIFLIISC*VLCIRKPVSELPHLLG F
2831	A	1	170	NSTTNCLVISNPQGLQYKGGANLHDSRDLGEFSNLTDFFEKSHVVHI LFVLHFYYS
2832	A	1243	5595	IMEIEEQKPKQLELLEQIEQQKLRLETD CFRAQLEEEKRRKKTQPTGV GCRKSHHYINHLVGIAPASCPIVSDSDSHROMIRNYQHQLLQONRLH RQSVETARKQLLEYQTMKGRCPSVSAPSLITDSVISVPSWKSERPT AISEHWDQGORLKLSPNKYQPIQPIQTSKLEQDHFQVARQNHFPQRQ VETTETLRASDILTNQALESQEHLRQFSQTETQQRDYKLVPKDSETL SRALSHDRQLISQDARKISETFGATTFSQLESQQLFSENSENISYHL TEPSSFVPLVPQHSFSSLPVKVESGKIQEPFSAMSKSTVSTSHSIIS QMHDRPPLLSENITAQQGNMKALQEQLDLQKKVLQATQEAQEQLLLC KQKEVEQQTGLSVFLPLVTPDSSALLPSAKADLGRIQES SPTKNNIA

				VSSDHHVISQLQDKRLSLSQPILSQNNFKFLQEQNLNIQKDSLQARR EAQEVLYVHKQSELDRRVCSEQAEPSPFPQVAQHTFTSLPSADTKSG KIQEQHSSKSEKGLVSCQSDIPISQDGSLSFLQQFLPLHDSLKLQ QLTKQRDTLQARHEAQVELLLHRQDRLGDSKSGLVSSSSSPVVQHS VASQASAKAEPRRIQELYLSEKENVGPSCHLIIPTFQDKSLSPQHS LAQQENLTILQEQSQIQRVILGAKEGTQEFVHTESELEKRISSEQTG TSSSLSQVDESERFQECISIKSDSTIPLSHPKIPRCQERLLRVSQHM LPLQDNLEEHQAWLDTEKEAFHFSQKTQENTSEQTGSSSFIPQLVQ LSFTSLASAESGTILEPLFTESESKIFSSHLQIPQLQDRLLRISQLI QPQDNLKALQEQLATQREAILARQEAAREELLHQSEWEGRISPEQ VDTSSLPLVPQHSFASLPLNESERNQEPSCINSNDNIVSSGHSEIPTL PDGLLGLSHLVLPQQDNLIALIEHLHAQTDFLPSIEKTQKELVLVSKP CKFEKVSSSEHFIQSHHGDQLALQQQLDTQKKAIRSIOEVQEEELLQ RLSELEKRVSESVQVSSSVFVSQVPVADSSERTQKSFPTKSNDTLPSSH REIPRLQDRLLSLSKPILPQQDNMTAQLDAQREVMYSYEKPQEELSL NKQRKLNKSESAEHTIPSLFLPKETEHSFIPLPFAEAKPKSTCELYS SQNEHAAPPSNPVPIPGFQDRLLSFSQS SVLTQQDNLGLQKQLDLQREV LHYSQKAQEKLLVQRQTALQQQIQKHEETLKDFFKDSQISKPTVEND LKTQKMGQLRDWFPNTQDLAGNDQENIRHADRNNSDDNHLASEDTSA KQSGEHLEKDLGRRSSKPPVAKVKCGLDLNQHELSAIQEVESPAIGR TSILEENLLPSREGPSGRIHLLIKEPLPSSSGSQVYVAMGLRQIP SFSKVFGIIRVATLLAVKGTSATVVNKAHAHMKTCLQREG
2833	B	2177	3174	MGKTTPMIQSRPSFDTWELQVPPSTCGDYNSSFikelRASQSNVIKP PGPVKLKESVVENHAVLSYAVEEEHAYLGPTVKPDDKAKTLSYEPLS SATVSTGSLLSYENTDLSLTDPESEHMDDSKQESTTSKEETNII SSIVPSTQDIYQRQNSSDVHKSLLPAVDETTGHTHFQQMIDKALYQ SGKPGTGHGIMEEPELTLISTTDTSAEMDFANLTLEEKSENEAKCF FQQSKTRLKRLKRVKHATFLPLATEASDYPAVSELSTIEKPTASTET PRRLTPVPGSLQEAFAIKRKKSFMERSHQKQEI RNKIHVSENSQIKT VKEKPSISSIL*
2834	A	2268	2547	KYLVDQHAGSPPGKSLCCLEKSQRMMNISQNLVDVLRV*TADDAN*E KCVPIILANLFFQVSNLLH*\VLVYHLLKVCVTTCSFIHCRQORFMNV
2835	A	137	716	TTTMSKKAKTKTKTKRP\QRATSNVFAMFDQ\SQIQGVQRGPFNM DQ\NRDGFHSDK\EKVLHDMLA\SLGKNPH*WHYLDAM\MNEAPGPI QFSPCFL\TLFG*GSLNGHQIP*RCSFRKRLAFALDE\EATGHPFRE DYL/REELLTNPWGDRVYQIEEVG*TCTGEAPI*QKGGNSNYHRSFT RHPNWKAPKAQR
2836	A	2	437	LVIIIESDLERAERAELSEG\KSDSWKNN*E*WIRP*KH*WLQRISK CAELEELKTVTNNLKSLEAQAKEYSQKEDRYEEEIKVLSDKLKEAE TRAFAERSVTKLEKSIDDLEDKFLCFTSPKTPSSSWMSHLSELICIC LFSS
2837	A	1	834	GSRVRRAAAGLSHCSPPARLP SGAMAGSSSLEAARRKIRSLQEQADA AEERAGTLQRELDHERKLRETAEA\DVASLN\RIQAWFEEFQFVP KERLATAF\QKL\EEAEEADESERGMKVIES\RAQKDEEKMEIQEI QLKEAKHIA\EDADRKYEEVARKLVIIIESDLERAERAELSEG\QVR QLEEQRLIMSD\KALMAEDKYSQKEDRYEEEIKVLSDKLKEAET RAEFAERSVTKLEKSIDDLEEKVAHAKEENLSMHQMLDQTLLELNNM
2838	A	9	1108	PDRATRPRPRARPADPALVLGPLAAVTMGAGKKMRMLKLDKENALD RAEQAEADKKAEDRSKQLEDELVS LQKKGTDRT*TGQIL*RLSKM PKEETWNWQEKKATDAEAD\VASLNR\RIQLVEEELDRAQERLATAL \QKLEEAEEADE\SERGMKVIES\RAQKDEEKMEIQEIPT*KRAKH IAEDADRK\YEEVARKLVIIIESD\LEPCRGSGAEELSEGKCAEA*KEE FENL*PNNFEVHLEGSRLRKYSQKERPDMEIEIKGFPDKA*RRLET RAWSFA\ERSVT*NLEKSIDD\LEDRAVTLQETEVQSHQRRSWDHAL NGYDFHISFFASLLPRLPRRSWMSHLSELFHLSYSPADPGSLS
2839	A	3	268	SGRCCECRIGTVISKSGIGGRDKLSRYQTVTCQAAQQLPSTCLSHR

				SLHGKKGKGGKDDGRGRGPGLVAPSPSALKLLNPVWLSLRD
2840	A	500	682	RTSLPCCSPAQEPCCRRTAWPTSMATTPTPSLRNTASGTCGSSSTSMW KRWTCRVTLKRN
2841	A	1617	2086	GLAASSRKHQMVDDADAVGGPGGPGMAGCDGLPGGFGSDIRPRLWLW LGPRLWSS*RGF\NIILASVPKLLLM/DCYALARDRTATLG\TFDA ISKSTASNWIPDLWKETVFTKFPYQEFTHL/VKTHTRVSKQKTQVPA VATTAARQTMEGQAPVEYI
2842	A	55	665	AMAEDHGLSNGDGPVEVTQGLELLVSAAAQDIVLLDGIQGLFRTLQF DNIWVNDHFLGKLPHRVFKGGGEKQHLAVPGQHPLDADALILVALSG YHDISLIQNKHLDLGINEL\DLEHQSSSTVPGVPMTICSLIFWPLSN LLPRTA*ASFSSG*NLPICSITFPV*SASSYVGERHRHWGYLSDGST RLSMAKTKAAVLPVPD
2843	A	43	548	LTGPITMAQAMIFCHTRKTASWLAELSKEGHQVALLSGEMMVEQRA AVIERFREGKEKVLVTTNVCARGEQRTCPTWSARLGVPGPIRARNPC IQGSRMVSGRWVGLVTLFSLRRDCLDFPEVVRTHTCQVRWLMIPAIPR QENCLNPGDRGCSEPRMCYSTPSWVTE
2844	A	1	876	MLKNEEPRRRPIMSNHTATHILNFALRSVLGEADQKGSVLAPDRLRF DFTAKGAMSTQOIKKAEIANEMIEAAKVTGSWERDPERTRVLSLDV GHAAGKGRMRGDKDLASHLQTVQPRPCSEWDLNNGHSRTLEEAPLSQ CCWGLRGLEPGALMRPVGGASLTLRSQHLISFPLTLEPVVVGGS LAFCAMAYPKVTSTHNVVTLGIDVEQVSVVINFDLPVDKDGNDNET YLHRIGRTGRFGKRGGLAVNMVDSKHSNMILNRIQEHFNKKIERLDT DLDEIEKIAN
2845	A	222	484	GNPLSSYSFCSMCLTELDPILTEVTLMNARSELYLRLFKKRISDFE VGDSMASEEVKQEHQKSLDKLLNNCLLSCTMQELIGLYVT
2846	A	3	218	SLFQLKTTKTQSRVMGAIYDSSWFQEDRQAAERFTDRSTHLRLRNAE AAA*TKPAQGGPSIPILPATPSSL
2847	A	322	452	LCCSI*IYLN/NLLIC*QSFSVLK*DFRVD*KKNPRMSHRVLNI
2848	A	3578	5288	TESREHFSPWYSVTAARRPQVASKAEENLLMVLGTDMSDRRAAVIFA DTLTLLFEGIARIVETHQPIVETYYGPGRLYTLIKYLQVECDRQVEK VVDKFIKQRDYHQQFRHVQNNLMRNSTTEKIEPRELDPILTEVTLMN ARSELYLRLFKKRISDFEVG\DSMVS*EVKQEHQKCLDKLLN*LAF LSCYHGRELIGLYVTMEEFMRETVNKAVALDTYKQGLTSSMVDDV FYIVKKCIGRALSSSSIDCLCAMLNATTELESDFRDVLCNKLRMGF PATTFQDIQRGVTSAVNIMHSSLQQGKFDTKGIESTDEAKMSFLVTL NNVEVCSENISTLKKTTLES DCTKLFSQGIGGE\QAQAKFDSCLSDLA AVSNKFRDLLQEGLTELNSTAIKPQVQAWINSFFSVFHNIEEEFND YEANDPWVQQFILNLEQQMAEFKASLSPVIYDSLTLGMLTSLVA\VEL EKVVLKST\FNRLGGLQFDKELRSL\IAYLTTVTW\TIRDKFARLS QM\ATIL\NLERVTEILDYWGPNSSGP\LTWRLTPAEVRQVLA LRIDF RSEDIKKAALVS
2849	A	233	801	VVTLTGSNLYFYCSLFIFSVLPDQDVSLV*ICYLSLPLDIVCFCNVK IQFFF\LSLESYY*FLTIFPHCFYLLKTPFKHRELFILVFGLLKIP Q/LC*FFYLILLRIFYFINFCFLDLFLFWIFIWYFVIACSWFIGV SLKFLLVPL/CSFFLRCRHSPLF*GAS*TDLYILGCIPFP*VCLLWE FCGGL
2850	A	170	495	LCSLTGQSGAGNNWAKGHYTEGAELVDSVLDVVRKEAESCDCLQGFQ LTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVVE PYNATLSVHQLVKN
2851	A	70	1474	RESGTWQPGKAGTQTGAKFWEVISDEHGIDPTGTYHGSDQLQERIN VYYNEATGGKYVPRAVLVDLEPGTMSVRSFPFGQIFRPDNFVFGQS GAGNNWAKGHYTEGAELVDVFL\DV*RKEA\ES*DCL\QGFQLTHSL GGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVVEPYNAI LSGH\QVENTDETYCIDNEALYDICKLTLK\TPPF\GDLNHLVS ATMSGVTTCL\RFPGQLNADLRKVAVNM\VPFF\RLHFFM\GGFAPT DQAGASQASTRALTVPRSSPKQ\MFDA\KNMM\AACDPRAWAAYLDG

				LPPCFRGPVPLKEVDE\QML\NVQKQKQPAIFVE\WIPQQCEKRAV CDIPLRLGLKNVRPPSFGKQARPIPGAFSKPHLPKQFHGPCFRRKAL PSFITGGEGMDEM\EFHPRPESNKN\LVSEYQ\QY\QDATAEE\EG EFEGRSLSGRKVA
2852	A	284	359	QQEANPSAPLQHVSTSN/CVLTCCGAEGLASCCYCHCLCNECCQG ACGPDTHLAHCCRCQHSSKPPGGPRI/ASTQTCYY*CPCRLPGGSRT *CLASCPYHWPWTSLPGSPVPNKAPP
2853	A	295	478	YYKRIPEAKRLTNTVFNFSIFSHSTHRTFGKQQWQQLYDTLNAWKQ LNKVKNSLLSLSDT
2854	A	1	1167	MVELLGSYTEDNASQARVDAHSCASSVARPSSSLFRSAWSCEWSVRCA RACTMSVPAFIDISEEDQQONEKYRVPQFDQSTIKNIESAKGLDVWD SWPLQADGTVAEYSGYHVVFALAGSPKADDDTSIYMFYQKVGDNIS DSWKNAGRVPFKDSKDFDANDPIMKDQTQEWSGSATFTSDGKIRLFYT DYSKGHYGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQN VQQFIDEGNYTSGDNHTMRDPHYVEDKGHKYLPNRGHARSSRRRQEI SKIREELKEIEIQKPLQKINESRSWFFKINRVDRLRLARLMKKREKN QIVAIKNDKGDMMTTDPTETIQTTVREYYKHLAYKLENLEEMGKFLDT YTLPLRNQEEVDL
2855	A	3	1328	SGILGTTTPSPFVGVVLRVECPLCPGPAPMSVPAFIDISEEDQAAEL RAYLKS KGA\EISEENSEGLHVDLAQIEACDVCLKEDDKDVESVM NSV\VSLLLIL\EPDKQ\EA\LIESLC\EKLGPNFREGEPPRLRLQ FVKATFSTGMD*EILPVKIHVSICSL\IKV\AASCG\AIQYHPQLEP GIKFRKWDFLNWN\LTTGKKSTPLLKTTFMKALVDCCKSDAASKGM\ VELLGSYPGGQCFPRARVDAHR\CIV\RAKDPN\AFPF\HLLTLK PRQVFWKGELI/HIVPF*PNFVSA*MGHHMSRFYDP*LRTFH*IPLG PVTMDPGIWPKMRLFLLLWGMGQ*ENR\EISFWTTPARNFRIGA\D D\VEAFVIDAGKELKMVYCQNSRPQRKVVVSHSTHR\TFGK\QQWQ QTV/YDTLNAWKQNLNK\VKNSLLSPSGYLKFLCL
2856	A	377	2393	FSLECLGHENR*D*ITIYKITS LGTGKVFNKIQHPFTIKNKK*KTLN KLGIEGNFLNLIKGIYEPMVSIILNGEGLDYFPLRSETRQGCLLWP FLFN/IVLDSQERAIRQENKIKVI*VGKEEV*LNR\MGDDMVLCIV IQGK\I*KIQRHLLINKFSKVTGYRI/NICRKLVI FHI*YQLNKSQ NDVKKTI*FSTMVKGGLC/RVIPTLWESEAERLLEARRPAWETVRS HLYKNKQTKNNKQTKN/TLDVMTLICRLSYSEAEV*GWLEPQSSKLQ *AITGSLQSSLDQRS*TLTQKTKKKRKL TASERVKYQYN*GSRNI D/PHLSSN*LENSA*GQFQWGGKIVFFIK*CLETWISTWQNNGNWD SYLILHIKINSELT*DLNVRANIVSIFKEN/MGVNLSDFELGNDFLN K*/PLKTQATKEENR*IKIKTICVSKDNIAKAKIQPTE*DNFF*NHV LVKGGICI*NM*RTVTII IKRHIIQFLKIQQGVWN*QFSKGGYTKGP LRHMEKVSQPSLAIREMQMRSTMRHYLT\PLE*TYNQSDNIKCW*GC REIGTLMHCWW\YPRDIKTNVYTKTCAQMFLPALFI*AQK*NGP*FL S\LTSALTKTWHIHT/MEYYSSQ*KKEMKVLIWPPTTMEKPLEKPYP SEECPRHERPTYMISIMKCPRTGEYI
2857	A	3	446	GEFADSF/SSMGSPVNAQDFCTDLAVSSANFIPTVTAISTSPDLQWL VQPALVSSVAPSQTRAPHFPGVPAPSSGAYS RAGVVKMTTGGAQSI GRRGKVEQETDQLEDEKSALQTEIANLLKEKEKLEFILAHRPACKN PDDLGFPE
2858	A	295	1622	DEMSVAGSFLFTAACGTGNSPHLCPEHARSRLSPSVLF*DFCTDLA VSSANFIPTVTAISTSPDLQWL VQPALVSSVAPSQTRAPHFPGVPAP SAGAYS RAGVVKTM\TGGA\QSIWQEGARWEQVRNF*RTLPGNVGA GWEAAPQM QEPSTEDEAT*WGLLAHP*LGALAPSPFHPNSDSEFSP* EVLS*FLP*VSYRMLSDWALLCSLAEDLILNASHT*SATAGQKWFHS GVPGSREAAGASSTGVGEWR*WQTLNLLNVGLFL*LF*LSPEEEKRR IRRERNKMAAAKCRNRRELDTLQAGRYSVGCSFLKLKGKVGRLH KGP*VRLCLYAFPLSLCIQ\ETDQLEDEKSALQTEIANLLKEKEKLE FIL\AAHRPCLARFP\DGPGAFPEEMSVASLDLTGGLPEVA/TPESE

				EAF/TLPLLLNDPEPKPSVEPVKASA
2859	A	3	1467	PHLQRATEKPRLSRRPRRSEAVTVLLPSSASQRPPVSAPRPLARLC LTATMMFSGFNADYEASSSRSSASPARD\SLSYHSP\AD\SFPSM GSPVNAQDFCTDL\AVSSANFIPTVTAIST\SPDL\QW\LVQPALVS /SLWAPSQTRAPSTFSESPPPTAGA\YSRAGVVKTMTGGRAQSIG\R RGKVEQLS\PEEEEEKRRIRR\ERN\KMAAAKC\RNR\RR\ELTDTLQ A\ETDQLED\RKSAEQTEIANLLKEKEKLEF/LSLAHR\PA\CKIP LIDLGLPRKE\MSVGS\LDLTGGLPEGS\TPE\SEEFTL\PLLNDP EAQGPQWEPVQGGISRHS*KDRGPFDDFLFPSIHGPGSGFLRTARS V\PDMGPILGPFYGRQIRGAFSHSGSLGMGAHGRGWEPLCTPVVTC TPSCNCLHVFPFRHLPRG*LLPQLCSCPPQGGQQQ*AFL*LAQLTHA AGPVRGQGRGSRHPQVPLPELVHYREEKHIFPRGFL
2860	B	1	196	MAEGNHRKKPLKVLES LGKDFLTGVLDNLVEQNVLNWKEEEKKKYYD AKTEDKVRVMADSMQEKQX*
2861	A	1	988	MGSLEGNHRKKPLKVLES LGKDFLTGVLDNLVEQNVLNWKEEEKKKY YDAKTEDKVRVMADSMQEKQRMAGQMLLQTFNIDQISPNKKAHPNM EAGPPESGESTDALKLCPHEEFLRLCKERAEEIYPIKERNNRTRLAL IICNTEFDHLPPRNGADFDITGMKELLEGLDYSVDVEENLTARDMES ALRAFATRPEHKSSDSTFLVLM SHGILEGICGTVHDEKKPDVLLYDT IFQIFNNRCLSLKDKPKV IIVQACRGANRGELWVRDSPASLEVASS QSSLENLEEDAVYKTHVEKDFIAFCSSTP\KYSWCCHLEEVFRKHCSQ
2862	A	12	914	GSFQRCCKGQRLFPMAEGNHRKKPLKVLES LGKDFLTGVLDNLVEQNV VLNWKEEEKKKYY\DAKTEDKVRVMADSMQEKQRMAGQMLLQTFNIDQ ISPNKKR**IGVTEAEITIVLQYPAHPNM\EA\GPPESSGRILP DCLK\LCPH\EEFLRLCKERAEEIYPIKERNNRTRLALIICNTEFDH LPPRNG\ADFDITG\MKELLEGLDYSVDVEENLTARDMESALRAFA TRPEHKSSDSTFLVLM SHGILEGICGTVHDEKKPDVLLYDTIFQIFN NRNCLSLKDKPKV IIVQACRGGEC
2863	A	12	1353	GSFQRCCKGQRLFPMAEGNHRKKPLKVLES LGKDFLTGVLDNLVEQNV VLNWKEEEKK\KYDAKT\EDKVRVM\ADSMQEKQRMAGQMLLQTFN \NIDQISPN\KKAHPIMEAGPPES\GESTDALTLCPEEFLRLC*RK ELKEIYPIKGRRKQPTHAGLFFI\CITEFDHLPPR\NG\ADFDITGM KELLEGLDYSVGVGRRFLTARGM\DSAL\RAFATRPEHKSSDSTF L\VLM SHG\ILEGICGTVHDEKKPDV\LLYDTIFQIF\NNRNLQPQ* RDKPQGSSIVQ\ACRG\ANPSGN*WV\RDSP\ASLGKWPSSQSSGEP WRKDAV*QDPHV\ERRDFIGFPGSFKRPHNRAPWERPAQWGSIFITQ \LITCLPRNIPWCC\HTLEEVFRKGTAIHLETTPR\AKAQM\PTIERT VR*QGYFYLPGEFENWEGHKQPSPSLNPTFKEAPFFVTACIF
2864	A	66	392	AQCLLLQSPGFEPWPVLAHPRALQSLQRKHGRSDCGGTGEEASGSS LES DAGFGPPGPGCAVPQVFQDCPVCLGNHHSQVLGGYCTEGPGLA AGSQACSPGLRVAP
2865	A	131	551	KIRGVSCPSAPKSGEQTGQHHNINTGFHPLPLGAVTSPVPQGPGRDL CPPPSSPEPAQPAQ/C*PCSDSGRSPGPGPKAWTVAPC\PEPSVFC LQSPGFEPWPVLAHPSSERRASSSGLDDDLPAQETGNGSGATRTC S
2866	A	943	1111	LMVLSDFIFKLKI/WPGAVAHACNLSTLGGRRWIT*GQQFETSPAS IVKPPSLLKI
2867	A	112	1078	ESSRQALLAKPLSACAEQPARAEVGAATALPVRWASGEMAPSGSLAG PLAALVLVLWGAPWTHGRR\TNVRVITDEN\WRELLEGDWMIEFYAP WCPACQNLQPEWESF\AE\WGEDLE\VNIKVDVTK\QPG\SGRFI I\TALPTIYH\CKDGEF*AVIQGPRTKKDFINFISDKEWKSIEPVSS WFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALA TLFSGLLGLCMIFVADCLCPSKRRRPQYPYPSKLLSESAQPLKK VEEEQEAEEDVSEEEAESKEGTNKDFPQNAIRQSLGSLATDKS
2868	A	1	448	HRGGLPGLKLPDFQDSIFEYFNTAFLLDLTFRTSSASEQETQAPKP EASPSMSVAASEQQEPKAHQFSIKSFSSPTQCSHCTSLMVGLIRQGY

				AGEVCSFACHVSCKDGAPOVCPIPEEQSKRPLGVDVQRGIGTAYKGH VKVPKPTG
2869	A	1	536	IISPHINKDEDVQRDLEHSLQMEAYERRIRRLQEKELELSRKLQEST QTVQSLHGSSRALSNSNRDKEIKKLNEEIERLNKNIADSNRLERQLE DTVALRQEREDSTQRLRGLEKQHRVVRQEKEELHKQLVEASERLKSQ AKSALSGPAPPSPATPLPSWAFCEWMTGVLVFTFLM
2870	A	1	5193	MAAAGTGTCWLLAIGSQKVKWPLSLPVAVVMKNTERIYAMKILNKW EMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLYLVMDYYV GGDLLTLLSKFEDKLPEDMARFYIGEMVLAIIDS IHQLHYVHSWTPKA FRVRKSVADQDPVGAPHRDIKPDNVLLDVNGHIRLADFGSCLKMND GTVQSSVAVGTPDYISPEILQAMEDGMGKYGPECDWWSLGVCMEML YGETPFYAESLVETYGKIMNHEERFQFPESHVTDVSEEAKDLIQRIC SRERRLGQNGIEDFKKHAFEGNLNENIRNLEAPYIPDVSSPSDTSN FDVDDDLVLRNTKSLKITNLVTACATVIEIRVCLLCFSDRGSLSIM QSNLTLDKDEDVQRDLEHSLQMEAYERRIRRLQEKELELSRKLQESTQ TVQSLHGSSRALSNSNRDKEIKKLNEEIERLNKNIADSNRLERQLE TVALRQEREDSTQRLRGLEKQHRVVRQEKEELHKQLVEASERLKSQA KELKDAHQQRKALQEFSELNERMAELRAQKQKVSRLRDKKEEEMEV ATQKVDAMRQEMRRAEKLKKELEAQLDDAVAEASKERKLREHSENF KQMESELEALKVKQGGRGAGATLEHQEISIKI SELEKKVLFYEEEL VRREASHVLEVKNVKKVHDSHQALQKEILMLKDKLEKSKRERH NEMEEAVGTIKDKYERERAMLFDENKKLTAENELCSFVDKLTQNR QLEDELQDLAAKKESVAHWEAQIAEIIQWVSDEKDARGYLQALASKM TEELEALRSSSLGSRITLDPLWKVRRSQKLDMSARLELQSALEAEIRA KQLVQEEELRKVKDANLTLCRSPWQPDFLCPLHEVAGIARLPVRVVL VLLGAATILPVMGKILMGLTAERPGPCVPPEEQRTLGLTRLGSKLKD EAKNRELLEEMEILKKKMEKFRADTGLKLPDFQDSIFEYFNTAPLA HDLTFRITSSASEQETQAPKPEASPSMSVAASEQEDMARPPQRP PLPTTQALALAGPKPKAHQFSIKSFSSPTQCSHCTSLMVGLIRQGYA CEVCSFACHVSCKDGAPOVCPIPEEQSKRPLGVDVQRGIGTAYKGHV KVVPKPTGVKKGWQRAYAVVCDCKLFLYDLPEGKSTQPGVIAVQVLDL RSAFGQHCPCSVNLPQLSLAKRTVTASLLGAPSKTSSLLILTENENE KRKWWGILEGLQSIHLKRNRLRNQVHVPLEAYDSSPLIKAILTAI VGCVLQVSEATALPAALQCPSENQMKVTGPFVDSFSMHVKKQTRP DADRIAVGLEEGLYVIEVTRDVIVRAADCKKHQIELAPREKIVILL CGRNHVHLYPWSSLDGAEGSFDIKLPETKGCQLMATATLKRNSGTC LFVAVKRLILCYEIQRTKPFHRKFNEIVAPGSVQCLAVLRDRLCVGY PSGFCLLSIQGDGQPLNLVNPNDPSLAFSLQSQSFDALCAVELESEY LLCFSHMGLYVDPQGRRARAEQELMWPAAPVACSCSPHTVTVSEYGV DVFDVRTMEWVQTIGLRRIRPLNSEGTLLNLLNCEPRLIYFKSKFSG AVLNVPTSDNSKKQMLRTRSKRRFVFKVPEERLQQRREMLRDP RSKMISNPTNFNHVHMGPGDGMQVMDLPLAAMLAETVPKAVPARL ALCSDLLALLSHKPVSAAELFTSTYPVTRPCAQASGRPGQ
2871	A	1	356	DPLWKVRRSQKLDMSARLELQSALEAEIRAKQLVQEEELRKVKDANLT LERCSPWQPDFLCPLHEVAGIARLPVRVVLVLLGAATILPVMGKILM GLTAERPGPCVPPEEQRTLGLTRLG
2872	A	1	401	RRCQTACFREERDVLVNGDCQWITALHYAFQDENHLYLVMDYYVGGD LLTLLSKFEDKLPEDMARFYIGEMVLAIIDS IHQLHYVHRDIKPDNV LDVNGHIRLADFGSCLKMNDGTVGIFVGDFFPGFGFGI
2873	A	151	5459	AGARRRGGEAPLLPGLAAAEPPEARPDGLAEPVVRGRRVGS GTMSAKVRLKLEQLL\DGPRNESALSVEITLLDVLCVLYTECSHS ALRRDKYVAEFLEWAKPFTQLVKEMQLHREDFEIK\VIGRGAFGEV AVVKMKNTERIYAMKILNKWEMLKRAETACF\RENDRDLVNGDCQ\W ITALHYAFQDENHLYLVMDYYVGGDLLTLLSKFEDKLPEDMARFYIG EMVLAIIDPIHQLHYVHRDIKPDNVLLDVNGHIRLADFGSCLK\M\ND DGTGAVPPVAVGTPDYISP\EILQAMEDGMGKYGPECDWWSLGVC

				YEMLYGETPFYAESLVETYGKIMNHEERFQFP SHVTDVSEEAKDLIQ RLICSRERRRLGQNGIEDFKKHAFEGLNWENIRNLEAPYIPDVSSPS DTSNFDVDDDLVRNTEILPPGSHTGFSGLHLPFIGFTFTTESCFSDR GSLKSIMQSNLTLTKEDEVQRDLHSLQMEAYERRIRRLQEKELELSR KLQESTQTVQSLHGSSRALSNSNRDKEIKKLNNEIERLKNKIADSNR LERQLEDTVLRQEREDSTQRLRGLEKQHRVVRQEKEELHKQLVEAS ERLKSQAKELKDAHQQRLALQEFSELNERMAELRAQKQKVSQRDRD KEEEMEVATQKVDAMRQEMRRAEKLRLKELEAQLDDAVAEASKERKL EHSENFCKQMESELEALKVKQGGRGAGATLEHQQEISKIKSELEKKV LFYEEELVRREASHVLEVKNVKEVHDSHQLALQKEILMLKDKLE KSKRERHNEMEEAVGTIKDKYERERAMLFDENKKLTAENEKLCFVD KLTAQNRQLEDELQDLAAKKESVAHWEAQIAEIIQWVSDEKDARGYL QALASKMTEELEALRSSSLGSRITDPLWKVRRSQKLDMSARLEQSA LEAEIRAKQLVQEELRKVKDANLTLESKLDSEAKNLEEMEILK KKMEKFRADTGLKLPDFQDSIFEYFNTAPLAHDLTFRSSASEQET QAPKPEASPSMSVAASEQEDMARPPQRPSPAVPLPTTQALALAGPKP KAHQFSIKSFSSPTQCSHCTSLMVGLIRQGYACEVCSFACHVSCKD APQVCPIPEEQSKRPLGVDVQRGIGTAYKGVKVPKPTGVKKGWQRA YAVVCDCKLFLYDLPEGKSTQPGVIASQVLDLRDEFSVSSVLASDV IHATRRDIPCI FRVTASLLGAPSKTSSLLILTENENEKRWVGILEG LQSI LHKNRRLRNQVVHVPLEAYDSSLPLIKAILTAAIVDADRIHVL EEGLYVIEVTRDVIVRAADCKKVHQIELAPREKIDVILLCGRNHVL YPWSSLDGAEGSFDIKLPETKGCQLMATATLKRNSGTCLFVAVKRLI LCYEIQRTKPFHRKFNEIVAPGSVQCLAVLRDRLCVGYPSGFCLLSI QGDGQPLNLVNP\NDP\ALAFSLHSSS\DALCAVELESEYLLCFSH MGLYVDPQGGRRARAQELMWPAAPVACSCSPHTVTVSEYGVDFDVR TMEVWQTIGLRRIRPLNSEGTNLNL\NCEPRL/VF*FKSKFFGKRV FQTWPD\TSDNSKKQMLRTRSKRRFVFKVPEERLQORREMLRDP RSKMISNPTNFNVHVMGPGDGMQVLMDLPLSAVPPSQEERPGPAPT NLARQPPSRNKPYISWPSSGGSEPSV\TVPLRMSDPPDQDFDKEPDS DSTKHSTPSNSSNPSPSPNSPHRSQPLPLEGLEQPACDT
2874	A	1	764	MEKIPILRSLRAREQQAGKDVTLQGEHQHLPPEPGCQOTVPLSVGRRP PDTGPGPETNSMEAAPGSPPGEGCPACSRCLRWEPPPPGRPC*PEESP AGT/PAPCPGSPG\GPAAQSLPPLPG/PLPQPSRPSA\SGPAPGH RHPEGGAGQAAEQ\GPRGQPRSSLQTSP\PRPLAAPVPM\PRGLA WQDVSEPPP\GCSGLNSSQKSPLSERPGPPVSGEA/GP/DGSSHSAQ RLQPPNRAGSGLESVSVLEQSGRGARD
2875	A	1	1641	MKVCSSIAEVSDTTNPPSRTNSGHMTSVLKQALKDPCRTRHRYRLVLW TLERTEVLDLFIERFCMTGGNSPICYLKAYHTNLYLSADAQKREAI DEGIAAATIFSPSRDVVSQSQRVAFDGDVLFSDSESRIVKATLD RFFEHEKAHENKPLAQEQGSTSFDPKVEAFRSPSVPLPITGHSANVY QTPTCARRRTTRPLVNWELIPRDNPPPLPPRQAFRDLGQSPAFSDAVA TTSAPVFGGDCHLSEVRGAETRQPAFAMKRPKEPSGSDGESDGPIDV GQEGQLRSSKLEKAEVLQMTVDHLKMLHATGGTGFFDARALAVDFRS IGFRECLTEVIRTPTIWLPLGRSKAVESQSQQFTGAHSTLGEPTAKK \A*SNPQVYMDIKIGNKPAGCIQTLLRSDVVPMTTENFLYMCTH/SK GLGFKGSSFHRIIPQFICQSDFTNHGGTRGKSIYKKKFDDENFIK HTGPGLRRHGTKCPMAHLALMEASKGQDQHPLLRKERAQQVHDVVK LTRGRGRGISLKRIARSLCKDKETGLCTLTWH
2876	A	1	949	LLLLGHASTSTGGGGRASKMATTKRVLYVGGLAEEVDDKVLHAAFI PFGDITDIQIPLDYETEKHRGFVFEFELAEDAAAAIDNMNESELF RTIRVNLAKPMRIKEGSSRPVWSDDDWLKFKSGKTLEENKEEGSEP PKAETQEGEPIAKKARSNPQVYMDIKIGNKPAGRIQMLLRSDVVPMT AENFRCLCTHEKGFSGKSSFHRIIPQFMCQGGDFTNHNGTGGKSIY GKKFDDENFILKHTGPGLLSMANS GPNTNGSQFFLTCDKTDWLDGKH VVFGEVTEGLDVLRLQIEKQESAITSQPRSWKLT

2877	A	185	339	LLLPPPPFGSSPWLNLHLHAALDHLPRPAAITCQKQGESAITSQPRS WKL T
2878	A	673	1085	GEPTAKK\A*SNPQVYMDIKIGNKPAGCIQTLLRSDVVPMTTENFLY MCTH/SKGLGFGKSSFHRIIPQFICQGSDFTN\HGCHQGSQA\HGK CPMAQFGPHGGLKRAGPAPSST\GKERAQQKQGESAITSQPRSWKL T
2879	A	141	1959	PRPANLLKKGGQITMSATVVDVNAAPLSGSKEMSLEEPKMTREDW RKKKELEE\QOKLGNAPAEVDEEGK DINPHI PQYISSVPWYIDPSKR PTLKHQRQPQPEKQKQFSSSGEWYKRGVKENSII T\KYRKACENC GA MTHKKKDCFERPRRVGAKFTGTNIAPDEHVQPQLMFDYDGRDRWNG YNPEEHMKIVEEYAKVDLAK\RTLKAQKLQEBELASGLVEQANS PKH QWGEEEPNSQTEKDHNSEDEDEDKYADDIDMPGQNFDSKRRITVRNL RIREDIAKYLRNLDPISAYYDPKTRAMRENPYANAGKNPDEVSYAGD NFRVRYTGD TISMGT\QV\FAWEA\YDKGSE\VHL\QADP\TKLELL YKS\FKVKK\EDFKEQOKESILEKYGGQEHL DAPPAELLLA\QTEDY VEYSRHGTVIKQERAVACSKYEEDVKIHNH THIWGSYWKEGRRGN\ KCCHSFSKYSYCTGEAGKEIVNSEECIINEITGEESVKKPQTL MELH QEKLEKEKKKKKKKKKKHRKSSSDSDDEEKKHEKLKALNA*EA\RL LHVKET\MQI\DERKRP\YNSMY*TSRP\IEEEMEAYRMK\RQRPDD PMASFLGQ
2880	A	711	1141	GVGVCFFPVPSSLRVLGRWAAFCALPGRSLRKSRLWGTGHTQS*E GELPWKAG/WQRCFWRGGRQTLPLTCS PRTRGCRAAQEGAGCKARG AWWVRSPGRAGRPLRRGGS RVTLNSQMGS DATGETEWIKEMPKPKKK KMS
2881	A	1	649	MAGALVRKAADYVRSKDFRDYLMRV TQQPYKVFNSGPWAFSSSYMS RPSAHISSLIVSRVSSSTSFQGG LGAGMGVEPLDPHENLYVDFYRG FIHNCQNL EANKMSFGRSQSEKAAYYL VPTTQ RSGKGKIMELVERSV VARVEHF WGPVANWGLPIAA INDMKKSPEIISGRMTF\VQPRNWLLF ACHATNEVAQLIQGRLIKHEMTKTASA
2882	A	1	389	FRAAGGLAGVSLALGSGSRGRDHSGSGVGTAMAGALVRKAADYVRSK DFRDYLMSTVRKLFPSISGFCRLSALTGLV TGLASFAYESLSSRHG WQVVKGAYCTLACPGEP RHELCD SHAPGAAPYSCF
2883	A	27	554	LAVGCRGVGLGVIGSGKRQQRQGPLGVSVSAQPCAGALVRKAADYVQ SK\DFRDYL\MSTH\FWGPVAN\WGLPIAA INDMK\KSPGDYSVGRM TF\ALC\CYS\LTFMEILPYKVQI*PLNWL/LCFACHGTNEVRPSFI QGEGRLIPNTRMDLKRASGINQWGKGKNKVFEGDSLCPGCC
2884	A	1	162	QCAEKIASNP KIVVAMAKESVNAAFKITLPEG\DDRKEGMTPFVEKR KANFKDQ
2885	A	1	196	FPGCYSSKFLKHWDHLTQFKKPVI AAVNGYAFGGGCELAMMCDIIYA GEKAQFAQPERTSAACQF
2886	A	148	427	CLLGFTTHSASHDQPLPAGAGGTQRLTRAVGKSLAMEMVLTGDRISA QDAKQAGLVSMICAVETL*CLLGFTTHSASHDQPLPAGAGGTQRLTR AVGKSLAMEMVLTGDRISAQDAKQAGLVSMICAVETLVGGAIQCAEK IASNSKIVVAMAKESVNA
2887	A	1	1484	EATLTRPRPAGGPAAGWYCPSAKTSGQLGAGFTFSPLERHCPLSPSH LAVHPAGAGPVQOANREAPASPIFGLACCSGPVPDLNAAGTPRIFTS PTLRP\LARGANFEYIIAEKRGKNNTVGLIQLNRPKALNALCDGLID ELNQALKTFEEDPAVGAI VLTGGDKAFAAGADIKEMQNLSFQDCYSS KFLKHWDHLTQVK\KPVIAAVNGYAFGGGCELAMMCDIIYAGEKAQF AQPEILIGTIPGAGGTQ\RLTRAVGKSLAMEMVLTGDRISAQ\DAKQ AGLV\SKI\CPF*DTGWKEAIQF\AEKIASNSKIVVAMAKESVNAGR SPNLSECIYLEGVAVPRACRWLEAGYSEESILKERRLLSPEVFGKV LPWERMLAPALEPQRLPPSAHLDLLCLASCKERAWNEQSQRRSWCRP RPALALVLSFLVFI LGYFSLFAAPLPPHSLSSRAQFAISPFIOFLSL LGAVGYRSVTFGGHSRAVGSARSPLGQCL
2888	A	1	946	GRGVQRAMAALRVLLSCARGPLRPPVRCPAWRPFASGANFEYIIAEK RGKNNTVGLIQLNR\PLPVNWLCDCL\ID*LNQGLKIFEEEDPAVGAI

				\VLTGGDKAFAAG\ADIQKQLQNLFSRDC\YSSKFFGRHWGPPSPR VKKPVIAAV\NGYAFGGG\CELCH*CVDIIL/YAGEKAQF\AQPBIL IGNLPRVRGGTQEDSPVPVGKSLAME\MV\LTGDPDPQPDQAQASRV LSSKICP\VELLVEEAI\QCAEKIA\SNSKIVVAMAKESVNAAFEMT LTEGSKL\EKKLFYFNLWPLDDRERRG*PRFVGKEKGPTFKDQ
2889	A	1	384	VRDYNLTTEEQKAIKAKYPPVNRKYEYLDHTADV/QWIVLHRA*YFF RLHAWGDTLEEAQEFCAMAMFGYMTDTGTVEPLQTVEVETQ/GWGEE FSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
2890	A	1	332	RDYNLTTEEQKAIKAKYPPVNRKYE*DDLQSLLFHFLDEWLYKFSADE FFIPREVKVLSIDQRNFKLRSIGWGEEFSLSKHPQGTEVKAITYSAM QVYNEENPEVFVIIDI
2891	A	3	425	SFMAQEEEDVRDYNLTTEEQKAIKAKYPPVNRKYEYLDHTADVQLHAW GDTLEEAQEFCAMAMFGYMTDTGTVEPLQTVEVETQV\HADEFFIPR EVKVLSIDQRNFKLRSIGWGEEFSLSKHPQGTEVKAITYSAMQVYNE
2892	A	91	598	LKNRRRSRPSIRQSIGSTSVSRWLTSFLTLDHTADVQ*V*REFIPL KPRQ*ED*MFQSWLHAWGDTLEEAQEFCAMAMFGYMTDTGTVEPLQT VEVETQDDQLQSLLFHFLDEWLYKFSADFEFFIP\GWGEEFSLSKHPQ GTEVKAITYSAMQVYNEENPEVFVIIDI
2893	A	359	938	IYFFRLHAWGDTLEEAQEFCAMAMFGYMTDTGTVEPLQTVEVETQCK *LQV\LLFHFDEWLYKFSADFEFFIPGKLCAIVF*KRL*RPGAVAYA CNPSTLGSRGWIT*QGEFETSLTNKEVKVLSIDQRNFKLRFN\GWG EEFSLSKHPQGTEVKAITYSAMQVYNEENPGSFCDHWTFTKTQKIKR LPTGKK
2894	A	220	345	LKKEKSLMEKHFF*QTDSSSVSNLEKNHEPSDIVNSLQWAMVS
2895	A	1	281	TLKYTGIRNKSSMVVIDVKMLSGFTPTMSSIEELENKGQVMKTEVKN DHVLFYLENSNLVFNIPAPAMVYDYEEKEEYALAFYNIDSSSVSE
2896	A	83	426	NPQSSRYLPWADLSFLLGHPITVLQATLKYNVLLPKKASGFSLSLE IVKNYSLTVFDLTVNLYKTGIRNKSSMVVIDVKMLSGFTPTMSSIEE LENKGQVMKTEVKNDHVLFY
2897	A	1	3600	MPRPASARTCAHPLTCAHCPALPSEMNPDPQNNRIFQRQNVTSFRN ITQLSFQLISEPMFGDYWIIVVKRNSRETVTHQFAVKRYVLPKFVETV NAPQTVTISDDEFQVDVCAKYNFGQPVGQGETQIRVCREYFSSSNCEK NENEICEQFIAQLENGCVSQIVNTKVFQLYRSGLFMTFHVAVIVTES GTVMQISEKTSVFITQLLGTNVFENMDTFYRRGISYFGTLKFSDPNN VPMVNKLLQLELNDEFIGNYTTDENGAEQFSIDTSDIFDPEFNKAT YVRPESCYPVSWLTPQYLDHFLVSRFYSRTNSFLKIVPEPKQLECN QQKVTVHYSLNSEAYEDDSNVKFFYLLMMVKGAILLSGQKEIRNKAW NGNFSFPISADLAPAAVLVYTLHPSGEIVADSVRFQVDCFKCHK VNIKFSNEQGLPGSNASLCLQAAPVLFALRAVDNRNVLKSEQQLS AESVYNMVPSIEPYGYFYHGLNLDGKEDPCIPQRDMFYNGLYYTPV SNYGDGDIYNIVRNMGLKVFTNLHYRKPEVCVMERRLPKPLYLET ENYGPMSRVSPIASSGIRGENADYVEQAI IQTVRTNFPETWMWDLV SVDSSGSANLSFLIPDTITQWEASGFCVNGDVGFGISSTTTLEVSQP FFIEIASPFSVVQNEQFDLIVNVFSYRNTCVEISVQVEESQNYEANI HTLKINGSEVIQAGGRKTNVWTIIPKLGAKASKQGVLDLPNDVVEG SARGFFTVDGILGLALQNLVVLQMPYGSQNAALLASDPTVLDYL KSTEQLTEEVQSKAFFLLSNAALDSGVTNGYNHAILAYAFALAGKEK QVESLLQTLQDQAPKLNVIYWERERKPKTEEFPSFIPWAPSAQTEK SCYVLLAVISRKIPDLTYASKIVQWLAQRMNSHGGFSSNQAPVDCKR PAFFVIPAAFGPLSDSKSQDQNTVTFSSSEGSSEIFQVNGHNRLLVQR SEVTQAPGEYTVDVEGHGCTFIQATLKYNVLLPKKASGFSLSLEIVK NYSSTAFDLTVTLKYTGIRNKSSMVVIDVKMLSGFTPTMSSIEEGFG RADSPFSVEQSNLVFNIPAPAMVYDYEEKGLIQRCPSRWSKGIAC AEDRPGRPMLASLLTSMAMAQEAFRSSCSGSAWKLQAVRERLPEP SVCHPRGTGVALGTCSLPLPELKPE
2898	A	1	197	GFGRADSFPFSVEQSNLVFNIPAPAMVYDYEEKGLIQRCPSRWSKG

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				IACAEDRPGRPLASLLT
2899	A	1	963	MGVTRARGEVGLALSSRLAATLKYNVLLPKKASGFSLSLKIVKNYSL TVFDLTVNLKYTGIRNKSSMVVIDVKMLSGFTPTMSSIEEEKLKSF VCVSAKLEPKDDMEALGGSPQVSMMLVNIREILCSRKWSRRVYKKS VFPDGLAGAVTKTHVMLGVETDKLFSAPCPSVREQLEQKVEREGQRT TSTCQTWAKSPKVDVPSYLTCLADLKYGASLGPSITHSALAPGSSRS SPAPATAVQAGQDDSSSIPFRRELSEATSVSFLDPWRIFCGVVVSL FTSGAGEGPGGESPYVRQQTVSANPQQPQAEEDDNWKS
2900	A	49	247	DLTRNHSPLQTVHVRWFMIFFQV*YRIKFVKRNASPSGI*NII*T INTFVCIYK*IFRYKMH
2901	A	1066	1768	NPQSSSSEGR*DFPRLTVTNRLLVQRSEVTQAPGQYTVDVEGHGCT FIQATLK\YNVLLPKKASGFSLSLKSKELLFDCF*P/RQVNLQYTG IRNKSSMVVIDVKMLSGFTPNPCHPIELENKGQSD*KSNDPCS FSYLENVFG/QPDSPPFFC*AEQPLCSTFQPGPSHGLTDYKEEYA LAFYQHRTVVVSE*DKAITRRVGEAISCNKLILLYQTWKIMNHLT S
2902	A	620	1124	ETPAPCLQAWVPOACREGPLAFRELLGGVLAALSTPGERCSVSVSEFE TRARCTQ/PCWGPSPKFLSPHAKPAITLRPELKEAPWPAPSLGPPG GLSTPPSGIPCPPQCCQGHVALCRGLRSPW*TE*PVCWKMPRCPEK LPPGIFGNETYLVPIVNWPTGTSFLSTY
2903	A	2	399	WKESQGRCEW*VARGL*ADLT*GFHWHLPGAPP\WGLLTGGGQGRGH GHRGGWALSGRPP\RGFHWHPGAPP\WGLLTGGGQGRGHGHRGGWA LSGIPPRLOSFQVWAEPLPQLPWGCVAGISVHTGVSWLP
2904	A	73	867	GRAEQTSDFHFFASTSACSHNLTMSCPNYCSGNSNSGSLRTSRHPL TSIDLCPSTSVSCGDVLYLPTSSQDHTWVTDNQETCCEPTSCQPVHC ETGNLETSCGS/SHC/CTTCGPCQGSFLPASFFSSCLPVSCRTT EVC/RPAAVRPLRAVVQ*FTSP*GDCVAQCL/RPQFCLSKSQPQNL LTSGCQPSSCLAYRPQSLHVVSSSLRPLGLPLFSGCQPLTHVSTVSS HLALEHGSFNICFLQSSILLHRSSSRVAVCSSALF
2905	A	1	478	VEKLVKGFQDNFEFIQWSKKFFDANYDGKDYNPLLARQQQDVAPPP NPVPQRTSPTGPPPCILRKNPPSARNGGHETDAQILELNQQLVDLKL TVDGLEKERDFYFSKLRDIELICQEHESNSPVISGIIGILYATEEG FAPPEDDEIEEHQQEDQD
2906	A	800	1209	LFSSGAVPQRTSPHQAPKN\QT\SGRLS\NVAPP\CILRKNPPSAR NGG\HET*CPNSLNSNQQLVDLKLTVDGLEKE\RDYFYSKLRDIELI CQEHESNSPVISGIIGILYATEE\GFAPPEDDEIEEHQQEDQDEY
2907	A	1	3961	MSSKHLKSEQIKDQIRVPVISLIPKIHSAQEEQLSSTAVCSCPARVF CAVTKVAVFQMWMLHDLVQMVPRSLQWLPHIFTLFSNPLILYHSHE LSAPSAEQRECKLAYMPVSSASAHLLQAFDFNLVSLSSLARNM LANSASVRILIKGGKVVNDCTHEADVYIENGIIQQVGRELMIRWGQ GKLVIPGGIDTSTHFMNATCVDDFYHGTKVMLLFAKGGFLFGF FILLGLLQTRLMASLAKSDWFSPEHQLFTADEELCTRVMQGGPG AEVTCLENLQNCYPYPCESHQVILGLHGGSMCSCNPDHKKPFMSGA LRSIMKRQNKQVPPPAVEPKPGNKKQPKKVATPPNQKQGRFRS LEEALKALDVADLQKELDKSQSVFSGNPSIWLKDLASYLNYKLQAPL SEPTLSQHTHDYPYSLVSRELGIIRGLLAKAAGSLELFFDHCLFTM LQELDKTPGESLHGYRICIQAQLQDKPKIATANLGKFLLELRSHQSR PAKCLTIMWALGQAGFANLTEGLKVWLGLMPLVGLIKSLSPFAITYL DRLLLMHPNLTKGFGMIGPKDFFLLDFAYMPNNSLTSPSLQEQLCQL YPRKVLAFGAQPDSTLHTYFSPFLSRATPSCPPMKKELLSSLTEC LTVDPASVVRQLYPKHLSQSRQVQKSLQETIQSLKLTNQELLRKG SRNNQDVVTCAMACKGLLQVQGPRLPWTRLLLLLVFAVGFLCHDL RSHSSFQASLTGRLLRSSGFLPASQQACAKLYSYSLQGYSWLGETLP LWGSLLTVVRPSLQLAWAHTNATVSFLSAHCASHLAWFGDSLTSLS QRWQLTMTIFLEKRNILAKGQSLRTAGQENWPVFKESTSGEAKGNVE QEOPKWPISGRAGFARRGRKAPVSAGRPLTVFRKTLLEPSGRSCPPS

				SPNDRSATCFPRSPIVGNSMIRCWVLKGAIFSSFLHTGTAATHGTL ESDRSWGMAVNVYSTSVTSENLSRHDMLAWVNDLSHLNYTKIEQLCS GAAYCQFMDMLFPGCVHLRKVKFQAKLEHEYIHNFKVLQAAFKKMGV DKVGACALGGPEEQCDPGEEDPPAQATGAAGVPIPIIPVEKLVKGKF QDNFEFIQWFKKFDA\NFDGKDYNPLARQQR/DVAPPPNP\G\D QIFNK/SPKKLIGTAS/VPQRTVPPTGPKKHARPSGRLSNVAPPICIL PEESLPSARNGG\HETDA\QILELN\QQLV\DLKLTSGWGWEKERDF LLQANFRDIELICQ\EH\ESENSPVISG\IIGHPLMPQRKGFAPPED DEIEHQEDQDEY
2908	A	48	310	NPRCGPGGSRFVSSWCSVFPEAGGG*RKEPGMRGAGYKQRMGS*SK GPFAFIMPFPRPRPGFVLPPPPHLPDLNKGPHFSQKKKKK
2909	A	3	214	WGIQKNRPAMNYDKLSRLRYYYEKGIMPKVAGERYSYKIVCEPEAL FSLAFPELAVPAQPFPGKGGYSY
2910	A	312	387	LLSAAQVPDSDEQFVDFHSENRE
2911	A	3	216	NCLLRPKNKSVRWGPAGAAALLRPSAALGAGSRACSVPPAAPAQTP RPQVSAPAWGPGRAARGSGRMERRMKAGYLDQVQPYTFSSKSPGNR LAR\TLIGPLGKLMDFGSLPPLDSEDLFQDLSHFQETWLAEAQVPDS DEQFVPDFHSENLAHSPPTTRIKKEPQSPRTDPALSCSRKPPLPYHH GEQCLYSSAYDPPRQIANQVPCPWCPDLSRPYSFPFGQSNGIS*DPL APPSPTLAMGTSGNIAPSSSSPWDICHSTFSGG/APG/HPSQAPYQ HQLSEPCFPYPQQSFQYHDPLYGTGGASQAVGTRGGGSMGAQ/R PGAGVVIKQEQTDFAVSDVTGCASMYLHTEGFGSPSGDGAMGYGY EKPLRPFPDDVCVVP\EKFEQDIKQEGVGAFFREGPPYQRRGALQLWQ FLVALDDPTNAHFIAWTGRGMEFKLIEPEEVARLWGIQKNRPAMNY DKLSRLRYYYEKGIMQKVAGERYVYKFVCEPEALFSLAFPDNORPA LKAEDRPVSEEDTVPLSHL\DESPA*PPYSLAPRPSVRAPGHARY PPRLQPRRPGLRSRPLGAPAVRREGAAGWSGG
2912	A	119	444	GFGVGTTPALTCPVTSPSPKARPS*T/ELEPPSRCPQPCQTLGPQA EGNQMSAPSLASPPSKQPLMANRCCCVPRSRHLCGIQNLGFWD SREERGGDATWVSVD
2913	A	1	576	APAEFRTSGEAAGSGERREQPSVTERVPTALGVPRMCVAQVLTALL PPRQALGSLCSPWAAPRVGPLPPAPAMVRISKPKTFQAYLDDCHRRY SCAHCRAHLANHDDLISKSFGQSQGRAYLFNSVNVGCGPAEERVLL TGLHAVADIHCENCKTTLGWKYEQAFESSQYKEGYIIELNHMIKD NGWD
2914	A	2	552	EFRLVRISKPKTFQAYLDDCHRRYSCAHCRAHLANHDDLISKSFGQS QGRAYLFNSV*VSGLPSCFP*PLL*PVTGILLRLPEFPAGARKL*A SFLGC*GQTQCLRGWAL*WQDPPWDYPMSPQ/VNVGCGPAEERVLLT GLHAVADIHCENCKTTLGWKYVNSSTPDPLWLAEPDLFNTFF
2915	A	1	574	GADGGGAFLRSGPGP*APPGPSSALMMPSSCPWRTGALGPSPAGSRA LGRCTSSVGPGRWLTRTSSPGCAYQNLNEDGAQASPEPDGGVGT RLGPGIPAE/PSIRSFVVLQHHSAAAPSAPTTAAAGPNTL*SRRT AEWCWPPSCSCCLGPGADPGRRGNWRRPPLPRCLQRQSSSCRAFLLL VPGV
2916	A	355	511	LFLETESCFVAQAGARWAVITHCSLKL/LGPCNPPISAL*VARTTGM SHHTEP
2917	A	1815	2152	INKEMSGQARWLTPVIPALWEVKVVDHLRPGVRD\HQPQQQSETPVS TTIQK*ARYGGMCL*S*LLRRLTQQNHLNQGGRCSELSRYCTPAW ARQSKTSSQEKKEKEMPW
2918	A	315	480	LFHCFHFHGGPRVGSFGPFLTSSVPDEELVKSFPQSTVLVIKDAPIV GLMLWSK
2919	A	1	1845	MWESLELPRDLLNGFAQNADSNMDNKVQAEVVLGDGDELGNWSKGL PGCKASVLTLLKVRQCATERVLQOCTGCGLWLLQVPWTTALGSTAP AAGLHGWLNFDCSIVSIFMGVQGWDLAACNKKEAKVLLHEAQFMGL GSSVMLQPFDDYDPNEKSKHKFMVQTI FAPPNTSDMEAVRCPSQSPAK LHGWSHRARARRSLTPSKHCTFINTATARILGSHNTPVLNINFLNQ

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				TLTRFTPAKASQGHSTSDICSSSFSEPKSWAFCLPALWSTTGGDRDKCR GHGTHGGGSQTEAKYICDLLTPPNASVSSLPVRAPPTPTTDDSTSQEC PHRHLLSPQEVLSFLLFPLDFESLYTAMVGSEKETGEGTPSVGKHA YERAHADGPPGLGEGINSPLPTCTGVRGLTQDIQDTGQESDSTLSTLG SEDDEKTAKPQGDTSSEVLPAVKNSPRTFQEDGDIPLPLGAANKSAQ KPQRLGRSLCVWLAKSHRGDLGPTFYFLRKGGAPAAPFAPGVQPTW ISPFQSPCSLELSPAQPDFSHNYALSVHFTVPKQTFDSLKNDEPSK AVPLNASKQDGPMPKPHSVSLNDTETRKLMEECKRLQGEMMKLSEEN RHLR
2920	A	407	802	VARSMLIPKTMGKMSPGHIRDLHSSPSHHRPRSPGGKSGFVGRAQG PCAMCSPGTWCSVSQQLQPWLKGANVQLGLWLHRVESPSLGSFHVVL SLWVHGSQELRFGNLHPDFRRACTVNLEKQPOTLNASL
2921	A	914	1134	QESLLLQFTKSSSCPSETTSARTLLSILLSAFWAKPFNKSLGSSKLS HIFLSSSDPSK/AVFTSAYYPVPKSLPH
2922	A	1	447	MWESLELPRDLLNGFVQNADSNIDNKVQAEVVSOGDEELVGNWSKAA PAVAEMRQCKAQAMVSEGLKWPQLPCGVEPENAQTSRIEVEWELP RFQKMYGSAWMSRQRFTAGLGLLWRTSARAVWEGNMRSEPPHRVPTG APPNGAVR
2923	A	218	544	SGFSLSLRGSISFSL/CFKVGMCVTYPRCYC*S\PVP*KPLIKPGWV SELPKPMNWASCSRTLASFLLQAARSHPWTPMKMETMEQSKLRSQPC KPAAGAVDPRAVVHGT
2924	A	3	260	VLTSVSLLPGHGTAGLISQSLCRLVKNHCWGASGLVWRCSGPWGSLKE RLQGDMPQPFWNGPSEGSSPHFHPGPRTCASHLLQCF
2925	A	1	534	MWKRLWNQVTDGTGWSLEGSEEDRKMWESLELPRDLLNGFAQNADSN MDNKVQAEVVSOGDEKLGNWSKGLLLLEEGMDPEAVGFQALPPDCR GPWTNPVGSVDNPRGLVNMKVPFVRPLHEDPNPLKIFMLSAAGNKS WIPGSLCLHVTATPTTAEPLGASRDGKVPACRVPV
2926	A	198	562	LKCGKQWSDPITSPQTESQLLSSQQQLHQHRLQGP*K*NRDSPLC FSLSSCPIPKTYTNRHILLP/SSSKSLCKFL*PA*ISPQKMGFSFLS QSVCKFSKLLCSASLIKLFNSIQVTS
2927	A	72	270	PRHPCPPLPLCLEHGPQGAHRAQPSSTGGPTEPEQDDHSLPLNTA LLLTRPQLVFLAATIHQC
2928	A	325	535	DSEEDRKMWESLELPRDLLNGFDQKPDSDNMDNKIQAQVVSOGDEELV GNWSKGDSCYVLAKRTGGILPLP
2929	A	492	696	VPSWLRQVQKMPINIERALSRSAAQIPTLGPPMKMETMGPSKVEKP THASQSAGAVDPRARGPRVL
2930	A	822	1759	SSAEPSPSSPAPSQQTAAAGAPPLCAVSPMASASGAMAKHEQILVL DPPTDLKFKGDG*VFIRPEQYYTV*KWCKRSKRHGFFRP\FTDVVTT NLKL RNP\SDRKVCVKTTVPS/RRYCVRP\NSGI\IDPGSTVTVS VMLQPFYDPN\ERSKHKFMVQTI FAPPNTSDMEAVV/WKEAKPDEL MDSKLR\VFEMPNENDKLNDMEPSKAVPLNASKQD/GPMPKPHSVS L\NDTETRKLMEECKRLQG\EMMKLSEENRHLRDEGLRLRKVAHSDK PGSTSTASFRDNTSP\LPSLL\VVIAAIFIGFFLGKFI
2931	A	2	417	FVAQQLQGDLSLHFMQALYQHFPIEVRYHLSQWIESQA/WNTYDRCP MELVRCIRHILYNEQRLVREANNNGSSPAGSLADAMSQKHLQINQTFE ELRLVTQDTENELKKLQQTQYFIIQYQESLRIQAQFGPLAQLSPQ
2932	A	1	855	MAIYPQILDSVSTPSKGILLRNLNAIVTLKKFSSDKGRVPPAVPDKV LWPQLCEALNMKFAEVQSNRGLTKENLVFLAQKLFNNSSSHLEDYS GLSVSWSQFNRENLPGRNYTFWQWFDGVMELVKKHLKPHWNDGAILG FVNKQQAHDLLINKPDGTFLLRFSDEIGGITIAWKFDSEAWERGL GSSGLLLNRNEGASAVLPESMSPSTILGTGSAHQPMGEATLLVQEG ALAGSSNSHNSLAVSECPQQWEEPPRARQGDSDNRGKTTVELQVGYH EST
2933	A	1	810	MLLWPLLLLLLLLLPTLALLRQORSQDARLSWLAGLQHRVANGALVWA ATWQRRRLEQSTLHVHQSQQALRDSVDLDNPQENIKATQLEGLVQ ELQKKAHQVGEDGFLKIKLGHYATQLQRI PCDDL PKNKLLPLSEH

				HALKLELPVNKQKMAGTGDRAKAVDGYVKPQIKQVVEFVNASADAG GAAPRLSGVVMCLDSRCESPDSDLTDGDFDLEDTMDVARRVEELLG RPMDSQWIPHAQSVTRDLSIVNFFIFTRRITLVDV
2934	A	224	2606	TMAVWIAQAQQLQGEALHQMQUALYGOHFPIEVRHYLSQWIESQAWDSV DLNPNQENIKATQLLEGLVQELQKKAHQVGEDGFLKIKLGHYATQ LQNTYDRCPMELVRCIRHILYNEQRLVREANNSSPAGSLADAMSQK HLQINQTFEELRLVTQDTENELKKLQQTQOEYFIQYQESLRIQAQFG PLAQLSPQERLSRETALQKQVSLEAWLQREAOQLTQQYRVELPEKHQ KTLQLLRKQQTIIILDELIIQWKRRQQLAGNGGPPEGSLDLVQSWCEK LAEIIWQNRQQIRRAEHLCCQLPIPGPVEEMLAEVNATITDIISALV TSTFIIIEKQPPQVLKTQTQKFAATVRLLVGGKLVNHNPPQVKATIIIS EQQAKSLLKNENTRNDYSGEILNCCVMEYHQATGTLAHSFRNMSLK RIKRSRRGAESVTEKFTI\LFESQFSVGGNELVFQVKTLSLPVVV IVHG\SQ\DNNTATVL\WD\NAFLQEPG\RVPFAVPDKVLWPQLCE ALNMKFKAQVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSGLSVSWS QFNRENLPGRNYTFWQWFDGVMVLLKKHLKPHWNDGPILGFVTKQQA HDLINKPDGTFLLRFSDEIGGITIAWKFDQSQRMFWNLMPFTRD FSIRSLADRLGDLNLYIYVFPDRPKDVVYSKYTTPVPCESATAKS/V LDGYVK\PQIKQVVEFVNASADAGGGSATYMDQAPSPAVC/PPQAH YNMYP\QNPD*VLDTDGDFDLEDTMDVARRVEEL\LRPMDSQWIPH AQ
2935	B	123	219	XPPTGMTMDKSELVQKAKLAEQAERYDDMAAA*
2936	A	1	1815	MTSRSPTLPSPLPYAAKQEMVVRGYCAGGAGFISSDKGGKADGSGVGO GGGVAITGDGEAVSSGKVSSEFTNSVSPALSGSSHTSPFQVAGSHS FPINALTLTVDTWLSMLVRAIGACLFGYPSWRMEGCAARRSGWAS SGISRSRRCKETASAKLACQQLQVAKRAGLGGGQSGRTVLRERVRI EIASTHIALAVECVSVRVWVPRLPSPRQKYAKHASQLVSNQKSEEEE YMKTFNISQQDLELVEVATEKITMLYEDNKHVGAARTKTGEIISA VHIEAYIGRVTVCABIAIGSAVSNQKDFDTIVAVRHPYSDEVDRS IRVIPTYGTDEWEQWNAFNEENLFCSEMPSSDDEATADSQHSTPP KKKRKGMTMDKSELVQKAKLAEQAERYDDMAAMKAVTEQGHELSNE ERNLLSVAYKNVKTNERNEKKQMGKEYREKIEAELQDICNDVLYSPP FPMVASCEQTAVIVVSLGSSCSASLPGSGLVLGVVCTESCDVNHL WVSQPAIPAPVSVAISEGAMDSVKVLSFGGLMFFVLIGLLPGGGAFQ KASAVVVRGIGGGQGPRTPLSSTTRVDRKGPPGGGGARSV
2937	A	1	510	KTERNEKKQMGKEYREKIEAELQDICNDVLYSPPFPMVASCEQTA VIVVSLGSSCSASLPGSGLVLGVVCTESCDVNHLWVSQPAIPAPVS VAISEGAMDSVKVLSFGGLMFFVLIGLLPGGGAFQKASAVVVRGIG GGQGPRTPLSSTTRVDRKGPPGGGGARSV
2938	A	107	961	VVGLGRKRSSRSGASLGRVFPVPCSPPTGMTMDKSELVQKAKLAEQAE RYDDMACSSERHVTEQG\HERLQPKRNLLS\VAYKNV\VGARRFLP GRVISSIEHENREGMKKKQMGK\EYP*EDRRQNLQDICK*CFWELL \DKYLIPN\AVTQES*GVLL*KLKGGYFRYLSEVAS*DNKQTTVSN SQPGFTREHFEISKEMQPTHPIRLGLALNFSVFYIEILNSPEKACS LAKTAFDEAIAELDTLNEESYKDSLIMQLLRDNLTLWTSENQDEG DAGEGEN
2939	A	208	1178	EGRGHLARSFARKGLCSLQPSHGRVSRDLGRYKKCILPIRLWIEKQE EHWTWSQGMTMDKSELVQKAKLAEQAERYDDMAAMKAVTEQGHELS NEERNLLSVAYKNV\GARRSSRVISSIEQKTERNEKKQ\MGKEY REKIEAELQDIC\NDVFE\LLEQISLFPNATQPRKVVFLLK*KGD YF\RYLF*KWQS*ROQTQPTCVETPQOSLPRKQFEISKEMQPT\THP IR\LG\LAPKFPQSFYIEIPKLPLKAW*AWAKTALCFRHF*SNLL NLDLTLEWKSLIKDSTSDSWQLLR\DN\LTLDWDIRKTRGDEGDAGEGE N
2940	A	1	461	IEIHIKCGGIPAVLAAPAMGLEFLDLVSPRAVYIFAKKNGIPLE LRTVDLVKGQHKSEFLQINSLGKLPTLKGDFILTE/SANRSVYLQ

				GGCWHITEMRFSKCKAEGPAKRSAILIYLSCYQTPDHWYPSDLQARARVHEYLGWHAD
2941	A	2	311	HEQTPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLI GVQVPEEKVERNRTAMDQALQWLEDKFLGDRPFLAGQQPVALGYELF EGRPRLAAW
2942	A	205	454	EEGVVLGSRWRARLEGSPSNAEKPPGPTGRWEQLGVNAWSQCPYSH CPFVPSSAILIYLSCYQTPDHWYPSDLQARARVHE
2943	A	5	437	AQESRDCGDHDRATALQPGQQSEILLQRLPPENAVD*VALEGSQPL *TLACLLSCKYQTPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPL WVQVRRANLPFLSFPLAPVPSLQLHVKLCTDKTSLVLSASILRCSI HTS
2944	B	307	447	XSAILIYLSCYQTPDHWYPSDLQARARVHEYLGWHADCIRGTFGIP L*
2945	A	2	385	TALSAFTAI PAVLAAPAMGLELFLDLVSQPSRAVYIFAKKNGIPLLEL RTVDLVKGGPSPFPRVSTNPVHPQAPALLCERLAARTAPSPPPAAS ATRECCGLSLGGITASLNLSPSEKEDNVTF
2946	A	1	1278	MPGLGFREKKGGSRTVIPASRGCGLPAPILCTKWELPLSGSSRCLAA AALQGTVWTAESSSLTAPAFQSRGWGLIPYFPARRDPATAAAHTALSA FTAIPAVLAAPAMGLELFL\DLVSQPSRAVYIFAKKNGIPLLELRTVD LVKGQHKSEFLQINSLGKLPTLKDGFILTESLAILIYLSC\KYQT A\DH\WYP\SDLQGFGARVHEVPWAW\HADLHPVGTFWYYPWVGQGV WGHS LGVQVPEEKVGTQTRTAMDQALQWLEDKFLGDRPFLAGQQVTL ADLMALEGS*CKPVALGYELFEGRPRL\AAWRR\VEAFLG\AELCQ EA\HTSIILSILEQAA\KKTLP\SP\EAYQAMLLRNRPGSPGSG MGAKEISNKDSFCYLLAPFYLSLLPQSLLSKLQCEALHRQRHSSVLW QVLLLLRCKHT
2947	A	298	458	NIYQLE*K*FKNGQVWLGA VVRACNPSTLGG R/WIPWGQEFGTSLAN MVKPRLY
2948	A	59	190	ARSFHSDAPQGHLECHWC PGVLEL*GHRNPDTCPHLEQGISSK
2949	A	319	462	HFSYIHWFYTEKYKIKITHQDYLOKFI IY/CTEEKHAYH*PNKILFI T
2950	A	78	3703	PQELGAREPFGNMYDADEDMQYDEDDDEITPDLWQEACWIVISSYFD EKGLVRQQLD SFDEFIQMSVQ RIVEDAPPIDLQAEAQHASGEVEEPP RYLLKFEQIYLSKPTHWERD GAPSPMPMPNEARLNLTY SAPLYVDIT KTVIKEGEEQLQTQHKTFIGKIPIMLRSTYCLNGLTR\RDLC ELN ECPSDP\GRYFII\NGSEKVLIAQRKMATNTSFCRLQKTDSKYAYT\ GECRSCLENSSRPTSTIWSMLARGGQ\AKKSAIGQ RIVATLPYIK QEVPIIIVFRALGFVSDRDILEHIIYDFEDPEMMEMVKPSLDEAFVI QEQNVALNFIGSRGAKPGVTKEKRIKYAKEVLQKEMPLPHVGVSD FCE TKKAYFLGYMVHRLLLAALGRRELD DRDHYGNKRLDLA GPLLAFLR GMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGN WGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPR QLHNTLWGMVCPAETPEGHAGLVKNLALMAYISVGSQPSPILEFLE EWSMENLEEISPAIADATKIFVNGCWVG IHKDPEQLMNTLRKLRRQ MDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQKLLKKRHI DQ\LKEREYNNYSWQDLVASGVVEYIDTLEETVMLAMTPDDLQKE VAYCSTYTHCEIHP SMILGVCASII PPDHNQSPRNTYQSAMGKQAM GVYITNFHVRMDTLAHVLYYPQKPLVTT RSMEYLRFKELPAGINSIV AIASYTGYNQEDSVIMNRS AVDRGFFRSVFYRSYKEQESKKGFDQEE VFKEPTREPCQ\MRHAIYDKLDD\G\LIAPRGFVVSGDDVIIGKT VTLP\ENED E/LWESTNRRYTKRDCSTFLRTSETGIVDQVMVTLNQE GYKFCKIRVRSVRIPQIGDKFASRHGQKGT CGIQYRQEDMPTCEGI TPD\IIINPHAIPSRMTIGHLIECLQGVSGLTRGEIG\DA\TPF*W MLFNVAGRFPNLFILDYGLSSSGGKWRSLYNGFTG\RKFTSQIFIGP TYYQRLKHMVDDKIHSRARGPIQIRO*TSMEGSSP\DGGLRF*\EM DRD\CQIAHGA\AQFL\RERLFEGHPEPHIQVPCFAN\LCGI\MAIA

				QHPGPHTYECRGCPQ*NPRFSLVRMPTACTL\LFQELMS\MSIAPRM MSV
2951	C	162	293	MGNLLKVLCTCTDLEQGPNNFFLDFENAOPTSESEKEIYNQVNVVAL*
2952	A	286	1327	AGAKFFP*F*KVADAQPTSESEKEIYNQVNVVLKDAEGILEDLQSYRG AGHEIREAIQHPADEKVAKKKAWGAVVPL\VGKLKKFYEFSSQRLEAA LRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFDLKMTP AIQNDFSYRRTL SRMRINN\YPAEGENEVANELANRMSLFYAEATP \MLKTLSDATTKFVSENKNLP IENTTDCCLSTMASVCRVMAGNT\EYR SQILQNEETVSFSLSWRAMVGC*S*SYDHRTSSGEAFCLKLPKFDKMG CIKVLKDQPPNSVEGLLK\SLR\YTTKHLEWMRLPPSKLKSMLPITI LGIKHPAVDRRQYSAMTENAVF
2953	A	75	478	AVKMCDF*DTA*FKEAFQLFDRDGDGKILYSQCG\DPKSDEMNVK VLDFEHFLPMLQTVAKNKDQGT*DYVEGLRVFDKEGNGTVMGAEIR HVLVTLGEKMTSEEVQMLVAGHEDSNGCINYEELVRMVLNG
2954	A	2	343	DFTEDQTAEFKEAFQLFDRTEMNVKVLDFEHFLPMLQTVAKNKDQGT YEDYVEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTSEEEVEMLVAGH EDSNGCINYEELVRMVLNG
2955	A	34	353	AVKMCDFTEDQTAEMNVKVLDFEHFLPMLQTVAKNKDQGT*YEDYVEG LRVFDKEGNGTVMGAEIRHVLVTLGEKMTSEEEVEMLVAGHEDSNGCI NYEAFVRHILSG
2956	A	2	303	LKFRPRRRRTFLPLLSCCLGLGGGLTAAGRGARGMENWSDSRWLLC KLTPGLVAVGMFPLMLPLQSGSPLALGVPLHSPVPWLIPFPLSTBLV RMVLNG
2957	A	1	999	MLYCFSSGNVSKSPTANNARTGRADYVSITDDEALEAFKTLCLHEGI I PALESSHALAHALKMMRENPDKEQLLLKERKEGAFVFPVTLGDPGI EQSLKI IDTLIEAGADALELGIPFSDPLADGPTIQNATLRAFAAGVT PAQCFEMLALIRQKHPTIPIGLLMYANLVFNKGIDEFYAQCEKVGK TVLVADVPVEESAPFRQAALRHNVAIFICPPNADDDLLRQIASYGR GYTYLMSRAGTVAKNKDQGT*YEDYVEGLRVFDKEGNGTVMGAEIRHV LVTLGEKMTSEEEVEMLVAGHEDSNGCINYEVLHTGPAHSRDLRSLSS VRLD
2958	A	255	528	ARYKIHTGKGTDSGETGKVLSHSAPCGRCSRPARHPRDSMPHKRFI VDTNQLLSSCPATSISTSSSVNLPRCD/FPEDQTAEFKEAFQLFDR TGDGKILYSQ\CGDVMRALGQNP THAE\VLKVLGNP\KSDEMNVKVL DFEHFLP\MLQTVAKNQDPGSPMGFMSKELRVFYK\EGNGT\VMGAE IRHVL\VTPG*\KLTEEEVEMLVAGHEDSN\G\CINYEAFVRHTPVG VTGPWAGASSAWC
2959	A	26	518	AVKMCDFTE\QTAEFKEAFQLFD/RKPGDGKIPCTAQCGDVMRALG QNPLPNAE\VLKAPGEPPRSDMSVKEH\DCHEF\LHILQT\VAQNQ G\QGT*Y\EDYVEDFRVFDKEG\NGT\VMGA\EIRHVLVTLGEED*QR KKVEMLVAGP*RTANGLVSNYEELVRMVLNG
2960	A	453	744	APSNLSHGHSQPYFFTGIARQWAGAVGGWPEDAADSEHNLVPPPHLG GPPLPLLLALLAGSLGSPGTVALRQVPMQAHPLHHCPOHVCQCLPAY CH
2961	A	736	1062	SWISDGTGRSAFIGIGFTDRGDADFNVSLQDHFQWVKQSEISQES QEMDARPKLDLGFKEGQTIKLCIGLCSKPGTTAIQLGPVLNGIGRTL RTDLRNKNDLEGITNL
2962	A	295	782	PLLCNPDPGWYWWVKQSEISKESQEMDARPKLDLGFKEGQTIKLCI GNITNKKGGASKPRTARGGGLSLLPPP*GKVITPPSS/VKLPSTN HVTPPSIPKSNHGGSDA\DILL\DLDSPAPVTTPTPTP\VSVSNDL \WGFSTASSVP\NQAPQPSN\WVQF
2963	A	192	326	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPPNVRDL
2964	A	1	1044	MAEIGEDLDKSDVSSLI FLMDYMGGRKISKEKSFLLDLVVELEKLN VAPDQLDLLEKCLKNHRIDLKTKIQKYQSVQAGTSYRNVLQAAI QKSLKDPSNNFREEPVKKSIQSEAFLPQSIPEERYKMKSKPLGICL IIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQFACMPEH

				RDYDSFVCVLVSRGGSQSVYGVDDQTHSGLPLHHIRRMFMGDSCPYLA GKPKMFFIQNYVVSDDGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVH READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERGTIPGSGI TESKDMHFSSSLGCILLDVL
2965	A	1	811	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLDILRER GKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYR VLMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVELEKL NLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQAGTSYRNVLQA AIQKSLKDPSSNNFRSIPERYKMKSKPLGICLIIDCIGNETELCGVR GPAGGQQPLGGGWASDEECGIQGSEARAVHSSPRS
2966	A	1	750	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLDILRER GKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYR VLMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVELEKL NLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSGWNGTWMTKASFS LWLEIASLYILHIPDLPTPLPCIFMISAKCCQAVLNISVFKKESGIC TGWQSYGHSGVLHVC
2967	A	493	1946	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLDI LRERGLKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV SDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVE LEKLNVLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQAGTSYRN VLQAAIQKSLKDPSSNNFRLHNGRSKEQRLKEQLGAQQEPVKKS IQES EAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRDFTTSLGYEV QKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDD QTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSDDGQLEDSS LEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSS PSLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWSNRVSAKEYYVW LQHTLRKKLILSYT
2968	A	539	1215	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLDI LRERGLKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV SDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVE LEKLNVLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQAGTSYRN VLQAAIQKSLKDPSSNNFRMITPYAHCPDLKILGNCSM
2969	A	414	1762	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDILLDI LRERGLKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV SDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVE LEKLNVLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQAGTSYRN VLQAAIQKSLKDPSSNNFRSIPERYKMKSKPLGICLIIDCIGNETEL LRDFTTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLV SRGGSQSVYGVDDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY VVSDDGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCT ADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWN SRVSAKEYYVWLQHTLRKKLILSYT
2970	A	449	1305	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDV\TPPNVR\DLL \DNLREGRGLKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRN PHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYMGGR\GKISKEKSFLD LVVELEKLNVLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQAGT SYRNVLQAAIQKSLKDPSSNNFRLHNGRSKEQRLKEQLGAQQEPVKKS IQESEAFLPQSIPEERYKMKSKPLGNLPLGLIDWHALRTELSFEDTF TSLGY
2971	A	473	1164	SKSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDV\VPNNVRD\LL DILRERGLKLSVGDLAELLYRVRRFDLLKRILKMDRKAVETPLFKDPP LVSDYGVLMMAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLV VELEKLNVL/APPDQLDL\LEKCLKNIPQK*P*RQKSQKYKQSV\QG AGTSYRNVL/QAAI\QKSLKDP\SNNFRMITP\YAHCP\DLKI\LGN CSM
2972	A	482	692	EKPL*SYLSSFFHFLEMGSHPRLVCSGVIVAHCSLQLLGSSDVPT

				S/ASR*LGLTGSHTTIPSLGLFLN
2973	A	1	358	AQLVEFGEHSMAPPAHFRALLYHPGTATLVPHPASISQHSPPSPWGNA /RG*PV*RQRHLTAPRSPPHPRFRHKPGKDPRENPSRWPEVPSLPQT HVVPQAAJWDTVNTTVCKNRSTKPD
2974	A	3	106	LPSGILVQTAARTVMMAPDAPSDGPYLPVATLPT
2975	C	109	294	MDTAGMILGWKFFDHAHLGGALFGIWWYVTYGHELIWKNREPLVKIW HEIRTNPGPKRRWL*
2976	A	3	131	IGRKIMASLPSGILVQTAARTVMMAPDAPSDGPYLPVATLPT
2977	A	788	1151	QPTLENKGPLRLES DVKI PGQWPAAEKVLS INRNTKEHLPANNTCQQ SAGPSTLGYSHPLVKSPFPESLPSFFVVLNAYPNPIQPFNTHPK*/P PGT/HWISSDSYCPNSS*SKMHKPKCPNK
2978	A	136	502	GTLPNSSLCESNNGHPRQRGRGSCPSRYTGPVSSPRLSRIQSWIR/H LHPPSPPTRPSYSSPQASASPVGLRGHPAQTTWTCRSVPSPVRFSS GSDGEKRLGQSCPHGNDPGAACISRPPYA
2979	A	242	9991	FKLELHQESDMFNNTTQEDVQERLAYAEQLVVELKDIIRQKDVQLQ QKDEALQEERKAADNKKLKLHAKAKLTSLNKYIEEMKAQGGTVLP TEPQSEEQLSKHDKSSTEEEMEIEKIKHKLQEKEELISTLQAQLTQA QAEQPAQSSTEMEEFVMMKQQLQEKEEFISTLQAQLSQTQAEQAAQL SSMQQVVREKDARFETQVRLHEDELLQLVTQADVETEMQKLRVLQR KLEEHEESLVGRAQVVDLLQQLTAAEQRNQILSQQLQOMEAEHNTL RNTVETEREESKILLEKMELEVAERKLSFHNLEEMHHLLEQFEQAG QAQAELESRYSALEQKHAEMEECTSHILSLQKTGQELQSACDALKD QNSKLLQDKNEQAVQSAQTIQQLQDQLOQKSKEISQFLNRLPQQHE TASQTSFPDVYNEGTVAVTEENIASLQKRVVELENEKGAALLSSIEL EELKAENEKLSSQITLLEAQNRGTGEADREVEISIVDIANKRSSAE ESGQDVLENTFSQKHKELSVLLEMEKAEQERIAFLKLQLOGKRAEEA DHEVLQKEMKQMEGEGIAPIKMKVFLEDTGQDFPLMPNEESSLPV EKEQASTEHSRTSEEISLNDAGVELKSTKQDGDKSLSAVPDIGQCH QDELERLKSQILELELNFHKAQEIYEKNLDEKAKEISNLNLIEEFK KNADNNSSAFTALSEERDQLLSQVKELSMVTELRAQVKQLEMNLAEA ERQRRLDYESQTAHDNLLTEQIHSLSIEAKSKDVKIEVLQNELDDVQ LQFSEQSTLIRSLQSQLQNKESVLEGAERVRHISSKVEELSQUALSQ KELEITKMDQLLLEKKRDVETLQQTIEEKDQQTVEISFSMTEKMVQL NEEKFSGLGVEIKTLKEQLNLLSRAEEAKKEQVEEDNEVSSGLKQNYD EMSPAGQISKEELQHEFDLLKKEQKRLQAALINRKELLQVRVS LEELANLKDSEKKEIPLSETERGEVEEDKENKEYSEKCVTSKQBEI EIYKQTISEKEVELQHIRKOLEEKLAAEEQFQALVKQMNQTLQDKT NQIDLLQAEISENQAI IQKLITSNTDASDGDSVALVKETVVISPPCT GSSEHWKPELEEKILALEKEKEQLQKKLQREALTSRKAILKKAQEKER HLREELKQKDDYNRLQEQQFDEQSKENENIGDQLRQLQIQVRESIDG KLPSTDQQESCSSTPGLLEEPLFKATEQHHTQPVLESNLCPDWPSHSE DASALQGGTSVAQIKALKEIEAEKVELELVSSSTSELTKKSEEVF QLQEQINKQGLEIESLKTVSHEAEVHAESLQKLESSQLQIAGLEHL RELQPKLDELQKLISKKEEDVSYLSGQLSEKEAALTKIQTETIEQED LIKALHTQLEMQAKEHDERIKQLQVELCEMKQKPEEIGEESSRAKQOI QRKLQAALISRKEALKENKSLQEELSLARGTIERLTKSLADVESQVS AQNKEDTVLGRLLAQEERDKLITEMDRSLLENQSLSSSCE\SPKL ALEGLTEDKEKLVEIESLKSSKIAESTEWQEKHKELOKEYEILLQS YENVSNEAERIQHVVEAVRQEKQELYGKLRSSTEANKKETEKQLQBAE QEMEEMKEMRKFAKSKQKILELEEEENDRLRAEVHPAGDTAKECME TLLSSNASMKEELERVKMEYETLSKFFQSLMSEKDSLSEEVQDLKHQ IEDNVSKQANLEATEKHNDQTNVTEEGTQSIPEGTEEQDSLMSSTRP TCSESVPKSAKSNPAVSKDFSSHDEINNYLQQIDQLKERIAGLEEEK QKNKEFSQTLNEKNTLLSQISTKDGELKMLQEEVTMNNLLNQIQE ELSRVTKLKETAEEEEKDDLEERLMNQLAELNGSIGNYCQDVTDAQIK NELLESEMKNLKKCVSELEEEKQLLVKEKTKVESEIRKEYLEKIQA

				QKEPGNKSHAKELQELLKEKQQEVKQLQKDCIRYQEKISALERTVKA LEFVQTESQKDLITKENLAQA\VEHRQKGTSONLASFK\VLLDDTQ SEAAARVIADNLLKKEQLQSNKESVKSQMKQKDEDLERRLEQAEEKHL KEKKNMQEKLDAALREKVLLEETIGETIQTTLNKKDKEVQQLQENLDS TVTQLAAFTKSMSSLQDDRDRVIDEAKKWERKFSDAIQSKEEEIRLK EDNCSVLKQDLRQMSIHMEELKINISRLEHDKQIWESKAQTEVQLQQ KVCDTLQGENKELLSQLEETRHLHYHSSQNELAKLESELKSLKDQLTD LSNSLEKCKEQKGNLEGIIRQQEADIQNSKFSYEQLETDLQASRELT SRLHEEINMKEQKIIISLLSGKEEAIQVAIAELRQHQHDKIKELENLL SQEEEBENIVLEENKKAVIDKTINQLMETLTKTIKENIQQAQLDSFVK SMSSLQNDRDRIVGDYQQLEERHLSIILEKDQLIQEAAAENNKLKEE IRGLRSHMDDLNSENAKLDAELIQYREDLNQVITIKDSQQKQLLEVQ LQQNKELNKKYAKLEEKLEKESEANEDLRRSFNALQESKQDLSKEIE SLKVSISQLTRQVTALQEEGTGLGLYHAQLKVKKEEVHRLSLKDFSSQ KRIAELEEEELVCVQKEAAKKVGEIEDKLKKEKLHLDHAGIMRNETE TAEERVAELARDLVEMEQLLMVTKENKGLTAQIQSFGRSMSSLQNS RDHANEELDELKRKYDASLKELAQLKEQGLLNRRERDALLSETAFSMN STEENSLSHLEKLNS\MLLSRDEQSLHLSSQLEDSYNQVQSFSKAMA SLQNERDHLWNELEKFRKSEEGKQRSAAQSTSPAEVQSLKKAMSSL QNDRDRLLKELKNLQQQYLQINQEIHELHPLKAQLEYQDKTKAFQI M\QEE\LRQEKPSWQHELHQLRMEKSSWEIHERRMKEQYLM\ISDK DQQLSHLHNLIRELRSSSSET\EPLKVQYQORQASPETSASPDG\SON LVYETELLRTQLNGQL*RKPHQKELRIQQLNSNFSQLEEKNTLSIQ LC\DTSSQLRENQQHYGDLNHCALVLEKQVQELQAVSKEKGPLNIDV APGAPQEKNGVHRKSDPEELREPQOSFSEAQQQLCTSRQ\EVNELR\ KLEEBERDQRAAENALSVPEEQIRRLEHSEWHSSRTPIIGLVGNQG AATVID\LTNSNCRRT\RSG\VGWKRVLRLSLCHSRDPECPLSSSHLT F*MIHVLLIMCYTGHL
2980	A	3	211	GDLPWEINPPSSCSLLREKDPPTTSGPEIDQPKHILTDFKSATPRGP GTLAQGSLLTDSFPDLLGLVAED
2981	A	1	519	MLLTQSLFGGLFTRTHMKFGAVTQIRGPPLGDKSPVLLLFALEQROR HVLSDMPKLRCSWRTGKAAPWCLIIAEMPDISPTFQRCQTTQGRLP WSFTLSSKSRFSGEGARACYKCQKSDHQAKECPQPGIPPKPCPICAG PHWKSDCSTHLAATPRAPGTLAQGSLLTDSFLA
2982	A	291	686	GLGTFAYISQDVWKSILYVQAEVCCGRVFLVCSGSCWSKSSRCEPP YAVLSIQVEAAHMEIWCRRSDRDLPE\SSCSLLLEKDDP/SGPQT DQPKHILTDFKSDKGDTFYPWTQNSGAGHGLGRQPSLG
2983	A	1	639	MWESLELNRYLLNDFDQKPDSDMDNKVQAEVSDGDEELVGNRSKET KETRFIRGPKTPALVTDWEGSLPLVFNHCREACLGPSPLAASPAFLG QGQDLINLAFKVYNNRKKLQFLASTVRQTPATSPAHKNFQTPPEQRP GVPPEPPPTGACYKYQKSDHQAKECLQPRIPPKPCPICAGPHWKLD STHLAATPRAPGTLAQGSLLTDSFSA
2984	A	2	425	GFLVLLTSRMKLRTLAKQRRHILSVDPKLRRRSRTGKAAPWCLIIA GTPLIIHPRFKGVPRCDACLGPSPLAASPAFLGEGQELATSARNLT TRPRNACSPGFLLSRVHLCGTPLFI*PPGQMPAAQDSS*AVSICAG PHWKSDCSTHLAAGTPRAPGILAQGSL
2985	C	80	106	MRMKFGLD*
2986	C	259	531	MSPAHKNFQTPPEPQRPPIPPPEPPPGACYKCQKSGHQAKECLQPRIP PKPRPICAGPHWKLDCTHLASTPRAPGTLAQGSLLTASQIFLA*
2987	A	3	505	TKETRFIRGPKTPALVTDWEGSLPLVFNHCREACLGPSPLAASPAFL GGQDLINLAFKVYNNRKKLQFLASTVRQTPATSPAHKNFQTPPEQRP PGVPPPEPPPTGACYKYQKSDHQAKECLQPRIPPKPCPICAGPHWKLD CSTHLAATPRAPGTLAQGSLLTDSFSA
2988	A	1	1056	MWKGPKGLDMYGKSSVSPKTSIDILGRDTHLLALKVQTVVLQACGEG HVAGNCGRPLETEGSLQLTATKKLRDSVLQPKSPEFCQFTRAWNRT QVPDETEAPAGTYAAQSGDLPEINPLSSCSLLHEKDPPTASGPQTD

				QPKHLTNFKSGFRGVRPRRDACLGPSPLAASPAFLGKGQVPQPLLS VSLPLLRLSGGQETPNPFSFTLSGKSAFLEEQVPQPRISVPQSLIST PRPLISVAQSLISAPQPLISLCPNPLFPCPDLLSLHPNPLFPRPNPF PAFLEGACYKCQKSGHQAKECLQPGIPPKLRPICAGPHWKSDCPTHL AATPRAPGTLAQGSLTASQIFLA
2989	A	1	1482	CSEYEDSSPAPVPATDLSSSTLSSSVQPQDTGTSSQQLHPLDPWHELL RAQELQGATNHKGYSHAHEHAGLVQGGNGALAFNSGHRHAVPTI SSGTGRRRTPSSSAFGLNLHQLWFVSGFQAFSDRLKAALSASLLLR GDSDWLPSSSACKCLMLGLHFVIVGNICATLKEYSSMLHLDVTMCK NGEKTRTLQKRKKGMPHPAYEDLNIAAITLPANVVLHQPSGFRSTSG QLDPVWWSLDTDAHEIWCQDPGLGSGDFPWEITPLSSYSLLHEKDP TTSGPQTDQPKKHLTNFKSKTKETGFIHGPKTPAPVTDWEGSLPLVF NHCRTSLIIHPCFKGVRPRRDACLGPSPLAASPAFLEKQDILINLA FKVYNNRKKLQFLASTVRQTAATSPAHKNFQMPPEQRPVGPPEPPPT GACYMCRKSGHWAKECPQPGIPPKPRPICVGPHRKSDCSTYLAATPR APGNLAQGSILTDSFPDLLGLAAED
2990	A	399	569	ACYKCWKSGRHVKECLQPRIIPKPCPICAGPH*RSDCSTHLAATPRA PGTLAQGSL
2991	A	1	468	MSSQRLFLTIDLPKTQCAQEKLRVIRGCRDQAMEALQMTKPCFFKST WSQNHVEKCVPHFSPPLYVALNHLMAKGSQKSPKNYNTVFTKIRNG ACYKCQKSDHQAKECLQPRIIPKPCPICAGPHWKSDCSAHLAATPRA PGTLAQGSILTDSFWA
2992	A	1	984	MSGAGFTGGIPGAGGGVKEGGEPRVGILDTVAVAQDEGLHLGEKLD CPAELLREEERGLGKWIDRCGFLVSLTSRMKPRTLAVSVTLKDG SGVCSFRCPDVSRASSFRWVHGLADFRSEAADLHKSRSFGLGSQVSR PSVHLQLLSVSVLCTAKVIEVETKETCFIREPKTPAPVMDWEGSLP LVFNHCRDASLMIHSRFGVRPRRDACLGPSPLAASPAFLGQGVPL NPFSTLSAHKNFQTPEPQQPGVPPPEPPGACYKCQKSDHQAKECL QPRIIPKPCPICAGPHWKLDSTHLAATPRAPGTLAQGSILTDSFSA
2993	A	1	900	MLTEGFLAFLGSSLTATSLSAVSIGESSWIQCHTSLWGCKGGQERAP GEVEEPWWAKAKAGITFGCHLAKQEMGQTPVAQTAPKDVSPQSTDDP YSQSGDLPREINPLSSCYLLHEKDPPTSNPQTNQPKHLTNFKSVR LIPNLSSFPPTCPHSPNPKRCFQSSFTDPSDLSLHPKIAPPQVYNN REELQLLASSLRESLATSAPAHKNFKMPKPQWPGVPSGLHPSGSCFTC WKSGLHWAKECLWPGIPPKLYPIYEGLHWKSDCPTHLATTAPRAGTLA QDILTDSFPDLLSLAAED
2994	A	1	522	MPILASWPHPPGPFLLLTLLGLTGPPMWTMLKNNIAEKNDIHSRDS HASQSGMASYMLHHLEASAFSLQHLRCSSSGSMKAGVANCYPEGMVP IGSCSSKDSGSCFKCQKFCFWAKECLQPRIIPKLCPICVGLHWKSDC PTHQAATPRAPGTLAQGSILTDSFPDLLGLVTE
2995	A	3	1150	WAPTPSKAGKNAGRVFKDSKLDANDRILKQDQTEWSGSATLPSDGK TRLFYTDYSGKHGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGD GKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTE NGYQGEESLFNKAYYGGGTNFFRKESQKLQQAQAKRDAELANGALGI IELNNDYTLKKVMKPLITSNTSLECDVPLPVSMCSHLGISRAARQVS TEEGLSLAQEYNCGFFETSAAALRFCIDDAFHGLVREIRKESMPSLM EKKLKRKDSLWKKLKGSLKKKGILLEPAAAACYKCPKSGHWAKECPQ PGIPLKLRPIWAGPHRKSDCSTHLAATPRARGTLAQGSILTDSFPDRL GLAAED
2996	A	3	501	LEGASYGETKADVAEGKSQKKATEWRSQGQRRKGEETSQKDKCKRTN QLSVKRTNQLSVIWTNQQDVGSYANPLMAAEPAAVKGWRPSPKPH IGDKSVSFWLLWMSGVQQGQKIGP/PSQGNACRPRNSS*SHVPCGGG PHWKLDSTHLAATPRAPGTLAQGSL
2997	A	3	605	GHSRPRNWSQWSRFLWLEAHRPSGSPDSAEIERSQVSDCLGTSRHG TGALFLALGIYAASCYVARFIRVRPHRDAYSLOGRSLDHSPTFQGCQ TTQGRLPWSFTLSGKSRSFSGEGATTSPAHKNFQTPEPQWPGIPPEPP

				PTGACYTCRKSGHWAKECPQARIPPKPHPICVGPB*KSDCSTHLAAT PRAPGTLAQGSL
2998	A	1	669	MDTVGRRLRDSLGRTVDLGLTGNHGVVHPSLADSANKFEENTYCFGR TVETLLLRFGKTIMEEQVLKRVANILINLYGMTAVLSRASRSIRIG LRNHDHEEGQGYLGLGVKVSMAQPHILHFLPIQQGSPGQERRHDQR QMSHSGICPMPLSRRLDRPGACYKCQKSDHQAKECPQPRIPPKPCPI CAGPHWKLDGSTHLAATPRAPGTLARGSLTDSFSA
2999	A	1	762	MENKEAFVFOAHKEEIFEREKQMEQDLTRRVRELGRDANNRLSPA ENEGTWLCWPFKNRQRRLHLSVDPKLRRQSRTGKAAPFWCLIIAGT PLLIHHPHFRGVRPRRDACLGPSPLAASPAFLKERQDLINLAFKVYN NRKTLQFLASTVRQTPATSPAHNFTQPEPQRPPIPEPPSPGACYK CQKSGHQAKECPQPRIPPEPCPIRAGPHWKSDDSTHLAATPRASGTL AQSLTDSFPDLLGLAAED
3000	A	1	519	MLKDLPRAIRQEKETKSGDLPWEINPPSSYTLCEKDPPTTSGPQT NQPKKHLTNFKSETKETRFIRGPKTPAPVTDWEGSLPLVLNHCRCAS LIHPCFKGACYKCQKSDHQAQDCRQPRIPPKPRPICVGPCHKSDCS THLAATPRAPGTLAQGSLTDSFPDLLGLAAED
3001	A	1202	1315	LITAVSALAATPRAPGTLAQGSLTDSFPDLLGLAAED
3002	A	1	930	MEEKEERKRRKRKRREERDGERKRMEKQKENQDKDPPTTSGPQ TDQPKKHLTNFKSETKETRFIRGPKTPAPVTDWEGSLPLVFNHSDRT SLIIHPGFRGVRPRRDACLGPSPLAASPTFLGKGPAAPRQTELGPN SSASAPPYPNPFIASPHTWSGLQFPMTSPPPPAQFTLKKVAGAK GIVKDLINLTFKVYNNRKKLQFLASTVRQTPATSPAHNFTQPELQQ PGVPPPEPPRGACYKFQKSGHRAKECLQPRIPPKPHPICVGPBHWKSD CPHHLAATPRAPGTLAQGSLTPSQIFLA
3003	A	132	248	LQNLSEFAGLAATPRAPGTLAQGSLTDSFPDLLGLAAED
3004	A	3	439	TSRSITTSPEKESDPAGPARQYYTKGNLVRICLGAVILIILAGFLAE DWHRRRLRHRGRAVQRPLPPLPPLPQTRKSHGGACYKCQKSDHQA KECLQPRIPPKPCPICAGPHWKSDCSTHLAATPRAPGTLAQGSLTPS RLSG
3005	A	1	357	MTSGPQTDQPKKHLTNFKSGVRPRRDACLGPSPLAASPAFLREGQVP LNPFSFTLSGACYKCPKSDHQAEECLQPRIPPKPCPICAGPHWKSDC STHLAATPRAPGTLAQGSLTDSFSA
3006	A	1	765	MVVSQNLVLSVDVQICLFLLPVGSWVLLTSGVKLQTFVSVTALKGG LSRVVHSSWLLLRSSQLGFRLLFFIKYENPAQFMAHLVATLKRFTAL DLEGSEGLFSLCILLPNLLPTLNKAQKLDGSGPQTPOQDLINLAFKVY NNREELQLLASAVRETSPATSPAHNFKTKPKQWSGLPSGPPPPGSCF KCQKSGHWAKECLQPRIPPKPCPICVGPBHWKDCPHTHLAATPRVPGT LAQGSLTDSFPNLLSLAAED
3007	A	1	1434	SVAFVFACPAVDYLVKISWELQGDDEEQDGLRNMWQTLQKTKDYED VRIQNAINIAQGASEAIGQRQSSAAKPRRSGKESVREPWARVPGALG VAARKYQKMGIEIKRRERLKCAGAKIERRKRLKDREVGEESKKRPLT GFEIEPPKVTVMKQNSFTGGSEVSIMCSATGYPKPKIAWTVNDMFI VGSHRYRMTSDGTLFIKNAAPKDAGIYGCLAKAPKLMVVQSELLVAL GDITVMECKTSGIPPPQVKWFKGDLELRPST/CFLLSILAP/PLQSL PSLNFSFHL\DFLAATPRAPGTLAQGSLTDSFPDLLGLAAED
3008	A	166	421	RPRSERLLWGTSPLS/CALTL*GDPPTTSGPQTNQLKEHLTNFKSGP HWKMDCPHTHAATPRAPGTLAQGSLTDSFPDLLGSAED
3009	A	1	434	MTSGPQTDQPKKHLTNFKSETKETHFIRGPKTPAPVTDWEGSLPLVF NHWRDASLIHPRFKGVRPRRDACLGPSPLAASPAFLGKGQELATSA RNLTTKARNACSPGFLLSRIPSVRDPTGNRTVQLTWQPLPEPELWLP KAL
3010	A	1478	2240	WQVPLSWGRGKYPSTPSPSPLAASPTFLGQGVPLNPFSTLSGKSR FPGAGASTPQPLLLHPQRQVPLSWGRGKYPSTPSPSPLAASPAFLGQ GQVPLNPFSTLSGKSRFPRGQETPNRLFPHNLLSLHPNPLFPHPD LLSLCPNPLFPCLNPFSAFLEGKNPPPLLRVSTLFSGLASFTMGACY

				TCQKSGHWAKECPQPGIPPKPCPISVGPB*KSDCSTHLAATPGAPGT LAQ/GLTDSFPDLLGLAAED
3011	A	1	624	MEFCISLGRKITFSNIFPYNGANWKVFLKKSQPLLNALVEQDDAERL FRFRRAAGDLPYGAFFEIFWETQCQEMQQLADRVIACRQPGQSMEID LACNGVQITGWLPQLWDAEGISFSVFSFGMLKGSASVSSALGCWSSL HMLEICHWAKECPQHGIIPKPRPICVGPFRKSDCSSHLAATPRAPGT LAQGS LTDSFPDLLGLAAED
3012	A	321	512	LRSGDLPWEINALSSCSLLHEKDPPTTSGSQTDQPKKHLTNFKSETK ETRFICGPKTPAPVTD
3013	A	1005	1251	KGGWSQRHSQGACYTCRKSGHWAKECPQPGIPPKPRPICVGPB*KSD CSTHLAANPRAPGT LAQGS LTDSFPDLLGLAAED
3014	C	18	56	MAINSIRSLQLM*
3015	A	188	365	VAYPPKKVCPEKGPWPVFSIHFGPNLYPQKKPWGEKGRKLNCPVKG PWTTTRQRMPPA
3016	A	602	2459	FWGEGEKATAFLICNLCLRCPCVDMNS\QGSDSNEEDYDP\NCE\E KEEEEEED\DP\GDIEDYY\VGVASDVEQQGADAFDP\EEYQFTCLTY KESEG\ALNEHMT\SLSFLSLKVSHSSWNLVNF\HWQVSEILDR YKNSAQLLVEARVQPNP/SQKHVPTSHPPHH\CAGCGMQVCAKREN LL\SLWACQL*FCRSCWEQHCS\VLVKDGVGVG\VSCMA\Q\DCPL\ RNTSGTFVFP\LLPNEEFEEKYRRYLFRDYVESHYQLQL\CPG\AD CPM\VIRVQEPRA\RARVQC\NRCNEVF\CFKCRQMYHAPTD\CATI \RKWLTKL\QDDSETANYI\SAHTKDCPKCNICI\EKDGG\CNH\MQ CSKCKHDFCWMCLGDWKTGSEYYECSRYKENPDIVNQSQQQA/RR EALKKYLFYFERWENHNKSLQLEAQTYQRI\HEKIQERVMMNLGTWI \DWQYLQNAAKFFGQGSFSSLLQCRYTLQYTYPY\AYYM\ESGPRK KLFEYQQAQLEAEIENLSWK\VERADSYD\RGDLENPDIIITEPTGG TNPCLKDF\HDTLSWDVDVPGVRKISLARS PRAHTACLAGSAFHDP QATAQGPTPERHWQHLVDFCFLLSLVSTQGRRPC
3017	A	103	769	GPCCIPIIQQLILQCFKHFSGLCFQLCKLMMPSKSLVMEYLAHPS TL\GLAVGVACGMCLG\WSLRV\CFGMLPKSKTSKTHDT\ESEASI LGRQPGSPG*FLVVRN*L*RWGKGERGCPSASHAAVSSPTKQISKKK SPEMAQNGEYVWASPKVGGSKVPDEETLIAL\LAHAKMLG\LTVSL IQDAGRTQI\APGSQTVLGIGPGPADLIDKVT\GHLKLY
3018	A	99	480	GGLWPQRAVASGSGKWRQEP SLHFAMSFLIDSSIMITSQIRQYVVQV IFSVTFAFSC TMFELIIFEILGVNLSSSRYPFHWMNLCVILLILVFM VPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFM
3019	A	2	87	NKPSGFWGMIKSVTTSASGESILCPSA
3020	A	1	921	MAKEPLAYICQDICWIPGVAYILNFLFHSQQHYFRATFPTSDAGRT RVSNLHVPIGPHCGNDISQLSNHLEQEYDLYMEDSVDPYHLHRKE VDALEELSRQLFLETADLYATKGTVVINVANDMTAMLIGKGGVILYT QRGFCPQAIFMSISFENGKLKAARGTYFSSSQYLLMMLEVFKAVKEE IQFRRVEKIVESFELERATKRVLYVFCLESTERELLELRKTVSKQ EWLLQSTAHLKIANQOKESMEQFIVSQRSPKLLRKSSKLIKDAFHN ELMGDENIKNYAYKLEMSLTGNNIK
3021	A	1	2203	MGGASARPAAPSGRWGVLPGRPFWFVMSPSARPPPRLGVPNSSLR TGHDDGGFVEQRRGKGDSEGQLGLRIKLVRVVFWSQLVMAFDKAE PSSPKVLVLTTRATGGVGLQTLRRLQERPGIGQLGALCLICTVRL CGHEEMTSTFNPCKLSKQEGQNYGFFLRIEKDTEGHLVRVVEKCS PAEKAGLQDGRVLRINGVFPVDKEEHMQVVDLVRKSGNSVTLLVLDG DSYEKAVKTRVDLKLQSQSQKEQGLSDNILSPVMNGGVQWTQPRLC YLKKEGGSYGFSKTVQGGKGVYMTDITPQGVAMRAGVLADHLEIV NGENVEDASHEEVVEKVRGPRRVGYGFDROQMAAALQKRGITVKNK QTESNNNINKRPHKNPIQSAASKIEELEKNYFKIQYGSKKEPVQV KTTVSKKNKAGGITLPDFKLYYKVTVTKTACSRYFHWKMNL CVILLI L/VFPMVPFLQLAYFIVSNIRLL\HKQRLLFSCLLWLTFMYFFWKLG DPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFVAVNCPYTYMS

				YFLRNVTDTDILALERRLLQTMDMIISKKKRLRGPVGVGFLLIYSPV GQIAEDLTLIQQEVDALAEELSRQLFLETADLYATKERIEYSKTFKKGK YFNFLGYFFSIYCVWKIFMVKFSQHSIFILVGIIIVTSIRGLLITL TKFFYAISSSKSSNVIVLLLAQIMGMFVSS
3022	A	2	215	QKMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFL VSALSSILFLYLAHKQAPEKQMAP
3023	A	50	1598	GGLWPQRAVASGSGKWRQEPSLHFAMSFLIDSSIMITSQILFFGFGW LFFMRQLFKDYBIRQYVQVIFSVTFASFCTMFELIFEILGVLNNS SRYFHWKMNLVCVILLIL\VFV\VPFYIG\YFIV\SNIRLLLSPLSQV A*TTDWLFSCLLGL\TFMYFFG\KLGDPFPILSPKHGILSIEQLISR VGVIGV\TLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSE NLTLIQEVDALAEELSRQLFLETADLYATKERIEYSKTFKKGKYFNFL GYFFSIYCVWKIFMATINIVFDRVGKTDVPTRGIEITVNYLGIQFDV KFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLL AQIMGMFVSSVLLIRMSMPLEYRTIITEVL/GEELQFNF/YIHRW\ F\DVIFLVRRLSLGILFPLFGLHKQAPEK\QMAPLNLKPYLQTDKRP SGFQKFRI
3024	A	1	158	AERHQFRDFRDLNKGHLYGSEVGHVWLPPAQDQPLVEANHLLHESD TDKVQ
3025	A	2	1067	AAELGTFAQTQSGAWRAERSWHNRGPMWRRPSVLLLLLLLRHGAQK PSPDAGPHGTGRVHQAPLSDAPHDDAHGNFYQDHEAFL*REVAKF DQLTPQESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHQRHIL DSVSAAWDTYDTRDGRVGWEELRNATYGHYAPGEEFHDVEDAETK KMLARDERRFRVADQDGDMSATREELTAFLHPEEFPHMRDIVIAETL EDLDRNKDGYVQVEEYIADLYSAEPGEEPAWVQTERQQFRDPRDLN KDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRL\TKAEI LGNWNMFVGSQATNYGEDLTRHDEL
3026	A	2	860	RRGPCNGRYHHPVYPHTAVQREPPAGPRACHSPCWHADAPVRSPGQ STSPHDAVTWPFLHGSREGPTPRRTRTPPAFRPHTQACPSTCYCHTL ASRRGPCNGRYHHPVYPHTAVQREPPAGPRACHSPCWHADAPADLRG ADQRPERLADSAWIWSSQRLATWKRVRTGQNTWASELSFEALANL PANMMQLPGHFSTFLVRAPHAAEKPLLHSILTHRPVHPLATVTLLP AEEAPVMADITAQSILTPQLCSGTLLLAHVAARAHAGTTLQHVGVCG PHYR
3027	A	2	1681	FGTLGSAFPESC PFQKEDGMIKFQIQGIHVQERVTFKDVAVVFTKV\ *LALLDKAQINLYQDVMLENFMNMLMWIPLPVSFQLSANGESQQEI QGRDKSEVRIFIPPGFSLEVAVEWLYSISIDQDAHPKTDPKLRPEE AQRKSLSRNVKMHCFVKPRAAPQTEPTLEPTLFPSYPGVRPVWRMR KEAYGLQSPESPARSSGHSQGYPGEDLHRAEQRPERFAGSAWTSLSQ RLATWKRIQRTGQNTWLEALANLLANMTQLPGHFSTFLVSAPHPAAE KPLLHSILTHRPVHLLATVTLLPAEEAPLMADITAQAILTPQLCSGT LLLAHVAARAHADTNLQHVGIAGDTTGDMSMTLLPGSDTVDLKDT APCIVAAPVPAMAKKGQIAQAIASEGANPRPWLPRTVGPVNVGEG KCGVGAPRVPTEALPSGAVRRGPPSSRPQTHQQLPPCAWKRCRHSSTP AHENSQVGYTLQSHRGRDAQGLGSSSLASACLDVRHGVKGDYFRTLR FNDPCPAGFQTGMGPAAPLFLCLISPFQNGGIYPKAVAPLYLGSN
3028	A	51	569	SLRTVPPHYLQSGPGTPIPPSSLGPASGTRRVES/CVAAPNEQEGSS KGGARPVTICDSQNRPCPPPPSPALPQADPSLKTWLLLNHIRWDTD SMICMEDSS**GFK/PNKDSIKVQVRLRGVQGVGHCMGGAALPSTSL SSCLTPFPAPLNSRHTTLAPPLPQENPAQRTTP
3029	A	2	396	KCHDCGAILEEYDEETLGLAIVVLSTFIHLSPLDAAPLLDDIMQSVG RLASSTTFNSQAESMMVPGNAAGVAKQFLRCIFHQLAPNGIFPQLFQ STIKDGTFLRTLASSLMDFNELSSIAALSQLEGLNN
3030	A	2	1038	GLLEPFSKLLSFVIQNAVFTLAYLVELCGLCYRAFTKERDKFYLSRS GCSKSFCRRLKLKSPLPDTNLLLLLVQFI\LPDAGTKLD*VNNPEQAD

				DSLCTWDVGT\AMECVRQYINEVLDFM\ADMHTLTCLKSHMKTC AS\DEDTFGGHLKVGLAQIAAMDISRGNHRDNKAVIRYLPWLYHPPS AMQQGPKEFIECVSHIRLLSWLLLSLTHNAVCPNASSPCLPIPLDA GSHVADHLIVILIGFPEQSKTSVLHMCSLFHAFIFAQLWTVYCEQSA VATNLQNEFSFTAILTALEFW\SRVTP\AILQLMG/HINKVMGRK WVLLSMWISLMGGNLPGNAIWT
3031	A	3615	5322	EVPPNPACYQHQ*SVCLCLHLKSSLTSSRR*/CTDKCHDCGAILEE YDEETLGLAIVVLSTFIHLSPDLAAPLLLDIMQSVGRLASSTTFSNQ AESWPPTASSRSCSKARSKVIHPLRIQAPQICLIPDTQTLNPIVDFP DGTFLRTLASSLMDFNELSSIAALSQLEGLNNKKNLPAGGAMIRCL ENIATFMEALPMDSPSSLWTTISNQFQTFQAKLPCVLPKSLLEPFS KLLSFVIONAVFTLAYLVELCGLCYRAFTKERDKFYLSRVVLELLQ ALKLKSPDPDTNLLLQYENKMNEKAERLVKLKLSAQQQFQFICA DAGTKLAESTILSKQMIASVPGCGTAAMECVRQYINEVLDFMADMHT LTKLKTSLHMCSLFHAFIFAQLWTVYCEQSAVATNLQNEFSFTA ILTALEFWSRVTPSILQLMAHNKVLIPMWLPMIQSNIKHLSAGLQLR LQAIQNHVNHSLRTLPGSGQSSAGLAALRKWLQCTQFKMAQVENPV LGKQPLNFILYEWTPSAPQCQHSGLAIMGLKTNNDPQAGWGNHIGY LYNPLS
3032	A	3	1078	FFSSVFPAAIEPGERASARRRVSRAAGCLALTLPALLLVTHQVPAEAA VSRMAEL\TALESLEMGFPRGRAEKALALTGNQGIEAAMDWLMH EDDPDVDEPLETPLGHIL\GREPTFSEQGGLKDLVLA\AGEGKPAL S*/EERQEQT\RMFGAWLAQKGSRE\REEREGRE\ALERERQRR\ RQGQE\LSAARQLQED\KMRR\AAAEERRREKAE\LAARQVRREK IERDKAERAKKYGSGVGSQPPQ\VAPEPGP\VPSSP\SQEPP\TKGE DDKCRIQ\VRLPRWDPH*PQTFRAREQLAAVRL\YVEL\HRGEBL\G GGARDPVQIASVAFF\RAFLRSLTMER\PLQELGMAAKTRNQD
3033	A	2	565	IHFQQEHWPSSQLLRESLEDMLHLSALGLCLLLVTSSNLAIATKKE KRPPQPLSRG\WGDDITGVQTYEESLLCSK*GSH*WVIHHLG\DC QYSQALKKVFQAQNEEQEMAQNKFIMLNLMHETTDKNLSPDGQYVPR IMFVDPSLTVRADIAGRYSNRLTYEPRDLPLLIENMKALRLIQSE L
3034	A	73	262	PLPARGKSTLPATFCSPAPELASMSVPPNRSQTGWPRGVTQFGNK YIQQTCKPLTLERTINL
3035	A	29	867	PLEGIADNRFPGETSTLPATFCSPAPELASMSVPPNRSQTGWPR GVTQFGNKYIQQTCKPL\TL\ERTINLYPLTN\YTFGTRAPLTRTS SV\AARF\QRIEGKNFDKIGMRRTVEGVL\IVHE\HRLTPWCYLLQL GTNFLPNYLGWLNLTPEGEDEV\EGKTA**PEIPGVSQDGV\QD\W GPLTDCHWVTW\RPKFLNPPSVSHIFPAHIT\KPKE/HIRKLFPGS SLQEKALVLQFPKKFTSW*PATPLFELYDNA\PGYGPIISSLPQLLS RFNFIYN
3036	A	2	817	RARIPKMAAVKDSGCG*GEMATGNRR\LHLGIPEAVFVYFYSY*RKM YHYFMKQPGNETADTVLKK\LDEQYQYKFMEINLAQKKRRLKGQIP \EIKQTLLEILKYMOKKKE\STNFNGRPRFFAGRLTLYLQKLSVPPT *RG\CLGLGANVMLEYDIDEAQ\ALLGKDL\STATKILDSRGRTLT FL\RDQFTTTEVNMARGLLIGDVKKEGNKD\STKNKALMLGQFKNV GLVFPPNMFIFKYPFIPYRFDINFGMFNQPRNFKEKINTILFIY
3037	A	3	468	ERIMEWHRHTMTECSAQEPKSHDIYLRLLVLYRFLARRTNSTFNQV VLKRLFMSRTNRPPSLSRMIRKMKLPGRENKTAVVVGTITDDVRVQ EVPKLKVCALRVTSRARSIRLARGGKILTFDQLALD/SPYVRSKGRK FERARCRRARRGYKN
3038	A	1	693	MGVDIRHNKDRKVRREPKSQDIYLRLLVLYRFLARRTNSTFNQV LKRLFMSRTNRPPSLSRMIRKMKLPGRENKTAVVVGTITDDVRVQ VPKLKHNTDVDVVKVPEVLRATAVSPGVLRVVNDSSVGYQGSAA PRQWRVCALRVTSRARSIRLARGGKILTFDQLALDSPKGCVLLSG PRKGREVYRHFGKAPGTPHSHTKPYVRSKGRKFERARGRRASRGYKN

3039	A	105	756	VDHPPYKRTKVRQSPKSYIYLSLLLKLYRFSGPPEPNSNIQTR VVLKRLFMSPHQTGPPLS\LSRMIR\KMKLSWPGKQRRAVVC/VGPI TD\DVGRSRRYPKLKVCCTAP*PSRAPQAAILKAGGK\ILTF\DLA LGLPLKG\CGTVLLSG\PSKG\RKVYRHRFRQRPQEPHKKHQNPTFR SKGRKFERARG\RRAS\RGYKKLTLDPTLLYKKIFA
3040	A	301	390	ENASMGPCLEFKTTSVSHLVEVVPQKLSWVI
3041	A	1	737	MWFAYSPTFCHDWKLPEASAEAKRMPALCFLYSLQHPLCEDGVCAH EAGVWGIGGLIAYVKGYEEVSQKFTSIRRVRGDNYCALRATLFQAM SQAVGLPPWLQDPELMLVVFVAILLHSHLECREPLLIPILSLYMGAL VRCTTLCGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALILA TQRISRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEI RAVYPAFDKNNPSNKLVSNTVTAAHIKKFTFVCMALSLTLKDSVQ KPDISLTGRLVQTLPTMRHQGESKDVAPLASWLSEPSTSSEASQT SSKLTINSQEGKAKQKLECGTLSIVLRSCENQERIKAAEKRNRSW TTLCLGAWRPLLFELPVIVQTPDQTNRFQFRYPAKTQSGLCSEFFHS FDLLTLEAFVKWVPGCLLILLCFVMFWTPNVSEKILIDIIGVDFAF AELCVPLRIFSFFPVPTVRAHLTGWL/QGPGAHAGCFCSHFASQS PGMPGAPAHDPDLLVHGRTCALHHPVPGLLQEHRSRHP*QKWPGAGG RCNNKKDAELLVAFGSNSGHTENQSAYCQPLCFPGPWWQFCSHRGS DFDSHPCGSHAIRLVDGNPCCVSCFRQE
3042	A	889	1577	RGKNTVLKKIRSQFTIRESFDLRYKEHIPLPKLEFPLDTKVFGLLG EDMVCTGPTGVALKGPWKYIGIIDEGKDLVNFYSQKLVFRTSWSTW LPRGPRVLLRDCSLKTPKPAQAQAEPT\VHLRPRRQGFSGSMRSLID WVSLTHSDGDVIVPIVLSNERYHWP\VLGWVGVDCEFFRVVLGEA RLH\LDGVAHQH*GKKEPFPTCSKTTSVSHLVEVVPQKLSWVI
3043	A	80	695	SPAASGGFRAGPRNQDPSRALAELWPTKAV\SVLKGDGP\VOGIINF E\QKESNGPSEG\WGKHLKGLTEGL\HGFBVHEFGD\NTAG\CTSAG \PHFIPLSRK\HGGPK\DEERHVEDLGQC*LLDKDGVGPMCLLKDS\ VIFTLQGDHLHLGRTLVPVWKKPDDLQQRVNE\ESSKTG\NAGKF VWACGVNLGSAPNKHSPWDVVLRRP
3044	A	2188	2706	RESIDQGSNFFFLRRSLDSVTQAGVQWHDLSLQPPPPGFK*K*F SCLSLSS*DYRSPATMPGLIFLYFFFLVETGGFTVLAR\MVSIS*P Q/CDPPASASQ\SAGIQKNSFFLETRVSAFVAQAGVQWCDLGSPQP PPPGV\QPFSCLSLPSWDYRRTPPGPANFAVCN
3045	A	33	198	CRHRQAQLQMVBHPRRLGGWWRIFARQEHICIRVPKVNKFYLLQC VHIHFHG
3046	B	6	125	MAGQFRIYLWDPDLLILSQIVLMQTVYYGSLGLWLALVDGL*
3047	A	1	110	YAQLGTRVPELASVTHFTPPLPINKCQPVSCSNLGS
3048	A	260	798	RPGHAQTLGSPSLALGMAGQFRSYVWDPLLILSQIVLMQTVYYGSLG LWLA\VVDGLLRISPSLDQMFDAEILGFS/TPFQGRLSMMSFILNTL NSA\LGILLYFIRRGK\QCLDFTVTVHFFHLLGLLSNSSPFSPPGG* TLVGLGPKPVVALHSLAVIGEYLCMRTELKEIPLNSAPKSNV
3049	B	1	528	MRRQDCPNPMKKIRSSSPVQQERVSSLYFQSARGGLGVDVSALGTVT HVSPPSSARVAMAMSAERGCSMGHIMGYRGVGRFTRGNGDHARVGYK GNPPEVSIISGYDDNWYLGRTDNLCDVRSNPEPTGYDWSSTSGTFP TSAVPRAPSWSSQWTVCSIHRLRHITNAVDGPR*
3050	A	31	206	GSSCRSRLVVVLSIVLEGPAAPAGDPQTPSPALDKLEFGNTLEDK ARELISRIKQSELSAKMRVPLRPRHEALPVAPGPGGGSVDRLGRPS SPRGPPDVSQCLG*ABGVWKHTGGQSGTHQPHQTE
3051	A	21	353	SAAGTGPEPEPEPHRHLNRPADRPPQSGPRASGRAQSPPGPSMARA AALLPSRSPPTPLWPLLLLLLLETGAQDVRVQVLPVVRGQLGGTVE LPCHLLPPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFSPKPK GSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATF PKGSVRGMTWLRVIAKPKNQAEAKVTFSDPTTVALCISKEGRPPA RISWLSLDWEAKETQVSGTLAGTVTVTSRFTLVPSGRADGVTVTCK VEHESFEAPALIPVTLVRYPPPEVSIISGYDDNWYLGRTDNLCDVRS

				SNPEPTGYDWSTTSGTFPTSAVAQGSQVL\IHAVDSL\FNTTFVCTS QPNPWALARAEQVIF\VRETPOALAPRCGPAGVGGRGDDTAGAAASG WGVGLHPCMRVRRRRKSPGGAGGGASGDGGFYDPKASGVKGWGPRL LDTSSPWSHGTRWQG*GGGGGGREGRERPHVASTPSTSRMTWSPSWT APSSHGG/PVYV*PGPPWPGPLPSCRRDRRRRRCCGRCCCCCSWKPE PRMCEFKCYPRCEASSGAPWSCRATCCHLFLDCTSPW
3052	A	1	1620	MARAAALLPSRSPPTLLWPLLLLLLLETGAQDVRVQVLPEVRGQLG GTVELPCHLLPPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFP SPKPGSERLSFVS AKQSTGQDTEAELQDATLALHGLTVEDEGNYTCE FATFPKGSVRGMT\WLRVIAKPNQAEAQKVTFSQDPTTVALCISKE GRPPARISWLSSLDWEAKETQVSGTLAGTVTVTSRFTLVPSGRADGV TVTCKVEHESFKEPALIPVTLVRYPPPEVAISGYDDNWDLGRTDATL SCDVRSNPEPTGYDWSTTSG\TFPTSAVAQGSQVLVIHAVDSLNTTF VCTVTINAVGMGRAEQVICVRETNPNTAGAGPTGGIIGGIIAIIATAV AATGILICRQQRKEQTLQGAEEDEDLEGPPSYKPPTPKAKLEAQEMP \SHLFTLGA*EHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPL HPGATSLGSPIPVPPGPPAVEDVSLDLEDEEGEEEEYYLDT\INPIY DALSYSSPSDSYQKGKGFVMSRAMYV
3053	A	408	2708	DPSSGHWLHWSIRPPAAGWSPRSGRAAARAQSPRRREHGAPGRTGPG GGPRLLLAVLLAAHPGAQDVRVQVLPEVRGQLGGTVELPCHLLPPV PGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVS AKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMT WLRVIAKPNQAEAQKVTFSQDPTTVALCISKEGRPPARISWLSSLD WEAKETQVSGTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEP ALIPVTLVRYPP\PEVSIISGYDDN\WY\LG\RTDAT/L*ACDVRSN PEPTGY\DWSTTSGTFPTSAVAQGSQ\LVIAHVN\SVLFNTTFV\CT VTNA\VGIGAGAE\QVIFVRETPRASPRDVGPLVWGA VGGTLLVLL LAGGSLAFILLRVRRRRKSPGGAGGGASGDGGFYDPKAQVLGNGDPV FWTPVVPMPEDGKDEEEEEEEKAEGKMLMPPPPALEDMMESQLD GSLISRAVYTTPSPVPGSAGAAVACTDPVPSSGVGHNDHKNSS MFRMKALAQLSPYKTPNTAGAGATGGIIGGIIAIIATAV AATGILI CRQQRKEQTLQGAEEDEDLEGPPSYKPPTPKAKLEAQEMPSQLFTLG ASEHSPLKTPYFDAGASCTEQVGAHGKTKEMPRYHELPTLEERSGPL HPGATSLGSPIPVPPGPPAVEDVSLDLEDEEGEEEEYYLDKINPIYD ALSYSSPSDSYQKGKGFVMSRAMYV
3054	A	115	467	VGCDLRSRRGGAQPLGTDDEDAIISVLAYRNTAQRQEIRTAYKSTIG RDLIDDLKSELSGNFQVIVGMMMPVTLYDVQELRRAMKGAGTDEGC LIEILASRTPEEIRIRISQTYQQQ
3055	A	315	433	SHGHGTDEDAIISVLAYRNTAQRQEIRTAYKSTIGRDLI
3056	A	53	444	PRVMAM/ATKGGTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVL AYRNTAQRQEIRTAYKSTIGRDLIDDLKSELSGNFQVIVGMMMPVTLYDVQELRRAMKGAGTDEGC LIEILASRTPEEIRIRISQTYQQQ
3057	A	186	1268	PRDMAMATIGGTVKAASGFNAMEDAHTLRKAMKGLGTDENAIISVLA YRNTAQRLEIRTAYKSTIGR\DLIDDLKSEL\SGNF\EQVIVG\MKM PT*RDDV\QELRRAMKGAGT\DEG\CLIEILASRTPEEIRIRISQTYQ QQYGRSLEDDIRS\DTSM\FKRVLV\SLSAGGRDEGNYLDDALVRQ DAQDLYEAGEKKWGTDEVKFL\TVLCSPEPKITLLHVDFEYQKDIHR RIIEPEVLNSETSGIFWKIALLGLI\VKCMRNKSAYFAEKL\YKS\M KGLGT\DDNT\LIRVMVSSSQMD\MLDIPAHTSKRLLWKSPLY\F IKNRVATSGD\YRK\VLLVLCGREMIKIKIPGRDREGSSTLLNFF
3058	A	1	4608	MKQLLPASGLPLSSSPLSPRQESPGVERAHEGCLSONLQVQRATRE GEIDRVAKSGGQERACASSETESEAGDIMDQQFEEMNNKLNVSVDPT GFLRMVRRNNLFSQAEYCAQPWGLSGEQQGPQPRSLHPAPLARPD IQSHPKSKEIEGVSADSSNPDPLEDEGNSRRSSRFNVEAVLCSSRGR PDSSMPDCCRNAALARSQSMSTLSFNTVSPTQDGTSSLP RRQSSF AKPPLRALYDILLIAPMEGGVVESTEPLGTSRAGFASGTALFWLGDN

				KAASPPGVSVSSLENNEDNTQCNRLQEQGYREAAVPDWTQDLALCLLP TLQSLKARTAPHLCPSSCYKAWYTLAVSKVSGMGLMHSSGPVGRHR QLILVLEGELYLIPFALLKGSSSNEYLYERFGLLAVPSIRLSVQSK SHLRKNPPTYSSSTSMAAVIGNPKLPSAVMDRWLWGPMPSAEEEEAYM VSELLGCQPLVGSVATKERVMSALTQAECVHFATHISWKL SALVLT SMDGNPASSKSSFGHPYTIPESLRVQDDASDGESISDCPPLQELLT AADVLDLQLPVKLVVLGSSQESNSKVTADGVIALTRAFLAAGAQC VLSLWVPVVAASKMFIHAFYSSLLNGLKASAALGEAMKVQSSKAFSH PSNWAGFMLIGSDVKLNSPSSSLIGQALTEILQHPERARDALRVLLHL VEKSLQRIQNGQRNAMYTSQQSVENKVGIPGWQALLTAVGFRDPP TSGLPAAVFFPSTDPGDRLOQCSSTLQSLGLPNPALQALCKLITAS ETGEQLISRLHQVLVQLQAGEKEQDLASAPIQVSVISVQLWRLPGCHE FLAALDMGKPAQMLAEGPCRHSMLHKEPYSAHVQDLESSRRKQML IFFVPLGFDLCEVGQEEVILKTGKQANRRTVHFALQSLLSLFGPDRS GHS GHVGLGDFQALGTHPARLMFLRAKLATVGRANAGLEGGYGLQVE PTESAEDSTELPKRLSLDSSSSLESLSAQSVSNALPLGYQPPFSP TGADSIASDAISVYSLSSIASSMSFVSKPEGGSEGGPGGRQDHRD KNAYLQRSTLPRSOLPPQTRPAGNKDEEEYEGFSIIISNEPLATYQEN RNTCFSPDHKQPQPGTAGGMRVSVSSKGSISTPNSPVKMTLIPSPNS PFQKVGKLASSDTGESDQSSTETDSTVKSQEESENPKLDPQBLAQKIL EETQSHLIAVERLQSGGQVSKSNNPEDGVQAPSSTAVFRASETSF SRPVLSHQKSQSPVTVKPKPPARSSSLPKVSSGYSSPTTSEMSIKD SPSQHSGRPSPGCDSQTSQLDQPLFKLKYPSSPYSAHISKSPRNMSP SSGHQSPAGSAPSPALSYSSAGSARSSPADAPDIDKLMAAIDEKVQ AVHNLKMFQSTPQHSTGPMKIFRGAPGTMTSKRDVLSLLNLSPRHN KKEEGVDKLELKELSLQHDGAPPKAPPNGHWRTETTSLSLSLPLPAG PPATAPARPLRLPSGNGYKFLSPGRFFPSSKC
3059	A	1	465	SPGVERAHEGCLSQNLQVQRATREGEIDRVAKSGGQERACASSETES EAGDIMDQQFEEMNNKLSNVTDPGTGFLRMVRRNNLFNSQAECYCAQPW GLSGEQGPQPRSLHPAPLARPDPIQSHPOKSKEIEGVSADSSNPDP LDEGNSRRSSRFNV
3060	B	109	192	GSSSNEYLYERFGLLAVPSIRLSVQSK*
3061	A	1	1542	MGITKMMNMVMEEAIGYFEQQLAMLQQLSGNESVLDRGRAYGNLGD YEALGDYEEAIKYEQYLSVAQSLNMQDQAKAYRGLGNHGRAMGSL QQALVCFEKRLVVAHELGEAFNKAQAYGELGSLHSQLGNYEQAI SCLERQLNIARDMKDRALESDAACGLGGVYQQMGEYDTALQYHQDLQIA EETNNPTCQGRAYGNLGLTYESLGTFERAVVYQEQHLSIAAQMN DLAAKTVSYSSSLGRTHALQNYSSQAVMYLQEGRLRLAEQLGRREDEAKIRH GLGLSLWASGNLEEAQHQLYRASALFETIRHEAQLSTDYKLSLFDLQ TSSYQALQVRVLVSLGHDEALAVAERGRTRAFADLLVERQTGQDSD PYSPTIDQILEMVNGQRGLVLYSLAAGYLYSWLLAPGAGIVKFHE HYLGENTVENSSDFQASSSVTLPTATGSALEQHIASVREALGVESHY SSIRNGHCRSLPCYLSLFHVSTAGHQDYKGTWVYDTHLKSLSHM
3062	A	1	4226	EAVLCSSRGRPDSSMPDCCRNAALEARSCQSMTSLFSNTVSPTQDGT SSLPRRQSSFAKPLRLALYDLLIAPMEGGVVESTEPLGTSRSGFASG TALFWLGDNGKAASPPGVSVSSLENNEDNTQCNRLQEQGYREAAVPD WTQDLALCLLP TLQSLKARTAPHLCPSSCYKAWYTLAVSKVSGMVEG KAWIILLLLAASTHALLQRPQEGDITPLAGSRAAAVSCQARPFSTFS GLMHSSGPVGRHRQLILVLEGELYLIPFALLKGSSSNEYLYERFGLL AVPSIRLSVQSKSHLRKNPPTYSSSTSMAAVIGNPKLPSAVMDRWL WGPMPSAEEEEAYMVSELLGCQPLVGSVATKERVMSALTQAECVHFAT HISWKL SALVLTPSMDGNPASSKSSFGHPYTIPESLRVQDDASDGES ISDCPPLQELLTAAADVLDLQLPVKLVVLGSSQESNSKVTADGVIAL TRAFLAAGAQCVLVSLWVPVVAASKMFIHAFYSSLLNGLKASAALGE AMKVQSSKAFSHPSNWAGFMLIGSDVKLNSPSSSLIGQALTEILQHP ERARDALRVLLHLVEKSLQRIQNGQRNAMYTSQQSVENKVGIPGWQ

				<p>ALLTAVGFRLDPPTSGLPAAVFFPTSDPGDRLQCCSSTLQSLGLPN PALQALCKLITASETGEQLISRLHQVLVQLQAGEKEQDLASAPIQVS ISVQLWRLPGCHEFLAALDMGKPAQMLAEGPCRHSMLHKEPYSAH VQDLESSRRKQMLIFFVPLGFDLCEVGQEEVILKTGKQANRRRTVHFA LQSLLSLFGPDRSGHSGHVGLGDFQALGTHPARLMFLRAKLATVGRA NAGLEGGYGLQVEPTGSAEDSTELPKRLSLDSSSSLESLASAQSVSN ALPLGYQQPPFSPTGADSIASDAISVYSLSSIASSMSFVSKPEGGSE GGGPGGRQDHRDRSKNAYLQRSTLPRSOLPPQTRPAS\NKDEEEYEGF SIISNEPLATYQENRNTCFSPDHKQPQPGTAGGMRVSVSSKGSISTP NSPVKMTLIPSPNSPFQKVGLASSDTGESDQSSTETDSTVKSQEE NPKLDPQELAQAQKILEETQSHLIAVERLQSRGGQVSKSNNPEDGVQAP SSTAVFRASETSAFSRPVLSHQKSQSPVTVKPKPPARSSSLPKVSS GYSSPTTSEMSIKDPSQHSRPSPGCDSQTSQLDQPLFKLKYPSSP YSAHISKSPRNMSPSSGHQSPAGSAPSPALSAGSARSSPADAPD IDKLKMAAIDEKVQAVHNLKMFQWQSTPQHSTGPMKIFRGAPGTMTSK RDVLSLLNLSPRHNKKEEGVDKLELKELSLQQHDGAPPKAPPNGHWR TETTSLSLPLPAGPPATAPARPLRLPSGNGYKFLSPGRFFPSSKC</p>
3063	A	2	4195	<p>ALDFPGRFRPTASFIWASVLFETIRHEAEVSTDYKLSLFDLQTSSY QALQRVLVSLGHHDEALAVAERGRTRAFADLLVERQTGQQDSDPYSP VTIDQILEMVNGQRLVLYSLAAGYLYSWLLAPGAGIVKFHEHYLG ENTVENSDDFQASSSVTLPTATGSALEQHIASVREALGVESHYSRAC ASSETESEAGDIMDQQFEEMNNKLSNVTDPTGFLRMVRRNNLFRNSC QSMTSLFSNTVSPTQDGTSSLPRRQSSFAKPPLRALYDILLIAPMEGG LMHSSGPVGRHRQLILVLEGEYLYLIPFALLKGSSSNEYLYERFGLLA VPSIRSLSVQSKSHLRKNPPTYSSSTSMAAVIGNPKLPSAVMDRWLW GPMPSAEEEEAYMVSELLGCQPLVGSVATKERVMSALTQAECVHFATH ISWKLALVLTSPMDGNPASSKSSFGHPYTIPESLRVQDDASDGESI SDCPPLQELLLTAADVLDLAAAL*RLVV\LGSSRESTSKFTADGVFA LTRAFLAAGAQCVLGSGLWVPVVAFAFKMFIHAFYSSLLNGLKASAALG EAMKVVQSSKAFSHPSNWAGFMLIGSDVKLNSPSSLIGQALTEILQH PERARDALRVLLHLVEKSLQRIQNGQRNAMYTSQQSVENKVGIGPW QALLTAVGFRLDPPTSGLPAAVFFPTSDPGDRLQCCSSTLQSLGLPN PALQALCKLITASETGEQLISRAVKNMVGMHLHQVLVQLQAGEKEQD LASAPIQVSIQVQLWRLPGCHEFLAALGFDLCEVGQEEVILKTGKQA NRRRTVHFALQSLSLFDSTELPKRLSLDSSSSLESLAS/SLSQSVNA LPLGYQQPPFSPTGADR\IASDAISVYSLSSIASSMSFVSKPEGGSE GGGPGGRQDHRDRSKNAYLQRSTLPRSOLPPQTRPAGNKDEEEYEGFS IIISNEPLATYQENRNTCFSPDHKQPQPGTAGGMRVSVSSKGSISTPN SPVKMTLIPSPNSPFQKVGLASSDTGESDQSSTETDSTVKSQEE NPKLDPQELAQAQKILEETQSHLIAVERLQSRGGQVSKSNNPEDGVQAP STAVFRASETSAFSRPVLSHQKSQSPVTVKPKPPARSSSLPKVSSG YSSPTTSEMSIKDPSQHSRPSPGCDSQTSQLDQPLFKLKYPSSPY SAHISKSPRNMSPSSGHQSPAGSAPSPALSAGSARSSPADAPDI DKLKMAAIDEKVQAVHNLKMFQWQSTPQHSTGPMKIFRGAPGTMTSKR DVLSSLLNLSPRHNKKEEGVDKLELKELSLQQHDGAPPKAPPNGHW\R TETTSLSLPLPAGPPATAPARPLRLPSG\NGYKFLSPGKIFSLLSK CLKHLLLPIDFEQACRWGPVCFSPSLSAFSPQPPAPS</p>
3064	A	8	665	<p>SAQMAVTTADPRVRPRVRTQLCSLATSNRHAWCILSPEEKSAVTALW GK\VNVD\VGKALGRLL\VVLPVPDRFFE\SFGDLSTP\DAVNG QTPKVKSWSRKCLGA\FSDGPGFTWDNLQGSPLPTLK*ACTC*QAC TWD*RTFRLPGGNVAGFVVAWAHSLGKEFQPHCKLA*SRKLVL VLAKCPWPHKYHLKLAFLAVQFLFKGFLWSLKTNY</p>
3065	A	8	531	<p>SAQMAVTTADPRVRPRVRTQLCSLASLIQTRMVHLTPVE\KSAVTAL WGKVNVD\VGKALGRLL\VVYPW\TQRF\FFE\SFGDLS\TP*SLLR ANP*GERLHGKKSASVPFSDG\LAHL\DN\LKGTFAHTEVSLHCDK\ LHRGSLKNFRLGQRAWVAVAGPIHFWKFNFTSCRLA</p>

3066	A	91	951	TPHFHQGTGKRAAWPTWFNPAGPGIFLRR*GPGKAQRRRSIAP\RPA VGFPSPGPIVRCPHGFGYPHERLRAGPRLPALRKL RVAGIHKEGWPGP IGI\SVDPKRPDQVPRSPLO\ANVQR\LKKYASNFI LFPQSRPRAPK KGDRS\AEELKLGHPSTLGP\VMVVRNVYKK\EKARVITEEEKNFKA FASLRMARANAPALRHTGQKEPREAAEQGC*KAHNKALPGDLESVGO SCWVSTWCVSWEQLGLGWGFTAVTSSCQGIWGFLEQSKPWIMLNL VLKPCWLFG
3067	A	1	1603	MKLLKSILLTILLDFSLHTCASLVPALQWILLITVLVVEGIAVAQ KTQDQGNIGIKHIPATQCGI WVRTSNGGHFASPNYPDSYPPNKECIY ILEAAPRQRIELTFDEHYIIEPSFECRFDHLEVRDGPFGFSPILDRY CGVKSPLLIRSTGRFMWIKFSSDEELEG LGISEQIIPFIPDPDFTYL GRYFKFPS/HDCQFE/HLRELDGDSAALVR*NKRRKQNGQAFD\CI WDL*/MPFQKLKIYLRFLDYQMEHSNECKRNFVAVYDSSSIENLKA KFCSTVANDVMLKTGIGVIRMWADSGRLSRFRMLFTSFGGASPAQA ALSFCHSNMCINNSLVCNGVQNCAYPWDENHCKEKKKAGVFEQITKT HGTIIGITSGIVLVLLIISILVQVKQPRKKVMACKTAFNKTGFQEVF DPPHYELFSLRDKESADLADLSEELDNYQKMRSSSTASRCIHDHHC GSQASSVKQSRTNLSSMELPFRNDFAQPQPMKTFNSTFKSSSYTFKQ GHECPEQGP GKDRVMGGRFPC
3068	A	163	392	HQELLLFLLSSRRLSRSPSEGSRTM/ALGEKKIGFPSLLWCPPPS AAGASSQIKWIQPCSGAPPLPGCSGKRA
3069	A	190	352	HQELLLFLLSSRRLSRSPSEGSRTMVLEKRR*GFHPHSCLRARWL KVCEGKS
3070	A	1	794	MSRERPPGTDIPRNL SFIAAL/DGARLLP*PAAQPRGGAGGGARRGR DAVRGPIPRSRTESGP/SGPDLHQPEAAGPGRP/CSRSPDTRKRVRF ADALGLELAVVRRFRPGELPRVPRHVQIQLQRDALRHFAPCQPRARG LQEARAALEPASEPGFAARLLTQRICLERAEAGPLGVAGSARVVDLA YEKRAPAAYAGPAPPPPRADRFARLPAPPIGGALLFALRYRVTGHE FWDNNGGRDYALRGPEHPGSGGAPEPQGWIFHI
3071	A	133	1079	ARRILQNFSLYPSGEDLKGKVIQAQTAFSANPANPAILTEA\SAPI PHDGNLYPRLYPE\LSQYMGLSLNEEEI\ RANVAVVSGAPLQGGQV\ ARPSSINYMGGLLLTG*LM LGIRRSR/II*GKGFREVILQDQDK\ IGL\RLKSIDNG\IFVQLVQANSSSLIGLV*EFGDQVLQINGENAG W\SSDKAPRWSNRPF*EKITMTIRDRPFERTITMHKSTGHVGFIFK NGKITSIVKDSSAARNGLL\TGPNLCGNSMGQNVIGLKDSQIADILS T\SGTVGTITIMP AFIFEHI IKRMAPSIM\KSLM\DH TIPEV
3072	A	242	512	AWVPCLLRHCDREPAPRGRTSPSLWPQEGT/P/GQDRGGGPWLQGPS LQ*QRSHGGHLPAPQGPLGGPHDNSSFRPGRGGAGRGQIEQGSK
3073	A	1	354	GTRWRPGSMAGLELLSDQGYRVDGRRAGELRKIQARMGVFAQADGSA YIEQGN TKALAVVYGPHEASGRAGWIVWPWELRGSRAERWLGD LRG NGRRASVYTADAQHRISLGVNASP
3074	A	3	756	VDPRVRVGRERTWRPGSMAGLELLSDQGYRVDGRRAGELRKIQARMG VFAQADGSAYIEQGN TKALAVVYGPHEIRGSR/LSKPCRTGALVNCQ YSSATF\STGERKRRPHGDRKS\VEMGLQLRQTFAAILTQL\HPRS QI*YLLLQVAYRADGGT*CSLCECSPRWAVLDAGIPMRDFVCACSAG C\VDGTALA\DFSHVEEAAGGPQLGPGPAAKPSGQIALLEMDGPAAR GPPGAGVGCCPRLPEMCTPS
3075	A	5	792	EDTGGIHMEEAPETYIPSRVSLFFNWKQEFRTLEVTLRDFSKLNKQ DIRYLKGFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEAS PLTIEDERHITSVTNLKTL SIHDLQNRQLPGGLTDSLGNLKNLTKLI MDNIKMNEEDA I KLA EGLKNLKKMCLFHLTHLSDIGEMDYIVKSLS SEPCDLEEIQLVSCCLSANAVKILAQNLHNLV KLSILDLS ENYLEKD GNEALHELIDRMNVLKQLNALELPLGL
3076	A	293	1303	GAAQLPPEAVL GARVFPERKGWGTSGRLAVRKAWEEVRALASGRPL PGCPCTPWRKAARAAPSELSESLRVGTSLADIFFTCSGFSSRIGPSAA SFAKAVRSLPEYPSVIL/QNSLIKLLWPISCTHYKYSVISSRLYTIK

				FY*KFSF*AS\IASCSPSLLSHKRLSTSSVITLRSSSSNCHPTSLAS CRKVNLDNTWLSFLTNAGSGRNSLVLSKNTNCLRFSTNTPMKASHPS LLTRFPAKFNCWKFFRFFPKNAPKILISVSLSLQFFNPSLTSCGTS SKCFNRLLRLPCTSQPQGSISAVSCSSTFILSTGRNKEQFRDWMVSK IDTNMRTEI
3077	A	1	3015	MEVARSGAISLSLSRAHTRGGARERRGPNSSEFLWWMACWRADVCCV LFRQHSPFNVLWTSSCLYVLPPMCSSRRPAALNFIKDNSRALIQRMG MTVIKQITDDLFVWNVNLNREEVNIICCEKVEQDAARGIIHMLKKGS ESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGLDDLAQDLKDLYH TPSFLNFYPLGEDIDIIIFNLKSTFTTEPVLWRKDQHHHRVEQLTLNGL LQALQSPCIEGESGKGKSTLLQRIAMWGSCKKALTKFKFVFFLR LSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVFLLDGYN EFKPQNCPEIEALIKENHRFKNMVIVTTTTTECLRHIRQFGALTAEVG DMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNLMKTPLFVVITC AIQMGSEFHSHTQTTLFHTFYDLLIQKNKHKGVAASDFIRSLDH CGDLALEGVFSHKFDFELQDVSSVNEVDVLLTTGLLCKYTAQRFKPKY KFFHKSFOEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITST YSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQES LQSVKNTTEQEILKAININSFVECGIHLHYQUESTSKSALSQEFEAFFQ GKSLYINSGNIPDYLDFDFEHLPNCASALDFIKLDFYGGAMASWEKA AEDTGGIHMEEAPETYIPSRVSLFFNWKQEFRTLEVTLRDFSCLNK QDIRYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEA SPLTIEDERHITSVTNLKTLSDHDLQNLRLPDIIISLSLQGPPEVLN KRVKLEVQVLESNCWSSKSRLFLPQPKPAVTETQRSASGHGRTAAP CVPPTVKAQLGTAAGLRLAYRTEWLVLRDGCMHCDADGLHLSLSYHPA LNAI LAVTSRGTIKVIDGTSGATLQASALSASRKLGFEGVSESHHR RALLGGVNLGPGTGLSDA
3078	A	1	3220	MNKKVSGLQELEASLKRKANTKKLYFKNMSWSPKKRAIGLLSQRPLQ ADTQAAGRREEHIGGRITYKQLDVQRTLKGECWRKSTQOTSARQQAII QRNDSEFGLVNFIIKDNSRALIQRMGMTVIKQITDDLFVWNVNLNREE VNIICCEKVEQDAARGIIHMLKKGSESCNLFLKSLKEWNYPLFQDL NGQSLFHQTSEGLDDLAQDLKDLYHTPSFLNFYPLGEDIDIIIFNLK STFTTEPVLWRKDQHHHRVEQLTLNGLLQALQSPCIEGESGKGKSTL LQRIAMWGSCKKALTKFKFVFFLRLSRAQGGL\KTFGDQLLDIP GTIRKQTFLAH\VLKHAARGGLGLLDGYDEFKPKQNCPEIEALIKENH RFKNMVIVTTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKE LAEGLVLQIQKSRCLRNLMKTPLFVVITCAIQMGEREVP\SYTQTTL FPLPFNE\RLVQKNKHKGVAASDFIRSPDHCGDLA\LEGVSPQF DFQH\DRMCPA*MSHVLLTTGLLCKYTAQRFKPKYIFFLKSFLC\FT AGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGS SV/VSHQGCYETTSQQVDQHGCLLGLSIA*RPLWRQESLQSVKNTTE QEILKAININSFVECGIHLHYQUESTSKSSLSRNLKLSFQGKAYIST* GTIPRLLI*LL*T/CCPIVQVPWTSNLWTFMGE/PMASWEKAAEDTG GIHMEEAPETYIPSRVSLFFNWKQEFRTLEVTLRDFSCLNKQDIRY LGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTI EDERHITSVTNLKTLSDHDLQNLRLPGGLTDSLGNLKNLTKLIMDNI KMNEEDA IKLGQISVLIFVSIFETIQSLNCSLFLPVRMNVLEQLTA LMLPWGCDVQGSLSLLKHLEEVQVLVGLKNWRLTDTEIRILGAF FGKNPLKNFQQLNLAGNRVSSDGWLA FMGVFENLKQLVFFDFSTKEF LPDPALVRKLQPKCYPKLTFLQEARLVGWQFDDDDLSVITGAFKLVT A
3079	A	184	562	QORGRGLRKSGSAGAGMMEHTHTEAHPHTWVCTSTHTCTHTLGD TD YMH LHVCVSIHMYV/CPHT/MSLALGMSAHTLHMFSTKLLSR*HAG RHVPMPKQVTCTYVPTSPHVLGHACGCRPHAS
3080	A	63	428	GLLFPQHCPAHRPRRCLRPRSSAGRGSAAPALSRRSALCHLCLPRSSL SAPRSVSPAATPHH*ALQGLVEPWGFLHSAPLHR*APASGPAGNVRA

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				WPACRGWCLSRPPLPGTVGEGAASRAF
3081	A	1	588	HYGRLDCKCITLQNTTNNRYKEFPLSEILTVEAQNFSLVPPGTN PHCFEIVTANATYFVGEMPGGTPGGPSGQGAEEARGWETAIRQALMP VILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVL GLGCPRTGISVGPVHHRTTTCRGWSASVFSEVLCPRPAAALHSGSS QDPSNELF
3082	A	81	289	DPVPPSPDAPAPGSELAALLGRDRLLQVPELERAASEAVSRADWIA AEVVALVTVRSKSPRLTSPPR
3083	A	3	387	EGGKAHSFLGHIPLMRVEQSVRHTTRKSSTTLREGRVHVHYSNKDTLK KRHYWRLDCKSITLQNTTNNRYKEIPLAEILTAEPANFSLVPPG TNPHCFEIGTANATYFVGEMPGGTPGGPSGHGA
3084	A	2	290	RPPGSPSRPPAPPPSSRRPL\PKMACCACCARVTAGVPVGLGWVG PGQSRSPVTRRARPPSGLLGFEARPLVPWTSRSPFRCQCTACGHLVEF VL
3085	A	2099	5383	VIQTSLSPPSPATNDRGHPFSLDNWTGKPVHSMVAHLDAVTCCLAVDPN GAFLMSGSHDCSLRLWSLDNKTCVQEITAHRRKHHEAIAHAVACHPSK ALIASAGADALAKAHKEQGGKRLHLPVEDDGFQAQAPPCWEEVPOGT NAQFLGCKGLCPSPAPGSEHTRKDGGRCCLDTQDMAAFCDWSHLPPFR KKGAELOSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHV KQLACSIQDKRPRVQVPRPPPLSQEPRKVLLPARPTPVGLPEVP ECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ\EGDLVEVVLAS ATFEDLQIRPHALTVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLN YHKRCAFSIPNNCSGARKRRLSSTSLASGHSVRLGTSESILPCTAEEL SRSTELLPRPPSSSSSSSSASSYTGRPIELDKMLLSKVKVPHTFLI HSYTRPTVCQACKLLKGLFRQGLQCKDKFCHKRCATRPVNDCLG EALINGDVPMEATDFS\EADKSALMDESEDGVI PGSHSENALHAS EEEEGEGGAQSSLGYPIMRVVQSVRHTTR\KSSTTLREGWVHVHYS NKDTLRKRHYWRLDCKCITLQNTTNNRYKEIPLSEILTVEAQNFS SLVPPGTNPH\CFEIVT\ANATYFVGEMPGGTPGGPSGQCG*GRP/V AWETAIRHALIPVILQDAPSAP\GHAPPKQASLGISVSNSQIQKNVD IATVYQIFPDEVLSRQFGV\YGGKHKRT\SRDVAVKAIK\LRFP TKQESQLRNEVAILQSLRTPGIVNLECMFETPEKVFVVMKLGDM EMILS\SEKGRLPRLTKFLITQILV\AFRQLHFKNI\VHCDLKPEI VLLASA\DPFPQVKLCDFGFARIIGE\KSFRSSVGGARRPYLGNPRL WL\NQGYNRSLDMWSVGVIMYVSLSGTFPFNEDEDINDQIQNAAFMY PWPAPWEATSSAGSHLTFIQQPCCRLKMR\KRYSDKSLSHPW\LQE YQTWLDLREL\EGKMGERYI\THESDE\TRWEQVC/EQSIRCPGWSA APRTGISVGACPTTGPRCTCKGLAERISVL
3086	A	2	426	EDGSLATFLGRRQFAFAEMRHSKRTHCPDWDSRESWGHEYSYRGSHKR KRRSHSSTQENRHCRPHHQFKESD/CCSMCIPLEASHSVEEDTHPSH YLEARSLNERDYDRDRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCS RS
3087	A	39	1514	GDGAAAILWGVCRSGRGGKTAVWRHFSAGPFAFAEMRHSKRTHCPD WGSIES\WGHEYSYRGSHKRTRISHSR\QENRHCKPHHQFKESDCHY LEARSLNERDYDRDRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSK SSVRSRRSSPKRKRNRHCSSHQSRSMKSVDTLGEGAFGKVVECIDHG MDGMHVAVKIVKNVGRYREARSEIQVLEHLNSTDPNSVFRVQMLE WFDHHGHVCIVFELLGLITYDFIKENSFLPFQIDHIRQMAYQICQSI NFLHHNKLTHDLPENILFVKSDYVVKYNSKMKRDERTLKNTDIKV VDFGSATYDDEHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILI ELYPWGSQFFRLQ**KEHLAMERNIRTPYPQHMI\QKTRKRKYFHP *PSLDWDEHSSC/AGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRML EYDPTQRITLDEALQHPFFDILLKKK
3088	A	2	175	TSVTSNLSRHDMLAWINESLQNLTKIEQLCSGAAYCQFMDMLFPG SIALKKVKCV
3089	A	1	534	MLFPGSIDLKKVKFQAKLEHECIQNFKILQAGFKKLGVDKIIPVDKS

				VKGKFQDNFEFVQWFKKFFDANYDGKIYDPVAARQVCCLEMEVKHAG DHAASFLDLWQREWSMKAIVTLGSARLGCFRGVGLVVFQEEDEERPEI AHPAPLPCEAMCSIRTLOKVPTSKEALTRCSPSTLDF
3090	A	1	325	LEKERDFY/FGKLR/NIELICQENEGENAPVLQRIVDILYATDEGFV IPDEGGPQEEQEEYSLGPAEQHGYSSSLQIMCLTVKYSLLLSLEDLSL VSFHKQKVPLLKVPVF
3091	A	3	930	SSRGRAGGVWRFERDEDGTGAGCGQWTRFCREPKMAVNVYSTSVTSD NLSRHDMLA\WINESLQLN\LTKEQLCSGAAYCQFMMD\LFPGSIA LKKVKFQAKLEH\EYIQNFKILQAGFK\RMGVDKIISVDKLLKGK\F QDNFEFVQWFKKFFDANYDGKDYDPVA\AR\QGQETAVAPSLVAPAL NKP\KPLTSSSAAPQR\PI\STQRTA\AAPKGWALGVVRKNPGVG\ NGDDEAAELMQGQRI*NLLFEDLGGKERDFYFGKLRNIELICQENE GENDPVLQRIVDILYATDEGFVILDEGGPQEEQEEY
3092	A	457	912	DSSNLVFPFGSTSNSSSLAVSTTSTVTSYNEILKLSVIKVRINFFQT PVNVAAILISFHETSVFLLASRMLNSFQKIFSLPRFWIWAQRPGILPN ICNAQESSSPTKD*QRKWFLEMRSTPGEDAANNVEMTTKDLNYDRNL VDKAVVGFEFRTDSNFERSTVG\NSIA*YREIVHGKSTWMQQTSL SYFKKLPQPLHPSATTTLVY*KPSISRQDSPPTK/RL*LTGSDDH
3093	A	337	903	CNRNTSTLRTCTNVCINTPRPAPPLA/PQATLHFQFP*/PPLPL* *QPQALSATRLSL/VCHGSGRLRLPLLQAAPGWLPISLPLSFCRG RVLLC*PGWSCYLGLKLSSHGLPKCWDPRPKPPSPASFEPATRPN PLPQHGTQSQCFLSVGEAPRPHSGSAYYTNQCLQCSRPCSERTRRLG VLLPK
3094	C	821	1051	MAMELINNKHWPSVRALCWNTVLAIVIGEGVNSGRSCLAQTLVTFFR KGSARFDWVLGPAPGGNGALRLFRKILFC*
3095	A	1	594	SSPLRVAVVCSSNQNRSMEAHNILSKRGFSVRSFGTGHVKLPGPAP DKPNVYDFKTTYDQMYNDLLRKDELYPSGLPFPKNPPCGPPWEGVTC GLGHRRTVTLCSANTGSSVFCESLVSISGARRIVHGSPGNLRLEKSL RISEELSGHVLVHPVWGTA TWLCSRRGLRRSRPGKYLPRSARTESS FSSLIRKDLV
3096	A	3	761	TSRGRVGTQAGEPRDLRPPPCSSPLRV\AVV\CLEQPERGAWEAHN IPQPNGDSAVRSFG\TGTHVKLPGPAPD\NPNVY\DFKTTYDQMYND LLRKDK\ELFTQNGILHIAG\RNKRIKP\GERPQCKDLFDLILT\ CEERVYDRVGWKI*ISR\EQGDLPSPVHVVN\LDIQDNHEEATLG/A RFLICE\VCQCIQHTEDM\ENEIDELLQEFEEKSGRFTL\HTV\CFI LFSFLDICF
3097	C	129	314	MSEVIGYEAFFLIFASLFIGXXXXXXXXXXXXFFAYSFLFFCSFWTL CVSFLRRPRTSGSYF
3098	A	1	1434	MGYQASMGQEYGNVLNVCLIRARSLVSLIRGQVVTDTGTPLVGVNVS FVKYPKYGYTITRQDGTLIQSTLIEEHVKSWMFGFQLSNIIPGFP RAKMYFVPPPYELSESQASENGQGFNPSHSPPTPTGILHKGTTGENQF LTQQPAIITSIMNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGS LYVGDFNYIRIRIFPSRNVTSILELRPSHRNHLGILGSFVCMKRIKY LGIQLTRDVKDLFKENYKPLLKEIKEDTNKWNLPKSWVGRINIVKM AILPKVTVKCLKEELLHGLASIKEVPANCDTAGRVVPHKGKDKDAMT GAAGMSLGALEKLPGGGVSCVPKPSSTTSFAMKPPVPISGYLLDISVS RQAPQTTNRKLNPLVLSNNFASGLFCHYRVSCVPKPSSTTSAMKPQV SVSRYPLDIISVSRQARQTTNRKLNPLVLSNNFASCLFCHYHERVP AQSNNTQR
3099	A	1	831	MPSTIKSGRGDKKESVQVKGAEQRKGYRVGVNTNRFPLRSVSPSDS SPCNPNAHKYYLAVDQVSGSLYVSDTNSRRIYRVKLSGKTDLAGNS EVAAGTGEQCLPFDEARCGDGGKATIDATLMSPRGIAVDKNGLMYFVD ATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQDHAYALPHS DVGLVLDKAVLCQLCTASPSQACLHLSRTRTAQAARPVSGDKERAWA SRLQFGFVQSHVTGAESALANFGLRGAEKHITLKKRPSRRQK
3100	A	1	1251	MGFSMLARILMQNASLRTSDSGMYRTGIPNCLGQFGLLQKQYHRLGG

				LNNKHLFLAVLEAGKSKIKAPADSVSDGLVDCLDPDCCQLSACQNSL LCRGSRDPLDIIQQGQTDWPAVKSFYDRIKLLAGKDSTHIIPGENPF NSSEHLSPGHASHVLHRSLSRHAWVHGRNLLSIDYDRNIRTEKIYDD HRKFTLRIIYDQVGRPFLLWLPSSGLAAVNVSYFFNGRLAGLQRGAMS ERTDIDKQGRIVSRMFADGKVWSYSYLDKDGCGKKSTGCLRKSRLCY QRQKSDSGHIAFIQYEAASPEQQLYVFNADGIHQYTVSLVTGEYLY IFTYSTDNDVTELDNNGNSLKIIRDSSGMPRHLLMPDNQIITLTVG TNGGLKVVSTQNLELGLMTYDGNTEGLLATKSDETGWTTFFYE
3101	A	1	5355	MAGWLRAWLDGWLTLGWLACMSEWMMDGWMDGWIDGWMGWNPIVPE TQVLHEEIELPGSNVLRYSRLSSRTAGYKSLKITMTQSTVPLNLRV HLMVAVEGHLFQKSFQASPNLAYTFIWDKTDAYGQRVYGLSDAVVSV GFEYETCPSLILWEKRTALLQGFELDPNSNLGGWSLDKHHILNVKSGI LHKGTGENQFLTQQPAIITSIMGNRRRSISCPSCNGLAEGNKLLAP VALAVGIDGSLYVGDFNYIRRIFPSRVNVTISILELRNKEFKHSNNPAH KYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGE QCLPFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVD QNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNS LYVLENNVILRITENHQVSIAGRPMMCQVPGIDYSLSKLAHSALE SASAIASHTGVLYITETDEKKINRLRQVTTNGEICLLAGAASDCDC KNDVNCNCYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRA VSKNKPVLNAFNQYEAASPEQEYLYVFNADGIHQYTVSLVTGEYLYN FTYSTDNDVTELDNNGNSLKIIRDSSGMPRHLLMPDNQIITLTVGT NGGLKVVSTQNLELGLMTYDGNTEGLLATKSDETGWTTFFYDYDHEGRL TNVTRPTGVVTSLHREMEKSITIDIENSNRDDVTVITNLSSVEASY TVVQDQVRNSYQLCNGTLRVMYANGMGISFHSEPHVLAGTITPTIG RCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDY DRNIRTEKIYDDHRKFTLRIYDQVGRPFLLWLPSSGLAAVNVSYFFN GRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWSYSYLDKSMVLLL QSQRQYIFEYDSSDRLLAVTMPVARHSMSTHTSIGYIRNIYNPPES NASVIFDYSDDGRIKTSFLGTGRQVIFYKYGKLSKLSEIYDSTAVT FGYDETTGVLKMNLSQSGFSTIRYRKIGPLVDKQIYRFSEEGMVN ARFDYTYHDNSFRIASIKPVISETPLPVDLYRYDEISGKVEHFGKFG VIYYDINQIITTAVMTLSKHFDTHGRIKEVLA/YEMFRSLMYWMTVQ YDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVACNDRPTWRY YELNGLHLLNPGNSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQ RGSDIFEYNSKGLLTRYNKAWSVQY\RYDGVRRASNKTNLGH LQYFYSDLHNPTRITHVYNHSNSEITSLYDLQGLHFAMESSGEEY YVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFH GGLYDPL\TKLVHFT*RDYDVL\GRWT\SPDYTMWK\NVGKGAGP PFKPYMFK\SNNPLSSELDLKNYVTGEDSATKDVKSWLVMFGQLSN IIPGFPRAKKYFVP\PPYELSESQASENGQLITGVQQTTERHNQAFM ALEGQVITKKLHASIREKAGHWFVTTTPIIGKGIMLAIKEGRVTTGV SNIASEDSRKVASVLNNAYYLDKMHYSIEGKDTYFVKIGSADGDLV TLGTTIGRKVLESQVNDL/VSKPTLLVNG\RTRRFT\NMEFRTSRW WFSIRYGNPRTLGRREKAVALDQ/ARRQALGT\AWAKEQQKARDG REGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSNIQF LRQNEGKR
3102	A	205	393	RCSMRVHQSQPLSSVESTGAHHEKMSYQSTHDGCGDFCLPEFKNKWL SWSLQTFGLCGMDRTA
3103	A	2	158	GRTCSEEARPGAVACRAGDMDPLFQQTHKQVHEIQSCMGRLETADKQ SVHSE
3104	A	1	1923	MRPPPALALAGLCLLALPAAAASYFGRQSRSLMPSRDPHAGALSAAI LASGEPSPRPSPPSAFALRSGDREGWVDGWDGLFPVSGQRIVRVQ GEWGKPRTSFAFDYNTKCFGILIREYANIRRAGNIYVFGPLMNDPQ QMASSLOAKTWAFAHQCSAAKGQLHTELLHEDALKKWTSPAMGWER SRSHDKPRRLSRPLVPPRPFPAPCAGSSRVRRGLADQKGQOFPQR

				SLLP TGSA SFTPD RGCAESWCLRP RALIGCSLTSSNPAAPRWAREGG GCGWR CASDKPESHFQSQVDFVPTIGGVAPPLHGRGQTSSSAPLLME PHLLGLLLGLLLGGTRVLAGYPIWWCWAQGCVAVNI FADIYLVWRAI LILHLYIHVILYAGKWSQWAMGAGEKVL RSEAE TRFFSVRQVPVPREH SGYPRQVHEIQSCMGR\DTADKQSGHIVENEIQASIDQIF\SRLER LEILSSKEPPNKRQNGR/LFRVNSLKYDVQHLQT\ALRNQ\HRRHA REQQ\ERQRERAF C/RSKPFTT*TTLDTTITNWDR IHLQF*LPSLPR KFHNGHGIDLILDG\HNI\LDGLRTQRL\TLKGTQKKILDIANMLGL SNTVMRLIEKRAFQDKYFMIGGMLLTCVVMFLVVQYLT
3105	A	1	566	FSGRPTRPRPGAVACRAGDMDPLFQQTHKQVHEIQSCMGRLETDKQ SVHIVENEIQASIDQIFSRLERLEILSSKEPPNKRQNAKL RVDQLKY DVQHLQTALRNQFQHRRHARE\QRRRQR\EBLLSRTFTTNGTQKKDPL TLPNMLGLS\NTVMR\LIEKR/AFPQDKYFMIGGHPA*PLWALFLWF QYRT
3106	A	53	151	PSSGLLP IHFQCLASYENYMKILNKSNAVVGW
3107	A	432	649	GSHFFAQAGVQWCVCSTLQP/LNS*SSNLSLHSCWDYKFKLVCICKG DGKEFLMHILKDVTLTEKLIPRYV
3108	A	2	678	PSPFQPQSDGRGDASGRNAAMAAQGEQQLVLVGDGGTGKTTFVKRHL TGEFEKKYVATLGVEVHPLVFHTNRRPIK\FNVWD TARQEKFGGLRD GYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKV DIKDRKVKAKSIVFHRKKNLQYYHICAKSNYNFEKPFLLWARKLIGD PNLEF/VAMPALAPPEVMDPAFASTYEHDL EVAQTAL
3109	A	1	549	MAAQGQPQVQFKLVVLVGDGGTGKTTFVKHHLTGEFEKKYVATLGVEV HPLVFHTNRRGPVKFNVD TAGLEKFSGLRDGYIQAQSTIIVFDVTS RVTYKNVPNWHRDLKNLQYYDISAKSNYNFEKPFLLWARKLIGDPNL EFVAMPALAPPEVMDPALAAQYEHDL EVAQTALPDEDDDL
3110	A	2	822	APALAPASAASPAFEFTLPPSFQPQSDGRGDASGRNAAMAAQGEQV QFKLVVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTN\ RGPIKFNVD TAWPWRNSSGL\RDGLYIPSPRVPIIMFD\VTSR\VT YK\NVPNWALGDLVTSV/CENIPHLCCVANKV\DIK\RKVKAKSIV F\HRKENF\QYY\DISAQVPTNLKKPFLLWALLGSLMGDP*LWNLLP MPLLSPPPR/EVMEPQLWPATSMKHDL\EVASDNCLPPDEDDDPVK K
3111	A	116	599	PQVISLPKCCDCRCEPLHLAAEKSLPTVRETTKVPGEAKSEFHKNKM DGRGGKPMGGCEGPDAMYVKLISSDG\HE\FIVKRDHGLT\SGTE*K PMLSGPG\QFAGGT KTH\EVNFR\EIPSH\IAIRKVCNVFFTYKV/R ATPNSSHPRFPEFPNLAPGNLHWELA
3112	A	84	350	KYTIKTKTVLKKSGIFSTCPKPKSCYDFVPLNAGPIPPKSILGTNGP THTLEMLD*RLNKPTPISQRSPLTQVGH*TRPTRRRRPT
3113	A	122	518	KSLEFFPPALSPSPALILCHLMQAPYHLKVSWEPTDPPT/ALEMLD* RLPLPHA*HKGETHTCGPLSDHTFKAPPDPLQICLLSHQGPASPSQQ THPYQPSEVTADSGGTQVDKANQBEATNTKHHEQEEEQD
3114	A	1	1452	MSAYCLQLGGLQALLALTQTPGHRDSL PDAQPAAVLVCGWPWLASF ERTIVGHKEWTIKDKLKNFKDEFDIVSLPCTLGSHPPQDPMLKLP WSITYGRCLAPGDHTVSLVIKLVESASLSLAVSNMLSDMI RWMPPAGC GRCLLGLQSESRAVCQCVCVMEQVCRVSGPHIRWIPQPLHSCFLFL YPSPYPLEPSSNTSFICPHSRTYNGSLLSCIPNSAAAAAAPTQATS FPSCPSPKQRLPTGRVVEGSDHRVHEARLPGNHSRSGVDSAPPTLA HAGLLLTEEKT LKENGRRAEALRVGVHWRHGT SQGPRTLWAEKV K HFRTRGQVYDASSAPVTEHTATELPAGNQGSQPGLQEGGLEGT VVTL VSWKVT/MVSRR C*CRYGQRPH/HHLKVLGNQR\PTHLEMLD*RLP LPQRLTPKGKHTPVVPLLI\QPFKAPPDPLQICLLSHQGPASPSQQ THPYQPSEVTADSRWDTR
3115	A	1	414	MSRQVVRSSKFRHVFQGPAKADQCYEDVRVSQTTWDSGFCAVNPKFV ALICEASGGGAFLVPLGKVINTLSDHHHRGTD FGGSPWLHVIIAFP TSYKVVITLWIVYLWEQAFESSQYKEGKYIIELNHMIKDNWD

3116	A	112	1655	QEHQORASPRLLQLLPPLPPPPPPAFGGSLSSLGSRMSRQV\VRSS KFRHVFGQPAKADQ\CYEDVRVSQTT\WDSGFWC/SVNP*VLWALIC EASGGGAFLVPLGKTGRVDKNAPTARR*HS/APVLDIAWCPHNDNV IA\SGSED\CTVMVWEIPDGGML\LPLREPVTLEGHTKRVGIVAWH TTAQNVLLSAGCDNVIMVWDVGP\GAAMLTGPEGPP\DANYRGDWE P\DGGLICTSCRDKRVRIIEPRKGTVVAEKDRPHEGTRPVRAVFVSE GKILTTGFSRMSERQVALWDTKHLEESPV\SLRKLHTRNGVPVAFPG P\DTNIVYLRGKG\SGPIRVFE\ITSE\APFLHYL\SMFS\SKESQR GHGLHGPNRGLEVNK\CEIAGFYKLHDGR\CVSPMPKPVPRKSDL\F QE\DLGPTQPQGPDPCLHGLKEWLGGRDAGPLPSSP\LKDG\YVPPK SREL\RVNRGLDP\GRRR\AAPEASGTPSSDAVSRLEEBMRKLQATV QELQKRLDRLEETVQAKL
3117	A	1	2964	MRRDPTPPRGLPRQRPTSPRTRSRGHQSQRPAKASEPQAPAAATPG GRRAWEPRAQAGCPPPPRAASPRRLVQGERPESGNRSRQAAYPRRAS RARTCTTRLPTLRQALRQPCSVPRTRNRKLRRGPGPITLRRPESC SRPAFATEAHDAQALPRPPGVIAQSAMHRALAALKNKPLNHVHKV KERLCPWLCSRQPEPFGVKFHHACKKFHSGKNGNDLHPLGGPVFSQV SDCDRLQNVKNEESQMFYRRLSNLTSSEEVLSFISTMETLPDTMAA GALQRICEVEKKDGDQGLPKEILENSIFQALCFQFEKEPSQLSNTSL VTALQALILLHVDQSSLLNLVAECQNRRLRKGGMVNRNLILGESL ITLHSSGCVTLELIINQLQGEKLETFTPEDIVALYRILQACTEKVDE HQTFLNKINNFSLSIVSNLSPKLI SQMLTALVVLDQSQAFPLI IKLG KYVVRHVPHFTNEELRRVLEAFIYFGHDTFFTKALEHRVAAVCLTL DPEVVCVMYCSRELILSKPILNAVAETFVCQTEKFSPRQISALME PFGKLNYPNASALFRKLENVLFTHFN\IVPPKSLLKLLHSCSLNEC HPVNFLAKIFKPLFLQRLQDVEIKLDEEGFVLPSTANEDIHKRIALC IDGPKRFCNSKHLLGKEAIKQRHLQLLGYQVVQPLLILSHLALPYP LHVRIQQTVLITLGTNLAPALGPNRKEPLPLRGLKQGSDDTKEARHS RGDCALQWQSYKFRSQQLKERASTEQTGASDETCLHVDPLGQFFKA SPGPSEFMTIHQLPSAVTWAGALDGGMEDDEEETTASTLRGKPRP PPVSAQSAFSYIPPRRLDPKEHSYYRPARVKKVFASPLLSAMITGI ISLYDCIFKRRLDYDQKLHRDDREHAKSLGLHVNEEEQERPVGVLT SVYGRINQPIEPLNRDFGRANHVQADFYRKNDIPSLKEPGFGHIAP S
3118	A	5	622	GETPRRPGASRGRRRAQGHAPGDTKAKGQRPSPPSPRRRPPEA EGRGN\PGASRLPTPAPGRLSQEISAGRAAGIREP*PTGSLPTPRQP GTNL\PTRLPPTLRQALRQPCSMHRALAALKNKPLNHVHKVKER LCPWLCSRQPEP\LGNSIMPVKSFIKRMEMTFIHSVDQCSLKYL ATGLNKMLKMRRVRCFTGD
3119	A	1425	2181	GMSHISLNEELRRVLEAFIYFGHDTFFTKALEHRVAAVCLTLDPEV VCRVMEYCSRELILSKPILNAVAETFVCQTEKFSPRQISALMEPFGK LNYPNASALFRKLENVLFTHFN\IVPPKSLLKLLHSCSLNECHPV NFLAKIFKPLFLQRLQKGESHLDTLSRAQLTQLFLASVLECPFYKPK NLAPCIPATPVMTKRQGTAWAVASEGVSPKSWQLPHGVEPVGAQKS RIKVWEPLPSFQRMENA
3120	A	408	1669	HIFYKSPRASCSCGCASRDPEVVCVMGVLO*EN*FFSKPILNAGA ETFVCQTEKFSPRQISALMEPFGKLNYPNASALFRKLENVLFTHF NYFPPKSLLKLLHSCSLNECHPVNFLAKIFKPLFLQRLQKGESHLDT LSRAQLTQLFLASVLECPFYKGPKLPLPKYQVKSF/PYPMFLPGDPCG FSAL*ICED\GLTNLLGARLYFAPKVLTPYCYTIGNCSLPEGKDSSE AFRARRPDVEIKLDEEGFVLPSTANEDIHKRIALCIGPKRFCNSK HLLGKEAIKQRHLQLLGYQVVQPLLILSHLALPYPLHVRIQQTVLIT LGTNLAPALGPNRKEPLPLRGLKQGLTSHSTLISGGPPRGAMTHMK EASHLQYMLPSFAVSPRAPRTPRRQDTPGETVRPWSGSGRTSSGVNN
3121	A	28	2034	ESDGMALITLRKNLYRLSDFQMHRALAALKNKPLNHVHKVVKERLCP WLCSRQPEPFGVRFHHAHCKKFHSGKNGNDLHPLGGPVFSQVSDCDRL

				EQNVKNEESQMFYRRLSNLTSSSEEVLSFISTMETLPDTMAAGALQRI CEVEKKDGDQGLPKGILENSIFQALCFQFEKEPSQLSNTSLVTALQA LILLHVDPQSSLLNLVAECQNRRLRKGMEVRNLCILGESLITLHSS GCVTLELIINQLQGEKLETFTPEDIVALYRILQACTEKVDEHQTFLN KINNFSLSIVSNLSPKLISQMLTALVVLDQSQAFPLIIKLGKYVVRH VPHTNEELRRVLEAFIYFGHDTFFTKALEHRVAAVCLTLDPEVVC RVMEYCSRELILSKPILNAVAETFVCQTEKFSRQISALMEPFGKLN YLPPNASALFRKLENVLFTHFNYFPPKSLKLLHSCSLNECHPVNFL AKIFKPLFLQRLQKGESHLDTLSRAQLTQLFLASVLECPFYKGPCLL PKYQVKSF/PYPMLFPGDPCGFSAL*ICED\GLTNLLGARLYFAPKV LTPYCYTIDVEIKLDEEGFVLPSTANEDIHKRIAL\VLMVQKRFCNS SKHLLGKEAIKQRHLQLLGYQVVQIPYHEIGMLKSRRELVEYL/RQR KPVSPQNTCPWGGQE
3122	A	200	470	RGGGAGPLTGHVGLLGHIAHAAADQFDRLAAGICGHSHPHPLPGPL HCCAPLWSGPQON*PTADVAESLQLVTVHQSETEDGEFTECN
3123	A	1	2520	MAAYLQWRRFVFFDKELVKEPLSNDGAAPGATPASGSAASKFLCLPP GITVCDSSGRGSLVFGDILRLELSPSRDPEIERLLDYPAHMEGQIW FLPRSLQLTGFQAYKLRVTHLYQLKQHNILASVGEDEEGINPLVKIW NLEKRDGFTDGSVTLNKGDI TRDRHSKTQILHKGNYPVTGLAFRQAG KTTHLFVVTTENVQHPVQSKTTFHPLPKYPKQTLQAPPNTLLLRH SVVPNGDCRDDHVFSLYFMI PFFFTLGLLYHNWYPSRVFVGDTFCY FAGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLLHIIPCPRHR IPRLNIKTGKLEMSYSKFKTKSLSLGTFILKVAESLQLVTVHQSET EDGEFTECNMTLINLLKVLGPIHERNLTL LLLLQVESVFETLVE DSAEESTLTCLKGNTISSLFGGGTPDAKENGTDTVQEEEESPAEGS KDEPGEQVELKEEAAPVEDGSQPPPEPKGDATPEGEKATEKENG KSEAQKPSEKAEAGPEGVAPAPEGEKKQKPKARKRMVEEIGVELVVL DLPLDPEDKLAQSVQKLQDLTLRDLEKQEREKAANSLEAFIFETQDK LYQPEYQEVSTEEQRBEISGKLSAASTWLEDEGVGATTVMLEKELAE LRKLCQGLFFRVEERKKWPERLSALDNLNHNSSMFLKGARLIPEDMQ IFTEVEMTTLEKVINETWAWKNATLAEQAKLPATEKPVLLSKDIEAK MMALDREVQYLLNKAFTKPRPRPKDKNGTRAEPPLNASASDQGEKV IPPAGQTEDAEPISEPEKVETEPEQEQTSGQKRPLKNDEL
3124	A	1	1950	MKKASSQEKDFRMPRGKKEPSYIVSGKDYPRVELDTHGCGLRCSALS DPSQDLQFIVAGDECYLYQPPDERGPCFAFEGHKLIAHWFRGYLIIV SRDRKVPKSEFTSRDSQSSDKQILNIYDLCKNFIAYSTVFEDVDV LAEWGSLYVLT RDGRMLFKKNLFEMAINLAKSQHLDSDGLAIFMQY GDHLYSKGNHDGAVQQYIRTGLPLGASPGLMIVQKAAIKGAWAGWR REQKKPNSADLGTVRAASRNCGQRLCVLAAQGYGYRTVIFSAMFGG YSLYYFNRKTFSFVMPSLVEEIPLDKDDLGFITSSQSAAYAISKFVS GVLSQMSARWLFSSGLLLVGLVNIFFAWSSTVPVFAALWFLNGLAQ GLGWPPCGKVLKWFPEPSQFGTWAILSTSMNLAGGLGPILATILAQ SYSWRSTLALSGALCVVVSFLCLLLIHNEPADVGLRNLDPMPSEGK GSLKEESTLQELLLSPYLWVLTGSSYMSALEVGLVGSIAAGYLS RAMAKAGLSNYGNPRHGLLLFMMAGMTVSMYLFRTVTSDSPKLWIL VLGAVFGFSSYGPIALFGVIANESAPPNLCGTSHAIVGLMAKCTIAK HYSWSTAFWVAEVICAATAAFLLRNIRTKMGRVSQEG
3125	A	1249	2166	MGAVYQAAALS KAFKVKPFVVRDAVVYPILVEFTREVEEBPGIHLK HNKRVLF SRMGYPYQKRVITFNRYSHDFNFHINYGDLGFLGPEDLRV FGSQNLTTVKLGVGDSFKKYPDYESKGIKAHFNLDSEGVLSLDRIF QTKCSICNSALELPSVHFLCGHSFHQCFESYSESDADCPTCLPEN RKVMDMIRAQEQKRDLDQFQHQKCSNDSFSVIADYFGRASPIIF MFVESVTQRTTYSQSNLRCVNGSGPPEPGADPQSAEEQQLWRQPLS RRQLCPLTPGPGKALGPAATMAVE
3126	A	1	2424	MVAIHSALLESSLLFQEQSQLLYLVLTWHENLNFMIAIGFTDGSVTLNK GDITDRHSKTQILHKGNYPVTGLAFRQAGKTTHLFVVTTENVQDLQ

				FIVAGDECYVLYQPDERDCRDDHVFSLYFMIPFFFTTL/VIALPQLV PITGVCGRYLLLLLCW\QTFVAVGILGHFSKTMLLFFMPQVFNFLYSL PQLLHIIPCPRHRIPRLNIKTGKLEMSYSKFKTKSLSFLGTFILKVA ESLQLVTVHQSETEDEGEFTECNMTLINLLL/QSPWAHT*EKPHIAP AAAAAFSFLCDHWHPGRFLPSADY*LDFTYGFLOLATLSLSIPSLQP \IGTIGKLEPSYVIRKFLDAQRIHNLTAYLQTLHRQSLANADHTTLL LNCYTKLKDSSKLEEFIKKKSESEVHFDVETAIKVLQRAGYYSHALY LAENHAHHEWYLKIQLEDIKNYQEALRYIGKLPFEQAESNMKRYGKI LMHHIPEQTTQLLKGLCTDYRPSLEGRSDREAPGCRANSEEFIFI NNPRELKAFLEHMSEVQPDSPQGIYDTLLELRLQNAHEKDPQVKEK LHAEAISLLKSGRFCDVFDKAWFQQIMHYHMQHEQYRQVISVCERHG EQDPSLWEQALSIFARKEEDCKEYVAAVLKHIENKNLMPPLLVLVQTL AHNSTATLSVIRDYLVQKLQKQSQIAQDELVRVRYREETTRIRQEI QELKASPKIFQKTKCSICNSALELPSVHFLCGHSFHQCFESYSESD ADCPTCLPENRKVMDMIRAQEQKRDLDHDFQHQKCSNDSFSVIADY FGRASPNFIYVV
3127	A	1	411	MAAYLQWRRFVFFDKELVKEPLSNDGAAPGATPASGSAASKFLCLPP GITVCDSGRSLVFGDILRLELSFSPSRDPBEIERLLDYPAHMEGQIW FLPRSLQLTGFAQYKLRVTHLYQLKQHNILASVGEDEEGINPL
3128	A	2	243	VVHLAQDQGLVKDVAEATTLQOQNGLCVKLLFDLERKEGRAAGQKKG ITRSLGTPVNSFPQSIPSSQRTIEPRGKVLV
3129	A	1	1176	MAWAGSEPRRVRRLGSTASEGEKQGVKEGPLAAAAAAG YPGGGRSGRGEGRRRRECAGRASPRAGRVPEADRLTGKLG EAAGRGRGTGQRRSPGHRRAARVPTAPGKPRPGFCARLPRPYAGAGR GQAGAGSAEPLGLRPLLEKRGKERRGVGDPKIFQKTKCSICNSALEL PSVHFLCGHSFHQCFESYSESDADCPTCLPENRKVMDMIRAQEQKR DLHDQFQHQEENSPKMRVIRVGTRKSQLARIQTDSSVATLKASYPGL QFEI IAMSTTGDKILDALSKGFTQALSVRQIGESLFTKELEHALE KNEVDLVVHSLKDLPTVLPPGFTIGAICKRENPHDAVVFHPKFVGGT LETLPKRVGPPGTIS
3130	A	2	496	HSPSGSRLGFGAELWAATSSGWNWGCWGSEIRHPVAGVTRTKGFS SWYSSPAGALQWRRFVFFDKELVKEPLSNDGAAPGATPASGSAASKF LCLPPGITVCDSGRSLVFGDILRLELSFSPSGSRRDRVRMKSVCRR GPCRAPLWFSWSSRVVLWSVSV
3131	A	2211	2568	GGRRABETWSRQTVPTITGVCGRYLLLLCWHDLCRGGHGLTLQDQD ILHAPGVQLPLLTASAPAYHPLSPPHQTQYQDRQTGDELQVQDQ EPLFLGHLYFKGGREPPAGDSTPE
3132	A	100	2726	AMMGPLPGPHLLLDPLLPSSFCPLPPGITVCDSCRGLVFGDMEGQIW FLPRSLQLTGFAQYKLRVTHLYQLKQHNILASVGEDEEGINPLVKIW NLEKRDGGNPLCTRIFFAIPGTEPTVVSCLTVHENLNFMAIGFTDGS VTLNKGDITDRHSKTQILHKGNYPTGLAFRQAGKTHLFFVVTEN VQSYIVSGKDYPRVELDTHGCGLRCSALSDPSQDLQFIVAGDECYVLY YQPDERGPCFAFEGHKLIAHWFRGYLIIVSRDRKVS PKSEFTSRDSQ SSDKQILNIYDLCKNFIAYSTVFEDVVDVLAEWGSLYVLTDRGRVHA LQEKDTQTKLEMLFKKNLFEMAINLAKSQHLDSDGLAQIFMQYGDHL YSKGNHDAVQYQYIRTIGKLEPSYVIRKFLDAQRIHNLTAYLQTLHR QSLANADHTTLLLNCYTKLKDSSKLE\EFIKKKSESEVHFDVETAIK VLRQAGYY\SHALDLAENHAHHEWYLKIQLEDIKNYQEALRYIGKLP FEQAESNMKRYGKILMHHIPEQTTQLLKGLCT*LSAQPRRQR*GGP RLAGPTLRSPIFI FANK/HPRDLKAFLEHMSEVQPDSPQGIYDTLLE LRLQNAHEKDPQVKEKLHAEAISLLKSGRFCDVFDKALDLCQMHDF QDGGLYLYEQGKLFQQIMHYHMQHEQYPAGQSA/CCERHGEQDPSL\ WEQALSIFARK\KEDCKEYVAAVLKHIENGNLMPPLLVLVQTLAHNST ATLSVIRDYLVQKLQKQSQIAQDELVRVRYREETTRIRQEIQELKA SPKIFQKTKCSICNSALELPSVHFLCGHSFHQCFESYSESDADCPT CLPENRKVMDMIRAQGT EPRFSMINSQHQLQVLQ

3133	A	11	707	AKMGAYKYIQE\LWRKKQSDVMRFLLRV\RCWQYRQL\SALHRGSRP HR/RPDKVHRLGYKQ\AKQGYVIYRIRVRYI*DSCSRDRRGGRKR \VSKGATFGKP\VHHGVNQAKWFPYPTSVAE\ERPGRH\CGALRVL NSYWVGEDSHLPNFLGVI PHGSHSHKAIR\RNP*PPQW\ITQTQSHK H\REMRGLTSARPERAVGL\GKGHKF\HHTIG\GSRRAAWRRRNTLQ APPLPLI
3134	A	1	333	DPMSLLYMNDCYSKLKLVPSPQNKVKSKMEILQHVIDYILDLOI ALDSHPTIVSLHHQRPQQNQASRTPLTTLNTDISILSLQVRPAPGSP PRRRTLPRSSGLSLGDP
3135	A	1	1530	MAVGKTGYNHSTCSDKYRPSFIKSSLLDNEKSNRSFQLTLGKGC KKSSFOGLPFFCVYMSFRGTVVTSLGSRPAHPAGIGCERGRTKPT RARAQWKRPLVLIDVPPSANGDEGLQRVAPASADKSRPAGLGLHS EPSVPSPAASSAGSGGLSFRAASSLPVSPSLAVSMKAFSPVRSVRK NSLSDHSLGISRSKTPVDDPMSLLYMNDCYSKLKLVPSPQNKVK SKMEILQHVIDYILDLOIALDSHPTIVSLHHQRPQQNQASRTPLTTL NTDISILSLQRGAVVWLIIPGGSPEGRRGVFPVAGYPRTWPPGPRH LSPAAAPADLCAAGREARSGNPPTASPPGEAQTPAARSPSHGDP VVRSDGPGERPRTEAVRAGLWGRPGPFRAPAGHRWRWRPRDPWSR GAAAPLGDFPRRQPRCPTPAVEPGRHLLADTRTAALARGLVGLGPG HWEPEEQSVGWRRSREKTPGSEDTEDAWEKELAGGPCGCV
3136	A	1	554	ILSQVRCQAQLAQAAGGGLSFRAASSLPVSPSLAVSMKAFSPVRS RKN/SALSDHSLGI\SRSK\TPVD\DPDGALLYNMKDCYS\KLKL VPSIPPEQRR*ARWEIL\QHVIRLTSDWLADSPWDLAFPLIVQPGI HQRTRGRNQ\RSRTPLGPPSTRDISILSFAGLLEFPSELM\SNDSK\A LCG
3137	A	193	561	GDSSGGSPWPDEKPKGKVTENNDHINLKVAG\Q\DGSVVQ\FKIKR H TPLSKLMKAYCE\RQGLSMRQIRFPI*PGNPINETDTPATVGKWKDE \DTID\VFQQARPGGVYLKKGTCFLYSQNSVSF
3138	A	3	251	NNGGGGGFGVSGSGSNFGGGSNNDFGNYNQSSNFGPMKGGNFGGRS SGPYGGGGQYFAKPRNQGGYGGSSSSSYGSGRRF
3139	A	1	1674	MRDPNTKRSRGFGFVTYATVEEVDAAMNTTPHKVDGRVVEPKRAVS R EDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGGKIEVIEIMTD RGSGKKRGFAFVTDDHDSVDKIVIQKYHTVKGHNCEVRKALPKQEM ASASSSQRRGSGNFGGGRGDGFGGNDNFGRGGNFSGRGGFGGSGC GGGYGGSGDGYNGFGNDGSNFGGGSYSDFGNYNQSSNFGPMKGGN FGGRSSGPYGGGGQYFAKPNQQAARCAARWLFRTEARLVFLQKFP P WAVEVTVIVAAPAAATATTRDGGGCSRNCNIPVFPPELLGCPNRR GPPGGVREKQQTNSKSTRRQETKTIAELKEITRKTLOKINESRS WIFYEKINKVDRLDLIKKKREKSQIDAIAKNDIGDIVDPAEIQTTI KEYYKRLYANELENLEEMDKFLATYSLHSLNQEVEESLNKPVTSSEV EAVTNSLPTKKSPGPDGFTVLLEVLAPAIRQEKEIKHIPIGREEVKL SLFADDVIVYLENPIVSAQNLLKLISNFSKLSGYKINVQKS
3140	A	1	650	MSLRKLTIMVEGKGGPNIPHACGRQRSSIKVSLLPVTSKSESPE K PEQLRKLFIGGLSFETTDESLRSHFEQRTLTDCAVMRDPNTKCSKG FGFVTYATMEEKYHTVNGHSCARKALSKQEVASASSQR/GRSGSG NFGGGHGGGFGGNDNFGHGENFRGHSSFGSGHGGSGYGGSGDDYSGF GNDGSNFGGGSYNDFGNYSNQSSNFGPM
3141	A	579	2102	SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVVRFG RDKA VKQPISLAYLGAVFSECL*K*LIAL*LCLCWQRNVLL*F*KLTS*I* G*WETGRFTFYKRLV*SFLLPYSKLK*QKLLRSDFVLHKLTLFSG\MR DPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSREV SGFFFFFLLNLLGYVLL*T*DSGVF*TYQNFLFEYRLC*SKPMVFL L\DSQRPQA\HLTV\KKIYVGGIKEDTEEHHL\RDYFEQYGGKI\EVV EIH*LDR\GQWPRKRGFAFVTDDHDSVDKIVSKYQIVAFSKGSTIC MAF*TLIPCCIVFFLVQKYHTVNGHNCEVRKALSKQEMASASSQR /GYACCLIKP*R*L*VTPV*MI*CLNFMS*GRSGSGNFGGGRGGGFG

				GNDNFRGCGNFSGR/GYVWFIYM*F*LLTIFAMKILQYGNCIQNVTL SPSHT*NLKLFLTGGFGGSRGGGGYGGSGDGYNGFGNDGKFFRNK
3142	C	42	152	MIXXXXXXXXXXXXXXXXXXVSPSAFAPXXXXXSLG*
3143	A	3164	3256	LLTNCISCDPPASASQSAGITGVSHSARP
3144	A	12	336	SPVQL*F*LFLVFC*LWSWSAVVYLGLTPSADAHT/AGLSKTPPH WAARARLDDVFLRFTSSHSLNMLVQDLTASAPMYSSTSRDPP/CL GLPKCWDYKREPPRAH
3145	A	602	745	TPASLKIPVE**NTLLAKMVIS*PRDLPASASQSAGITGVSHRARC
3146	A	269	484	DKTSRGITRQQHSRFTKIRCSAATAADTQANRVWSGPLANSNRPAE GPRDPPASASQSAGITGVSHRAWP
3147	A	2	988	KYPPPAVLWFFGFFVLRRSLALSPRLECSGMISAHCKLCLPGSRHSP ASASRVAGTTDVHHHAQLI/L/YVFLVETGFHRVSQDGLNLLTRLHL PKCWDYR/R*ATTPGLCFVF*KKRNAREGGRQPPDHKS*FL/VFFFL FFLKWSL/DSVSKAGVQWHGLSSLQAPPRGFTPFSCLSLPSSWDYRR PLPRPANFFVFL**\DGGFTVLARMVLIS*PRDLPASASQRAQ\ITG LSHCAWSEFF/CFFKTGSHSVTHARVQRHN\LDSSLEA*TPGLN*SS RLSLPSSWDYRSTPPSPANF\CSFSRDGVSPC*PGWSRSSDLVIRPP RPPKVPGLQA
3148	A	2	608	RDSPPRSLDSGARRDAPPHSPPAECRAHAATWRLKPRPHRPHSLTAP LPVHWAGTTEPLSPRPATGTREPRPLHFPATPRSHS/WRLARPCRQ PGPS*DRLFSAGAGPGVVSCLDREEKNAGHWLSSAFALVWLWLTEHW LLLVGFIGYVKAGSVYPGCRACFFWAVLAGLCLPAVSGIPRERFW VFPRLHLVPWLALWE
3149	A	131	454	VFTSAIKMGRIFLDHIGGTRLFSCANDTILTNRSELISTRFTGAT GRAFLFNKVVNLQYSEVQDRVMTGRHMVRDVSCKNCSKLGWIYEF ATEDSQRYKEGRV
3150	A	403	787	MGRIFLDHIGGTRLFSCAN\CDTILTNRSELISTRFTGATGRAFLFN KVVNLQYSEVQDRVMTGRHMVRDVS\CKNCN\SKLG\WIYGVWPLK DSQRF*GKGRR*SGER\VLVSEELRALEE\VPDENS
3151	A	171	382	KNSYKCEECGKIFNEYSHLIARK/RIYT*EKLYQYKDCEKAINVCSH LTHQQRV/H*KKYYKFNYCQKVQKI
3152	A	76	195	VHLLNPQHMLPSTHKQRRRTL*KGHAHLQYYLNNQKLS
3153	A	2	634	WWESLNREDLWPCFLRRILGSSYSTAEMVSGQTLQRAHLREAASI SLNSQGVWRKSARFASHQLERGTEEQQLQIPDLGQHPSSKAPVFPQVQ AHPRFQTGPHGHKLQRNQDPGQLQ*IPMLGQTPWTQATGPTI*TOPS GRSPCSHYSGMSTDSGFMLAHSITQVSSQPTCRLLLEACPWTSSGGL PRISGWTDRQVFGSVDRDLISP
3154	A	275	464	GKFFSLCETLFPSPGVGSFFSSCTMDSSRSLGVGSKNSHFSLA*NTDL RLSLCPFPGWKEDIKF
3155	A	5904	7919	FMFINMSVCRLITTKYLLLLFLHESLILLSNLNRKD\VEAVTGSPAS QTSICIGILLRSABLALLLHPVDQANTLKSPVSESVSPVDPDYLPT NGDFLSSKRKQISRDINRISVTNVHMSDNRSMSVDLSHPLKDP FKSA\SDTNLAKRAFPMDYLSDKHLGKI\SEDESSGLVYKSG\SGE IGSETSDKKDSFYTDSSSILNYREGFRIYLSFG*VMGNQNILS\STL TSKGNET\IESIFKAEDLLPEAASLSEN\DISKEETPPVR\TLK\S QSSLSGESLRERLPHPNLGF\PLVFSYKNMKRSSSQMSF/EATISLD SMI\LEEQLLES DGS DSHMFLEKGNRKNSTNYRGTAESVNAGANLQ NYGETSPDAISTNSEGAQENHDD\LMSVVVKITGVNGEIDIRGEDT EICLVNQVTPDQLGNISLRHYLCNRPVGSQKAVIHSKSPEISLR FESGPGAVIHSLLAEK\NGFLQCHI\ENFSTGFLTSSLMNIQHFL ETVATVMPMKIQVSNTKINKDDSPRSSTVSLEPAPVTVHI\DHLLV ERSDDGSF\HIRDS\HMLNTGNDL\KENVKS DSVLLTSGKYDLKKQR SV\TQATQTS PGVPWPSPQSANFP\EPFSGHLGELMEENESLKQEL \AKAKMALAEHL\EKDALLHHIKMTVE
3156	A	149	382	ARHCGSCP*SQHF\GRSR*AEHLRTGV*DQPAQRGETPSLWQNTKIR RAQWWCPPIPATSGGLRQENYLNPGRQRLQ

3157	A	162	342	TYSECEDGTYSP EISWHHRKGTGKSEDSPPKHAGNNESHSSRRNRH SKSKVTNGVGKK
3158	A	1	1995	FRLVTPGVPAFSGCGRHRGRTGRRAMASCVGSRTLSKODVNYKMHF RMINEQQVEDITIDFFYRPHTI\TLLSFT\IDSLMYFAFTTDDSVP* DNIWRGILSGILLFLIIKV*AFPNGPLTRPHPALWRMVFLSELYFL FLVFLLFPEFEQAKSLMDWLDPNLRYATREANVMEYAVNCHVITWER IISHFDIFAFGHFWGWAMKALLIRRYGLCWTISITWELTEFFMHLL PNFAECWWDQVILDILLCNGGGIWLGMVACRFLERRTDHWASFKDIH TTGKIKRAVLQFTPASWTYVRWFDPKSSFQRVAGVYL\FMIIW\QL T\ELNTFFLKHI FVFQASHPLSWGRILF\IGG\INSFPQLRQYYAYL TDTQCKR/L*GTQCWVFGVIGFLA\AIVCIKFGQ\DLF\SKTQILYV VLWLLCVAFTTFL\CLYGMIWYAEHYGHPRKRPTPECEDGT\YSPEI SW\DRKGTGKSEDSPPKHAGNNESHSSR\RRNR\HSKSKVTNGRWE RNEKPWNKMFPECLGTEEGKWEHLGLTPRGGSRAHRGKPGRGEG TLGVIILRSLSLCPPTDLGRVQADHRLGGPFANVGSLLTSALDMRSP VAARCVERETVAISFHSCQEQLRAMLDRGCSVNIFFSDEALTPWLMD WSPVFNFI FYESTFPID
3159	C	410	538	MKMDTRIQEQVSSKSSLYSCFLSQPHTNRENTLCLCLLWMLAC
3160	A	4	334	FFPKALIFCREVGPISPPPKIRFP/SPKFPGNRFSPPRVVKPPPGP/ SPFKRPPIRKKILPCQPP*TLAPPRIL*KGPP/PSSSSG*NPYYLFI QQKTEYLLWSRPPCWHEQR
3161	A	1	1130	PLLPTSLSVEDAAILLQQVMRAFASKQASTVVFSDTVVVSEKF\INDC TELFRELMHQKAEKEMKNPVHLITEEDLKQISTLESVSTSKDKKD ERRRKATEGSGSMRGGGGGNAREYKIKKVKKKGRKDDSDDESQSSH TENEESGYDKKDENILEDVKWGKTSQFLEIFQDIEKARDKTLEADSE LESVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEGMKFFAD DTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPAAITSEIRKK ILSKLSEETKVALTKLHNSLNEKDQHALLVKYQGLVVKQLVSQSKKT QGQDYPLNNELDKEDVASTTRKELQELSSSIKDLVLKSRKSSVTE E
3162	A	20	2478	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATORLSERNCI EIVNRLIAQKQLEVVTLDGKEYITPAQISKEMRDELHVRGGRVNIV DLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQL\IDENYL\DRVGQ EVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLAIIIGHIDL NRGVIFTEAFVARHRARIRGLFSAITRPTAVNSLISKYGFQEQLLYS VLDELVNSGRLRGTVVGGRODKAVFVPDIYSRTQSTWVDSFFRONGY LEFDALSRLGIPDAVSYIKKRYKTQLLFLKAACVQGLVDQVEASV EEAISSGTWVDIAPLLPTSLSVEDAAILLQQVMRAFASKQASTVVFS TVVVSEKFINDCTELFRELMHQKAEKEMKNPVHLITEEDLKQISTL ESVSTSKDKKDERRRKATEGSGSMRGGGGGNAREYKIKKVKKKGRK DDSDDESQSSHTGKKKPEISFMFQDEIEDFLRKHIQDAPEEFISEL AEYLIKPLNKTYLEVVRVFSSTTSASGTGRKRTIKDLQE\EVSNL YNNIRLFGKRGWKFF\ADDTQGWLLPKHLLEVQCVLISLNL\I\FNF\ LGFGILMDGQ*DDPGRPPTS\ELRKEI\LSKLSEETKVALTKLHNSL NEKSIEDFIFC\LDSAAEACDIMVKRGDKKRERQILFQHRQALAEQL KVTEDPALILHLTSVLLFQFSTHMLHAP\GRCVPQIIAFLNSKIP\ EDQHALLVKYQGLVVKQLVSPSKKTGQGDYP\LNNELDKEDVAST T\RKELQ\ELSSSIK\DLV\LKSR\KSSVTEE
3163	A	1	390	IPSEISRSVAFSL/LPLLSVSGLEAIQRTPKNQVYSRHPPENGSKF LNCYVSGFHPSPDIVGDLNMGERIE*A*HSDLAFRKDWAFYLLDYTE FTPT/EKDEYACRVNHVTLSPKICKWDRDMLASMEA
3164	A	2	409	RPRVRPRVRSIRAEMSRVALAVLALLSLSGLEAIQRTPKIQVYSRH PAENGKSNFLNCYVSGFHPSPDIEV\DLLKNGERIEKVEHSDLSFSKD WAFYLLYYTEFTP\TEK\DEYACR\VNH\VTLSQPKI\VKWDRDM
3165	A	26	299	VVEFTTAVVSGTVKQSGEVLVNVKEHSRQINDIQLSRDMTMTFVTASK DNTAKLFDSTTLEHQKTFRTERPVNSAALSPNYDHVREPHLPSC

3166	A	11	487	RVTAGMKPILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNG ERLGYTMGHTGAVWCVDADWDTKHVLTSADNSCRLWDCETDNNPEY MKIPCNDISKITSAVWGPLGECI IAGHESGELNQYSAKSGEVLVNVKE HSRQINDIQLSRDMTMF
3167	B	198	282	XPSLEDLSNSIQKLHLAENAEPEEQSAA*
3168	A	80	827	AQQAVALARSKLESCLRELHGHNRSLKEEGVQVQAREEEEEKRKEVTSHF QVTLNDIQLQMEQHNERNSKLRQENMELAEERLKKLIEQYELREEHID KVFKHKLQQLVDAKLQQAQEMLEAEERHQREKDFLLKEAVESQR MCELMKQQETHLKKQLALYTEKFEEFQNTLSKSSEVFTTFKQEMKEM TKKIKKLEKETTTMYRSRWESSNKALLEMAEEKTVRD/ERTGGPAGKN PTAGEAVPGTADRAQ
3169	A	1	2511	MEPELLVRKVSALQALGRGFLVRRQFQSVRAEYEAIVRKVEGDLGTL QWTEGRI PRPRFLPEKAKSHQTKAGDRVANPEQGLWNHFPCEESEGE EATWEEMVLKKSCESSANQGSCLRDHSSWLQMKQNRKPSQEKTRDIT RMENPDRGFVPGKECSFEQLEHVREMQUEKLARLHFSLDVCGEEEDDE EEEDGVTEGLPEEQKKTMDRNLQDQLLSNVGSCLGALVPGGMRGGEG EGTKPVQDGRPGWEEGLVQSATILDGHSQKLHLAENAEPEEQSAAWP QTLSTRTVPSQDPPVDAKKPILLQGHERSITQIKYNREGDLLFTVAKD PSGPLVIEKVRNYSPLWSVLSVGSTQEEALSRCPOEQCPWLPTSAR RPNPRKPLLPGDGEGLMPSQRPMDKKKKRSPKPCLAQPAQAPGTLR RVPVPTSHSGSLALGLPHLPSPKQRAKFKRAS PAGELHAPGGGLWGL GAKHGQLAESAGRLPLTVTCKAGTEHHLPGSPGHGELFDSTTLEHQB TFRTERPVNSAALSPNYDHVVLGGGQEAMDVTSTTRIGKFEARRKA LQDAVNALCATSPPGSQRCPPPI TRNGKQLALLKTNSAVRTCGDFDG GNIIMFSTDKQMGYQCFVSFFDLRDPQIDNNEPYMKIPCNDISKITS AVWGPLGECI IAGHESGELNQYSAKAVGEDEDEDEEGESLDSVKALT AKLQLQTRRPSYLEWTAQVQSQAARRAQAKPGPGGPGDICTGFDSDMS ALEWLRRELRQEMQAQDRQLAGQLRLRLRAQLHRLKMDQACHLHQELLD EAELELELEPGAGLALAPLLRHLGLTRMNI SARFTLC
3170	A	93	517	GRGHLGG/VWC*RSQERAQQIKEASAEIT/CSWLQMKQNRKPSQEK RDTTRMENPDRGFVPGKECSFEQLEHVREMQUEKLARLHFSLDVCGEE EDDEEEEDGVTEGLPEEQKKTMDRNLQDQLLSNVGSCLGALVPGGMR GGE
3171	A	3	348	FFAFLGLIPFNAPLPHSTWGAAEHPPESVKSHSLKMRGAVW/CLR GTPTQR/HCSSGSFAFSARCSFWIELLRSSRLSSWSRLRSAIVFFCS SGKPLSDPNPLPLHRPPPHTHPG
3172	A	2618	5946	PGCNFSLDVCREEEDDEEEEDGVTEGLPEEQKKTMDRNLQDQLLSNA RGRAYQLAPMEPELLVRKVSALQACVRGFLVRRQFQSLRAEYEAIVR EVEGDLGTLQWTEGRI PRPRFLPEKAKSHQTKAGDRVANPEQGLWN HFPCEESEGEATWEEMVLKKSCESSANQGSCLRDHSSWLQMKQNRKP SQEKTRDITTRMENPEATDQRLPHSQPQLQELQYHRSHLAMELLWLQ AINSRKEYLLKQTLRSPEAGPI REEPRVFLEHGEQACERDQSQPSA PLEDQSYKRQDHWARTGGMTPTVGVKSPHRFPGSFGHYTKKHLGA KPREPCYSKSGPPSSIPSNSQALGDRLTKGPDGRTFGGTCLLQMK ILEDQTPRGLKPRNHCPKRSRTQLSALYEDSNIKEMSPRKL DHKEPD CRTVRTQELGLSEDHIIWDGGSPAARVVVYRNGDPFFPGSQLVVTQ RRFPTMEAFLECVTS AVQAPLAVRALYTPCHGHPVTNLADLKNRGQY VAAGFERFHKLHVFRNGDLVSPFSLKLSQAASQDWETVLKLLTEKV KLQSGAVCKLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPLYLELL VPSPSLPRGCWYAQGHRAQVTQPSKPEPDRIKPSAFYARPQQTIQPR SKLPTLSFSPSGVIGVYGAPHRRKETAGALEVADDEDTQTEEPDQTV QGKGTLMATRKQNSCRGKGRMGKGRVLTHSGEMSGSKELTQVASNTK QNSSKPGPTCRCQGEVIEKGSTLVEEKGHQKPILLQGHERSITQIKY NREGDLLFTVAKDPRTRARVNFVIFLNNSSGDTKHVLTGSADNSC\R LWDCETGK\QLALLK\TNSAVRTCGFGLWGATFIMFSNGQSRWGYQC FVELFWTWRDSEARFDNNEALHGRFPCNDK\ITSA\WVGPLGE\CI

				IAGPWRVGEINQYSAKS\GEVLVNVKEHS\ROI\NDIPVYSRDM\TM FVTASKDNTAKLFDSTTLEHQKTFRT\ERP\VNSA\ALSPN**QRWF WAGGQEAMD/V*PTTLHPGLGKFEARFLSIWPF\EEFPG\RV\KGHF GP\INSVAF\HPDGKS\YSSGGEDG/YTSPHIFRPHQYFEFEV
3173	A	3	1131	ENSPLPKAVRGVRPRTSLIGRTSPLVTLFCLSWQRIKAAAAALGTAL PRLCYPWLGGPAKQLLRAAPGRLLAAKEASVLCRLQGGDQKAESTAGD AGASAVHQRSTDTLSSSVMASIIARVGNSSRLNAPLPWHAHSMRLSL GRSLGPIMASMADRNMKLFSGRVVPAQGEETFENWLTQVNGVLPDWN MSEEEKLRLMKTLRGPAREVMRVL\QATNPNSLV\EIFLRAMKLG FGGV*KQF*LSPWVNFNTLTCLKGEKASLYVIR\LEVQLQNAIQAG IIA\RMQGTGTRLQQLLLGGELSRDLRLRLKDFLRMYANEQERLPNF LELIRMVREEEDWDDAFIKRKRPKRSESMVERAVSPVAFQGSPPIVI GSA
3174	A	16	319	LGTRPAHRSSQ*KGSPLPPGAPLISRGAGKEGGPGDRAAHADFLPA EEGAHEM/RGSHGSLIAPLPTYPHPPSGLFPLGALPLARPRHQGAA LGSVHEIQ
3175	A	2	458	NWAGTGHSLOQVTHGDHYNADLKPIDGFNGRFGYRRNTPALRQSTSV FGERPDRMVSVLNRKLSAEELERKROEMMENAKWREERLNLILKRHA KDEEREQRLEKLDSDRGKFIHRMKLESASTSSLEDVRKRNISLQRT SVALEKNFMKR
3176	A	91	521	SLISQKKMANSSPVLSKVPGYGLQVRNSDRNQGLQGPLTAEQKRGHG MKNHSRSRSSSHSPRHASKKSTREAGSRDRRLSLGRRSRSPRPSK LHNSKVNRRRETQTRSPSPKKEVYQRRHAPGYTRKLSAEELERKROE MM
3177	A	3	1636	RPSEATVVGMAYLSECLRLLEKGFILDGVAVSTAARAYGRSRPKLWS AIPPYNAQEDYHARSYFQSHVVPPLLKRTDQSLRTLVDCVFSMGNAS DYAWLASHTTPRGMGKPRGHSLQQVTHGDHYNADLKPIDGFNGRESG TSGNVATRSSQNETSTAKASTAEPGLQNLQVTPTSQSATEPCTSS RDADAMCERLLEENLAIVEDILPSHACLGYNLKKSWHPQTLRNVE KVWKAQKHEAERKKIEELQRELR\KERAREEMQRYAEDVGAVKTRK KEEKLDLDVPGSWWDG*TVNEYLLGRPIDKYVFEKMEKEAGCSSET GLLPGSIFAPSGANSLLDMASKIREDPLFIIRKKEEKKREVLNPNV KMKKIKELLQMSLEKKEKKKKKKKKKKKKKKHSSSSDRSSSEDEH SAGRHNKSV\KGERQAKLGAHHLKRRSTKGDMPLDTPENSLQRN*SE NGQEMMENAKWREERLNLILKRHADEEREQRLEKLDSDRGKFIHRM KLGEICILLSSLGSGLKRISSYFYRELR
3178	A	11	301	NVDLLIPNSSITLLSDRPASILLRTFIFSSKFSVVYFPLLFILNLTL NHQQEKTGKALMNWQKKKPTFFKQNLAESPKRHGHCIGG*WTEGAN HD
3179	A	915	2482	SLEGLVPAHRVAVAVSCSPWGKRRTATSVLRCRAAFPGPSLAGVKF SMNKRKGYTTLNLEEKMKVLSRIEAGRSLKSVMDEFGISKSTFYDIK KNKKVILDFVLEPDMPLIGAERKRRTTGAKYGDVDDAVYMWYQKRS AGVPVRGVELQAAA*RFARCDRTDLIASTGWLFRPNRHAIGNRIG CGEQVLSSSVSENVFPFRQKLSMIKEEKLCLAQLYSGDETDLFWKSM PENSQASRKDICLPGKKINKERLSAFLCANADGTHKLKSIIGKSKL PKRVKEDTSTLPVIYKPSKDVWFTRELFSEWFFQNFVPEVRHFQNLG LRIHDEDVRALLLDSCPAHPSESSELTSEDGRICKMFFPHNTSTLIQ PD\DOGVILSCKRLYRWKQLEESLVIFEESDDEQEKGDKGVSKIY NIKSAIFNWAKSWEEVKQITIAHAWENLLYKKEPEYDFQGLEHGEYR EIS*KTGGSWNLSSWMKIGCWLNGDEEKGCLLKTGGITKGSCKRRR S*EADC
3180	A	417	736	YGLGAVAHACNPSTLGGQAGQITRLAVQDQPDQHCETPSLIKMQKN/ LPGHGGVCLQSOLLRGLRQGNCLNQGGGSCSEPRSHQCTPAWAI*E SVSKKKKKKKLVV
3181	A	1	2061	MGAVRDELHSLVVPPLMGRGAQTPMAAAALRDPAQGCVTTFEDVTIYF SQEEWVLLDEAQRLLYCDVMLENFALIASLGLISFRSHIVSQLEMKG

				EPWVPDSVDMTSAMARGAYGRPGSDFCHGTEGKDLPSEHNVSVEGVA QDRSPEATLCPQKTCPCDICGLRLKDILHLAEHQTTTHPRQKPFVCEA YVKGSEFSANLPRKQVQNVHNP IRTEEGQASPVKTCRDHTSDQLST CREGGKDFVATAGFLQCEVTPSDGEPHEATEGVVDFHIALRHNKCCE SGDAFNNKSTLVQHQRHSRERPYECSKCGIFFTYAADLTQHOKVHN \KENPYECFEGGKFFKPAL\SLVKHRRVHTGESPHVCGDCGKFFSRS SNLIQHKRVTGKPYECSDCGKFFSQRSNLIHHKRVTGRSAHECS ECGKSFNCNSSLIKHWVHTGERPYKNECGKFFSHIASLIQHQIVH TGERPHGCGECGAFSRSSDLMKHQRVHTGERPYECNECGKLFSSQS SLNSHRRLHTGERPYQCSECGKFFNQSSSLNNHRRLHTGERPYECSE CGKTFRQRSNLRQHLKVHKPDRPYECSECGKAFNRPTLIRHQKIHI RERSMENVLLPCSQHTPEIS\LRTDLIRALSSTMLNLVHPSTHTGEV P*EC*LCWKLSGDKLHSLTVEFISVFSLLGL
3182	A	441	1074	QRVQRSLKK*CWG/FNWGHSGGKI*KQIGPYLNTG/TRLKSKWIIVP QNCIISRROQGRV\HLGLGKDFLNPTPKAQSM/RGKIDKLYFIKIE NFSLKGITIRRTKRQAVEWQK/IYLNISDK*VASRLHKEVSKLNKVK PIVDLMRCF/RPELAASGPCSLSFSICFQH*IQNVLLEIQVRSHQPS ELSNRRPWHSKVHNSLQCWAKHEAPLFSLL
3183	C	1	900	MGHVSSDDGHSDEDELRSLSSELVDDKFGTGKKTIVTRILDGGNPFLD VPQALSATTYKHGVLTRKTHADMKGKRTPRGRRGWKKFYAVLKGITIL YLQKVRDCPRDLTHPGASDYSKKS NVLKLKTADWRVFLFQAPSKEEM LSWILRINLVAAIFSAFPAFPAVSSMKKFCRPLLPSCCTTRLCQEEQL RSHENKLRQLTAELAHRCHPVERGIKSKEAEEYRLKEHYLTFEKS YETIYIHLAMKIKVGSDDLRIEARLATLEGDDPSLRKTHSSPALSQ GHVTGSKTTKDATGPD*
3184	A	178	490	VSSTVFGNTVRNKTEDDSGGNWEPPRTILQASGKLKNPKARLASECL SPFDSTGKAIHLQVCGRASRSHYSLGHH/MRHSVGE*S*KCPGCG KGFSTKLDLRW
3185	A	7	310	KKRSHCAQAGLELLSGQLG*TSSVQKIRKLAGCGGVHPWSQLLERLR WEDS\LPQGGQGCSEP*SHHCTPAWATE*DPVSNNNKQKQPKESNL SRATSRP
3186	A	65	203	KGDFQGHQGPWDAPP*PAFWWQREARGEGEAMSQSPCRGRGNAEMYR PSAQPETGPASG**TEAARGSSGWAEPWPRG*KPPEFPMRLGWPFPT PGAFSLPILCDEERP*QORSSGCESQQLRSPRETELQVTSPTCFSA GPRRPGPAPGGPQAARAYCCHLKTSSPTFHQAPTQAEVSWEFSPA/ PPADKEMTSMATPEKCPSTQ\APAIRKAALPHPERGNYFLSAAWPQ APFPLWGSASPFVALPWSPRAGAAPLCPGKAPPSKTRLGRAVTFP*A EGGTGRGRGHVAVPLPWERQGRNV
3187	A	210	951	ARSCRAALSEASAGRPLPPFPGRAKETCRAAAMEAIWLYQFRLIVIG DSTVGKSLIRRFTEGRFAQVSDPTVGV\DFFSRLVEIEPGK\RIKL QIW\DTAGQERFRSITRAYRNSVGGLLSITNRSSFQNVHASWQE PKLHVQPYQIVLVLVGH\KCDLDTQRQVTRHEAEKLAA\DTAMKYIE TSARDAINV/EESPSQT*PRDIYELVKRGEITIQEGWEGVKSGFVFN VHSSEEVVKSERRCLC
3188	A	1	2559	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEQAIAGMA ADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQPNFDH WTADRHGDLCLGEHMERVGMDCRRRPIPCLPFRVASRCMEPGHLDL NGSRRHLANGFTTTPRIGANQFLRRTVNAQTNPWQONISIASAISSRT RRISGSVGSWPRSGNAEVSALHHYVVDLHRRMLLATLWNTYICINEA LALTLSDFSLVPPHPYRQLFTLTTFHNRACSSSVTRIVSILSRFIGI ITPMNRNPPTTEASVTQKKTALNMARFIRSQTLTLEKLNELDADE QADICESLHDHADELYRSCLARFGDDGATQAFKENNQKAYKETYG VSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDNISDSW KNAGRVFKDSKFDANDPILKDQQTQEWSSATFTSDGKIRLFYTDYS

				GKHYGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQ FIDEGNYTSGDNHTRLDPHYVEDKGHKYLVFEANTGTENGYQGEBSL FNKAYYGGGTNPFPRKESQKLQOSAKKRD AELANGALGI IELNNDYTL KKVMKPLITSNTVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINS NDIYMLGYVSNSTLGPYKPLNKTGLVLQMG LDPNDVTFTYSHFAVPQ AKGNNVITSYMTNRGFFEDKKATFAPSFLMNIKGNKTSVVKN SILE QGQLTVN
3189	A	259	3222	NFRLVGQTSVDRLLQLSQAQAVKGNQLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLL PVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPN TQTASPRALADSLMQLARQVSRLESGQSCSTPPPN TDKQSKEKCPMK FTFQQVETNMTGDVAGMDDIPQEARQYRHNQAYAYS IQGDGAEDDDE RIVRFHTRVTVDSDTLASDAARLT CRHGLGNQILNVMAGESGCEENC GNGGGGNKGNRNKRKQIRKRRKRAEPRKGPTRKGTPTPTTEARRARV ARSEESTETPERRHQQRRTGDPQAPGARPC TAMRTTRNETQEKTLRA PTKPAKHKGGTESGKKHLAQTPRATAWTAYKRKTRKTSFSNLGLEGG TRFKRTKDDQHQRTPRVYAPQRAKRRARTGDT PKHLKRAYRVI PFVV TPTRDSADMIGPPKDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQ WKLRLLLKAVKEKKAQFYPALIHICARLMNVHRRFRMAIKDGF IENMF FVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMLPAIQ VHHAVCDGFHVGRMLNELQQYCDEWQGGADFADFGTTIKQDFRLLGQ TSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESG Q
3190	B	114	2876	MDKFLDITYTLPRLNQEEVESLNRPI TGSEIEAI INSLPTKKS PGPDG FTSEFYQRYKETVVCRLSPPSFNGGLPLGSDLVFYAPGPQKI IWVMV HVGALALKDGFSPLDVGVHGF CRFRNHHQTGFSPAGANQRDPLAATL SGPGGEGQSAVARLTGEKKNHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAVSATQLMVKDDVTYAIKLS CWPGLDIIPSC LALHRIETELMG KFDKGRLPHTPHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCA ADVLI VPTPAELLDYTSALQFFDMLRDLLKNVDLKGFE PDVRILLTK YSNSNGSQSPWMEEQIRQAWGSMVLKNVEFCRFRTPHQP GFSPAGAN QRGPLAATLSGPAGEGQSAVARLTGEKKNHPGAQYANRLSPRVGRFI NAAGTTGFPTGKRAGIREISDLMIIGETVITRSP TGRSPVGQFLAV WGGKLPSPAFGSGSRDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESG QAWSLCTPIMWFYPRAFSRLRQLTRYSSSGGVAGCHSGKPSRK LSTL GFASLVQHS TSLSRATLLIYKGFCRFRNPHQTGFSPAGANQRGPLAAT LSGPGEQSAVARLTGEKKNHPGAQYANRLSPRVGRFINAAGTTGF PTGKRAVSATQLMDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLARQVSRLESGQLAGFP RQALNRGLPL GFRFSALRHLDPKKLDLGDGSRSGPSP*
3191	B	1	2640	MEIRGRVEQRVGYTIEQINHM RDVFGTRLRRAEDVFPFVIGVAAHKG GVYKTSVSVHLAQDLALKGLRVLLVEGNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSC LALHRIETELMGK FDEGKLPTDPHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYPSALQFFHMLCDLVKNVDLKGFE PGELAPLYGC WGLRTGIAVACAPHHASLNLHGLNQIRNVKKQSVYLMNLRKSGTLGH PGSVDETTYERLAEESLDSLAEFFEDLADKPYTFEDYDVSFGSGVLT

				GKLGRLATYVINKQTPNKQIWLSSPSSGLKRYDWTEKNWVYSHDCV SLHDVLAELTKALKTKLDLSSSLAYSGKELDAQPGYYMLHAQYMLRP PLSSPMQHRAPETGPTSRNSVLNAVTPPAPTTPPSPLFDSRGSRRK TYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFRKESQKLQOSAKKRDAELANGALGIIIE LNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGKWYLFDSRGSKM TIDXGSPXKIRLFYTDYSGKHYGKQSLTTAQVNVSKSDDLKINGVE DHKTI FDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYL VFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQOSAKKRDA ELANGALGIIELNNDYTLKKVMKPLITSNTAAANQESSHVQQQALAL EQQFLERTQALEAQIVALERMRAADQTTAKQGMCTQVHLTNTSRHAG RPSKCQFCSTRQRHRLSDPKQDLGNRRFSPPP*
3192	A	1	454	MERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAADGVTFSPVPT PHTFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEYTKVFALDVAA RHRAIR\VPROQGDYRTRIWKFEGLSNVLVIQNLKLIICVMCLVRD CDVLKTYFHL
3193	A	2758	2946	DGQQLI ALHRLALRELQQAVHAGLPQQA KILFDGGSEIGKIPGVPT PAKANRRRGYNPPFGL
3194	A	2372	3570	EALLPGDQDSQSGKGVAAREVWFLPSSFAPVLLRLVGNHHVGDNSID SWKNAGR/VFKDSDKFDANDPILKDQTQEWSSSATFTSDGKIRLFYT DYSGKHYGKQSLTTAQVNVSKSDDLKINGVEDHKTI FDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTNFFRKESQKLQOSAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIERANVFKMNGKWFAD/SRNHHQTGFS PAGANQRGPLAATLSGPGGEGQSAVARLTGEKKNHPGAQYANRLSPR VGRFINAAGTTGFP TGKRAVSATQLMDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLES GHNYSKGQSKVSFKTRQVPSAYEPVKS KAGGCFRVAP NRAFKSRRDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLL PVSLVKRKTTLAPNTQTASPRALADSLMQARQVSRLESQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPN TQTASPRALADSLMQARQVSRLESQIVRSATGQLIHNWTQRTQGF SPQPAGNPKRQVFSDASLEVAKVRYPLSTIGGPPSRGPGLPKWEGRG CKGSLVSPVFFCTCTFALGWKSSRRRQLNRQLEKRGPFKDSKDFDA NDPILKDQTQEWSSSATFTSDGKIRLFYTDYSGKHYGKQSLTTAQVN VSKSDDLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRK ESQKLQOSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQARQVSRLESQ DFADFGTTIKQDFRLLGQTSVDRLLQLSQGQANHLMTQFSEPVLIIE QRTTDEE
3195	B	1	2232	MKLMTLNQCINAGHEMTKAIAIAQFNDDSPPEAR KITRRWRIGEAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMRDVF GTRLRRAEDVFPFVIGVAAHKGGVYKTSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIIPSCALHRIETEFMGKFDEDNAGMVRVLQPFSTDEKKS VI STLTFPGKHLRRDKSLTTAQGCDKINNKTSPPTSPLALALKGLRVLL VEGNDPQGTASMYHGWVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTC WPGLDIIIPSCALHRIETELMGKFDEGKLPTDPHMLRLAIETVAHD YDVIVIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDML RDLLKNVDLKGFE PDVRI LLTKYSNSNGSQSPWMEEQIRDAWGS MVL KNVEPENGEVGKXGSPQLINQEKMFRI RNSYIDRDS EYLLQENEP DGTLDQKLLLEDLQKKNDLRYIEMQPPPLVSSSRVWVKRGELTAYVE DTVLF SRRTSKQVYFFL FNDVLIITKKRRSDSSLREGDNQKAYKE TYGVSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVSD

				AGMVPVLQPLHLTEKSGYSTLTIPVNLQRQTSLTQRKVMCQNLVTHLK STEWKHKTIIVDGERKTYQKRSVAVFRMKGILHSATTIR*
3196	A	1260	1340	LPMALAVGFCRFRNHHQTGFSPAGANQRGPLAATLSGPGGEGQSAVA RLTGEKKNHPGAQYANRLSPRVGRFINAAGTTGFPTGKRAGFCRFRN HHQTGFSPAGANQRGPLAATLSGPGGEGQSAVARLTGEKKNHPGAQY ANRLSPRVGRFINAAGTTGFPTGKRAGFCRFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLTGEKKNHPGAQYANRLSPRVGRFINA AGTTGFPTGKRAQAQAK*WHYREPLLLRAQLTNPPSGQQLKSVDQWP VQKQFSSGSDLYQLHPFHVQHFLPCFPFRHPEFAPPSTGTESHYYCW IW
3197	B	200	2602	MQLARQVSRLESQGVKHEGQHTKMSQVLWRSQEENPATLGNNIQLFD WIPQNDLLGHPKTKAFITHGGTNGIYEAIYHGVPMVGVPMFADQPDN IAHMKAKGAAVEVNLNTMTRPGGEGQSAVARLTGEKKNHPGAQYANR LSRVGRFINAAGTTGFPTGKRAVSATQLMDFADFGTTIKQDFRLLG QTSVDRLLQLSQQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQ AVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLES GQILPDFGPHHQTEFSPAGANQRGPLAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFINAAGTTGFPTGKRAVSATQLIPKVDK TTKIGKKQSRKTGNSKNQSASPPPKESSSSHATEQNWTENDFDELRE EGFKRSNCSELQEEVQTHGKEVKNLEKKLDEWLTRITNEEKPLKOLM ELKTKAQELRDKCTSLSSRFNQLLEERVSVMEDQMNMKREEKFREKR IKRNEQSLQEIWDYVVKRPNLRLIGVPESDGENGTKLENTLQDIIQDF ADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLPVSLVKRKTTL LAPNTQTASPRALADSLMQLARQVSRLESQHQAQCMKSNALIVILG TVTLDAVGIGLVMPVLPGLLRDIVHSDSIASHYGVLLALYALMQFLC APVLAALSDFRGRRTVLLASLLGATIDYAIMATTPVLWIYPLVNSPS C*
3198	B	1	3198	MKLMETLNQCINAGHEMTKAIATAQFNDDSPARKITRRWRIGEAAAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMARDVF GTRLRRAEDVFPVIGVAAHKXSPVIGVAAHKGGVYKTSVSVHQAQD LALKGLRVLLVEGNDPQGTASMYHGWVDPDLHIHAEDTLLPFYLGEKD DVTYAIKPTCWPGLDIIIPSCALHRIETELMGKFDEGKLPTDPHLML RLAIETVAHDYDVIVIDSAPNLGIGTINVVCAADVLIPTPAELFDY TSALQFFDMLRDLLKNVDLKGFEPCDRIILLTKYSNSNGSQSPWMEEQ IRDAWGSMLVKNVRETDEVGKAVINHKKRKNSPRIVQSNLDTEAAY SLSRDQKRMLYLFVDQIRKSDGTLQEHGICEIHVAKYAEIFGLTSA EAKDPRGVYKTSVSVHQAQDLALKGLRVLLVEGNDPQGTASMYHGWV PDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIIPSCALHRIE TELMGKFDEGKLPTDPHLMLRLAIETVAHDYDVIVIDSAPNLGIGTI NVVCAADVLIPTPAELFDYTSALQFFDMLRDLLKNVDLKGFEPCDI NAGHEMTKAIATAQFNDDSPARKITRRWRIGEAAADLVGVSSQAIRD AEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMARDVFGTRLRRAEDVF PPVIGVAAHKGGVYKTSVSVHQAQDLALKGLRVLLVEGFIEENMFVS ANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLMPLAIQVHH AVCDGFHVGRMLNELQOYCDEWQGGADYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQNEFAGNISALADAENISRKIITRCINT AKLPKSVVALFSPHGEALSARSGDALQKAFTDKEELLKQQAASNLHEQK KAGVFIRDKLMERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAA DGVTFSPVPTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEVEY TKVFALDVAARHRVQFAMPESDAVAMLKQLS*
3199	A	1	2259	MKLMETLNQCINAGHEMTKAIATAQFNDDSPARKITRRWRIGEAAAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMARDVF GTRLRRAEDVFPVIGVAAHKGGVYKTSVSVHQAQDLALKGYVFCWS KCINAGHEMTKAIATAQFNDDSPARKITRRWRIGEAAADLVGVSSQA IRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMARDVFGTRLRRAE

				DVFPPIGVAAHKGGVYKTSVSVHLAQDLALKGLRVLLVEEPPSAPN LGIGTINVVCAADVLIPTPAELFDYTSALQFFDMLRDLKNNVDLKG FEPDVRILLTKYSNSNGSQSPWMEEQIRDAGSMVLKNVRETDEVG KAAPMVDSLIARVGMARGNAITLPCGRDVKFTLEVLRGDSVEKTS RCDNLKTCHTSHGSVMAETAVINHKKRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTLQEHGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFRLSETKEITNPHYAMRLYESLCQYH PLTIEKVMKPLITSNTVTDEIERANVFKMNGKWYLFDTSRGSKMTID GINSNDIYMLGYVSNLSLTGPYKPLNKTGLVLQMGLDPNDVFTTYSHF AVPQAKGNVITSYMTNRGFFEDKKATFAPSFLMNIKGNKTSCLKP H
3200	A	1	2418	MAETAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIR KSDGTLQEHGICEIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPWFIKRAHSPSRGLYSVHINPYLIPFFIG LQNRFTQFRLNLFVQKSRLVDLALKGLRVLLVEGNDPQGTASMYHGWV PDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCALHRIE TELMGKFDEAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHGICEIHVAKYAEIFGLTSAEAIABYNGYHVVF ALAGSPKDADDTSIYMFYQKVGDNISWSKNAGRVPKDSKDFDANDP ILKQDTQEWSGSATFTSDGKIRLFYTDYSGKHYGKQSLTTAQVNVSK SDDTLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQ KLQQSAKKRDAELANGALDLTTAQVNVSKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGTNFFRKESQKLQQSAKKRDAELANGAL GIIELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGKWYLFDTSR GSKMTIDGINSNDIYMLGYVSNLSLTGPYKPLNKTGLVLQMGLDPNDV TFTYSHFAVPQAKGNVITSACGAESTFYVEDPPGWSQTPGLKRSS CLGLPKC
3201	A	1907	5097	TSKKIVQAPVLTFTTA/LLAGGAIQAFAKENNHKAYKETYGVSHT RHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQAD GTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDNISWSKNAGR VFKDSKDFDANDPILKQDTQEWSGSATFTSDGKIRLFYTDYSGKHYG KQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQFIDEG NEGILPISEPPIKQDFRLLGQTSVDRLLQLSQQAQVKNQLLPVSLV KRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQQAQVKNQLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLL QLSQQAQVKNQLLPVSLKPYACQIPGCTKRYTDPSSLRKHVKAHSS KEQQARKKDHNSSPAREHNWTANEFDELTEVGFRDFADFGTTIKQD FRLLGQTSVDRLLQLSQQAQVKNQLLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQ LSQQAQVKNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQV SRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAQVKNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQQAQVKNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSV DRLLQLSQQAQVKNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAQVG NQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDF ADFGTTIKQDFRLLGQTSVDRLLQLSQQAQVKNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLARQVSRLESGQ
3202	A	891	2136	GATQAFAKENNHKAYKETY\ESAKGLDVWDSWPLQADGTVAEYNGY HVVFALAGSPKDADDTSIYMFYQKVGDNISWSKNAGRVPKDSKDFD ANDPILKQDTQEWSGSATFTSDGKIRLFYTDYSGKHYGKQSLTTAQV

				NVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHT LRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFR KESQKLQSSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYVSNLSLT GPYKPLNKTGLVLQMG LDPNDVFTTYSHFAVPQAKGNVNVITSYMTN RGFFEDKKATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN
3203	A	1	3987	MILKPKDGNIEEVNSLRKQRAGSSSSKMNLSLGFRCFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQSAVARLTGEKKNHPGAQYANRLSPRVG RFINAAGTTGFP TGKRAVSATQLMDFADFGTTIKQDFRLLGQTSVDR LLQLSQGQAWKIPKTI FDGDGKTYQNVQQFIDEGNYTSGDTHTLRDP HYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQ KLQSSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLF TDSRGSKMTIDDTSLSTPAAPMVDSL IARVGM ARGNAITL PVCGRDVKFTLEVLRGDSVEKTSRVWVSGNERDQELLTED ALDDLIPSFLLTGQQTAFGRRVSGVIEIADGSRRRKAAALTESDYR VLVRKLFVLVHCSELSTILVGNIPAMVPNLLILPLHCYDIVHPKRSE VISPSYRILYHHEKEDVGCLIDVNILDNLGLQPVLSQSISILVQQSE FSLEVTQYQEREPLVRASPCSDVTERAGSSLSQSPLLSADLTAAQ TPSEFLALTEDSVSEMDAFSKSGSMASHCDNFHNDSTSQMSLNSAA VTKTTTELGTGTPCAIMSPGKYRLEGQCSTESNSLPETSAANQKEVL LQIAELPATSVSHSESNLPADSEREENIGLQNAACSWGRGDTSTPVV TPTGTMLGQTRSQNSTGSFPRPAIATTYLYVCSRRALQSAELEKTT LKFIWSQKRACIVKSILSQKNKAGGITLPDFKLYKATVTKTAWDFA DFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLARQVSRLESGQAIKNHSLPRKTLQCLPY ILTGFRRGQSEYF S ILSNKALADTVMFLDFADFGTTIKQDFRLLGQT SVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQSPQSGLKHAFSQLLCFDYLLSTKSLFTTWPQL SALTALSTVGHNPFSEQSALLDQYGDQTQEWSGSATFTSDGKIRLPY TDYSGKHGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQG EESLFNKAYYGGGTNFFRKESQKLQSSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIERANVFKMNGKWYLF TDSRGSKMTID GINSNDIYMLGYVSNLSLT CYPLPSPGILHAVLFFIIHVVDPTNGILS SNKRKNVLKQATT
3204	A	2	247	QGAGFSSSLRMASIFS IHSVGT RDLSRLSTILSPLYNTVAPGAN*CR ELKLVL DADDVLSTE VKRVITSSASNITPAFFCS
3205	A	1099	2224	DGQQLIALHRLALRELQQAVHAGLPQQA KILFDGGSE/TRQNPLQQL VHMGLPRPLDKKNFQEP
3206	A	1366	2673	CDNLKTCHTSHGSVMAETA VINHKKRKN SPRIVQSN DLTEAAYSLSR DQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWF I KRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRLSETKEITNPYAMQSPYTDYSGKH YGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNK AAYGGGTNFFRKESQKLQSSAKKRDAELANGALGIIELNNDYTLKKV MKPLITSNTVTDEIERANVFKMNGKWYLF TDSRGSKMTIDAGISHKK RKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDG ICEIHVAKYAEIF
3207	A	1	7035	MLIGAFQISDFQIWDAQPMFQKEQVDPLQMKLQQVNLGGQLIQSAG KDCDVQGLEHDMEEINARWNTLNKKVAQRI AQLEALLHCGKFQDAL EPLLSWLADTEELIANQKPPSAEYKVVAQIQEQKLLQRLDDRKAT VDMLQAEGGRIASAE LADREKITGQLESLESRWTELLSKAAARQKQ LEDILVLAKQFHETAEPISDFLSVTEKKLANSEPVGTQTAKIQQII RHKALEEDIENHATDVHQAVKIGQSLSSLTSPAEQGVLS EKIDSLQA RYSEIQDRCCRKAALLDQALS NARLFGEDEVEVLNWLAEVEDKLSSV

				<p>FVKDFKQDVLHRQHADHLALNEEIVNRKKNVDQAIKNGQALLKQTTG EEVLLIQEKLDGIKTRYADITVTSSKALRTLEQARQLATKFKQSTYEE LTGWLREVEEELATSGGQSPTGEQIPQFQQRQKELKKEVMEHRLVLD TVNEVSRALLELVWRAREGLDKLVSDANEQYKLVSDTIGQRVDEID AAIQRSQQYEQAADAELAWVAETKRKLMAFGPIRLEQDQTTAQLQVQ KAFSIDIIRHKDSMDELFSHRSEIFGTCGEEQKTVLQEKTESLIQQY EAISSLNERYARLERAQVLVNQFWETYEELSPWIEETRALIAQLPS PAIDHEQLRQQEEMRQLRESIAEHKPHIDKLLKIGPQLKELNPEEG EMVEEKYQKAENMYAQIKEEVQRALALDEAVSQSTQFHDKIEPMLE TLENLSSRLRMPPLIPAEVDKIRECISDNKSATVELEKLQPSFEALK RRGEELIGRSQGADKDLAAKEIQDKLDQMVFVWEDIKARAEEREIKF LDVLELAEKFWYDMAALLTTIKDTQDIVHDLSPGIDPSIIKQQVEA AETIKEETDGLHEELEFIRILGADLIFACGETEKPEVRKSIDEMNNA WENLNKTWKERLEKLEDAMQAAVQYQDTLQAMFDWLDNTVIKLTMP PVGTDLNTVKDQLNEMKEFKVEVYQQQIEMEKLNHQGELMLKKATDE TDRDIIREPLTELKHLWENLGEKIAHRQHKLLEGALLALGQFQHALEB LMSWLTHTEELLDAQRPISGDPKVIEWELAKHHVLKNDVLAHQATVE TVNKAAGNELLESSAGDDASSLSRLEAMNQCWESVLQKTEEREQQLO STLQQAQGFHSEIEDFLELTRMESQLSASKPTGGLPETAREQLDTH MELYSQLKAKEETYNNQLLDKGRMLLSRDDSGSGSKTEQSVALLEQK WHVVSCKMEERKSKLEEALNLATEFQNSLQEFINWLTLAEQSLNIAS PPSLILNTVLSQIEEHKVFANEVNAHRDQIIELDQTNQLKFLSQKQ DVVLKKNLLVSVQSRWEKVVQRSIERGRSLDDARKRAKQFHEAWKKL IDWLEDAESHLDSLEISNDPDKIKLQLSKHKEFKQTLGGKQPVYDT TIRTGRALKEKTLLPEDSQKLDNFLGEVRDKWDTVCGKSVERQHKE EALLFSGQFMDALQALVDWLYKVEPQLAEDQPVHGDLDLVMNLMDAH KVFQKELGKRTGTVQVLKRSGRELIENSRRDITWVKQQLQELSTRWD TVCKLSVSKQSRLEQALKQAEVFRDTHMLLEWLSEAEQTLFRFGAL PDDTEALQSLIDTHKEFMKKVEKRVVDVNSAVAMGEVILAVCHPDCI TTIKHWITIIIRARFEEVLTWAKQHQRLETALESELVANAELLEELLA WIQWAETTLIQRDQEPQPONIDRVKALIAEHQTFMEEMTRKQPDVDR VTKTYKRKNIEPTHAPFIEKSRSGGRKSLSQPTPPMPILSQSEAKN PRINQLSARWQQVWLLALERQKRLNDALDPSIVSPKCRPPGGRQAYP LVNSSGSKRQIAKNRGATQAFAKENNQKAYKETYGVSHTRHMLQI PKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQADGTVAEYN GYHVVFALAGSPKDADDTSIYMFYQKVGDNIDSWKNAGRVFKDSK FDANDPILKDQQTQEWSSGATFTSDGKIRLFYTDYSGKHGKQSLTTA QVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDN HTLRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNF FRKESQKLQSSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNT VTDEIERANVFKMNGKWYLFSDSRGSKMTIDGINSNDIYMLGYVSHS LTGPYKPLNKTGLVLQMGDPNDVFTYSHFAVPQAKGNVNVITSYM TNRGFFEDKKATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN</p>
3208	A	1	2328	<p>MKLMETLNQCINAGHEMTKAIAIAQFNDDSPPEARKITRRWRIGEAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMEDVF GTRLRRAEDVFPPIGVAAHKGGVYKTSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWVPLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIIPSCALHRIETELMGKFDEGKLPTDPLMLRLAIETVAHDY DVIVIDSAPNLGIGTINVCAADVLIIVPTPAELFDYTSALQFFDMLR DLLKNVDLKGSKQKTVHTEGDMNMNIKKIVQATVLTFTTALLAGGAT QAFAKENNQKAYKETYGVSHTRHMLQIPKQQQNEKYQVPQFDQST IKNIESAKGLDVWDSWPLQADGTVAEYNGYHVVFALAGSPKDADDT SIYMFYQKVGDNIDSWKNAGRVFKDSKFDANDPILKDQQTQEWSSG ATFTSDGKIRLFYTDYSGKHGKQSLTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLV FEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQSSAKKRDAE LANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGKWY</p>

				LFTDSRGSKMTIDGINSNDIYMLGYVSNLSLTGPYKPLNKTGLVLQMG LDPNDVTFYSHFAVPQAKGNVITSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQGQLTVN
3209	A	1	2328	MCELDILHDSLYQFCPELHLKRLNSLTLACHALLDCKTLTLTELGRN LPTKARTKHNIKRIDRLLGNRHLHKERLAVYRWHASFICSGNTMPIV LVDWSDIREQKRLMVLASVALHGRSVTLYEKAPPLSEQCSKKAHDQ FLADLASILPSNTTPLIVSDAGFKVPWYKSVEKLGWYWSRVRGKVQ YADLGAENWKPI SNLHDMSSSHSKTLGYKRLTKSNPISCQILLYKSR SKGRKNQRSTRTHCHHPSPKIYSASAKEPWVLATNLPVEIRTPKQLV NIYSKRMQIEETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIALMLQ LTCWLAGVHAQKQGWKHFQANTVRNRNIPKQQQNEKYQVPQFDQST IKNIESAKGLDVWDSWPLQADGTVAEYNGYHVVFALAGSPKADDDT SIYMFYQKVGDNIDSWKNAAGRVFKDSKDFDANDPILKDQQTQEWSSG ATFTSDGKIRLFYTDYSGKHYGKQSLTTAQVNVSKSDTLKINGVED HKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYL FEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQSSAKKRDAE LANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGKWY LFTDSRGSKMTIDGINSNDIYMLGYVSNLSLTGPYKPLNKTGLVLQMG LDPNDVTFYSHFAVPQAKGNVITSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQGQLTVN
3210	B	1	2541	MPRQVSGSGPGLLVAGQAAGVTGGKSLCQYRKPDGSGIVSLKIDW IIERYQLPQSYQHRKAGECLLHEYEDLVPIRDTLRLFPGGRYLPRAK HVAPSEPDPDEQDEQKLRFADFGTTIKQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLE SGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLL PVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPN TQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPVSLDDVTYAIKPTCWPGLAIPSCAL HRIETELMGKFDEGKLPTDPHMLRLAIETVAHDYDVIVIDSAPNLG IGTINVCAADVLIPTPAELFDYTSALQFFDMLRDLKKNVDLKGF PDVRILLTKYSNSNGSQSPWMEEQIRDAWGSMLKNNVRETDEVGKG QIRMRTVFEQAIDQRSSTGAWRNALSIWEPVCNEIFDRLIKPRWEIR *
3211	A	1	3849	MCELDILHDSLYQFCPELHLKRLNSLTLACHALLDCKTLTLTELGRN LPTKARTKHNIKRIDRLLGNRHLHKERLAVYRWHASFICSGNTMPIV LVDWSDIREQKRLMVLASVALHGRSVTLYEKAPPLSEQCSKKAHDQ FLADLASILPSNTTPLIVSDAGFKVPWYKSVEKLGWYWSRVRGKVQ YADLGAENWKPI SNLHDMSSSHSKTLGYKRLTKSNPISCQILLYKSR SKGRKNQRSTRTHCHHPSPKIYSASAKEPWVLATNLPVEIRTPKQLV NIYSKRMQIEETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIALMLQ LTCWLAGVHAQKQGWKHFQANTVRNRNLIYSHMVTWGNYEIGISQ YQVPQFDQSTIKNIESAKGLDVWDSWPLQADGTVAEYNGYHVVFAL AGSPKADDDTSIYMFYQKVGDNIDSWKNAAGRVFKDSKDFDANDPIL KDQTQEWSSGATFTSDGKIRLFYTDYSGKHYGKQSLTTAQVNVSKSD DTLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHY VEDKGHKYLVEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKL QSSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERA NVFKMNGKWYLFETDSRGSKMTIDGINSNDIYMLGYVSNLSLTGPYKPL NKTGLVLQMGDPNDVTFYSHFAVPQAKGNVITSYMTNRGFFED KKATFAPSFLMNIKGNRGTEGKQGIQYFPHKPLGVGSPHIFDYLLV

				SILPSIRNPTGKFVVKDLAKRKNYAPVAMLOSAMTRTHNHRSCPEPV KDMLLAFPNDRAATIRSKDHHKHFRDFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQL ARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAHAI TGDVGMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVT VSDTLASDAARLTCRHGLGNQGTAPMYHGWVPDLHIHAEDTLLPFY LGKDDVTYAIKPTCWPGLDIIPSCALHRIETELMGKFDEGKLPTD PHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCAADVIVPTPA ELFDYTSALQFFDMLRDLLKNVDLKGFEVDRIILLTKYSNSNGSQSP WMEEQIRDAWGSMLKNVVRETDEVGKGQIRMRTVFEQAIDQRSSTG AWSNALSILGTCLQ
3212	B	1	6724	MDNFFAPVFTMGKYTQGDKVLMLAIQVHHAVCDGFHVGRMLNELQ QYCDWQGGADFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQ LLPVSLRKQNTSRPPSMHVDDFVAAESKEVVPQDGI PPPKRPLKVSQ KISSRVENLNTLNLKELMLCHHQEEGAGEDLDRVYDLMIFFVREN TQVDHHLCMWMTLLLLKVKWFLKMEYLHQNGHSKYHRRFLPVVGQ AIEEDGVLSTVRIGFSHLLQKALQNFQRTGFIQHVHRIGMAERMWC DRNRERHTVSSSGGNRLPNPGPGGEGQSAVARLTGEKKTTHPGAQYAN RLSPRVGRFINAAGTTGFPTGKRAVSATQLMDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLE SGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMRDVFGTRLRRAEDVFPVIGVAAHKG GVKTSVSVHLAQDLALKGLRVLLVEGNPDQGTASMYHGWVPDLHIH AEDTLLPFYLGKDDVTYAIKPTCWPGLDIIPSCALHRIETELMGK FDEGKLPTDPHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFDMLRDLLKNDFRLLGQTSVDRLLQLS QGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTI KQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLACKTTTFQACSPYLKLEEYSFQSEEDQ RNTKLYQQLVRNSYDHDYEFELGTHMDNFFAPVFTMGKYTQGDKVL MPLAIQVHHAVCDGFHVGRMLNELQYCDWQGGADFADFGTTIKQD FRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQ LSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQV SRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLGFCFRFNHPK QDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLGFCFRFNHPKQDF RLLGQTSVDRLLQLFSGPGGEGQSAVARLTGEKKNHPGAQYANRLSP RVGRFINAAGTTGFPTGKRAVSATQLMDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLM QLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLHEDGI CEIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYSVHINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKPDSGIVSLKIDWIIERYQLPQSYQR MPDFRRRFLQVCVNEINSRTPMRLSYIEKKKGROTHICKLVEANNP QAISQQLVHMAIQIACGMSYLARTEVIHKDLAARNCITDDTLQVKI TDNAVSWTITVWKTMTKGQFVGWLLKVWLITSFLALVMCGAFGVMLW

				ELMTLGQTPYMDTDPFEMAAYLKDGYRIAQPINCPDEPFAVMACCWA LDPGERPKFQQL*
3213	A	532	1232	SDNMCELDILHDSLYQFCPELHLKRLNSLTLACHALLDCKTLTLTE LGRNLPTKARTKHNIKRIDRLGNRHLHKERLAVYRWASFCISGNT MPIVLVDWSDIREQKRLMVLRSVALHGRSVTLYEKAPLSEQCSKK AHDQFLADLASILPSNTTPLIVSDAGFKVPWYKSVEKLGWYLSRVR GKVQYADLGAENWKPI SNLHDMSSSHSKTLGYKRLTKSNPISQIILL YKSRSKGRKNQRSTRTHCHHPSPKIYSASAKEPWILATNLPVEIRTP KQLVNIYSKRMQIEETFRDLKSPAYGLGLRHSRTSSSERFDMILLIA LMLQLTCWLAGVHAQKQGWDKHFQANTVRNRNLKIYSHMVTWLGNYE GISQTQAFAKENNQKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPK DADDTSIYMFYQKVGDNIDSWKNAAGRKFDSKDFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYSGKHYGKQSLTTAQHTVNARGLQSKD MKSYNQPPYVLWSSWSHTGTENGYQGEESLFNKAYYGGGTNFFRKE SQKLQSSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDE IERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYVSNSLTGP YKPLNKTRLVLQMG LDPNDVTFTYSHFAVPQAKGNNG
3214	A	8749	11698	CSWHDRFPDWKAGRILPISEPPSNRIFACWGKPAWTGLLQLSQGQAV KGNQLLPVSLGFRGPPASNPGGAPGSASVAAAAA VAAAAAAPPV DNAAPHSAAKLEERRKPDPRRDFADFGTTIKQDFRLLGQTSVDRLLQ LSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQV SRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDF ADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKT LAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLDLVLKGLRVLLVEGNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGEKDDVTYAIKPTCWPGLDII PSCLALHRIETELMGK FDEGKLPTDPHMLRLATETVAHDYDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFDMLRDLLKNVDLKGFEVDVRILLTKY SNSNGSQSPWMEEQIRDAWGSMLKNVVRETDEVGKGQIRMRTVFEQ AIDQRFSTGAWRNAPSIWEPGCMEIFERLNKPKLSKLFHVRPVTQGD VYRAETEEIPKIFQILWPIKHKKGAGGNEPSEQFSKTLFGESASGYL EIFKDFTGNRNIFRQYRGNEGQMRELQDQLEAEQYFSQONEKYQVPQ FDQSTIKNIESAKGLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPK DADDTSIYMFYQKVGDNIDSWKNAAGRKFDSKDFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYSGKHYGKQSLTTAQVNVS KSDDTLKI NGVEDHKTFIDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEESLFNKAYYGG\GTNFF\RKESQKLQSS AKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERANVF KMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYVSNSLTGPYKPLNKT GLVLQMG LDPNDVTFTYSHFAVPQAKGNVIVTSYMTNRGFFEDKKA TLGDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLL PVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADLG

				TTIKQDFRLLGQTSVDRLLQLSQQAQVKNQLLPVSLVKRKTTLAPN TQTASPRALADSLMQLARQCLEPRPLSPVFFVPLMFEEQGS
3215	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGAGHAGEYGAELERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDL HAHKLVRDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3216	A	24	609	GIPQTQREPTMVLSPADKTNV\KAAGKVGAGHAG\EYGAELERMFL SFPTTKTYFPHFDLSHGFCPLRATGKKVADALTNVAHVDDMPNAL SAL\SDLHAHKLVRGPGSTFKLLSHLPCW*TLGRPPSPAEPQPLAVA RLPWKFPGLFVEAPLLDLQITFKVGSFGWPLFFCFFGPPSPSSPF LHPYPRGL
3217	A	3	583	EPRLRKAGLLSRSRQNDQEGREGAQGWPAAYGPARGVVPQFWQTGT WQNGTQQRVPQLPPHPPPIHLVSRHRGKLRHGFLRPMPEPRGLESCK T/GQCSGSCSMYVTMRKRPEWEGGHDLTQQGGCRSSVCGRRAHEAL RPRVWCGEQPQWTW\CAVCP\NRSAPGAGLAD\RQHPGESRAWGETR LGEAGGAE
3218	A	3	398	QTPEKRHKSCPGGLHFLSRSINLHFPKLSISGTYKLRVLRNLGITK IFSNEADLSGVSQEAPLKLKSAVHVAVLTIDEKGTEATGPPHLEKA WSKYQTMFNRPFVLIKDDITNFPLFIGKVVNPTQK
3219	A	1766	3896	NTKLDQAQQAPEDHYPIISLLPSHMAIGLLMAQEGHCKDSSAMGEEA HHPLTPATPPFPPLSPDWGHMQPDDFFVPVAVPAVFRGPPQLQCHGRR LFLNSPCAQKSSSGLVVEPGLSRTLLEMVKLTSMRGQFLEAQIPTGI SLTLQYQLYQKQTNKNMSYSFVFLKQWVALGQGRAGYPSLEDADSR RFNGRSRSLITVIGITLTVEIVTSGMMKGTRVRWSGAGNEGMMGLEE GRNERSVKEAPPRRAVEAQPKDRTWDVGKGQGTGEGRGLEVEGQOH QGSEPGTIPFSVSWGVLLLAGLCCLPSSLVDPQEDAAQKTDTSHH DQGDWEDLACQKISYNVTDLAFDLYK\SWLIYH\NQ\HVLVTPTSVA MAFAMLSLGTKADTRTEILEGLNVNLTETPEAKIHECFQOVLQALS PDRQLQLTGSSFLVNMKMLVDTFLEDTKKLYHSEASSINFRDTEE AKEQINNYVEKRTGRKVVDLVKHLKDDTSLALVDYISFHGKWQDKFK AERIMVEGFHVDDKTIIRVPMINHLGRFDIHRDRELSSWVLAQHYVG NATAFFILPDPKMWQLEEKLTYSHLENIQRAFDIRSINLHFPKLSI SGTYKLRVPRNLGITKIFSNEADLSGVSQEAPLKLKSAVHVAVLTI DEKGTEATGAPHLEEKAWSKYQTMFNRPFVLIKEYITNFPLFIGK VVNPTQK
3220	A	3	1226	MRRNKPRQGRVREARPAGGAGPGWRGARC SGAGEGGGGERRGSPAA LALAPASGPRRNFPDARCLIQYQIHQGAFLLAGSASLSAVTGVPEG EARFTEDYCPEEKMFGFHKPKMYRSIEGC\CISGAKSSSRFTDSKR YEK\DFQ\SCFGLHETRSGDI\CNACVLLVKRWKKL\PAG\SKKNWN HVVDARAGPS\LKTTFEPK\KVKTLSG\NRK\STQISKLQKEFK\R SNSDAHSTTSSASPAQSPCYSNQSDDGSDTEMASGSNRTPVFSFLDL TYWKRKICCGIYKGRFGEVLIDTHLFKPCCSNKKAAAEKPEEQGP EPLPISTQEWTECPDLSLVSWRPPLSSLPAGCSLHGLAADWTTDMI TVTTSKREPSQQEGSFQRRKAFPKRLPKMAEVQVLLL
3221	A	1	269	GGGGPLGSGRNGGSMNAPPAFESFLLFEGEKQLLQDPQVLFAGYKV PHPLEHKIIIRVQTPDYSPOEAFNTAITDLISELSLLEERF
3222	A	240	377	SNTHRVPTFTDAWEVEMVTSLSLQSFLLLPHIHCLKLQ*DPLHSP
3223	A	47	263	LTVLQAVQEAWLGRPQETDNHGRRRRGSRHVWPCWSRRDRESEVGG HAFKQPDPTSAHSISREQQGSRPP
3224	A	416	498	KRLSLQSFLLLPHIHCLKLQ*DPLHSP
3225	A	1	305	RTRGRTRGGDGGHLSGSRNGGSMNAPPAFESFLPLRG/QRRITIN KDTKVPNACLFTM\NKEDHTLGNIIKSRACFPFAFCRDCQFPEASPA TLPVQPAEL
3226	A	74	562	GSGGGGGHLSGSRNGGSMNAPPAFESFLLFEGEKK/ISDAGCGGP RITINKDTKVPNACLFTINKEDHTLGNIIKSQRLKDPQALFAGYKV PHPL\EHKIIIRVQTPDYSPO\RAFTNRQSPDL\ISELSLLGGSFAF

				RGGHKKTSQERNLSRGARGGLCSGL
3227	A	3	146	LKNKKNIYFCKLSECRDVLNPNVTQISSPKRNEQKTEKELYQMCS
3228	A	45	592	PSPPPPARAPSARTRRAPIPAAGQGRARPPRTVSRCSAAMATKIDK EACRAAYNLVRDDGSAVIWVTIKYDGGSTIVPGEQGAEYQHFIQQCTD DVRLFAFVRFTTGDAMSKRSKFALITWIGENVSELQRAKTGTDETTLV KEVVQNFANEYVISDRKELEEEFIKS\ELKKAVGANYDAQTE
3229	A	1	2661	MRQKVNKDIOELNSALHQVDLIDYRTLHPKSTEYTFSSAPHLTYSK IDHLVSSKALLSKCKRTEIIRNCLSDHSATKLELRIKKLTQNRSTTW KLNNLLNDYWVHNEMKAEIKMFFETNENKNTTYQNLWDTFKAVCRG KFIALNTHNRKQERSKIDTLTSQKEPEKQDQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFKINKIDRPLARLIKKEGEKNQIH TIKNDKGDLTNNPIEIQTTIREYYIHFYANTLENLEEMDKFLNTYTL LRLNQEEVESLNRRTGSEIEAIINSLPTKSPGPDAEKAFAFKSQQR FMLKTLNKLIGIDGTYLKIIRAIYDKPIANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIQEKEIKGIQSGKEELKLSLFADDMI VYLENPILSAQNLLKLIGNFSKVSQKINVKQSAFLYTKNRQTESQ IMSELPFTIASKRIKDLGIQLTRDVKDLFKENYKPLLEEIKEDTNKW KNIPCSWIGGINIVKIAILPKPCGKCLKDPFLTPYTKINSRWIKDLH VRPKNVKTLEENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIK LKSFCVTKEITTIRVNRQPTWEKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIYAARKHMKKCSASLAIREMQIKT MRYHLTPVRMATIKKSGNNRGYMTMLEQESFFLSLNIAYDSVLLPVI LPVPPFGVPDFPQQVPGSSHWDWLDSECSPWRCSTLGRHLPGVGNRH LIEVGAPLGRSFQRKDQAAIFAVLQPLLVIIPRQTASGVDLRQPPTDL QEHNSSPAREENWTENEFDELTEVGFRRLVITKFSSELKEDV
3230	A	1	1454	MIISIDAFAFDKIQQPFMLKTLNELVLEVLARAIQEKEIKVIQLG KEEVKLSLFADDMIVYLENPISVSAQNLLKLISNFSKVSQKINVKQS QAVLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKILCSWAGRINIVKMATLSKVIYRFNAIPIKL PMTFFTELEKTTTLKFIWNQKRACIAKSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQKRDIQDQNRTEPSEITPRIYNYLIFDKPEKNKQW GKDSL FNKWCWENWLAICRKLKDRFLIPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMSKTPKAVATKAKIDKWNLIKLSFC TAKETTIRVNRQPTKWEKIFATYSSDKGLISGIYKELKQIYKKKTNN PIKKWAKDMNRPFPSKEDIYAARKHMKKCSPLAIREMQIKTTMRYHL TPVRMAIIQKSGNN
3231	A	1	2364	ETLIDWCDEKELNLILTGGTGFAPRDVTENS AVNPSGPGLFLVL EVLARAIQEKEIKGIQLGKEEVKLSVSADDMIVYLENPISVSAQNLL KLISNFSKVSQKINVKQSAFLYTNNRQRAKSIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRFN AIPIKLPMPFFTELEKTTTLKFIWNQKRARIKSILSQKNKAGGITLP DFKLYYKATITKTAWYWYQNRDIDQNRTEPSEITPHIYNYLIFDKP EKNKQWQKDSL FNKWCWENWLAVCRKLKDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKWDLI KLKSFC TAKETTIRVNRQPTKWEKIFATYSSDKALISRIYNELKQIY KKKTNNPIKKRAKDMNRHFSKEDIYAARKHMKKCSPLAIREMQIKT TMRYHLTPVRMAIIKSGNNSTPAATGCMAWRENLCIERNSTVIV RRSIGHSAALSQKATPGLTQLNTAHRGTIWTSPQRGTTNPCDWKE SSGWHQVNAALGRSFQRKELAAIFAVLQPLLVIIPRKTGSRVDIQQTP ADLQQRGLTVRRKTNEQRGIASTSTKRISTQKPHPKVTNIKEQSEYY KYLANKLENLEEIVKFLDYTPPRLNQEEVKS LTRPITSSEVEAVI NSIPTKKSPEPDRFTAIFYQKYQELVPFVLKLFQTTKEGILLNLL YEASIIILIPKPERDTTKKISGQYPRGTWMHKSSIKY
3232	A	1	1368	MQNQEQKSAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLKEIKEDTKKWKNI PCSWVGRINIVKMAILPKVIYR FNAIPIKLPMFTFFTELEKTTTLKFIWNQKRAHIAKSILSQKNKAGGIT

				LPDFKLYYKATVTKAPWYQNRDIDQWNRMEPSEITPHMYNYLIFD KPEKNKQWGDLSLFNKWCWENWLAICRKLKLDPFLLTSYTKINSRWIK DLNVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKWD LIKLSFCTAKETTIRVNRQPTKWEKIFETYSSDKGLISRIYNELKQ IYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMKCSPSLAIREMQI KTTMRYHLTPVRMAI IKKSGNNRSEAADLRGECYSSEGGSVGVHSS RWARALAGSGVKLQTFVVSVAHKGSDPKSEQ
3233	A	114	1474	VKGDRFGALRFNDPCAGIKLPMTFFTELEKTTLKFIWNQKRARIAS ILSQKNKAGGSTLPDFKLYYKATVTKTAWYQNRDIDQWNRTPGSE ITPHTYNYLIFDKPEKNKQWGDLSLFNKWCWENWLAICRKLKLDPFL TPYTRINSRWIKDLNVRPKTIKTLEENLGITIQDIGMGKDFMSKTPK AMATKDKIDKWDLIKLSFCTAKETTIRVNRQPTKWEKIFATYSSDK GLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMK CSSSLAIREMQIKTTMRYHLTPVRMAI IKKSGNNRCWRGCGEIGTLL HCWWDWKLVPWKSVMRFLRDLELEIPFDPAPILLGIYPNDYKSCC YKDTCTRMFIVALFTIAKTWNQPKCPTMIDWIKMWHIYTMYYAAI KNDEFM/SFVGWTMKEIIILSKLLQEQKTK
3234	B	1	1890	MDKFLDITYTLPRLNQEEVESLNRPIITGSEIVAIINSLPTKKSPGPDG FTAIFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEASIIILIPKPGR DTTKIENFRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGFTPG MQGWFNICKSINI IQHINRTKDKNHMII SIDAFAFDKIQQHFMLKT LNKLGIDGTYLKMIRTIYDKPTANIILNGQKLEAFPLKTGTROGCP SPLLFNIVMELLARAIRQEKEIKGIQLGKEEVKLSLFADDMIRIKYL GIQLIRDMKDLFKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMA ILPKVIYRFNAIPIKLPMTFFTELEKTTLNFIWNQKRARTAKSILSQ KNKARGIMLPDFKLYYKATVTKTAWCWYQNRDIDQWNRTEPSEITPH IYNYLIFDKPKDNKQWGDLSLFNKWCWENWLAICRKLKLDHPFLTPYT TINSRWIKDLNVRPKTIKTLEENLGNTIQDIGMGKDFMSKTPKAMAT KAKIDKWDLIKLSFCTAKETTISVNRQPTKWEKIFATYSSDTGLIS RIYNELKQIYKKKTNNPINKWAKDMNRHFSKEDIYAAQHKMKNHHH WPSEKCKSKHNEIPSHTS*
3235	A	1	2677	MKAIEIKMFFEINENKDTTYQNLWDAFKAVCRGKFIALNAHNRKQERP KIDTLTSQLEKEQEQTHSKASRRQEMTKIRAELEKEIEIQKTLQKI NESRSWFFERINKIDRPLARLIKKKREKNQIDA IKNDKGDITTDPT IOTTIREYYKHLANKLENLEEMDKFLDITYTLPRLNQEEVESLNRPI TGPEIVAIINSLPTKRSPGPDGFTAIFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIIILIPKPGRDTTKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVVQHINRTKHKNH MIISIDAFAFDKIQQPFMLKTLNKL SIDGTYLKIIRATYDKPTANI ILNGQNLEAFPLKTGTROGHPLSPLLFNIVLEVLAIRQEKEIKAQ NLLKLISNFRKVSVKINVQKSQAFLYTNNRQTESQIMRELPTIAS KRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNI PCSWIGRI NIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTILKFIWNQKRAHIA KTILSQKNKAGGIMLPDFKLYYKATVTKTAWYQYQNRDIDQWNRIEL SEIIPHIYNHLIFDKPKDNKQWGDVFNKRCWENWLAICRKLKLD FLTPYTKINSRWIKDLHVRPKAIKTLEENLGITIQDIGMGKDFTSKT PKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTKWEKIFAIYSS DKGLISRIYKELKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAHRM KCCSSSLAIREMQIKTTMRYHLTPVRKAI IKKSGNNRCWRGCGEIGT LLHCWWDCKLVQP\LWKTVMQFLRDLELEIPFYPAIPLLGIYPKDY
3236	A	1	3045	MDKFLNTYTLPRLKQEEVESLNRPIITGSDIEAIINSLPTKK\SPGPD GFTAIFCQRYKEE/LEKEGILPNSFYEASIIILIPKASDTTKENFR PISLMNINAKILNKILAKQIRQHIKKLIHHDQVGFI PGMHGLFNICK SVNIIQHINRTNDKNHMIISIDAFAFDKIQQHFMLKTLNKLQNL KLIGNFSKVSQYKINVQKSQAFLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLNEIKEDTNKWKNI PCS\WEKTTLK

				FIW/NQKRAHIAKSIISQKNKAGGITLPDFKLYCKATVTKTAWYWYQ NRDIDQWNRTESEIMPHIYNHLIFDKPDKKKWKDLSFNKWCWEN WLAICRKLKLDPFLTPDTKINSRRIKDLNVRPEMIKTLEENLGNTIQ DIGMGKDFMSKTPKAMATKAKIDKWDLIKLKSFCTAKETTIRVNRQP TEWEKIFAIYSSDKGLISRIYNELKQIYKKKTNNPIEKWAKDMNRHF SKEDIYAAKHKMKCSSSLVIREIQIKTTMRYHLTPVRMAIIKKSNG NRCWRGCGEIGTLLHCWWDCKLVQPLWKSVWRFLRDLELEIPFDP PLLAAPSLPSGLRSPSKSSPSPSRCTLVIIILLHVFDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGYTVGFSTFEALRLGLSRYWLP SACRRPIVGLQLVMINSNGNFQVIAMEGTVASECCHGNGKLTWHRP SVCSFSRCTVQAAGGSAILEDGDPLLTAPLGSTPQAACVCRGPRGREL RAAPADSHLFQRDLWPFNKVIVHGEKGSNQTSQGLLNTGSEMTIVLE NPKYHSGPPVRVSPDGGQVIEVLADPSYTGPTALNNVFFAFQCNFY FDHIPENCGFSDPDPQNLQKGEGCPSLVRASTAPPQEKATEQPILL KTTESPFGMTVGPCTDETLDHGAPSKHVPGTAHNELALLDLRVIKSA GSAAVHHKLKVLHWRSSLSNNKGTGRLYEQVA
3237	A	1	2142	MLKTLNKLRIIDGTYLKIRAIYDKSTANIMLNGQKLEAFPLKTGTRQ GCPLSTLLFNIVLEVLARAIROEKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSAQNLLKLIGNFSKVSQYKINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIHLIRDVKDLFKENYKPLLNEIKEDTNKWK NIPCSWIGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKF IWNQKRARIAKSVLSQKNKAGGITLPDFKLYYKATVTKTARYWYQNR DIDQWNRTEPSEIMPHIYKYLIFDKLEKNKKWKDLSFNQWCWENWL AICRKLKLDPFLTPYTTINSRWIKDLNVRSKTIKTLEENLRIAIQDT GMGKDFMSKTPKAMATKAKIDKWDLIKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKHKMKCSPSLAIREMQIKTTMRYHLTPVRMAIIKKSNGNS TFDFGQHEFELHRSTYTRIVFSKITPILEVLRARAIROEKEIKGIQLG KEEVKLSLFADDMIVYLENPIVSAQNLLKLIGNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIKL PMTFFTELE
3238	A	1	1552	MRFKEKIHLHNIKEPSEAAASADGGAVASYPDLAKIVDEGRYKAEVMQ LRCGWRAPASDCVHSVAVVGVDVLEVLARAIROEKEIKGIQLGKEE VKLSLFADDMIVYLENPTVSAQNLLKLISNFSRVSGYKINVQKSQAF LYTNNKQTESQIMSELPFTIASKTIKYLGIQLTRDVKDLFKENYKPL LNKIKEDTNKWKNIPCSWIGRINIVKMAILPKVIYRFNAIHIKLPMT FFTELEKTTLKF IWNQKGVHIAKSILSKKNKAGGIMLPFKLYYKAT VTKTAWYWYQNRYTQCNRTEPSEIIPHIYNHLMFDKPKDKKKWKGD SLFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVRPKPIKT LEENLGITIQDIGMGKDFMSKTPKAIATKAKIDKWDLIKLKSFCTAK ETTIGVNRQPTELEKIFAIYSSDKGLISRIYKELKQIYKKK\NNPIK KWVKDMNRHFSKEDIYAVNRHMKKCSSSLVIREMQIKTTMRYLTPV
3239	A	1	1459	GLSGDLLGAHQLPDVLGCVQPLPDLLLPPQNLLALQSLQDDLLWALD PAAAAPWAMDRGAATQWAVGPVSDPWVMEAVASLPSAMDLDAAQP TWLLGAASLLVTDQPMQPSADQLAEFPDLSKVSQSLRIKYLGIKL TRNVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELENTTLKFIWNQKRACIAKSILSQKNKA GSIMLPDFKLYHKATVTKTAWYQYQNRDIDQWNGTEPSEIMSHIYNY LIFDKPEKNQKRGKDSLFSKWCWENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKI IKTLEENLVNTIQDIGMGKDFMSKTPKAMATKAKI DKWDLIKQSFCTAKETTIRVNRQPTWEKIFAIYSSDKGLISRIYK ELQQIY\RKKTNPIKKWAKDMNRHFSKEDIYAANRHMKKCSSSLAI REMQIKTTMRYHLTPV
3240	A	1	2028	MIISIDAEKAFDKIQPFMLKTLNKLIGIDGRYLKIRAIYDKPTANI ILNGQKLEAFPLKTGTRQGCPLSPLLFIHVLEVLARAIROEKEIKGI

				QLGKEKVKLSLFPDDMVVYLENPIISAQNLLKLISNFSKVSQYKINVT QTSQAFLYTNNRQTESQIMSELPFTTASRKIKYLGQILTRDVKDLFK DNYKPLLKEIKEDTNKWKNIPCLWVGRINIVKMAILPKVIYRFNAIP IKLPMFTFFTELEKTTTLKFIWNQKRARIAKSILSQKNKAGGITLPDFK LYYKSTVTKTAWYWYQNRDIDQWNRTEPSEIMLHISNYLIFDKPDKN NQWGDLSLFNKWCWENRLAICRKLKLDPFLTPYTKINSRWIKDLNVR PKTINTLQENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKLS SFCTAKETTIRVNRQPTWEKIFAIYSSDKGLISRIYNELKQIYKKK TNNPIKKWVKDMNRHFSKEDIYAAKHKMKCSSSLATREMQUIKTMR YHLPVRMAIIKKSGNNRPLWPTMPGDSQRGBDKLRDGGTPGKDHFP PFAFQAPIHPTESHLHSPSLPAFTILQVHGFECTAAKQTSHTPVAS PTGESGNFLASVTSRLSGGNVKIILDWKMRIMNKEDYGTISVIRRSY NRTLKQDGGSKAEENKQR
3241	A	2	1547	SNISLYSVVSLRPLPADYVPSIVMLPGTCQTDVEVSEETVEPSDEL IEYDSPEQLNEQLVTLSELLPESRWKNLLNLNDVIKRALELRYNINVO KQAFLYTNNRQTESQIMSELPFTMASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFSAIPK LPMFTFFTELEKTTTLKFIWNQKRARIKVSILSQKNKAGGITLPDFKLY YKATVTKIAWYWYQNRDIDQWNRTEPSEIMPHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVRPK TIKTLEENLGITIQDIGMGKDFMSKTPKAMATKPKIDKWDLMKLKSF CTAKETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQIYKKKT NPIKKWAKDMNRHFSKEDIYAAKHKMKCPSLAIREMQUIKTMRHY LPPVRMAIIKKSGNNRCWRGCGEIGTLLHCWRDCKLVQPLRKTW
3242	A	3	1945	NYPDQHFPPIFHGIKEKSPRTGSWLIETSERPFKTSQCQDPVYPSC HYSQSSLFMDPGYNEPPEIAPVNEAVGIQIRGPGAASCARFCEQLAT ACRMLEFLARAIRQEKEIKGIQLGKBEVKLSLFPDDMVVYLENPIIL AQNLLKLISNFSKVSQYKINVOQNSQAFLYTNNRQTDQIISELPFAI ASKRIKYLGIQLTRDVKNLKFENYKPKQLSEIKEDTKKWKNIPCLWVE RIYIVKTAIQAKVIYRFNAIPKIPMTFFTELEKTTLNFIQNRKRAR ITKSILSQKKKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNR TEPSEITPHIYNYLIFDKPEKNKQWGKDSLFNKCYWENWLAICRKLK LDPFLTPYTKINSRWIKELNVRPKTIKTLEENLGITFQDIGMGKDFMS KTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTKWEKIFATY SSDKGLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAK HMKKCSPLAIREMQTKTMRYLTPVRMAIIKKSGNNSLITIREY YKHLIYANKLENLEEMDKFLDITYTLPLKSEEEVESDMLSFYTTGSKD CSPNFDTKNALLMYTPVKTRTKIQLQIRTLHKALTV
3243	A	1	2124	MAQELRDECTSLSSRFDQLEERVSEMEDHMNEMKREEKFRKKGIKRN EQSLQEIWDYVVKRPNRLRIGVPETQNLKLISNFSKVSQYKINVOQS QAFLYTNNRQTESQIISELPFTIASKRIYLGQILTRDVKDLFKENY KPLLNEIKEDTHKWKNIPCSWIGRINIVKMAILPKVIYRFNAMPKIL PLTFFTELEKTTTLKFIWNQKRARIAKSILSQKNKTGGITLPDFKLYY KATVTKAAWYWYQNRDIDQWNRIEPSBIIPHIYNYLIFDKPEKNKKW GKDSLFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLHARSKT IKTLEENLGNTIQDIGIGKDFMSKTPKAMATKAKIDKWDLIKLSFC TAKETTIRVNRQPKWEKIFAIYSSDKRLISRIYEEIKQIYKKKTNN PINKWAKDMNRHFSKEDIYAAKHKMKCSSSLVIREMQUIKTMRHYL TPVRMVIKKSGNNRSLFHVIPKTCELGSLPRLAHEGHLQVTRGVQK WGHQLEFGPRVWIPKQESCSMALFCYAAEGLYFGSKGSQGDKLCCG GTFARFNILQEDDLSLRVVRLEDKERGSGENGHTYNTCELKQLIFI MKKSTKDGAAWPLPHAGSCRCKGRTTANGTEKVPACIIQEPEDRPAP PTTATASACGHCLGPEDKPVSPIIKATCTQACHPGICLLQPALHTI GEA
3244	A	1	2250	MGEFLDHTTLARLNQEEIESLNRPIITGSEIVAIINTLPTKKSPPGPDG FTAKFYQSRAETQPKKNFRPISLMNIDAKILNKILANQIQOHKKLI

				HHQVGFIPGMQGWFNICKSINVIQHINRTKDKNHMISIDAFAFD KIQQPFMLKTLNKLGTDTYLKIIRAIYDKPTANIILNGQKLEAFPL KTGTQGCPLSPLLFNIMLEVLARASQEKEIKGIQLGKEEVKLSLF ADDMIVYLDNPVVSQAQNLKLI SNFSKVSQKINVOQSQAFLYTNNR QTESQIMRELFFTIAASKRIKYLGIQLTRDVKDLFKENYEPLLEIKE DTNKWKNVPCSWVGRINIVKMAIVPKVIYRFNVIPIILLPMTFFTELE KTLKFIWNQKRARIAKSILSQKNKAGGITLPDFKLYYKATVTKTAW YWYQNRDIYQWNRTQPSSEITPHIYTYLIFDKPEKNKQWGKDSL FNKW CWENWLAICRKLKLDPLTPYTKINSRWIKDLNVPKTIKTLEENLG ITIQDIGMGQDFMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLISRMYNELKQIYKKKTNNSIKKWAKDM NRHFSKEDIYAAKHKMKCSPSLAIREMQIKTTMRYHLTPVRMVIK KSGNNSLGDKARPCPKKRKEKMFVTGTSLEEKAEGRISVSLV KEYLKVSKILPALEYWTPSSSVLELGLALLAPQPADGRLWDLVIL
3245	A	2	2483	GKYYKLSSGTAPTCSVLGWLARGDSAAPALGSRTSACAPCSHG TWK LSLEPSDRLSPCDRSSEEAHTHAPHRLLALVASLPWSRLPLLAPQSH SEAEATSQPTGVENHHQKTRYVKAGGPVICRSLPESRGFLWASEGRK CMLIGSWAAMGRLRKSTISSRFGPQTLAGTGRPQAI PVLKXHSDAVL LGVCFLKLLHQHHELGELGENADSQTLPQTHWEFILSEYDNKMPVKYQ QVLEVLARAMRQEKQIKSIQLGKEEVKLSVFADDMIVYLENPIVSAQ NLLKLI SNFSKVSQKINVOQSQAFLYTNNRQTESQI ISELPTIPS KRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNI PCSWVGRI NIMKMAILPRVIYIFNAISIKLPMTFFTELEKTTLKFIWNQKRARIA KTLISQKNKAGGITLPDFKLYYKATVTKTAWYWYQNRGVDQWNRIEP SEIIPHIHNLIFDKPDKNKKWGKDSLFTKWCWENWLAICRKLKLDP FLTPYTKINSTWIKDLNVRPKTIKTLEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTWEKIFTIYPS DKGLIPRIYKELQ\IYKKKSNNPIKKWAKDINRHFSKEDIYAA NRH MKKCSSSLVIREMQNKITIR/YHLTPVRMAI IKKSGNNRDMDEAGNH HSEQTIARTENQAPYLLTHRWE LNNTWTQVEEHHTLGPIVGVICR KVFPNGSGPSKPSGLHFSQPLPQVTSVVAKITIVPWEMKLIAMGVQD ELNIAFHKNHLLMNDTTIHMTPIYIOPAPKS
3246	A	1	2622	MDKFLDITYTLPRNLQEEVECLNRPITGABIVAI INSLPTKKSPPGPDG FTAIFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEASII LIPKPGR DTTKKENFRPISLMNIDAKILNKILADRIQQHIKLIHHDQVGFIPG MQGLEFNIRKSINVIQHINRAKDKNHMNISIDAFAFDKIQQHFM LKT LNKLADKHFSKVSQKINVOQSQAFLYPNNRQTESQIMSELFFTAS KRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRI NIVKMAILPKVIYRFNAILIKLPMPFFTELEKTTLKFIWNQKRARIT KSILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNRTPE SEIMPHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLN FLTPYTKINSRWIKDLNVRPKTIKTLEENLGITIQDIGMGKDFMSKT PKAMATKDKIDKWDLIKLSFCTAKETTIRVNRQPTKWEKIFATYSS DKGLMSRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKM KKCSPSLAIREMQIKTTMRYHLTPVRMAI IKKSGNNSKLPFEP SRNK RVMPEPCAHTILSSSLARPASKMHSPLSMEPSAGPGGSQNFPEEAB DRPRTLNFEGSETWALTGPDARYFNYTREARGENSLVSGGCRPLAAG RARASTSGWAAKRVGT LQGGPLTWAMPAPISPPMTVTCLTI IFLAE AEA VDEEDTERMNCLVT KAMVWQRRRQRGDPGREDARGGQPRKARLW GRGPTRPCSPRAPGVVTPQGGGGASSPALPIGP GCNVPALSGYTRA GSQLSAAGARVSAGLRPAEQDLAAGVL
3247	A	853	2831	YPESTMNSNKFTRKKQTTPSKSG*RI*TDTSQKKTFMQPKDT*KNAQ HHWSLEKCKSKPQ*DTISHQLEWRSLSQDRKD*QSTLLAILIKKKG QKNQIDT/IKNDKEGITTDPREIQTITREYKHYLTNKVENLEEMDK FLDITYTLPTLKQKKEVKTLNRPITGSEIEAI INSLPT/KKSPGPD RF TAEFY\R/DIRSSGQGNQARERNKGYSIRKRGSIQVPVCR*HHCIFR

				KPHHLSPKSS*ADKQLQQSLRIQNQSAKITSIPHIHQ*QTNREPNEH* TPIHNCFKENKMPRNPTYKGCESLQGELOTTAQ*NKRGHKRMEEHS MLMDRKNQYRENGHTAQGNL*IQCHPHQATNDFHHRIGKNYFKVHME PKKSPHRQVNPKEQSWRHHTT*LQTILOQYSNQNSMVLVVPKQRHR PMEQNRAPGNNTIHLQLSDL*QI*QKQEMGKGFP**MVLGKLANHM *KAETGSLPHILYKN*FKMD*RLKC*T*NHKNPRKPRQYHSGHRHG QGLHD*NTKSNNGNKSQN*OMGSN*TKELLHSTRNYHQSEQATYRMGE NFCNLLI*QRANIQNLOQT*TNLQDKNKQPHQKVGKGYEQTLKRRH LCSQKTHEKMLIITGHQRNANQNHNEIPSHTS*NGDH/SNQVRKQQV LERMWRN
3248	A	1	4954	MVFSIDAQKAFDKIQHRFMLKTLNKLIGIDGYLKIIRAIYNKPTGNI ILNGQKLEAFPLKTGTRQGCPLSPLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDIIVYLENPIVSAQNLLKLIGNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKNLFK ENYKPLLNEIKEDTDKWKNI PCSWIGRIHIVKMATLPKVIYRLHAIH IKLPMTFFTELEKTTLKFIWNKKRARIKSI LSQKNKGGGITPPDFK LYYKATVTKTARYWYQNRDIDQWKTREPSEIIPHIYNHLIFDKPDKN KKWGKDSL FNKWCWENWLAICRKLKLPFLTPTTKINSRWIKDLNIR PKTIKTLEENLGNTIQDKGVGKDFMSQTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQPTWEKIFAIYSSDKGLISRIYKELKQIDKKK ANPNINKWAKDMNRHFSKEDIYAANRHMKKSSSSLAIREMQIKTTMR YHLTPVRMVIKKSNNSEGLNPGYKGFPTI IAPLPVAQSKDSGLA SLNSDPDIPSMLECSLKAPQLYRSKNVGQVFI ISSASQAFTKKARIY ARLRVSQALKTLCKSSCHDGWSFERLARIQEVSLPISPDILCSEAY HYGTPQWLVAATGTAQTFLELNQKSQQYQKQEQTHSKASRMQEITK IRAEKIEIETRTLQKIDESRSWFFERINKTDRPLARLTQKREKNQ IDAIKNGKGDITDPTGIQITIREYYKHLYAKKLENLEEMDKFLDTY TLPRLNQEEVDSLNRPTGAEIVAI INSLPTKSPGPDGFTAIFYQR HKEELVPFLLKLFQSI EKEGILPNSFYEASII LIPKGRDTTKKENL RPISLMNIDAKILSKILANRIQQHIKKLIHHDQVCFIPGMQGWENIR KSINVIQHINRAKDKNHMI ISIDAQKAFDKIQOTFMLKTLNKLIGIDG TYFKIIRAIYEKPTANI ILNGQKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVKLSLFADDIIVYLENPIVSAQNL LKLISNFSKVSQYKIYKIDVQKSQAFLYTNNRQTESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFK\ ENHKPLLNEIKEDTNKWKNI FIPCL WVGRINIVKMAILPKGIYRENAIPIKLPMTFFTELEK\ TTLKFIWNQ KRARITKSILSQQKNKAGGITLPDFKLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNKKWGKHS LFNKCWESWLDICR KLKLDPTYKFTPTTKINSRWIKGLNVRPKTIKTLEDKPIQVFNTIQD IGMGKDFMSKTPKAMATKAKIDKWDLIKLSFCTGKETTIRVNRQPT EWEKIFAIYSSDKELISRIYKELKQIYKKK\ TNNPIKKWAKDMNRHF SKEDIYAANKHMKK\ CSSSLAIREMQIQTMMRYHLTPVRMAI\ IKKS GNNRCWRGCGEVGTLLHCWDCNLVQPLWKS VWRFLRDLELEIPFDP AIPLLG IYPKDYKSCCYKDTCTRMFIVALFTIAKTWNQPKCPTMMDW IKMWHIYTM EYAAIKNDEFMSFVGTWMKLEII ILSKLSQEQKTKH RIFSLIGGN
3249	A	25	527	EFHRLRENPPMAVASCPTKTNVKA\AWG\KVGAAVSRMCAEALERM FLSFPT\TKTYPPHFDL\SHG\SAQVKGATGKKVADALTNANVANV\D DMPNVAVRPEATLHAHKL RVPV\NF\KLLKPLACLVDPGPAHLPRP SFTPGGATSSLGQSFLGFLKHKRCLNLPNYR
3250	A	97	1360	SACAWRLPSPGPSAMWPLWRLVSL LALSQALPFEQRGFWDFTLDDGP FMMNDEEASGADTSGVLHPDSVTPT\YSAMCPFGCHCHLRVVQ\CS LGLKSVPEISPDTTLLDLQNNDISELRKDDFKGLQHLYALVLV\NN KISKIHEKAFSPLRKLQKLYISKHNLVEIPP NLP\SSLV\ELRIHDN RIRKVPKGVFSGLRNMNCIE\MGGNPLENSGF\EPGAFDGLKLN YLR ISEAKLTGIPKDLPETLNLHLDHNKIQAIELEDLLRYSKLYRLGLG

				HN\QIRMIENG\SLSFLPTLREV\HL\DNNKLARVPSGFP\DLKLLQ VV/YILHSNNIHQSGVFNFLFPWGFGEAGPYYNH/ISLFNNPVP YWEVQ\PATFR\VVTDRLAIQFGQLQKVEAAAATLVSQWGS LGNRAR HPDGEAEPGS
3251	A	1	2535	MAERGQCTAQAVASEGGRSKPWQLLRGIEPAGAOKSRIEVWEPLPRF QKMDAQAIVLLQGGQTHGEPLAASYPSSGQIQRRYQGLALRTLGI FL SFYSTAAELTPKPKDKLLILLSRFLKQRNLSWPPLPQACSKYCKA VADIHSRSGSLVSLWSMLIGLISLQGNGLPSGPEIKRVKLISNKG TETDNDPSCVHPIIKRRQCRPEIRMWQTREKAKFSDGEKCRREAFRR LGNGVSDDLSEEDGEARTQMILLRRSVEGASSDNGCEVKNRKSILS RHLNSQVKKTTTRWCHIVRDSDSLAESEFESA AFSQGSRSVSGGSR SLNMSRRDSESTRHDETEDMLWDDLLHGPECRSSVTSDEGAHVNT LHSGTKRDPKEDVFQQNHLFWLQNSSPSSDRVSAI I WEGNECKMDM SVLEISGIIMSRRFLFAKLFSHITSARKARKYEIPHFRLKKVENIKI WLSLRSYLKSMCKNMLTEAPGSSYSVDSVVLGVRQIIAAADRLAGQQ VGCHLSAKLVGVGHEDQVPGGDLPLLCASRTRFKAFVTIEDYNGYVG LGVSAAPRRGVGTVLAPVPRNLLLMVVTHHCCTLTGDCAAATLANFAKG TFDAISKTSYFTPNLCCGKLNHKLKCLDSPLAGIKTYLSRKVMTA ETSEIPTCLFTCTGALSSAKANEWCFRRSKSFSNWVGDI VEINGEP TQGITHTRAELIQAGGNKVL LLLRP GTGLIPDHVIAIVLYLMPIV NISEVLGPLCLMLLMGTVHCQIVSTQITRPSGNNGNRRRRKLKRTVN GDGSRNGNNSDKVRGIETLESVPIIGGFWETIFGNSICYRLSPA
3252	A	5	2333	NPILWLETQMASNERDAISWYQKKIGAYDQQIWEKSIEQTQIKGLKN KPKKMGHIKPDLDIDVLRGSTFAKAKPEIPWTSLTRKGLVRVFFP LFSNWWIQVTS LRIFVWLLLYFMQVIAIVLYLMPIVNISEVLGPL CLMLLMGTVHCQIVSTQITRPSGNNGNRRRRKLKRTVNGDGSRENGN NSSDKVRGIETLESVPIIGGFWETIFGNRIKRVKLISNKG TETDNDP SCVHPIIKRRQCRPEIRMCQTREKPKFSDGEKCRREAFRR LGNGVSD DLSSEEDGEARTQMILLRRSVEGASSDNGCEVKNRKSILSRHLNSQV KKTTRWCHIVRDSDSLAESEFESA AFSQGSRSVSGGSRSLNMSRR DSESTRHDETEDMLWDDLLHGPECRSSVTSDEGAHVNTLHSGTKR DPKEDVFQQNHLFWLQNSSPSSDRVSAI I WEGNECKMDMSVLEISG IIMS RVNAYQQGVGYQMLGNVVTIGLAFFPFLHRLFREKSLD\QLKS ISAEILTLCGAPPVTPPIIVLSIINFFERLCLTWMFFFMCMCV\AER TYK\QRFLFAKLFSHIYFCQGLGKYEIPHFRLKKVENIKIWLSLRS YLKRRGPQRSVDVV\VSSVLLTSLIAFICCAQVLQG\HKT\SWNDA Y\NWGVFDLGETALLFLRLASLGSETNKKYSNVSILLTEQINLYL KMEKKPNKKEQLTLVNNVLKLS TKLLKELDTPFRL\YGLTMNPLIYN ITRVVILSAVSGVISDLLGFNIRLWKIKS
3253	B	73	358	XVPGSRGPETKLWDDFSMSQATKRKHVVKEVLGEHIVPSDQQQIVRV LRTPGNNLHEVETAQGGQRFVSMPSKYRKNIWIKRGDFLIVDPIIEG EK*
3254	A	80	201	TSEPMFLTKTPCHPSVKGPSSEQSWVLSLPSKELRRRS
3255	A	498	748	FLPRRGDNDSSYPQ/WTKACRRRRRTCW*T*TWIRSGQRKMWSCGRR SLTTCMPMRTRTAARLMACGSGSWRRSGPSCGRLSP
3256	A	1	1764	MTTSQKHRDFVAEPMGEKPVGSLAGIGEV LGKKLEERGFDKAYVVLG QFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLRE/WCAKSRPAAB VSELKADSKEGPQAQGPQERTGL
3257	A	842	1186	FLPRRGDNDSSYPQ/WTKACRRRRRTCW*T*TWIRSGQRKMWSCGRR SLTTCMPMRTRAWTTWRSKNLALSCPSMTKSLKSGSHIPSAWSRAAR LMACGSGSWRRSGPSCGRLSP
3258	A	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGEKPVGSLAGIGEV LGKKLEERGFDKGL /YVVLGQFLADIEKMKTSFREWLKDTCGANAK\QSRDCFRMPF EKWCEALLVDALLGKFSIPPAPQSRSLASRSDSSPCPSYEGKD\CY C\RTHL\RRYFRGSFGEFSPLNHFQLFFGILRSWHAFFRPFFFPWVVS WVTVYQLFLEWDFPGPIPHPHPHFQSV

3259	A	35	407	TFMFVFLSSAGNMPVTCWCWEAPRCNQKCTDPAARRPDPQTCASQDR LRCAPCTCHQPLASRYTPPPACPPSHVSLHTLATSLQHFLNKNYKNY IAKMCKLSILSLSFLKEGAGDKNSSEPNLG
3260	A	3859	4052	ASCPNPKEFAPPRAGPPWFPGPPLARVNPG\LGGPFSGTRPTPPQPL PEQRVTLTSTNPWLAASV
3261	A	493	712	AHGRQLRKYSQQQGCWSRLPFCGCHAVSGGGCGKCC\SPANGPCGAA \CLGFQPHNFPDPCETC/CGCHAVSGGGCGKCCISSKWSLWCSPAWV SSHSTSRIPVKLAGLPSPLPG
3262	A	51	541	MGSLSLNLPFVVTVLLMCLSRSRKGDASQFLVFCQKHRDEVVAEHP DASGEEIEELLRSQWSLLSEKQRRARYNTKFALVAPVQAEEDSGNVNG KKRNHTKRIQDPTEDAEADTPRKRLRTDKHSLRKRDTITDKTARTS SYKAMEAASSLKSQAATKNLSD
3263	A	742	4858	ERKHLGWMEFSIKQSPLSVQSVVKCIKMKQAPEILGSANGKTPSCEV NRECSVFLSKAQLSSSLQEGVMQKFNGHDALPFI PADKLKDLTSRVF NGEPGAHDAKLRFESQEMKGIGTPPNTTPIKNGSPEIKLKITKTYMN GKPLFESSICGDSAADVSQSEENGQKPKENKARRNRKRSIKYDSLLEQ GLVEAALVSKI SSPSDKKIPAKKESCPNTGRDKDHLKYNVGDVWS KVS GYPWWPCMVSAADPLLHSYTKLKGQKKSARQYHVQFFGDAPERAW IFEKSLVAFEGEGQFEKLCQESAKQAPTAEKIKLLKPI SGKLAQW EMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAES LGEMAESSGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESH DIGKSTPQKTAADPRRGVGSPPGRKKT TVSMPSRKGDAASQFLV CQKHRDEVVAEHPDASGEEIEELLRSQWSLLSEKQRRARYNTKFALV PVQAEEDSGNVNGKKRNHTKRIQDPTEDAEADTPRKRLRTDKHSLR KRDTITDKTARTSSYKAMEAASSLKSQAATKNLSDACKPLKKNRAS TAASSALGFSKSSPSASLTENEVSDSPGDEPSES PYESADETQTEV SVSSKKSERGVTAKKEYVCQLCEKPGSLLLCEGPCCGAFHLACLGLS RRPEGRFTCSECA SGIHSCFVCKESKTDVKRCVVTTQCGKFYHEACVK KYPLTVFESRGFRCP LHSVCVSHASNPSNPRPSKGKMMRCVRCVAY HSGDACLAAGCSVIASNSI ICTAHFTARKGKRHHAHVNVSWCFVCSK GGSLCCESC PAAFHPDCLNIEMPDGSWFCND CRAGKKLHFQDI IWV KLGNYRWWPAEVCHPKNVPPNIQKMKHEIGEFFVFFFGSKDYWTHQ ARVFPYMEGDRGSRYQGV RGIGRVFKNALQEAARFREIKLQREARE TQESERKPPPYKHIVKNKPYGKVQIYTADISEIPKCNCKPTDENPCG FDSECLNRMLMFECHPQVCPAGEFCQNCQFTKRQYPETKIIKTGKG WGLVAKRDIRKGEFVNEYVGELIDEEECMARIKHAHENDITHFYMLT IDKDRIIDAGPKGNYSRFMNHSCQPNCE TLKWTVNGDTRVGLFAVCD IPAGTELTFNYNLDCLGNEKTVCRGASNC SGFLGDRPKTSTTSLSE EKGKKTXXXTRRRRAKGEGRQSEDECFRCGDDGGLVLC DRKFCTKA YHLSCLGLGKRPFGKWECPWHHCDVCGKPSTSPCHLCPNSFCKEHQD GTAFSCTPDGRSYCCEHDLGAASVRSTKTEKPPPEPGPKPGKRRRRR GWRRVTEGK
3264	A	2	658	AFLRMLFPESWMETR RGAPAPPAPRSETSHDLVATLMRCTPHYIR*S NPTRPRGPETGRRTA*TRSPQVPHLQHLPPTPRLVTPHPEGTQPTLP TRSSTRWNTWA*RTSGCESRLRLPPPVRQIPAEYAILTPETWPRWR GDEPRAS9TCFGRSTWSPTRPDGEHQGLCQEPRVAFPPGGGAKRKFD GFARTIQAWRRTWLSGSTRRCGRKLPTSC
3265	A	1	4095	MEFSIKQSPLSVQSVVKCIKMKQAPEILGSANGKTPSCEVNRECSVF LSKAQLSSSLQEGVMQKFNGHDALPFI PADKLKDLTSRVFNGEPGA DAKLRFESQEMKGIGTPPNTTPIKNGSPEIKLKITKTYMNGKPLFES SICGDSAADVSQSEENGQKPKENKARRNRKRSIKYDSLLEQGLVEAAL VSKI SSPSDKKIPAKKESCPNTGRDKDHLKYNVGDVWSKVS GYPW WPCMVSAADPLLHSYTKLKGQKKSARQYHVQFFGDAPERAWIFEKSLV AFEGEGQFEKLCQESAKQAPTAEKIKLLKPI SGKLAQWEMGIVQA EEAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAESLGEMAES SGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESHPDIGKSTP

				QKTAEDPRRGVGSPPGRKKT TVSMPSRKGDAASQFLVFCQKHRDE VVAEHPDASGEEIEELLRSQWSLLSEKQRRARYNTKFALVAPVQAEED SGNVNGKRRNHTKRIQDPTEDAEABDTPRKRLRTDKHSLRKRDTITD KTARTSSYKAMEAASSLKSQAATKNLSADACKPLKRRNRSTAASSAL GFSKSSSPSASLTENEVS DSPGDEPSES PYESADETQTEVSVSSKKS ERGVTAKKEYVCQLCEKPGSLLLCEGPCCGAFHLACLGLRSRRPEGRF TCSECASGIHSCFVCKESKTDVKRCVVTVQCGKFYHEACVKKYPLTVF ESRGFRCLHSCVSCHASNPSPRPSKGKMMRCVRCVPAYHSGDACL AAGCSVIASNSIICTAHFTARKGKRHHAVNVSWCFVCSKGGSLCC ESCPAAFHPDCLNIEMPDGSGWFCNDCRAGKKLHFQDIWVKLGNRYR WPAEVCHPKNVPPNIQMKHEIGEFPPVFFGSKDYEWARTQARVFPYM EGDGRSRYQGVGRIGRVFKNALQEAABARFREIKLQREYHREBTQESERK PPPYKHIVKNKPYGKVQIYTADISEIPKCNCKPTDENPCGFDSECLN RMLMFECHPQVCPAGEFCQNCQFTKRQYPETKIIKTGKGWGLVAKR DIRKGEFVNEYVVELIDEEECMARIKHAHENDITHFYMLTIDKDRII DAGPKGNYSRFRMNHSCQPNCE TLKWTVNGDTRVGLFAVCDIPAGTEL TFNYNLDC LGNEKTVCRCGASNC SGFLGDRPKTSTTSSSEEKGKTK KKTRRRRAKGEGKRQSEDEC FRCDGGQLVLCDRKFCTKAYHLSCLGL LGKRPFGKWECPWHHCDVCGKPSTSFCHLCPNSFCKEHQDGTAFSCT PDGRSYCCEHDLGAASVRSTKTEKPPPEPGPKGKRRRRRGWRRVTE GK
3266	A	26	173	RDTITDKTARTSSYKAMEAASSLKSQAGNVVSALSFLASGCPGWAGW VG
3267	A	387	1443	PHRKQAEPPRHHERLGRVRHHRHARGRSRPDTAAEAAGCGDPRAF QQLERRLRHPPLRWQGLLRQRLREEPRRSLLRPHRADAVQ*PGLP PDALPREAGWRQEGAPQHRLQDYETCQLTWWPH**GAHPTTSAALN PTRPRGPETGRRTESSTRWNTWA*RTSGCAEPASPTA/SQFAKFLQ RYAILTPETWPRWRGDERHGVQHLLRAVNMEPDQYQMGSTKVFFVKNP /VVAFPFGGGARAKVRWLCPNHPEGLAAPRGCPVEVRGDA/RRKLPTS C*TRRSGGATASIGTSSGTTGWGRSGPSCVSSWARRSGWTSPIRSPS TTAASSPSSGT*S*RPSVCM*LGERR
3268	A	1	4496	MEGNVNAHRASGAQIRTCRAPPGATGCTALFKANSPEFTGLKSAQRG RGPVVGAPKRKFSGLRGHREAERTLGWGSQAPPPAAQAHTPAAGDS TLLLRSAVPGTCLLYAPHPQDFPPAGFLREQWWPRLLTLQVFLHLRT GGRVGPVDWVLLGGGRLLGGRMPGPCNLAEAVLLREARWPWGEAGG SEEGEPSSGSGVGCNCQRRPLPSAHPEAQQGVGLVGRGMVAPAASY FADEGRPNGDHPARQPRGLPLGAHGRRHLKSFDPDTGSLNLEEEQN NVQDILGELREKVGECEASAMLPLECCQYLNKNALTTLAGPLTPPVKH FQLKRKPKSATLRAELLQKWPCRSGVHANVHISTAAQRVMTKHLQRA DEHPHFCVEEWHSGLISAFYYCEKHLAENHILDRIIDAGPKGNYSRF MNHSCQPNCE TLKWTVNGDTRVGLFAVCDIPAGTELTFNYNLDC LGN EKTVCRCGASNC SGFLGDRPKTSTTSSSEEKGKTKKTRRRRAKGE KGRQSEDEC FRCDGGQLVLCDRKFCTKAYHLSCLGLGKRPSPDHIP LKNGFVASCLLFCGDCGLQTPAAPYCCTSGVLHLSTVDISGRIALLR GHPVRCRRCSSIHDRNPSES VVKCIKMKQAPEILGSANGKTPSCEVN RECSVFLSKAQLSSSLQEGVMQKFNGHDALPFI PADKLKDLTSRVFN GEPGAHDAKLR FESQEMKIGITPPNTTPIKNGSPEIKLKITKTYMNG KPLFESSICGDSAADVQSSENGQKPENKARRNRKRSIKYDSLLEQG LVEAALVSKISSPSDKKIPAKKESCPNTGRDKDHLKLYNVGDVLVWSK VSGYPWWPCMV SADPLLSYTKLKGQKKSARQYHV\RFFVYAPERAW IFEKSLVAFEGEGQFEKLCQESAKQAPTAKAEIKLLKPI SGKLRQW EMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAES LGEMAESS*VSEEAENPKSVREECIPMKRRRRRAKLCSAETLESHP DIGKSTPQKTAEDPRRGVGSPPGRKKT TVSMPSRKGDAASQFLVFCQKHRDE VVAEHPDASGEEIEELLRSQWSLLSEKQRRARYNTKFALVAPVQAEEDSA

				PLKGIPKQAPFRSPTAPSVFSPTGNRTPIPPSRTLLRKERGKAGLC LSWQLLDISELDMVGAGREARRRKTLDAEVVEKPAKEETVVENATP DYAAGLVSTQKLGSLNNEPALPSTSYLPSTPSVVPASSYIPSSSTPP APSSREASRPPEEPSAPSPTLPAQFKQAPMYNSGLSPATPTPAAPT SPLTPTTPPAVAPTTQTTPVAMVAPQTQAPAQQPKNLSLTREQMF AAQEMFKTANKVTRPEKALILGFMAGSRENPCQEQQDVIQIKLSEHT EDLPKADGQGSTTMLVDTVFEMNYATGQWTRFKKYKPMTNVS
3269	A	911	2827	ERKHLGWMEFSIKQSPLSVQSVVKCIKMKQAPETIL\GSANGKTPSCE VNRECSVFLSKAQLSSSLQEGVMQKFNGHDALPFI PADKLDLTSRV FNGEPGAHDAKLRFESQEMKIGITPPNTPPIKNGSPEIKLKITKTYM NGKPLFESSICGDSAADVSQSEENGQKPKENKARRNRKRSIKYDSLLE QGLVEAALVSKISSPSDKKI PAKKESCPNTGRDKDHLLKYNVGDVW SKVSGYPWWPCMVADPLLHSYTKLKGQKKSARQYHVQFFGDAPERA WIFEKSLVAFEGEGQFEKLCQESAKQAPTAKKIKLLKPI SGKLRQA WEMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAE SLGEMAESSGVSEEAENPKSVREECIPMKRRRRRAKLCSSAETLESH PDIGKSTPQKTAEADP\RRRGVGSPP\GRKKTT\VSMPSRSGDAAS QFLVFCQKHRDEVVAEHPDASGEEIEELLRSQWSLLSEKQRARYNTK FALVAPVQAEEDSGNVNGKKRNHTKRIQDPSENA\DLEDTPRKGLRT DKHSLRKRDTITDKTARTSSYKAMEAASSLKSQAATKNLSADCKPLK KRNASTAASSALGFSKSSSPSASLTENEVK
3270	A	3	114	SCSGDMAGVKALVALSFSGAIGLTFMLGCALEDYG
3271	A	328	471	GFNPSFLVFQIKGGACAVVLAGNAVIFLTIQGFLLIFGRGDDFSWEQ W
3272	A	1	190	GTSRSGLGRLPGPWQEGSSRGPSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGCTSLK
3273	A	2	479	SGLGRLPGPWQEGSSRGPSSGDMAGVKALVALSFSGAIGLTF/LHM LGCALEDYG VYWPFLVL\FFHAI SPHPFI AKRVTYDS DAT\SSACR ELAYFFTGTIVVSLWISPVILARVALIK\WGAC\AFVL\AGNAVIF PYNRSGFSLYLGRGDDFSW\EQW
3274	A	3	586	ARAMGISRDNLHKRRKTGGKRKPYHKRRKYELGRPAANT\KIGPRRI HTVRVRGGNKKYRALRLDVGNFSWGSECCTRKTRI IDIVYNASNNEL VRTKTLVKNCIVLIDSTPYRQ/WTPEEEBILNKKRSKKIQKKYDERK KNAKISSLLEEQFQGGKLLACIASRPGQCGRADGYVLEGKELEF\YL RKIKARKGK
3275	A	2	727	LFPASAEQMGISRDNW\HKP\RKTGGPRESFYQAEAKMSMLGRPAA\ NTKILAPRRIQHSPVCRGG*QVNTVPLRFD\VGNFWSG/SKECCTRK TR\IIDVVYNAI**PSWVRYPRPLVERICI\VLIDEQHPY\RQWVRS PTYAL\PLGPQRKGAKLDSL RKEEIFKPKTDLK*IQKKYD*/ERKKV CQNSASLPGRSSFQGGKASLRCAFK/RPGQC\GRA\GYMTRGHRV RSYYLRKIKARQSKINT
3276	B	48	209	XKNQCETRTMQENGYSSHAVDGTGPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX*
3277	A	2	353	GYRAGIPGSSWLREKKAALSMFKSVLAPATDGGLNLSSTFLRKNQCE TRTMLLQPAAGSLGSYSYRSPREWGLHRPPGPSLGATLAGTTLGQPPA AEIHVGVDGDCPTSVRGKGQAWA
3278	A	3	676	SAVEFPPLSHTTGTTRPTPILLQQENGYFIHTLWMGLALLGVLGDL SGQHRRRPRSPCQPNFQDKFLGRWFKRG\LASNSSWLREKKAALSMC KSVVAPAT\DGG\FNLSTFLQEKTSVETRTML\LQPRGVPSASLQL TGVPHWQA/HYSVSVVETDYDQYALLY\TRASKGPGEDFRMATLYS RTQTP\RAELKEKFTAFCKAQGFEDTIVFLPQTDKCMTEQ
3279	A	154	522	HVACGLLWIVVSPSAHLNLDGTITTK/ENLGTVNEILLGSNPTEAEL QDMINEVMSDNGTIDFP\EFLTMMARKMK\DTDSEGRKL\EEAF\R VFGLRVGNGLYLVACRNFRHVDGQTLGGGSLPD
3280	A	1	1446	MELEQLMTLISAAREYEIEFIYAISPGLDITFSNPKEVSTLKRKLDQ TLTSSHLNIPKRM SVKGGGDFKQGDQEDLVDNFGSEHTPSGPSLGN

				SGTGCSWPWASAEESEKEVRGMATGTARNQKWLGVDRDCASPLMGGAGTG RGSPALCVSGAEFEEGSYSMAAGCELSGHTRSFTFKVEEEDDAEHVL ALTMLCLTEGAKDECNVVEVARNHDHQEIAVPVANLKLSCQPMLSL DDFQLQPPVTFRLKSGSGPVRITGRHQIGHPPGPTKKALKQRFLKLL PCCGPQALPSVSESKCLSCASGGGARC VHSVDDEFELSTVCHRPEGL EQLQEQTKFTRKELQVLYRGFKNECPSGIVNEENFKQIYSQFFLKED FVAGLSVILRGTVDDRNLNWFNLYDLNKGDCITKEEMLDIMKSIYDM MGKYTPALREEAPREHVESFFQKMDRNDKGVVTIEEFIESCQKDEN IMRSMQLFDNVI
3281	A	774	3564	VLSKGNERSQPRSPRLRLAPQLKAEAAADKGLAPVPPPFSSGHSGPC \ERELEGQRGRGRSRRGAHLELKPSPLRAGAPTDRGRGGPAEVA GGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAGEDNPA GAGGA AVAGAAGGARRFLCGVVEEQLMTLISAAREYEIEFIYAI SPGLDITFSNPKEVSTLKRKLDQVSQFGCRSFALLFDDIDHNMCAADKEV FSSFAHAQVSI TNEIYQYLGE PETFLFCPT EYCGTF CYPNVQS SPYLRTVGEKLLPGIEVLWTGPKVVSKEIPVESIEEVSKIIKRAPVI WDNTHANDYDQKRLFLGPYKGRSTELI PRLKGVLTNPNCFEFANYV AIHTLATWYKSNMNGVRKDVMTDSEDSTVSIQIKLENEGSDEDIETD VLYSPQMALKLALTEWLQEFVPHQYSSRQVAHSGAKASVVDGTPLVA APSLNATTVVTTVYQEPIMSQGAALSGETTLTKEEEKKQPDDEEPM DMVVEKQEETDHKNDNQILSEIVEAKMAEELKPMDDTKESIAESKSP EMSMQEDCISDIAPMQTDEQTNKEQFVPGPNEKPLYTAEPVTLEDLQ LLADLFYLPYEHGPKGAQMLREFQWLRANSSVSVNCKGKDSEKIEE WRSRAAKFEEMCGLVMGMFTRLSNCA NR TILYDMYSYVWDIKS IMSMVKSFVQWLEDEDGICGYALGTVDVTPFIKKCKISWIPFMQEKY TKPNGDKE LSEAEDCASPLMGGAGTGRGSPALCVSGAEFEEGSY SMAAGCELSGHTRSFTFKVEEEDDAEHLAL TMLCLTEGAKDECNV VEVARNHDHQEIAVPVANLKLSCQPMLSLDDFQLQPPVTFRLKSGS GPVRITGRHQIVTMSNDVSEEESEEEEDSDEEBVELCPILPAKKQGG RP
3282	A	51	672	VLSKGNERSQPRSPRLRLAPQLKAEAAADKGLAPVPPPFSSGHSGPC \ERELEGQRGRGRSRRGAHLELKPSPLRAGAPTDRGRGGPAEVA GGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAGEDNPA GAGGA AVAGAAGGARRFLCGVVEEQLMTLISAAREYEIEFIYAI SPGLDITFSNPKEVSTLKRKLDQ
3283	B	506	2416	MNPSAPSYPMASLYVGD LHPDVTEAMLYEKFS PAGPILSIRVCR DMI TRRS LGYAYVNFQQPADAERALDTMNF DVIKGPVRIMWSQR DPSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDE NGSKGYGFVHFETQEA AERAIEKMNGMLLNDRKVFVGRFKSRKE RAELGARAKEFTNVYIKNFGEDMDDERLKDLFGKFGPALSVKVM TDES GSKSGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGR AQKKVERQTELKRKF EQMKQDRITRYQGVNLYVKNLDDGIDDER LRKEFSPFGTITSAKVMMEGGRSKGFGFVCFSSPEEATKAVTE MNGRIVATKPLYVALAQRKEERQAHLTNQYMQRMASVRAVPNP VINPYQPAPPSGYFMAAI PQTONRAAYPPSQIAQLRPSPRWTA QGARPHPFQNMPGAIRPAAPRPPFSTMRPAS SQVPRVMSTQR VANTSTQTMGPRPAAAAAATPAVRTVPQYKYAGVRNPQQHLNA QPQVTMQQPAVHVQGQEPLTASMLASAPQE QKQMLGERLFLPI QAMHPTLAGKITGM LLEIDNSELHLMLESPE SLRSKVDEAV AVLQAHQAKEAAQKAVNSATGVPTV*
3284	A	183	3080	PRRCSTGNSGRPKIIRRAEAENEDRTLGRLLPGNERSQPRSPRLRL APQLKAEAAVDKGLARVPPPFSSGHSGPC\ERELEGQRGRGRSRR GAHLELKPFSGL\RAGAP\TDR\GRGGPAEVAAGGRRMVQKESQAT LEERESELSSNPAASAGASLEPPAAPAGEDNPAGAGGA AVAGAAG GAR RFLCGVVEGFYGRPWMEQRKELFRRLQKWELNTLYAPKDYK HRMFWREMSVEEAEQLMTLISAAREYEIEFIYAI SPGLDITFSNP KEVSTLKRKLDQVSQFGCRSFALLFDDIDHNMCAADKEV FSSFA HAQV\SI TNEIYQYLGE PETFLFCPT EYCGTF CYPNVQS SPYLRTVGEKLLPGI

				EVLWTGPKVVSKEIPVESIEEVSKI IKRAPVIWDNIHANDYDQKRLF LGPKYGRSTE\VIPRLKGVLTNPNCFEFANYVAIHTLATWYKSNMNG \VRKDVMTDSEDSTVSIQIKLENGSDEDIETDVLVSPQMALKLAL TEWLQEFQVPHQYSSRQVAHSGAKASVVDGTPLVAAPSLNATTVVTT VYQEPIMSQGAALSGETTTLTKEEEKQPDDEEPMVMVEKQETDHK NDNQILSEIVEAKMAELKPMDDTKESIAESKSPMSMQEDCISDIA PMQTDEQTNKEQFVPGNEKPLYTAEPVTLEDLQLLADLFYLPYEHG PKGAQMLREFQWLRANSSVSVNCKGKDSEKIEEWSRAAKFEEMCG LVMGMFTRLSNCA\GRILYDMYSYVWDIKSIMSVKSFVQWLGCRS HSSAQFLIGDQEPWAFRGG LAGEFQRLLPIDGANDLFFQPPPLTPTS KVYTIRPYFPKDEASVYKICREMYDDGVGLPFQSQPDLIGDKLVGGL LSLSLDYCFVLEDEDGICGYALGTVDVTPFIKKCKISWIPFMQEKYT KPNQDKELSEAEKIMLSFHEEQEVLPTFPFC
3285	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGAGAHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDL HAHKL RVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3286	A	26	526	NSTDSETHPWLLSPADKTTVK/APAWGKVGAGAHAGEYG\SEALERM LSFPTTKTYFPHFDLSHGFCPLRATGKKVADALT KRRGAPLDDMPN ALVRPL\SDLHAHL\RVGPGSTFKLLKPLACL\LTLPALHPRPSF TPGGCKASLGQSFLGFLKXRCLNLPNYR
3287	C	410	484	MRTGSAXXFXSXCXSGXGXQFXXS
3288	A	3	170	IRGSVVLSSLNFLNTFFTP*RSFISTSVMF*KPFIFSFLMLLL*VFI FSLKILSY
3289	A	831	1559	IAWAFKINWLPIIFLIFSVLFYPIFGFIFYLLYFSNTCLSLFFHFL SETLDNIFIFYLVSIQFSSKFVHFAISFMFSPSLSFFFCFILSRFKF IFFSSKKYVFIFLISLSF\IPF
3290	A	253	414	VRSLVISMTCKTAVSFLTSRVCSNRHGLIRKYGLNMCRQCFRQYAKD IGFIKLD
3291	A	3	225	CTAESKMGHQQLYWSHPRKFGQSRSCRVCNRRHGLIRKYGLNMCRQ CFRQYAKDIGFIKKDLSCLPWHCLWR
3292	A	218	602	SFLLLPRCTAEKQRWGHQ\QLYWSHP\RKFGQG\SRS\CRVCNRRH GL\IRKYGLNMCRQCFRQYAKDIRFHLSTKCSSFRGLSGASTSMKK PWINSFVYIIHFEKATEKKRKKNEIKRGPFCFKGPL
3293	A	33	494	QPQTD TMVHLTPEEKTAVNALWGKVNVDVAVGGEALGRLLVVYPWTQR FFESFGDLSSPDVAVMGNPKVKAHGKKVLGAFSDGLAHLNLKGTFQS LSELHCDKLHVDPENFRLLGNVLVCVLARNFGKEFTPQMQAAYQKV AGVANALAHKYH
3294	A	1	609	PLKRS DGCNDGRPTRPPTRPDTTVFTSNLQTRMVHLTPEEKSAVT LWGKVNVDVAVGGEALGRLLVVYPWTQRFFESFGDLSTPDVAVMGNPK KAHS\KKGLRGAFSDGLAHL\NLKGTFATL\SEL\HCDKAAPWIE ELQAPWATCLVCVAVPITFGKRISTPPVAGLPNQENWLAWCWLNALG PTSNHLSLAFLAGPISN
3295	A	8	519	SAQMAVTTADPRVRPRVRTQLCSLASLIQTLVHLT\PEEKSAVTAL WGKVNVDV\VGKALGRLLVVYPWTQRFL\ESFGDLSTPDVAVMGNPK VKAHS\KKVLG\AFSGGPGCTWDNLKGTFATTEVSLHCDK\LRHGL KNFRLLGQRAWVAVGPIHFWQKNFNPTSCRLA
3296	A	3	333	GRGGPAAEPCSGEAPPCFPWPSRGRARTRPSRAGSPPLDSCDPHRT PTRARRMMKLKSNQTRTYDGDGYKKQASYFETLRQGYSANNGTPVVA TTYSVSAQSSMSGIR
3297	A	35	717	RRSSPSLLPLAERGGAARGRPERAPHPSTPATRTAPPPWARRMMKL KSNQTRTYDGDGYKKRAACLCFRSESEE\EVLLVS\SSR\HPDRWIV PWKEGMEARRKEAKCGKQVREVCEGRLGVKGT\LGRLVGIF\ENQER KH\RTYV\YVLIVTE\VLEDWEDSVNIGRKREWFKIEDAIKVLQYHK PVQASYFETLRQGYSANNGTP\VV\ATTYSVSGFRASMFRAFRWT
3298	A	81	426	PSFHYAVLPLHNCLGFFPSLRHRWLHSMTDDPPTTKPLTARKFIWTN

				HKFNVTG\PQNNMYLILPLERRFRSGSHLQHLTSKDNEEQLKHAKEYG AFHVITLLLLFTIHYNSQLKLCD
3299	A	180	484	RQQAIFWHRWLHSMTDDPPTTKPLTARKFIWTNHKFNVTG\PQNNMY LILPLERRFRSGSHLQHLTSKDNEEQLKHAKEYGAFHVITLLLLFTIHY NSQLKLCD
3300	A	591	942	MAKTHFWDVDGSMVPPPEWHRWLH\SMTDDPPTTKPLTA\RKFIWIDG TIKFQRLGHPRNNM\YLILPLE\RRFRSGSHLQHLTSKDNEEQLKHA KEYGAFHVITLLLLFTIHYNSQLKLCD
3301	A	1	508	NFALEAKNSARAISYVQTPMGHFTRGGRPTITSLWGK\VNVE\DA GGETPGKGSLLVVP\WT\QRFDSFGNLSSAFPCSWPTPKVKAHGK\ KVL\SLGDAHKSTWDDLKGHLLPKPEVNCTVDKPAWDPENFKAPG EMLLVTRFGQSLFRQKNFTPEGCRASLGKKDG
3302	A	3	452	QTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAELERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKGVADALTNAVAVDDMPNALSALS DLHAHKLVRDVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3303	A	1	627	TLVLPQDSERTHPWLLSPADK\TNVKA\AWGKVGGAHAVRSMCAEAL ERMFLSFPTTKTYFPHF\DLSHG\SAQVKGATGKKVADALTKRAGAPL DDMPNAL/SSALEATLHAHKL\RVGPGSTSKLLKPLACLVDPGPAHL PRPSSTPGGCNVFPGTKFPGLFVEAPLLEPSKLPLKLGSLRLAIVFL PLWGFPPAPPPLSCTRTPVVFEEKS
3304	A	131	406	EAMGILKLQVFLIVLSVALNHLKATPIESHQVEKRCNTATCATQRL ANFL\VHSSNNLGGILSSTNVGSNTYGKRNAVEVLKREPLNYLPL
3305	A	154	1702	IGHRDPARGRSCRGYYSRMVCEKLAPQSEMASAG\VSRLATILCL LAWAGLAAGDRVYIHPHFLVIHNESTCEQLAEANAGKPKDPTFIPAP IQAKTSPVDEKALQDQLVLVAAKLDTEDKLRAAM\GMLANF\LGFP YYMGHSE\LVGV\VHG\ATVLSPTAVFGTLASLYLGALDHTADRLQ AILGVPWKDKNCTSRDLAHKVL\QAVTGLLVAPGRADKQA\QLL \LSTVGVFTAPGLHLKQPFVQGLALYTPVVLPRSLDFTELDVAET ID\RLMQAVTGWKTGCSLTGAKADSTLAFNTYVHFQGMKMGFSLLAE PQ\EFVWDNSTSVSPMLSG\MGTFQHWSDIQ\DNFSVTQVPFTD\S AFLLLIQPHYASDL\DKVEGLTFQON\SFNWMRKLFPRTIHLTMPLN LVLQGSY\DLQDLRPGSSCPPFLHTELNLRISGN\DRIRVGEVLN SIFF\BLEADEREPTTESTQQLNKP\EVLE\VPLTRPF\LFAVY\DOG ATALALSWGRVKGPA
3306	C	223	417	MHVFLKLSVGVTQMVLISEAEKLTGXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXQAGRHAGKQG
3307	A	3	742	HEASCRSERRQMAFDYDDRAYSSFGGGRSGRS\AGGHGSRSQ ELPTEPPYTAYVGNLPP\NTVQGDIDAFKDLIRSRLVRDKD FKGFCYVEFDEVDSLK\EALTYD\GALLGDRSL\RVDAEGRKQDKG GF\GF\RKGGPDDR\GFRDDFLGGRG/GLSRPGDRRTGPPMGS R\FRDGPPLRG\SNMDFREPTEERAQRTTTPALKPRTVATPLNQVANPNS S\IF\GGARPREEVVQKEQE
3308	A	1	861	MVPSEGLWRGLREMLDQSNQWGGTALVVPFAFEIRRARRMPMNKNE LVQLYQVGEVRPFYGLCTPCQAPTNYSRWVNLPEESLLRPAYVYFQAR LAGAGNSTARILSTNHTGPEDAFNFWNVTLTLLSQLPLLLFTLLNSFL YQCVPETMAKLPREREILSEAPQWLLGHGEGSLPKARTVPEASSSH HVPTGEGAGADEFLPLLSVLHAHCDLPELLLEAAYMSLEPSLLTG EGGYLTSLASLALLSGLGQAHTLPLSPVQELRRSLSLWEQRRLLPA THCFQ
3309	A	1	2076	MVKAQLRTALASGGVLDASGDYRVYRGLLKTMTDPNDVILATHASVD NLLHLSGLLERWEGPLSVSVFAATKEEAQLATVLAYALSSHCPDMRA RVAMHLVCPSTRYEAAPDPREPGEFALLRSCQEVFDKLARVAQPGIN YALGTNVSYPNLLRLNLAEGANYALVIDVDMVPSEGLWRGLREMLD QSNQWGGTALVVPFAFEIRRARRMPMNKNELVQLYQVGEVRPFYGLC TPCQAPTNYSRWVNLPEESLLRPAYVVPWQDPWEPFYVAGGKVPTFD

				ERFROYGFNRISQACELHVAGFDFEVLNEGFLVHKGFKEALKFHPQK EAENQHNKILYRQFKQELKANWLRYSPELGVGGSGPASPLARRGEMA ADEGHRLOSTEPSPGSLQAEGLRECRPVTMETGPRYPSPMRDQTVQL VQMPVQPPSKDTEEMEAEGDSSAEMNGEEEESEEBERSGSQTESEEBES SEMDDDEDYERRRSECVSEMLDLEKQFSELKEKLFRRERLSQLRLRLEE VGAERAPEYTEPLGGLQRLSKIRIQVAGIYKGFCLDVIRNKYECLO GAKQHLESEKLLLYDTLQGELQERIQRLLEDRQSLDLSSGPYIVYML QEIDILEDWTAIKKPGGPSEQALHHPGFSSSSCRQADPQAPQGLPSQ APVVLGPPTPSGTGLDSSSALLEACTAVAVELT
3310	A	34	657	SDGRCCGCCAPRAPRAMHMSFAIS/RCAFYQLLLAALMLVAMLQLLY LSLLSGLHGQEEQDQYFEFFPPSPRSVDQ\VKAHVRTALASGGVLDV SGD\YRV\YRGLLKTTM\DPNDVIL\ATHASVEQTCLEH\SGLL\ER W\EGPAVPCSVFAA\TKEE\AQLATVLAYALSSHCPDMPAR\VAMHL VCPSRYEAAVDPREPGEFALLRSCQEVFDKLARVAQPGINYLGTN VSYPNLLRNLALEGANYALVIDVDMVP\TEGLWRGLREMLDQSNQW GGTALVVPFAFEIRRARRMPMNKNE\LVQLYQVGEVRPFYGLCTPCQ APTNYSRWFNLPEESLLRPAYVVPWQDPWEPFYVAGGKVPNFRSSGF RQYGFNRISQACELHVGGFDFEVL\NEGFLVHKGFKEALKFHPQKEA ENQHNKILYRQFKQE\LKAKYPNS\PRRRAQLATVLAYALSSHCPDM PARGRHAPRVPLALRGSRARPPGAGGVCPAAVLPGGL
3311	A	160	441	PPGRTAILSRMKIFLPVLLAALLGVERASSLMCFSCNLQKSNLYCLK PTICSDQDNYCVTVSASAGIVNLVTFGHSLSKTCFPGCPIPESGNVG
3312	A	107	691	RTAILSRMKIFLPVLLAALLGVERASSLMCFSCNLQKSNLY\CLKP TICSDQ\DNY\CVTVSAS\AGIG\NLVTFG\HSL\SKTCFPCLAPFP BGRSMLGV\ASMGHSAFCQSFLVAIFSCGPMAGLRGKRSPLLGARAC CLSLAGRALL\RFGPLDRPEPCSPDPPAQEGKPSFWIPQCMGAPDS SRALICALGPRSG
3313	A	388	525	PSLLQVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
3314	A	194	1131	PQHGGHFPRIKSCSWQARPLEDEATLGQCGEALTTLEVTRPACLE VKSMVPWPVLEKVRGQTPKVAKHGEKKKKKTGRAKRRMQYNRRFVNV VPTFGKKKGTTFTKIFVGGGLPYHTTDASLRKYFEGFGDIEEAVVITD RQTGKSRGYGFVTMADRAAAERACKDPNPIIDGRKANVNLAYLGAKP WCLQTGFAIGVQQLHPTLIQRTYGLTPNYMYPPIVQATVVIIPAAPV PSLSSPYIEYTPASPAYAQYPPATYDQYPY\AASPAT\VRSFVGYSS PAAVPQALSAAPAGTTFLQYQAPHVQPDHMH
3315	A	1	407	DAERQEALGIVRRIGTDTAATEPAGATVPAAAAAAARIGTVGPQPPA MPRRKRNAGSSSDGTDSDSTDLHTDSSDGTSSRSARVTRSSA RLSQSSSRISRSCSKSGSLLALRSLTLPEE*PVVSSSLPQ
3316	B	78	316	XSYLLGQWPRDADGAFTCC'TNDKATQTPLSWQELEGERASSCAHKRS ASWGSTDHRKEISKLKQQLQRTKLSRSGKEKERX*
3317	A	1	2319	GHPAFLEDGSPSPVLFAAASPRPNHSYIFKREPPEGCEKVRVFEEAT TRGKYGEGAKQETFTFALTTLVFIQCVINAVFAKILIQFFDTARVDR RSWLYAACSISYLGAMVSSNSALQFVNYPTQVLGKSCKPIPVMLLGV TLLKKKYPLAKYLCVLLIVAGVALFMYKPKKVVGIEEHTVGYGELL LLSLTLDGLTGVSQDHMRHYQTGSNHMLNINLWSTLLLGMAVSCP DQGPVLPVPCFPVQALEKPSWKNLHQQLDFATCYWHNEGESCVSCHG KTLSSKTQGGILFTGELWEFLSFAERYPAIYINILLFGLTSALGQSF IFMTVVYFGPLTCSIITTTTRKFFTILASVILFANPISPMQWVGTVLV FLGSTQIILDNLKILNTSAKTLLYKTPLSWQELEGERASSCAHKRSA SWGSTDHRKEISKLKQQLQRTKLSRSGKEKERGSPLLDH/VASGST EGVPS/RASPGPLSCDSAPACT/VSEGLNQELEEVFVKEQGEEL LRILDIPDGHRAAPFPQSGSCDHPLLLLEPGNLASSPSMSLASQPC GLASHEEHRGAEEELASTPNDKASSPGHPAFLEDGSPSPVLFAAASP RPNHSYIFKREPPEGCEKVRVFEEATTRGKYGEGAKQETFTFALTTLV FIQCVINAVFAKILIQFFDTARVDRTRSWLYAACSISYLGAMVSSNS ALQFVNYPTQVLGKSCKPIPVMLLGVTLKKKYPLAKYLCVLLIVAG

				VALFMYKPKKVVGIEEHTVGYGELLLLLSLTLDGLTGVSQDHMRAHY QTGSNHMMLNINLWSTLLLGMVSCPDQGPVLVPRCPFVQALEKPSW KNLHQQDLFATCYWHNEGESCVSCHGKTLSSKTQGGILFTGELWEFL SFAERYPAIIYNILLFGLTSALGQSFIFMTVVYFGPLTCSIITTRK FFTILASVILFANPISPMQWVGTVLVFLGSTQIILDNLKILNTSAKT LLYKTPLSWQLEGERASSCAHKRSASWGSTDHRKEISKLKQQLQRT KLSRSGKEKERGSPLLGDHAVRGALRASPPSPSGSPVLRLSPCLHR SLEGLNQEELEEVFVKEQGEELRLILDIPDGHRAAPPQSGSCDHPL LLEPGNLASSPSMSLASPQPCGLASHEEHRAAEELASTPNDKASS PGHPAFLEDGSPSPVLAFASPRPNHSYIFKREPPEGCEKVRVFEEA THQRRDSFDIREKVAELRKKRNSGLSKEQKEKMEHRQTYGNTREPL LENLTSEYDLDFRRAQARASEDLKRLQGGQITEGSMIKTIAGFR YELDTWYHSPYEEYARLGRLYMCEFLKYMKSQTLRHMDSGSL
3318	A	845	1343	LSLGDSAQCLLPHASWCQVAGHPAFLEDGSPSPVLAFASPRPNHSY IFKREPPEGCEKVRVFEEATS/RRVLTGPFLLTSCDPK\NKVHFQP\T GSAFCPVNLMKPLFPGMGFI FRNCPSNPGISSSPGQPQATTSESGS LQGLPTAIRAMAVAPHLQMSLCFSRAP
3319	A	44	499	GGILEELERRRKEEEEERRRABEEKRRVEREQECRWREMEEHRQAERL QRQLQQEQAYLLSLQHDHRRPHPHQHSQQPPPPQQERSKPSFHAPPEK AHYEPADRAREVPVRTTSRSPVLSRRDSPLQSGGQNSQAGQRNSTS IEPRLLWERY
3320	A	1	164	SGERFRVRSSSKSEGSPSQRLNAVKKPEDKKEVFRPLKPAVRIVQD QFYLFQT
3321	A	2	439	ARAARVFLHRSSNLNSNGETESVKTMIHVHDDVESEPAMTPSKEGTLI VRQTQSASSTLQHKHSSSFTPFIDPRLLQISPSGGTTVTSVVGFS DGMRPEAIRQDPTRKGSVVNVNPTNIRPQSDPPEIRKSGKG*L*ILG AGLW
3322	A	3	174	RAVEDVRPSHKVTDYSSSSSEESGTTDEEDDDVEQEGADESTSGPEDT RAASVPGLF
3323	A	2	4978	RRTSAVSRGLLFMSFVQPLLQPPVHLLTARVRVPGYLQIDGVKIKEH NGKLMNCFKTKMTYYFMCVGLPAQLTIGFSGPSRETGSDPRAARR GEDPQSKDRGDLSEQTEAQRSGVHCPRSQVLGELAGQSPRTIPAAL RVCLYLLCITSYNHTSKDESSKDEEEIKLEINMLKKYSHHRNIATY YGAFIKKSPPGHDDQLWLVMEFCGAGSITDLVKNTKGNLTKEDWIA ISREILRGLAHLHIHVHHRDIKQNVLLTENAEBVKLDHHPHPIGWD AEVTEKSAEVPASALGSLKALKVVVHSGKPLLVTVGEAGEAARSRPHR SFQTVDFGVSAQLDRTVGRNRTFIGTPYWMAPVIAADENPDATYD RSDLWSCGITAIEMAEGAPPLCDMHPMRALFLIPRNPFPRLKSKKWS KKFFSFIEGCLVKNYMQRPSTEQLLKHPFIRDQPNERQVRIQLKDH DRTRKKRGEKDETEYEYSGSEEEEEVPEQEGERPSSIVNVPGESTLR RDFLRQQENKERSEALRRQQLLQEQQLREQEYKRQLLAERQKRIE QQKEQRRRLEEKLLDVFQQSKKEDDKDSREVCCQKYRMTGKQSVSK NKERIPDFNCVERSVMQQRREARRRQEREQRRREQEERLEEL ERRRKEEEERRRAEEBKRRVEREQEYIRRQLEEEQRHLEVLLQQLLQ EQAMLLECRWREMEEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPHQ SQPPPPPPQERSKPSFHAPPEKHAHYEPADRAREVEDRFRKTNHSSPE AQSKQTGRVLEPPVPSRSESFSGNSESVHPALQRPAPQDPCPPSR SEVLSQSSDSKSEAPDPTQKAWSRSDSDEVPPRPVVRTTSRSPVLSR RDSPLQSGGQNSQAGQRNSTSSIEPRLLWERVEKLVPRPGSGSSSG SSNSGSQPGSHPGSQSGGERFRVRSSSKSEGSPSQRLNAVKKPED KKEVFRPLKPAGEVDLTALAKELRAVEDVRPPHKVTDYSSSSSESGT T\DEEDDDVEQEGADESTSGPEDTRAASSNLNSNGETESVKTMIVHD DVESEPAMTPSKEGTILVRQSTVDQKRASHHESNGFAGRIHLLPDLL QQSHSSSTSSSSSPSSSQPTPTMSPQTPQDKLTANETQSASSTLQK HKSSSSFTPFIDPRLLQISPSGGTTVTSVVGFS CDGMRPEAIRQDPT RKGSVVNVNPTNTRPQSDTPEIRKYKRFNSEILCAALWGVNLLVGT

				ESGLMLLDRSGQKQVYPLINRRRFQQMDVLEGLNVLVTISGKKDKLR VYYLSWLRNKILHNDPEVEKKQGWTTVGDLEGCVHYKVVKYERIKFL VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLDLTVEEGQRL KVIYGSCAGFHAVDVDSGSVDIYLPHTIQCSIKPHAIILPNTDGM ELLVCYEDEGVVNTYGRITKDVVLQWGMPTSVAYIRSNQTMGWGE KAIEIRSVETGHLDFVFMHKRAQRLKFLCERNDKVFFASVRSQSSQ LQNSLSLNDVSVLWVSDSGDDEHAVGFIGSGHKEAFHKMKHATVNTLV YISREEGKAQVENS KRPRGRHRRRANLGPCSQCWHLALVSRAARAAS SSIRHINKPLRVSS
3324	A	197	332	DPVSKKKEKKRKKKKQAQWLTPVIPTLWEAEVGGSPVSRSPA
3325	A	1	1788	MPVIPATQEAEEESLDPGRRRLRTIGKLEPSYVIRKFLDAQRIHNL TAYLQTLHRQSLANADHTTLLNLCYTKLKDSSKLEEFIKKKSESEVH FDVETAIKVLRQAGYYSHALYLAENHAHHEWYLKIQLEDIKNYQEAL RYIGKLPFEQAESNMKRYGKILMHHPQTTQLLKGLCTDYRPSLEG RSDREAPGCRANSEEFIPIFANNPRELKAFLEHMSEVQPDSPQGIYD TLLELRQLQNAHEKDPQVKEKLHAEAISLLKSGRFGVDFDKALVLCQ MHDFQDGVLYLYEQGKLFQQIMHYHMQHEQYRQVISVCERHGEQDPS LWEQALSYPARKEEDCKEYVAAVLKHIENKNLMPPLLGTWEDRWDEL RVRRYREETTRIRQEIQELKASPKIFQKTKCSICNSALELPSVHFLC GHSFHHQCFESYSESDADCPTCLPENRKVMDMIRAQEQKRDLDHDFQ HQPPKDDKKKKDAGSAKKDKDPVNKSGGKAKKKKWSKGVKRDKLNN LVLFDKATYDKLCKEVPNYKLITPAVVSERLKRIGSLARAALQELLS KGLIKLVSKHRAQVIYTRNTKGGDAPAAGEDA
3326	A	3	111	HAYEGLIKLVSKHRAQVIYTRDTKGGDAPAAGEDA
3327	A	220	425	HEELKSGPYLLTFRDCFLHFWALVSKR/LALNFM*TSAPT*KALSK RNICLVNKNRNIKIPYPKKKKK
3328	A	273	501	RSGVRDQPGQHGKITSLKIQKLARRGGACL*SQLLRRLRQENRLNP GGGGCSEPRSCHCTPAWETEQDSISKIK
3329	A	1	1176	MAWAGSEPRRVRLGSTASEGEKQGVKEGPLAAAAAAAAAAAAAAG YPGGRSRGEGSGRRRECAGRASPRAGRVPADRLTGKLG EAAGRGRGTGQRRSPGHRRLRAARVPTAPGKPRPGFCARLPRPYAGAGR GQAGAGSAEPLGLRPLLEKRGKERRGVGDPKIFQKTKCSICNSALEL PSVHFLCGHSFHHQCFESYSESDADCPTCLPENRKVMDMIRAQEQKR DLHDQFQHQEENSPKMRVIRVGTRKSQLARIQTDSVVATLKASYPGL QFEI IAMSTTGDKILDALSKGFTQALSVRQIGESLFTKELEHALE KNEVDLVVHSLKDLPTVLPFGFTIGAICKRENPHDAVVFFHPKFVGKT LETLPKRVGPPGTIS
3330	A	245	394	GPGCIPAALLQPPKDDKKKKDAGKSAKKDKDPVNKSGGKAKKKVEIR PL
3331	A	458	701	GPAPTRRGPAHPGAHTR**PAGTARAACGSA*SAGTASPAHKGKGGH PGSRASGTGPGPCQRRRRSDHSSAGKWPLREASL
3332	A	365	814	AALRSSSENSRHRSLVKMSDKKAKDPVN\KSGGQGPKRKNWSKGKSS GTSFMN\LVLFDKATYDKLCKEVPNY\NLITPAVGSERL\KIRGSLG QGKPFQELLS\KGFI PNWFSKHRASSYFTPGITKGG\DAPSLLGEDC MNRSNPPVHLEK
3333	A	41	565	APSPRRPWGHFTEED\KATIK\NLWGKGEMWKDAGGKNPWERLPWLS YPMGPQRFDDQLLANLSLCPLPIMGNPPKVKGTPWRKVLTSLG\SAH KSTWDDLKGHLLPKPEVNLHC\DKPAMWDPENFKAPGEMLLVTRFGQ SHFRQKNFTPGGCRASWGRKMGDLELASALVPSRYH
3334	A	399	593	KCIHFPGPPTPKFVCGVIVVTAVP/TFGM*TVYV**LPFSILAQNVG* RDDCDPGWKLNLFYAKKKK
3335	A	28	312	HITNIDPSAINKSGQETWPHGVGLGTALLGRGPSAMLWGALGPDLSR LWAAVSELRAQPAHTGAHRTATSSQKLQKSGPRRGPOEQVPPADRET Q
3336	A	26	417	QEQQDQVFHTRDQAKTRLPLPLLGPHCPQKAAAVIMGNIFGNLLKSLI GKKEMRILMVGLDAAGKTTILYKLLGEIVTTIPTIGFNVETVVAVL

				LASESFPCPHKPFYSLFAFPLPPSPCFTWKLHGPLC
3337	A	16	3567	EPSSQSKPGKEQEGATVFPSPCQKRLSSSRLHQPDDGGRGGEAEGG RPGDSTLEERTFRILGLPAPEVNLRDAPTPGSPPEHQALGPAASGAQ GRAEGSEVAVVQRRAGRGWARTPGPYAGALREAVSGIRRHRTAPDSDT DEAEELSVHSGSSDGSDEAPGASWRNERTLPEVGNSSPEEDGKTAE LSDSVGEILDVISQTEEVLFQDKSSSLVGLPSPKLSGPILPGSFPSD DRLSRPPPPATPSSMDVNSRQLVGGSQAFYQRAPYPGSLPLQQQQQQ LWQQQQATAATSMRFAMSAFPSTPGPELGRQALGSPLAGISTRPLG PGCNCAESCCFFCSSFFSCSNRSSMSRGNLATSELSILSSSSPDAA GPPGKVKAPLSSSNFSSREDPPGPLSGLVSSFCEDAVLWAPVCAG CALSSETAAHNLLRKPGNDSKMLVCETCDKGYHTFCLKPMPMEELPAH SWKCKACRVCACGAGSABELNPNSEWFENYSLCHRCHKAQGGQTIRS VAEQHTPPRMLRLFLQSRSPGECMQAVEPLHRGRLEQAADGFDVCS CQPYVVKPVAPVAPPELVPMKVKEPAFSESLHAKLVGYTELNLQNH LQQLMVQOGIPQADAVVQYDVELIALIRANYWLKLVKGLPLKEKMA KTPLSDEKQLLLFQQKLLAEEEMAKKKERLLSQFLKNNLSNPPTPPS SLPPTPPPSVQQMVNGVTPSEELGEHPKDAASARDSERALARRETRF STAGTGFRLLFHNAHANSRAWLLPAPLDRPILCFAYTWRAVYQPPR VTMETGASASIPELICEAMRIWSSSPALDGCCELLCCGRGHRTRTQR VTERCNCTFWCCHVSCRNCTHTRVLHECLGIVNVASSTNLLTDSKS LQLVLEPSLQLLSRKQRRIRQNPGLHSVSGGLQSAVRECKWQFRN RRWNCPTAPGPHSSARSSTEPQHCGTYLPPSHSLFDAVSSLIIRNKI HRLPVIDPESGNTLYILTHKRILKFLKLFKAAAVIMGNI FGNLLKSL IGKKEMRILMVGLDAAGKTTILYKLLGEIVTTIPTIDEENKERRQA ILQETCNWPHTLNSTSMSKAYQSTFTGETNTPYSKQFVHSKSSQYRR LRTEWKNNVYLARSRIQGLGLYAAKDLEKHTMVIEYIGTIIRNEVAN RREKIYEEQ
3338	A	6385	6599	HMPLIGHSHGWSQALLEGMSWWLGGHQWLQGTWLSGTCKTQGKLLL GPSQTGRRALMWQRHGLGRAWCRQ
3339	A	2	758	ERGGFFSPEGEPDPSWTGSGGTTPTSTPTTTEGEDGLSYNQRL QRWEKDEELGQLSTISPVLYANINFPNLKQDYPDWSSRCQIMKLWR KVPAADKAPYLPGSPEHQALGPAASGAQGRAEGSEVAVVQRRAGRGW ARTPGPYAGALREAVSRIRRHRTAPDSDTDEAEELSVHSGSSDGSDE APGASWRNERTLPEVGNSSPEEDGKTAE LSDSVGEILDVISQTEEV FGPPPIRGTOQQGNRKQ
3340	A	116	627	RLFPVIVIAAPLLDSPWTSRPAATGLAGSRTARVGRARDPHSRRPAGP GPPGCCRRRPTGGRGPWPRSELGSKRKGKRRRRSGRPRRPSEKGARL VGPDGAPRVDPARSPATPLGWPSWQGSLLPCGRSAWRLWGERPVHPR SRRATQGRGRGPGEVGGPGPQATRLTCC
3341	A	1830	2259	GDWQEKVPRGKGAGRVLQEVGPRAVAHPDWRHCRYTCAEWVALGRGS PVSGGSRCLVASSGYSQPTLHQ TASANQGQCLGSCLPDPF PSHQDPQ LPPSLAQCLPGRGSLGTAPHRSWGSSCSAAPPLPPSRHSGSCLQQQR L
3342	A	1	619	FPCRPTRPKARKPSRAPLAMETVISDSSPAVENEHPQETPESNNS VYTSFMKSHRCYDLIPTSSKLVVFDTS LQVKKAFFALVTNGVRAAPL WDSKKQSFVGM LTI TDFINILHRYK SALVQIYELEEHIETWREVY LQDSFKPLVCISPNASLFDVSSLNSGTRSTSLAVIDPRIQAILCTI LNPQAHSGSSSKLFNTGG
3343	A	1830	2258	GDWQEKVPRGKGAGRVLQEVGPRAVAHPDWRHCRYTCAEWVALGRGS PVSGGSRCLVASSGYSQPTLHQ TASANQGQCLGSCLPDPF PSHQDPQ LPPSLAQCLPGRGSLGTAPHRSWGSSCSAAPPLPPSRHSGSCLQQQR L
3344	A	290	1377	RSFRAIGEVGSIRGWGGGYAAQLQSPSRLPVLGGGKKGSGRGVGGQS SRAEVGLGSQRERSGTCGAEEEEAAQLIAGTGSSLPYQGPQNQTA IAPTCAPLSPCKAAAVIMGNIFGNLLKSLIGKKEMRILMVGLDAAGK TTILYKLLGEIVTTIPTIGFNVETVEYKNISFTVWGCGVARDK\IR

				PL\WRH\YFQN\TQGFILWSDSN\DR\ERVNEA\REEL\MKNAGAE TSLRDAVLLVFGQTNRICPNAMNAAG\IQDKLG\LHSLRHRNWYI\Q ATCATRGN\GLYEGHLWLANSVPKQEVESRTALTKHSTSPITYLLSP CPQFLPLLSMQGLARAWGIMSTLPSRTLPLPLTSLPFSCPI
3345	A	292	574	VTENSGGQTQCGKQDRIQVPRHPARRGPPGSQY/PVTPPVPPGPLH ATQLPPGPPIPLGKRKAGQERRLDPRPTTCQAAAPTRSSPFCPPQKVR R
3346	A	3	142	TISSIIRKARKP\QDLLNNYTPRSSPLRSSGRTRMYKGKNVRPGNSS
3347	A	1	1418	MAAALFVLLGFGALLGTHGASGAGEERARKQPCGKSRFQGHSEALAT RFSAGNTGFVQAPLSQQRWVGGSVELHCEAVGSPVPEIQWWFEGQGP NDTCSQLWDGARLDRVHIHATYHQHAASITISIDTLVEEDTGTIECRA SNPDPRNHLTRAPRVKVVRAQAVVLVLEPGTVFTTVEDLGSKILLTC SLNDSATEVTGHRWLKGGVVLKEDALPGQKTEFKVDSDDQWGEYSCV FLPEPMGTANIQLHGPPK\VKAVKSEHINEGETAMLVCKSESVPV TDWAWYKITDSEDKALMNGSESRRFFVSSSQGRSELHIENLNMEADPG QYRCNGTSSKGSQDAIITLVRSHLAALWPFLGIVAEVLVLTIIIFI YEKRRKPEDVLDALRRCTWPGLMSCPEPPLGVTEGRAGSTDAPARGL SGASADRLSSRPLFHGGGPSSDDDAGSAPLKSSGQHONDKGKNVRQR NSS
3348	A	3	896	SCRGRRRQRLEVVRGFRRGIGIMAAALFVLLG\FALLGTHGASGAAG TVFTTVEDLGSKILLT\CSLNDSEATEVTGHR\W\KGGVVLKEDALP GQKT\EFKVDS\QWGEYSCVFLPEPMGTANIQLHGPPRV\KAVK\ SSEHINEGETAMLVCK\SEFVPP\VTWAWYKITDSEDKAL\MNGSE \SRFFVNSSQG\RSELHIENLNMEA\DPGQE\RCNGTSSKGLRPRPL QFLVRSHLAALWPFLGIVG\EVLVLTIIIFIYEKRRKPEDVLDLDDDD AGSAPLKSSGQHONDKGKNVRQRNSS
3349	A	870	997	KWASNTYVISSNEESMIS*LSGRQ*NLRVWRLRKTWWLNLWTL
3350	A	2	225	GILKGLYYPLATNSFPATCWRL*VSPAHSKDPNAATVHLSFFSPSG GPRYLLGHTTWQOGLGKRGRRTTEQHS
3351	A	1	336	FLLSSRWGWPMASTAGCPQGQVCGMTGNAGVHNVGAALWHS LGWVK GEQNTKGPFGDQNRPVQAIWASPFRTSWVKFPRPWRQMPAILGPWGT YCLSLAREGERRPAAQSG
3352	A	1193	2524	SKPPAASFAPRRPPATSRTLSAACAFRSRCRLAACSFVRPLPHTDTN MNGQLNGFHEAFIEEGTFLFTSESVEGEGHPDKI\CDQIS\DAVLDAH LQQDPDAKVACETVAKTGMILLAGEITSRAAVDYQKVREAVKHIGY DDSSKGFYKTCNVLVALEQQSPDIAQGVHLDRNEEDIGAGDQGLMF GYATDETEECMPLTIVLAHKLNAKLAE LRRTGLPWL RPSKTQVTV QYMQDRGAVLP IRVHTIVISVQHDEEVCLDEM RDALKEKVIKAVVPA KYLDDVTIYHLQPSGRFVIGGPQDAGLTGRKIIVDTYGGWGAHGGG AFSGKDYTKVDRSAAYAARWVAKSLVKGGLCRRVLVQVSYAIGVSH LSISIFHYGTS\RKSERELLEIVKKNFDLRPGVIVRDLDLKKPIYQR TAAYGHFGRDSFPWEVPKCLKY
3353	A	346	461	TLHKKTFFYLEQLILKYG MHQNTLRIKEIHGELKLKSI
3354	A	3	1632	MTEQLEPILMQAFIKSTAGLEARKLKAYRTMEYMAKSTDRSPGHILC CECGVPISPANICVACLRSKEDISQGI PKQVSI SFCKQCQRYFQP PGTWIQCALESRGTFLLWCLEKNPKPLWSKVRLVDAG\FVWTEPHF\ KRLKVLTIQKEVMNGAILQQVFVVDYVVSQMC GDGHESEKLKDFW K\AVIQVRQKTLHKKTFFYLEQLILKYG MHQNTLRIKEIHGGLDFY SSKQHAQKMVEFLQCTVPCRYKASQRLISQDIHSNTYNYKSTFSVEI VPICKDNVCLSPKLAQSLGNMNQICVCIRVTS AIHLIDPNTLQVAD IDGSTFWSHPFNSLCHPKQLEEFIVMECSIVQDIKRAAGAG\MISKK HTLG\EVWGTEGHLEMNRIKQYFCRT\HLGTSC LNPGD\RVLGFDL AN\CNLNDEHVNMNSDRVPDVVLIKKSYDRTKRQRRRNWKLKELAR ERENMDTDDERQYQDFLEDLEDEAIRKNVNIYRDSAIPVESDTDD GAPRISLAEMLEDLHFSPGCPLVKEGASMLT
3355	A	35	378	PRSVPSRFSGGRTHEGREGAQA*GEASNPGNPRRG\QSGGGT*GDS

				SKGER\KQDRNKEKKEALS KVVIRRLPPTLTKEQLQEHLQPMPEHDY FELFSNDTRLHYAHMDARSLHQL
3356	A	11	1379	PRSGQAASAGYVSMKEEKEHRPKEKRVTLTPAGATGSGGGTSGDSS KGEDKQDRNKEKKEALS KVPGRPLARERAGRVRTAGRMAGNGAAPFL SQVLLLSLRLNGSRIILVHPFTRNGESPSRPNPGWGLYPHMYARAYI NFKNQEDIILFRDRFDGYVFLDNKAKKTTPLLSPLKNKQORMREEK/K RRKEEERNRKKTKRRREEEME\EEERKRKRDIEKLKKIDRIPERDK LKDEPKIKVHRVSVTSCSEKS/RSRSQKKGDEKELDKREKAKKLDK ENLSDERASGQSC TLPKRSDSELKDEKPKRPEDESGRDYREREREYE RDQERILRERERLKRQEEERRRQKERYEKEKTFKRKEEEMKKEKDTL RDKGKKAESTESIGSSEKTEKKEEVVKRDRIRNKDRPAMQLYQPGAR SRNRLCPDDSTKSGDSAAERKQESGISHIKEGCEE
3357	A	3	1015	IRHEEIIKVTPLOQMLASCTGAILTSVIVTPLDVVKIRLQAQNNPLP KGKCFVYSNGLMDHLCVCEEGNKLWYKPGNFQGTLD\AFFKII RN EGIKSLWSGLPPTLVVAVPATVIYFTCYG\QLSALLRSKLGNETCI PIVAGIVARFGAVTVISPLELIRTKMQSKKFSYVELHRFVSKVSED GWISLWRGWAPT VLRDEPF\ SAMYWYNYGILKKWLCEKSGLYEPTF\ MINF\TSGALSGSFAAVATLPFDVVKTKQKQTQLWTYESHKISIMPLHM STWIIMKNIVAKNGFSGLFPG\LIPRL/ILKLAPACAIMISTYEF GK AFF\QKQNVRRQQY
3358	A	231	877	PKPGGYSQCRTTSSRATERNRIDYVSSAVPYLTTPPDLRPREV\ VFI G\RSNV\GKSSLIKALFSLAPEVEVRVSKKPGHTKKMNFVKVGHFT VVDMPGYGFRAPEDFVDMVETYLKERNLKR TFLLVDSVVG IQKTDN IAIEMCEEFALPYVIVLTKIDKSSKGHLLKQVLHIQKFVNMKTQGC PQLFPVSAVTFSGIHLRLCFIASVTGSLD
3359	A	3	234	GSVLKKTTGLVGLAVCNTPHEEPDVKKLEDQLQGGQLEEVILQAEHE LNLARKMREWKLWEPLVEEPPADQWKWPI
3360	A	25	546	QSGDLGGRLSRSENC SQRVVRHRVVGAVMAGVLKKTG\LVGLA\VC NTPH\ERLRILY\TKI\LDVLEEIPK\NAAYRKYTEQITNEKLAMVK AEPDVKK\LEDQL\QGGQL\EEVIL\QA\EHELNLAKKK*GEWKL\W EPL\VE\EPPA\DQ\WKWANI I IKLTLVVFMGKLDVIKIFYCI
3361	A	2	368	YAGFSLSAQKCPGAMAE*SYAKSTKLVLKGTKTSSKKKSKKEKKRKR EEDDEETQFD/IVGTIAIEMDEGTYIHALDNGLFTLGAPHKEG\KMAL LASNGCFIRCNEAGDIEAKSKTAGEEEMIT
3362	A	268	393	DGRRKEKWHKVERRHRPYLLSSLSQHRW*TVTNFGEISGTIAIEVDE GTYIHALNGLFTLGAPHK/ERIALKPGYGKYL SINSDELVV/GRSD AIGPREQWEPVFQNGEVRNGGPAEMGEEKRNGTKWREDTDHTSFPLF PSTGGQPKAHSNWRKVCH
3363	A	6	223	TVTNFGEISGTIAIEMDEGTYIHALDNGLFTLGAPHK/ERIALKSGY GKYLGINSDLVGHSDAIGPREQWEH
3364	A	329	877	RPWKQDRRAGDPWPRTHEFRSSEASLQASACKKKKSKKEKKRKEEDE ETQFDMFGIW*TVTNFDEISGTIAIEMDEGTYIHALDNGLFTLGSST QRRIALKSGYGKYLGINSDLVV/GRSDAIGPREQWEPVFQNGACAA VFTVIGSEKQSECSLLRESRAKYHGCTHGQISSSLKQHPRWY
3365	A	97	704	AGFSLSAQKCPGAMAE*SYAKSTKLVLKGTKTSSKKKSKKEKKRKE EEDDEETQFD/IVGIW*TVTNFDEISGTIAIEMDEGTYIHALDDGLFTL GAPHKEG\KMALLASNGCFIRCNEAGDIEAKSKTAGEEEMIKIRSCA ERETKKKDDFLEBDKGNVKQCEINYVKKFQSFQEHKLKISKEDSKIL KKAQKDGFLHETLLDR
3366	A	24	981	AIQRLGEDGGGFYRDVGCQGVFISRPLLFLRAPVLPRLTYSSRTGLS LSAQKLPGAMAEYSYVKSTKLVLKGTKTSSKKKSKDKKRKEEDEE TQLDIVGIWTVTNFGEISGTIAIEM\DKGTYIHALDNGLFTLGAP HKE\SDEGPPPEQFTA\VKLSDSRIAL\KSGYGKYLGIIRDGLVVG \RSDA\IGPREQWEPVFK\MGKMALSTSNCSFIRI\HEAEDIEAKSK TAGEEEMIKIRSCAERETKKKDDIPEEDKGNVNKCEINYVKKFQSFQ DHKLKISKEDSKILKKARKDGFLHETL\LDRRA\KLEAD\RYCK

3367	A	1	555	PLKRS DGCNDGRPTRPPTRPDTTVFTSNLKQTRMVHLT\PEEKSAVT ALWGKVNVD\VGKALGRLL\VVYPW\TQRFEE\SFGDLSTP\DAV \MGNPKVK\AHGKKVLG\AFSGGPGCTWDNLKGTFAHTEVSLHCDK\ LHRGSLKNFRLG\NVLGLCCLAHSLGKEFQPHQLQACLIKIGWL GVG
3368	A	1	390	WEEIQELNEVARHRPRSTLVMGIQENRQIRELQENKELRTSLEEH QSALELIMSKYREQMFRLLMASKKDDPGIIMKLKEQHSKELQAHVDQ ITEMAAVMRK\PLKLTNSRVARNKNEYFNLNKKTKA
3369	A	769	912	FPTPIPLFQELQAHVDQITEMAAVMRK\PLKLTNSRVARNKNEYFNL K
3370	A	1	463	MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCR SSQSLVHGIGNTYLHWYQQKPGKAPKLLIYKVSNRFSGVPSPRFSGSG SGTDFTLTISGLQPEDFATYYCQHYDSLPTYTFGQGTKLE\IKRTVAA PSVFIFPAHLMSS
3371	A	2	166	GDSPLNLSPPFYQYNAFDGFAAYGGLNEKS FVDGLNFSLNNMQYSNQ FQPVMAN
3372	A	39	1200	FCGVAAMQLEIQVALNFIISYLYNKLPRRRVNI FGEELERLLKKKY\ EGHWYPEKPYKSGSFR\CIHIGEKVDPVIEQASKESGLDIDDVRGNL P\QDLESFRIDPFVSYQIGEKGPVKVLYVDDN\NENGCE\LDKEIK NSFNPEA\QVFMPI SDPASSVSSSPSPFGHSA\AVSPTFMPRSTQP LTFTT\ATF\AATKF\GSTK\MKNSG/RGSSRFARTSPINLRGMWN DLLEGRKAISSS\MHSLYGLGLG\SQQQPQQQQAQPPPPPPPPQQ QQQQ\TSALSPNA\KEFI FPNMQGQGSST\NGMFP\GDSPLNLSPL QYSNAFDVFA\TYGGLNEKS FVDGLNF\SLNNMQYSNQFQPCYGLT KKKKMYRTKLKCTGPRGIFFFSPP
3373	A	1	1197	MEYYATIKKNIISFAAAWMLDAITLSKLTQKRKTKYRMFLFVSEG RPPWAVGRESGWRPPVPFSSVLLLRDPGTGVLKDLNNQEVDGEHEDG ALQANHLLPDEFGALESVKAASELYSPLSGEVTEINEALAE NGLV NKSCYEDALTFYFDKYYKHRSNPSNSLANFHF KALTIASKHHQIVK MDLRSRYLDSLKAIVFKQYNQIATVLRLLRVMEHVQTLLLGKLPGA LTACCHPLHLCVHKQAKCVTIAYS IQYSNMLYRFVAQEORLYHTAKV KVTVLEDNDPFAQYHYLVTVYTGHRGAATSSKVTVTLYGLDGEREP HHLADPDTPVFERGAVDAFLSTLFLPLGELRSSGCGMTTQGTARAS TCDVLKVTQLASMEQGLCILEAK
3374	A	66	632	RRDPRT PANMALRVRSVRALLCTLRAPLPA\APCPPRPWQLGVGA VRTLRGTGP\ALLSVRKFTKQESGNNQEKSMNQLGSGNFAQ\EALGD VVYCSLPEVGTKLNKQ\DE\FGALESVKAASELYSPL\SGEVTEIN\ EAL\AENPGTCKTNFCY\EDGWLKMTLSNP\SEL\DELMSEEAYEK YIK\SIEE
3375	A	162	552	VASEHSPKIGASQGLDYEPLLVVAKVWYLTRPTGT KAGSVFSQYLPP LEPGILGPASLPWLRQTLTGKEIEIDIEP\TDKVERIKERVEEKEG\ IPP\QQQRLHLQVAKM\NDEKTASWITKILRWVQSFT
3376	A	77	427	GRDKEGEYPPAPSSGWGKSVGIMLTELEKALNSI IDVYHKYSLIKGN PHAVYRDDLLKKLLETECPQYIRKKGADVWFKELDINTDGAVNFQEF LILVIKMG\WQPTKKAMKKATKSS
3377	A	1	143	GKSVGIMLTELEKALNSI IDVYHKYSLIKGNFHLCSNIYFKKFYVF
3378	A	200	899	GKSTGPVCVHMSLCEWTL SLATRVSLSSHPSHQSHSLLVWLFGESR PGQGLRLGHESAYCPGQM QIPCHGIPQKVLF FRWGKSVGIMLTELE KALNSI IDVYHKYSLIKGNFHAVYRDDLLKKLLETECPQYIRVRRGLG WRGLSAWSWGCPGPAVL PATLHRWLCGLS*DL*TLASSSSILT\KK GADVWFKELDINTDGAVNFQEF LILVIKMG\WQPTKKAMKKATKSS
3379	A	99	498	RESGGKRLNIYHQTVYH\KYSL\IKGNF\HAVYR\DDLKKLLET\EC PQYIRKKGADVWFKELDINTDGAVNFQ\EF LILVIKMG\WQPTKK\A MKESHKGVSLSLGPGK WALGGHVTCRI IKVINTSKKKKKVDAA
3380	A	1	282	PLKRS DGCNDGRPTRPPTRPDTTVFTSNLKQTRMVHLT\TPEEKSAVT ALWGKVNVD\VGKALG\RLL\VVPLGPPKGPLKSFGGICPNLSL

				AG
3381	A	24	452	APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDSFGNLS SASAIMGNPKVKAHKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMTGVASALSS RYH
3382	A	3	549	FCPRGQEFGEKNKLLVPDA\MGHFTEED\KATI\TSLWGK\VNVE\D AGGET\LGRL\LVVYP\WT\QRFDD\SFGNLSASAI\MGNP\KVKA HG\KKVLTFLGRCQQSTLDDLKGHLLPKPEVNCTVDKPAWDPENFK APGEMLLVTRFGQSHFRQKNSPPGGCKASWAERWVT\GV\ASALVPS RYH
3383	A	347	716	REPCVSRSTCCPLPWMEPRAMCPPVGAMRGSRRDPASSSLSPDHLA QLQPAGFLFCSAPALSGSFPPRPSPOGHLATAGSWL/ CPPVQAQPO APALCGPRRGVAWVGIAWEDSGKSVGEVAS
3384	A	1	1362	MEKSLLFPPLTTSAGNDRDSRSRSGGESSGETGSESGPRAPGGPMT PPSPARGSLLSPALTCLPFPPTPRRIQVQDVEKPMLGQQROGLPAGRS PTVAAAILLELETSGGDEEPPGRDHLRGVGTVLSEGDGGHACTPRLSG AKFYSEIIAIMVNLLQIVRDHVVHVLVPMGFVIGCYLDRKSDERLTA FRNKSMFLPKRDGSSGSGREFQLARODACQWAYSWSVGSLRGKRTEQHP QWQEGSLCAQHCLNNLLQGEYFSPVELSSIAHQLEDEERMMAEGGV TSEDYRTFLQWFNLNLLTGPELISDTYLALFLAQLQOEGYSIFVVK GDLPDCEADQLLQMIQVQMMHRPKLIGEELAQLKEQVRHKTDLERVL EANDGSGMLDEDEEDLQALALSQRQIDMEDEEADLRRAIQLSMQGS SRNISQDMTQTSNTLTSEELRKRREAYFEK
3385	A	284	540	KLFQKKNKSSCISDNFFLLAIMVNLLQIVRDHW\ VH\VLVPMGFV IGCYLDRKSDERLTAFRNKSMFLKSFPHRELQPSSEVTWK
3386	A	194	353	KVPATTADMIREHLPA PGDDVLVLLCGPPPMVQLACHPNLDKLGYSQ KMRFTY
3387	A	57	880	DPHSVSSTGGPLPIWFWPLSSGPGAVAADPAQSGSPTVDAGVPIPH IRARDSARLPLCPWHASALELGIATPGTVTTQAPGSYPAWSRCLLY PQSPVLLASLGVLVTLGLAVGSYLVRRSRRPQVTLDPSEKYLRL LLDKTVSWGRKGQEGGDQSAPGM*GTAPTUVGMSKGRGSARRAW*N TCVLHPP\TVSHNTKRFRFALPTAHHTLGLPVGKESVEWAPFGYPQ KVTPLLGSHETRCFNRFAPHTISPSPTWLCILQAVRCHWA
3388	A	430	483	NQPCLTLPTRKSECTDTVISWSLSFGFLFTRWVTGMAVLLRLSLRQA EYTHSQQLLPLDT*RLGNVVKFRGP\SGLLSYTGKGFHN IQPNKKSP PEPRVAKKLGMIAAGGTGITPMLQLIRAILKVPEDPTQCFLLPATQTE KDIIILREDLEELQARYPNRFLWFTLDHPPKGILPISGHPTIPSSSK SKPCPFVNNSGFIEINLASHCQLGSLSAQTQ
3389	A	3	1007	HACAHASAHASGRLVRWGRKRRSVMGIQTSVLLASLGVLVTLGL AAGSYLVRRSRRPQVTLDPNEKYLRLNKTTVSHNTKRFRFALPT AHHTLGLPVGKHIIYLSTRIDGRVR\IKPYTPVTSDEDQGYVDLVIK YKGV\QPKFSEG\GKMSQYLDLKVGDV\VEF\RGPSGLLTYTGK HFNIQPNKKSPPPE\RVAKKLGMIAAGGTGITPMLQLIRAILKVPEDP TQCFLLFANQTEKDIIIFAGGLKRNQARYPNRFLWFTLDHPPKQWA YSKGFVTADMIREHLPA PGDDVLVLLCGPPPMVQLACH\PNLGQTGV TSQKMAISPY
3390	A	2568	2783	RSPGRPPHDPPNAPV/RRPASCHS/AAESQHGGWKKSKISASRKLQL KTLQLQIAKQE/ LERAEERRGEKGRAL
3391	A	2	410	SSSPEETDGPWDPEGHPGGPTEPPNAPVLALPPAIPGLRLSMADGS SDAVREPRPAPTPIRRRSSNYRAYATERRGEKGRALSTRCQPLELAG LGFAELQDLCRQLHARVDKVEERYDIEAKVTKNITEIADLT
3392	A	3	492	SSPEETVGPWDPEGHPGGPLTDPNAPVLALPPAIPGLSLIMADGSS DAVRAAG*GVAGTPRARAREPRPAPAPIRRRSSNYRAYATEPHAKKK SKISASRKLQLKTLQLQIAKQELERAEERRGEKGRALSTRCQPLEL AGLGFAELQDLCRQLHARVDK
3393	A	2023	2613	TLQTPLSLSSLPPIAIPGLSLSMADGSSDAAREPRPAPAPIRRRSSNYR

				AYATEPHAKKSKISASRKLQKLTLLQIAKQELEREAEERRGEKGR ALSTRCQPLELAGLGFAELQPDHTWFDGSSTRPNRHTPAKAGYAIV SSTSIIEDTALPPSTTSQQAELIALTQALTLAKGLRVNIYTDISKYAF HILPHHAVI
3394	A	150	848	VSAWRNGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKIS\A SRKLQKLTLLQIAKQE\LEREAEERRGREGARSLAPRC\QP\LELA G\LGFAADLPGLCCRQFHARV\DKVDEERYDIEAKVSKNITEIAN\LT \QKIFDLRSKFKRPTL\RRVRI SADAMMQALLGARAKESLDLRAHLK QVKKEDPEKENREVGDWRKNIDALSGMEGRMKKWRELSLPAYCPCPE EGH
3395	A	1	2880	MSKIKTLLQYSPSSTNSQPWHFIVGSKAFVESVRAEHPDARHHCVAW VAGAPDDSQQLGFSDDGEPAGTAGKPMLAQLMGSGVGEITAVVVRY GGILLGTGGLVKAYGGGVNQALRQLTTQRKTPLTEYTLQCEYHQLTG IEALLGQCDGKIINSYQAFVLLRVALPAKVAEFSAKLADFSRGS HAPARLASISAGCRFPTQDRSKSMNCSYGAMVPAITKNPNERASLA AWRQGGATLGLLLCTVGFVPMNLIENQQLGYIFAATLFSLFGLLF MWICYSGVKERYVETQPANPAQKPGLLQSFRAIAGNRPLFILCIANL CTLGAFNLAIQVYYTQYVLNDPILLSYMGFFSMGCICIGVFLMPASV RRFGKKKVYIGLLIIVLGDLLNYFFGGGSVSFVAFSCLAFFGSAFV NSLNWALVSDTVEYGEWRTGVRSEGTVYTGTFFRKVSQALAGFFPG WMLTQIGYVNPVQAADHTIEGLRQLIFIYPSALAVVTIVAMGCFYS NEKMYVRIVEEIEARKRTAFLPAPLAFNVNIYAEFASGFFQIFRSHI GVSNTRRRTGRYADDSWRVGKRGRRLRASLVIQRREQLIRRRRLYTR PNLIIRKARGGSCACAGSCKCKCKCTSCCKSECGAISRNGLWLRL LDSIETEKGRSLFYIFRVTPVSCEQKSRYALAIRANSREETMDNDK IDQHSDEIEVESEEKERGKKIEIDEDRLPSRAMAIEHHRQDGEKEL DARIALGVENIIESCTVVSROGKDADIMIIGGIPDKLKDDKQIDLLV QATESWVKTPMRQTPFPPIVDPDES DRAAETRSTLTSSGMAAVIGFQ SPYNDQRSVIALLADSPRGYEMLNDVNDSGKRATMFGSVAVIRESG INSLRVGDVYVGHLPWFERVWYALANHPILLAVLAAISVILLAWVL WRLRLIISRRRLNPDNEIYE
3396	B	61	5070	MGPTSGPSLLLLLLTHLPLALGSPMYSIITPNILRLESEETMVLEAH DAQGDVPVTVTVHDFPGKKLVLSSEKTVLTPATNHMGVNTFTIPANR EFKSEKGRNKFVTVQATFGTQVVEKVVVLSLQSGYLFIQTDKIYTP GSTVLYRIFTVNHKLLPVGRVVMVNIENPEGIPVKQDSLSSQNQLGV LPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFVKEYVLPSPFEVI VEPTEKFYIYNEKGLEVTITARFLYGKKVEGTAFVIFGIQDGEQRI SLPESLKRIPIEDGSGEVVLSRKVLLDGVQNLRAEDLVGKSLYVSAT VILHSGSDMVQAERSGIPVTSPIYQIHFTKTPKYFKPGMPFDLMVVF TNPDGSPAYRVPVAVQGEDTVQSLTQGDGVAKLSINTHPSQKPLSIT VRTKKQELSEAEQATRTMQALPYSTVGNSNNYLHLSVLRTEL RPGET LNVNPLLRMDRAHEAKIRYYTYLIMNKGRLLKAGRQVREPQDQDLVVL PLSITTD FIPSFRLVAYYTLIGASGQREV VADSVVVDVKDSCVGS LVKSGQSEDRQVPVPGQMTLKI EGDHGARVVLVAVDKGVFVLNKKNKL TQSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLTFTSSSGQQT AQRA ELQCPQPAARRRRSVQLTEKRMKVKGYPKELRKCCEDGMRENPMRF SCQRRTRFISLGEACKKVFLDCCNYITELRRQHARASHLGLARSNLD EDIAEENIVSRSEFPESWLWNVEDLKEPPKNGISTKLMNIFLKDSI TIWEILAVSMSDKKGCIVADPFVTVMQDFFIDLRLPYSVVRNEQVE IRAVLYNYRQNQELKVRVELLHNPAPCSLATTKRHHQOTVTIIPKSS LSVPYVIVPLKTGLQEVEVKAAYVHHFISDGVRSKLVVPEGIRMNK TVAVRTLDPERLGREGVQKEDI PPADLSDQVPDTESETRILLQGT PV AQMTEDAVDAERLKHIVTPSGCGEQNMIGMTPTVIAVHYLDETEQW EKFGLEKRQGALELIKGYTQQLAFRQPSAFAFVKRAPSTWLTAY VVKVFS LAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQE MIGGLRNNNEKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDF

				LEANYMNLQORSYTVAIAGYALAQMGRLKGPLLKNKFLTAKDKNRWED PGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQRYGGYGST QATFMVFQALAQYQKDAPDHQELNLDVSLQLPSRSSKI THRIHWESA SLLRSEETKENEGFTVTAEGKGQGTLSVVTMYHAKAKDQLT CNKFDL KAAGPMVLTDTSPMSLDKAFSDRNTLIIYLDKVSHEDDCLAFKVH QYFNVELIQPGAVKVYAYYNLEESCTRFYHPEKEDGKLNKLCRDELC RCAEENCFIQKSDDKVTLEERLDKACEPGVDYVYKRLVKVQLSNDP DEYIMAIEQTIKSGSDEVQVGQORTFISPIKCREALKLEEKHYLMW GLSSDFWGEKPNLSYIIGKDTWVEHWPEEDECQDEENQKQCQDLGAF TESMVVFGCPN*
3397	A	3	560	EGKGQGTLSVVTMYHAKAKDQLT CNKFDLCLPGSRQKVEVFLGPCLO PGTFLWSRNRRLVGFPSMNGEDMGLLFLCSEWERSSEGWL CNREGGS GHSIEPHCCTFLHLTHRS LAFSLLAGVSC TCASSCKCKE\CKCTSCK KSECGAISRNGLWLKVGREP KAVPEVRASGEPAFLCPCRLSLPV
3398	A	3	1584	SNQPLRREAFPETPKGLRQGIPEGEPENGDRSHFFSFDVTAVMILYKE SQALTGNLPGPQLPRLRAAGRGGHPSVPAPSRRGALSRFPASGRSA VPTIGWLCRSHYPHSIRGANGWDRQELVRASHTMSATAQT NHRAEKA GRELSQANNDRTGR LAHPAPPPSQARQVPRLEHLASPRCRWPAVISR PFRSWHCILEIRFRKGKLGGRASPENEGAGEIRVKVPKORDWLTAKL QGDLT TVSQ TAKLED MVLTAKSTQDFLTPTARSYSPTTKLGKGVNT KSPTLLTPTARGRHYLLGAPIASWRCHTSTIRYHTVVMSMTL TESE HQAGSVDM SANDYAHYSGASGDNEMCVVIACPTPLFS PRAWKPCDA GSKVKNWGIENGNLVHTVLSSTQHGDPEHVHAPFGMEAEYAHPLETL ILGTGFFIGIVLLCDHVILLWAWVTIRLLETIDVHSGYDIPLNPLNL IPFYAGSRHDFHMH\NFIG\NYGFQHFTRW\DNWFLGTD SQYNAYN EKRRKFEKKTE
3399	A	2	873	GRVGEMSQGRGKYDFYIGLGLAMSSSIFIGGSFILKKKGLRLARKG SMRAGQGGHAYLKEWLWRAGLLSMGAGEVANFAAYAVAPATLVTPLG ALSVLVRAILSSYFLNERLNLHGKIGCLLSILGS\IVMVIHAPKEEE IETLNEMSHKLGDPGFVVFATLVVIVALILIFVVGPRHGQTNILVYI TICSVIGAFSVSCVKGLGIAIKELFAGKPV\GIPWAWILLSLIVC VSTQINYLNR\PWDIFNTSIVTPIYYVFFTTSVLTCSAILFKGVGKD MPVGRCPVL
3400	A	90	458	HFSRGYLEAFSEISNIRFVPPHSVTVVVVFACFLCILGIWPWACL P GPGGEGSGGFGEGRGSEAGRLGSVELTP\ATLPLQAPEAYPVFEPVP PVPEAAQGD TEDSEGAPPLKRICPNAPDP
3401	A	3	787	PGSTISWRPGLARSLSPDPGRRPRRGLGPGPSPASMAGRTVRAETRS RAKDDIKVMATIEKVRRWEKRWVTVAA TPFRILNWVA\VVDPQEE R\RRAGGAERSRG\RERRGRGASPDGGG/PLFILLDL\NDENSQR FPLRKGS LQRGTE\PSPGGTPK\PNRPCVTLPDPPEGGPCTRAQPPT /RLGQEERSPGGITV\GSTDEPP\MLTKEEPVPELLEAEAPEA\YPV FEPVPPVPEAAQGD TEDFGSAPP\LKRICPNAPDP
3402	A	1	172	DCVRKQLKKERPIILD PADPTLNVAEGYWLGLGIYGIQDSDTLILSK KKGEALFPAS
3403	B	1	5501	MVSKLSQLQTELLAALLESGLSKEALIQALGEPGPYLLAGEGPLDKG ESCGGGRGELAE L PNLGETRGSEDETDDDGEDFTPPILKELENLSP EEAAHQKAVVETLLQEDPWRVAKMVKS YLQQHNI PQREVVD TTGLNQ SHLSQHLNKGTPMKTKRAALYTWYVRKQREVAQQFTHAGQGGLIEE PTGDELPTKKGRNRNRFKWGPASQQILFQAYERQKNPSKEEREAQGLG SNLVTEVRVYNWFANRRKEEAFRHKLAMDTYSGPPPGPGPALPAH SSPGLPPPALSPSKVHGVRYPATSETAEVPSSSGGPLVTVSTPLH QVSPTGLEPSHLLSTEAKLVSAAGGPLPPVSTLTALHSLEQTSPGL NQQPQN LIMASLPGVMTIGPGE PASLGPTFTNTGASTLVIGLASTQA QSVPVINSMGSSLTTLQPVQFSQPLHPSYQQLMPPVQSHVTQNPFM ATMAQLQSPHALYSHKPEVAQYTHTGLLPQTM LITDTTNLSALSLT PTKQVFTSDTEASSESLHTPASQATT LHVPSQDPAGIQHLQPAHRL

				SASPTVSSSSSLVLYQSSDSSNGQSHLLPSNHSVIETFISTQMASSSQ *
3404	A	158	755	RGGRPAWPCGSRAMVSKLSQLQTELLAALLESGLSKEALI QALGEPG PYLLAGEGPLDKGESCGGRGELAEPLNGLGETRGSEDETDDGDEF TPPILKELENLSPEEAAHQKAVVETLLQEDPWRVAKMVKS YLQQHNI PQREVVDTTGLNQSHLSQH/HQQGHSHEDAEAGRPHVHLVRPQAARGG AAVHPCRAGRAD
3405	B	133	2369	MVSKLSQLQTELLAALLESGLSKEALI QALGEPGPYLLAGEGPLDKG ESCGGRGELAEPLNGLGETRGSEDETDDGDEF TPPILKELENLS EAAHQKAVVETLLQEDPWRVAKMVKS YLQQHNI PQREVVDTTGLNQ SHLSQH LNKGTMPKTKRAALYTWYVRKQREVAQQFTHAGQGG LIEE PTGDELPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEE CNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEEAFRHKLA MDTKVHGVRYGQPATSETAEVPSSSGGPLVTVTPLHQVSPTGLEPS HSLSTEAKLVSAAGGPLPPVSTLTALHSLEQTSPLNQQPONLIMA SLPGVMTIGPEGASLGPTFTNTGASTLVIVPTLDQSLCYISDTWVN QTDQNLSNSSREAGTKHNTSILWYLRRLPGLHAGTECAGHQHQQPD HLQP VQFSQPLHPSYQQPLMPPVQSHVTQSPFMATMAQLQSPHX*
3406	A	1	2112	MMKLGKAHCS ILDFGFLDLQCSTNSAAEFIRSWEDPWRVAKMVKS YL QQHNI PQREVVDTTGLNQSHLSQH LNKGTMPKSKRAALYTWYVRKQ REVAQPHIPIPI PENSTGTEWLIELTWLDPHTAKNDQEHRTDSPVNY GKKKGKENKNLKPPEVYVSLIKACGGPGNFCPSFSELQRNFVKHRP TKLKSLLRLVVKHWYQQWLQPHREWKEEVLDAVRTVEEFLRQEHFQK RGLDQDVRVLKVVKVGSFGNGTVLRSTREVELVAFLSCFHSF/QEAA KHKDVLRLIWKTMWQSQDLLDLGLEDLRMEQRPDALVFTIQTGT AEP\ITVTIVPAYRALGPSLPNSQPPPEVYVSLIKACGGPGNFCPSF SELQRNFVKHRPTKLKSLLRLVVKHWYQQYVKARSPRANLPPLYALEL LTIYAWEMGTEEDENFMLDEGFTTVMDDLLEYEVICIYWTKYITLHN AIIEDCVRKQLKKERPIILD PADPTLNVAEGYRWDIVAQRASQCLKQ DCCYDNRENPISSWNVKRARDIHLTVEQRG\YPDFNLIVNPYPIRK VKEKIRTRGYSGLQRLSFQVPGSERQ\LLSSR\CSLAKYGFISHTH IYLLLETIPSE\IQVFVKNPDGG\SYAYAI\NP\NSFILGLKQQIED\ HQGLPKK\QQQLEF\QQQ\VLQGLVGWGFYGIQD\SDTL\ILS\KK KGEALFPAS
3407	A	108	442	ALLSWEMSAACWEEPWGLPGGFAKRVLTGGAGF\IR*WRR*PSSGS PETPTFSRSSACPSASHMIVSLVEDYPNYMIINLDKLDYCASLKNLE TISNKQNYKFIQGDICDS
3408	A	115	1196	ALLSWEMSAACWEEP\WGLPGGFAKRVLTGGAGF\ISASHMIVSLV EDYPNYMIINLDKLDYCASLKNLETISNKQNYKFIQGDICDSHFVKL \LFETEKIDIVLHFAAQTHVDLSFRTCPWSFTHVNV/YMGTHVLVSA AHEARVEKFIYVSTDEVYGGSLDKFDESSPKQPTNPYASSKAAAE\ CFVQSYWEQYKFPVITRSSNVYGP HQYPEKVIPKFISLLQHNRKCC IHGSGLQTRNFLYATDVVEAFLTVLKKGKPGEIYNGTNFEMSVVQL AKELIQLIKETNSESEMENWVDYVNDRPTNDMRYPMKSEKIHGLRWR PKVPWKEGIKKTIEWYRENPHNWKVNEKALEPPFV
3409	A	359	532	IVMCHCLELVIGEPCHICGSVCVCVYAAVCVLCVCHTCICFGACV /CVCVCRRCVPCVCLCTYLYLLWGLCVVCYQVRVFWK
3410	A	27	1389	GQPRSQQGAGSWGKRRQESYRAREGDGGSGSLTGLLRATAAGWLLPAR ASPRERATRHVPVRSQRRARRSLQRGPERPRRDPPQTAWAARMCTKM EQPFYHDDSYTATGYGRAPGGLSLHDYKLLKPSLAVNLADPYRSLKA PGARGPGP\EGGGGGSYFSCQGS DTGPSLKLASSELE\RLIVPNSKT A\ITTTPTPP\GQYFYPRGGSGGGAGGAWGGVTEEQEGFADGFVKA LDDLHKMNHVTPPNVSLGATGGPPHGP/GIRASPEPP\PVYTNL SYSPASASSGAGAAVGTGSSY\PTTTISYLPHAPFFAGGHPAQLGL GRGASTFKEEPQTVPEARSR\DATPPVSPINMERPRAPSKLEPSGLR NRLAGHSAGKRK\LKR FARLEDKV\KTLKA\ENAGPVEVPPGLPPG

				SRLAQATRKVIDPRVSNGLSSLLFGV\RGHAFNLVPCPL
3411	A	1	3589	IRRPLDQRRGIPLRKKPLEDLVCKLADISINYVNERKSEQHLRFLST LLDSFSSSRVFIKMLLGDEKQSIQAKPLEIAKLQKNPAVQFLYQKL IGWLNEDQ\RKDFGFLVDILYSALRCCDNDMERKKVLDLTKVDLKW NSLLKIEKACPSSDKHALVTPWLKGDILGEKLVNLADCLCNEDLES RVSSSESHFSESWTLLSLVLSQHVKNLYLIGDVYVERIIVRLHETLFLK TKKLSEAESDSSVSFICDVAYNYFSSAKGCLLMPSSDILLTLFLQ CAQSKEKTHLPDFLICKLKNTWLSGVNLLVHQTDSSYKESTFLHLSA LWLKNQVQASSLDINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSV MPNDSEWEKMRQSLPMQWLHRPLLEGRLSLNYECFTDFKEQDIKTL PSHLCTSALLSKMVLIALRKETVLENNELEKIIABELLYSLQWCEELD NPPIFLIGFCEILQKMNTITYDNLRLVGNLNTSGLLQLLFNRSREHGTW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCPFLS KEEKKESPAQCIPALLGWTKKDLCTNNGGFGHLAIPMSYMLRKTKSLNK GELLHGILKIIISWKKEHEDIFLFCNLSEASPEVLGVNIEIIRFLS LFLKYCSSPLAESEWDFIMCSMLAWLETTSENQALYSIPLVQLFACV SCDLACDLAFAFDSTLTDITGNLPLVNLISEWKEFFSQGIHSLLLPIL VTVTGENKDVSETSFQNAMLKPMCELTLYISKEQLLSHKLPARLVAD QKTNLPEYLQTLNLTAPLLLFRARPVQIAVYHMLYKLMPELPQYDQ DNLKSYGDEEEEPALSPPAALMSLLSIQEDLLENVLGCIPIVGQIVTI KPLSEDFCYVLGYLLTWKLIILTFPKAASSQLRALYMSYMLRKTKSLNK LLYHLFRLMPENPTYAETAWEVPNKDKPKTFFTEELQLSIRETTMLPY HIPHLACSVYHMTLKDLPAMVRLWWSSEKRVFNIVDRFTSKYVSSV LSFQEISSVQTSTQLFNGMTVKARATTREVMATYTIEDIVIELIQL PSNYPLGSIIVESGKRVGVAVQQWRNWMQLSTYLTHQNGSIMEGLA LWKNN\VDKRFEGVEDCMICFPVIGHGFNYSLPKKAC\RTCQKKF\HS A\CLYKWTSSNKSTCPLCRETFF
3412	A	112	828	PVFKTLPSSHRAHAALDILLGASSSDPHADSGTGNAEVDPGSAQH LPRPSSQLPHFLLSGGGPGQCRRGQORGEGLLPSSGGTATPCAPRGLGW GLRSCALRAAAAAPPTAPQTLRRAPRPARPRAGPGLAPQPSISRDFL GQAACASGTMLRWLRDFVLPTAACQDAEQPTRYETLQALDRNGDGV VDIGELQEGLRNLGIPLGQDAEEVGRRRGAA* A*GGLRALGTLRGPR RAAA
3413	A	1	1413	RDARRYSGTTPHPSISRDLGQAVCASGTMLRWLRDFVLPTAACQDA EQPTRYETLQALDRNGDGVVDIGELQEGLKNLGIPLGQDAEKEIFT TGDVNKDGKLDPEEFMKHLKDHEKMKLAFKSLDKNNDGKIEASEIV QPLQTLGLTISEQQAELILQSIDVDGMTVDWNEWDRDYFLFNPVTDI EEIIRFWKHSTGIDIGDSLTPDEFTEDKKSGQWWRQLLAGGIAGA VSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVEGGIRSLWRG NGTNVIKIAPETAVKFWAYEQVMKTRLAVGKTGOYSGIYDCAKILK HEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFADKSVNP GVMVLLGCGALSSTCGQLASYPLALVRTRMQAA\MLEGSPLNMVG LFRRIISKEGIPGLYRGITPNFMKGLPAVGISYVVYENMKQTLGVTO K
3414	A	1	222	AKRLLFLLLTIVFCQILMPQEGVPAPLPPEDAPNAASLAPTPVSPVL EPFNLTSEPSDYALDLSTFLQQHAAAF
3415	A	2	528	SRVDPRVRHSARLTMCHSR\SCHPTMTILQAPTAPSTIPGPRRGSG \PEIFTFDPLPEPAADP\AGRPSASRGHRKRSRRVLYPRVVRQLP\ VEEPNP\AKRLLFLL\LTIVFCQILMAEAGVPAPLPP\EDAP\NAAS L\APTP\VSPVLEPFNLTSEPL\DYASWNLSTFLQQH\AAAF
3416	A	1623	2346	TFPSGAKPPLAASHHHRHLRDASRLWGRSGGPSVTRRPTFLPSYPP APAHAPASAPGPS\SDSCSPPSRRRSPTRTDSCFVCRPVCFPFIVP PGRAPSRMAEVLLLLLLLLSLPSAAAKIQGYTDCPCPGPQLSRDILSSGD GWWAGLSGHHRVCGGPGVQEPQTTVVHNATDGIKYIHHRLIHLTPAD YDDFVNARSARSFAFCLTPMGMQFNDILQNLKRSKQTKELWQRVSL EMATFSP

3417	A	256	658	KGLSLSKKAGENHYFYLPHSFPEKAPPGAIGHLSPRGTIEEALDLFS ARIVAEFIVLPASHHPRHLRDASRLWRGRSGGPSVTRRPTFLPSYPP APAHAPASAPGPS\SDSCSPFSSRRRSPTRLARMRGLLGF
3418	A	294	575	SHLLGLHEPSRHNRRASPGSLFCTHRRGIHSASSKPSSPTSP*CKSPR PSPGAAPRRG*LE*AGLLGFSTGFRGFPNRARRRRLGVAIAHQAP
3419	A	1	931	MTLEELVACDNAAQMQTVTAAVEELLVAAQRQDRLTVGVYESAKLM NVDPSVVLCLLAIDEEEDDIALQIHFTLIQSFCNDNDINIVRVSG MQRLAQLLGEPAETQGTTEARDLHCLLVNPHTDANKSHGLVEVASY CEESRGNNHTTPPKQPNPRGPSGAESLETEEEEEEEKGSRPPPGRR SRSWRPPIRWRRGDPGQQTGPPLRPWDGAEAGVAGHAAAFPIREG PDCPLGGGQLRDRFITKPGRRATTVTGCAGANPKLWAHMEAFQREGV LAAAPDRLGGHRSRSGSVKGA PGTTQR
3420	A	640	757	TPLPPSTTPPKQPNPRGPSGAESLETEEEEEEEKGSERT
3421	A	865	1314	TPLPPSTTPPKQPNPRGPSGAESLETEEEEEEEKGSRPPPGRRSR\ SLRPP\IRWRRGDP\GQ\QETGPP\KLRP\WDGAEA\GVA\GHAAAF PH/ITEGPRLVPLGG\GVRLTPSP\TL\LRTGAGLLHYERLWLNLVG P\CLHP\QDHTLGLGSWG
3422	A	2	310	ARDVHPLPLPFSLGNSLALGMQMRPQLLSRCRCLPATCASSCKCK ECKCTS/TARKKSCCSLNPCGLVPKCAPRACICKRGHRRSASLLRLM TGTAALLPTYK
3423	A	41	317	LLLKFFFETGSHSFIQVGQWCDHDSLDLPGSGDPSS/AS/RVAGTA GMHDHTWLIF\VFLVRRWSLTVLLRLVFNWSAKVILHLGLPKGWGLQ V
3424	A	1	3560	MLHHPSQGFRTGTRESSAEDYVRQSFPEMHEYMRRYNVPATPDGVE YLKNDPEKLDAFIMDKALLDYEVSIDADCKLLTVGKPF AIEAFFLL SQERGADEARFRTFVDSWPYTTAHMDMSLEFSDPSHLLDCPLGKTLN LYPCGFSSWNSCKLQGLPLHGMKCEVHLGPVNSFQDSQGVPLPGTRNT CFPGVDHLTSFTGKRLSSSAKMSGIGNKRAAGEPGTSMPEKKA AVE DSGTIVETIKLGGVSSSTEELDIRTLQTKNRKLAEMLDQRQAIEDEL EHIEKLERRQATDDASLLIVNRYWSQFDENIRIILKRYDL\SRAWET YSQNEKPL/CVPEPEPDSDSNQERKDDRERGWEGQEPAFSFLATLA SSSSEEMESQLQERVESRRRAVSQIVTVYDKLQEKVELLSRKLNSGD NLIVEEAVQELNSFLAQENMRLQELTDLLQEKHRTMSQEFSLQSKV ETAESRVSVLES MIDDQLQWDIDKIRKREQRLNRHLAEVLERVNSKGY KVYAGSSSLYGGTITINARKFEEMNAELEENKELAQNRLCELEKL RQ DFEEVTTQNEKLKVELRS AVEQVVKETPEYRCMQSQFSVLYNESLQL KAHLDEARTLLHGTRGTHQHVELIERDEVSLHKKL RTEVIQLEDTL AQVRKEYEMLRIEFEQTLAANEQAGPINREMRHLISSLQNHNLKLG EVLRYKRLREAQSDLNKTRLRSGSALLQSQSSTEDPKDEPAELKPD S\GTYPSPSPQQRHLRRMPKSSLNGMKKNENEGGRRRGNEKE/TR EKEKEREREKQKLKESEKERDSAKDKEKGKDDGRKKEAEI IKQLKI ELKKAQESQKEMKLLLDMYRSAPKEQRDKV\QLMAAEKSKAELEDL RQRLKDLEDKEKKENKMADEDALRKIRAVEEQIEYLQKKLAMAKQE EEALLSEMDVTGQAFEDMQEQNIRLMQQLREKDDANFKLMSERIKSN QIHKLLKEEKEELADQVLT LKTQVDAQLVVRKLEEKHLLQSNIGT GEKELGLRTQALEMNKRKAMEAAQLADDLKAQLELAQKKLHDFQDEI VENSVTKEKDMFNFKRAQEDISRLRRKLETTKKPDNVPKCD EILMEE IKDYKARLTCCCNMRKDAVLTKCFHVFCFECVKTRYDTRQRKCPK CNAAFGANDFHRIYIG
3425	A	94	203	PLNFRPIFPVIFGISCSRIFKQVFRACVRPSHSDFL
3426	A	3	343	RSAAGIRHEVSSAPGLGFGGAGMRSLLSVGLPPIPIGRGCHFTLITA FLYCTRVGRKGTCAVPPDLPVSASTFGTSCLRQEAAAEGRPVVRGW WWPARLISSKEQGFPALIL
3427	A	2	256	FVGKSGEGIVSIIKSVA VGGTNAPTTEAGRKLSSGARAQRPELPK QRGFGDGGFVRNRTKSRWWGIFDILRSRTTG AHETD
3428	A	245	691	CGGGRGVAGASVCRGGRVPVRVSSAPGLGFGGAGMRSLLSVGLPPIPI

				IGRECHFTLITVFLYCTRVGRKGTVCAPPDLVPSASTFGTSCLRQEA AAEGRPVVRFDKIQSCQVKT\VR\REMEGSWDLIDDALEKTSCL MRMSAIPLN
3429	A	781	949	LLCLGLAYRRHFEMSLWLGMAHVCNPSAWGGRRGGQIT/R/QGEFET SLVNMVKTCLY
3430	A	3	1029	RAFRFDDTMAGGGCRAGPGATCSGDAGSDQRQNEEIEAMAAIYGEE WCVIDDCAKIFCIRISDDIDDPTWTLCVHMLPNEYPCAPPIYQLN APWLKGQERADLSNSLEEIYIQNIAESILYLWEKIRDVLIQKSQMT EPGPDVKKKTEEDVECEDDLILACQPESLKLALDF\EVSEARTEVE VEELPPIDHGIPITDRRSTFQAHLPVVCCKQVKMGLSKLYENKKIA SATHNIYAYRIYCEDKQTFLODCEDDGETVAGGRLLHMEILSVKDV MGVRARWYVGMGLGPDRFKHINNCV\RNILVEKNYTSSLEESSKALG KNKKVRKDKKRNEH
3431	C	153	224	MVAHACNPSTLGDRGGFRTRSGD*
3432	C	20	58	MTQLTKRKETIL*
3433	A	837	1125	LDVTTSKNQFVLRWTWKIPGNCYRRHFFFFETESCSVAQAGVQWHNL SSLQAPPPG\SRHSPTSAS\QAAGTYRYPAHHAWPNFVFLVETGF HPC
3434	A	3	474	DGSIMASMQRKRLQKELLALQNDPPPGMTLNEKSVQNSIT\QWIVYME GAPCTLYEGEKQLLFKCRRRYPFDSSQGMFTGENITDHPHVYSNGH MCLSILTKNWFPAHSVQSVCL\SIISMLSSCKE\KTTHDPDNSFYVR T\CNKNPKKTKWYHDDTC
3435	A	1	993	MAATPPHRAGPNPCRHSRHLSEGREETRTHPHSPHTHGGGVEGPAPP ASRLQORDKVTHPGARQRCALTRARRPRASDAGSSSSSRRRRRRHL RPSTSADGGRERVAALKRVLYLVWAFIPESWLNSLGLTYWPQKYWAV ALPVYLLIAIVIGYVLLFGINMMSTSPLDSTHTITGHERNTNVLQTM GSSVFEGHDQFSVTVTGDPMARAGRSQLEPHSDSDATLQLHCSQPTC VIKPVYTKPSILEAAVSQPASAAAAAPRGPSLPVILWFLRQPLNLV SECTMGGHILGKVQSLTPHHHSVKDLRTWQELKCSVYLIADGARFSS AA
3436	A	157	501	SPRKNGGKFTVAIARKSDLWLCFSLKLPWLQKSEGISCLLSVPCAS TSLGGFSLYKLYSTRDGKVDKAWVPALKEVVVLWRRQTVLYLVWG \FIPESWA*TL*GLTYWPPKY
3437	A	48	544	GGENGSMVSRSTSLTLIVFLFHRLSKAPGKMVENSPPSPLPERAIYGF VLFLKLP\GFILYLWALIPESWLNSLGLTYWPQKY\WAVALPVYL LIAVVIGYVL\FGINMMSTSP\PTSHTITDNYAKNQKKYQEEA IPALRDISISEVNQMFFLAACKELYTKN
3438	A	56	291	SAFGLLLAWFRFLAAKQAKNVALDCGGVSRLVIFVSWRNPQVAPSTA HQNRPSRNPVSRPPNTQVRARRKHYALADGY
3439	A	468	993	VLLACFWPGSDFWPRSRRKTYGTAPQSCYSFYVALDCGGVSRLVIFV SWRNPQVAPSTA HQNRPSRNPVSRPPNTQVRARRKHYALADGYTERR WTNAPCRAESSFPNCPSAAPIPDSYDK*PSRATLFTSHLTVEAFPV WSYLYPGETPRLHPRAHTRTPAAIRYPDRQTPNGLRGANTMHSQMD TLNGDGRTHLAGQRARSPTARPQQRQYRIHTTSDLPGLVRKYASGCC LRIWYCCAWIERALSLQVGGGVFGDPLSEGQAECDHGST
3440	A	1	3114	MLQQDSNDDTKDVSFLDAEEETTNRPRVKIRHPVASFFHLFFRVSA IIVCLLCELLSSSFITCMSKKWLAVVIVGVVLQGANLYGYLRCKGQE VRETFAEPSLQATQMKLKRARLADDLNEKIAQRPGPMELVEKNILPV DSSVKEAIIIGKTLKIYYLGAPAEAAATKEDERTTSGPGHHATNYHFL KDFDYLWHLFVHKDAILSGHPLVRLSTRVLRGPNDVFHGVSSVDS VLAIFVLAEPMGSLASLENQLEAFDGTLPANEIPPLQSSSEDRE PFSLIEDLQNDLLSHSGMLDHSHPMETSETQFAAGFRLLRQNRKP GQKQPKGTLEQTSEYPGNRGIPIIRQSLVFRVSVTGTTVNFCDASTN HNRVFKVLQALPLDSLHNVLVFLSMPVVAFSVINIVLTLSSFLWLN PLACLFILARLHQYFIMTYGIVIDRSMIANIIDTTAPESYALMTTPM SSTLGFSGVLAALIAEWIQUIKPATSRRLSVLFRGANILVSVLLILV

				AALFYKDYASLFRNNKELVKSLSPSNSIVASWSWYSHQRLANLPLVR IGEDAHNRNPLMQNEQRKNLTILMVGATSRAENFSLNGYPRETNPRLA KDNVVYFPNTASCGTATAVSVPCMFSDMPREHYKEELAQHQEGVARI SFSEASTVLWNDNDGGCKGACDRVGCLNLVYIGEACNDHLAKKPPK GQREKHLPGATTEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAE NYIPNRVAQQLAGKQSLIGVATSSSLALHAPSQIVAAIKSRADQLGA SVVSMVERSGVEACKAAVHNLLAQRVSLIINYPLDDQDAIAVEAA CTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLA GPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTML NEGIVPTAMLVAFRLRVCAVVTSPSLSPSLAPVPSVAAAALLVLSLS PVKTKPVVEHKYAGGQCLVHIQALMNEDTEKHQVHYSTPKCGRHAQW SDAY
3441	A	3	401	TSSLSLSGKSGRYIVFLRRSVGIQSPSAVATVRLLLAGSDRRFAAGS AGCAVLSRAERS*EPGCCYRIRRSARLRAIGSIRNRDKPVAWPDTS GDNTEVYFRAHQAGILPDTVLGPAQRVAVSGGTPVDW
3442	A	2874	3062	GNRAGALPGATLLILAGFLPSAHQNRPSRNPVSRPPNTQVRARRKH ALADGYTERRWTNAP
3443	A	2766	3323	MPDLVEGREKSDKGAQPQRTQSRARSARTNGSGVRILHSLWRIIGIPL LLGYSLVCSRVLLACFWPGSDFWPRSRRKTYGTAPQSCYSFYVALDC GGVSRLVIFVSWRNPQVAPSAHQNRPSRNPVSRPPNTQVRARRKH ALADGYTERRWTDAPCRAESSFPNCP*QRYRIHIVDASVCGP
3444	A	968	1441	PESFSCIAAERFLARRRKKSEVTSRPKQARAWRPVLKASDGKARL AVCCRRWSRDLALSPGRPPAPVPGIRSPRMSSEFFLGLFGHSWPVAT ERTFFPARVSPAGDSGLLSRDAGTPVACEASFIFIAPSSPCRIIPG SGRNEGLLLLASTGTS
3445	A	3	640	LSVVRSRIHMGVGVGVCVPVRYRNQDDHELQITHGNKILCGIVCDKG AQPQRTQSRARSARTNGSGVRILHSLWRIIGIPLLLGYSLVCSRVLLA CFWPGSDFWPRSRRKTYGTVPQSCYSFYVALDCGGVSRLVIFVSWRN PQVAPSAHQNRPRNPVSRPPNTQVRARRKHYPADGYTERRWTI APCRAESSFPNCP*SAAPIPDSYDK
3446	A	1	3140	MVYKMRYSQHPYSIKEKQMKSEVLSVKEKIGYGMGDAASHIIFDNV MLYMMFFYTDFIGIPAGFVGTMLFLVARALDAISDPCMGLLADRTRSR WGKFRPWVLFALPFGIVCVLAYSTPDLSMNGKMIYAAITYTLLTLL YTVVNIPYCALGGVITNDPTQRIISLQSWRFVLATAGGMLSTVLMMP VNLIGGDNKPLGFQGDLSPMFSTPEBIARPGPYENDVHVVGASSLAA GHKTLIPELVRSAEQHMGTTRYLRGRRVAVIIPPTGLRLPARARQWR FMVQHTRPBGHDAGGKASPRHQALSTQLLDAIMPYCGNTLRLGVGTGP GAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSILGDKTRMND LARAEEAFIRPVPSSGHLGGASQRARELMLLCEAGYDVIVETGVV GQSETEVARMVDCFISLQIAGGGDDLQGIKKGLMEVADLIVINKDDG DNHTNVAIARHMSRVPCIFCDDRLCIVFLETLRSTCFLEPLWPICCP RTAMATLGPRNRYGFDPLAVSSGTRSCSLGVPRHRFALAGSRDPGY THKRVLAIFQAFNAFPEPPANTPEDPAGLSLLPSGHTSAREPGLCLP INSLCPIVQSLWPSSLRSTQPLTPLPSCPSQAHPGSAVPCGAAWYP AGHTRKLPGVFSQRPRSHGGGTRWHSSTSVGTDQAAGTGADSPGRS DARRQGSAGKRAAGPSLQSQDGDPTSRQQGHSAAAGNRGRAGFG QRHRAERQQLWGPSSREGGVGAREEQEQFGDRGSGVAGLESGRSGD WLPQFAGQWPRLEAVSQRRAAHAGRTAAACGYCTHFGGLSEYLCY WGIRWFVLECFWPAFGLVPIFGRRSRKTYGTVPQSC*LFLLRT*\R GGVSRLVIFVSWRNPQVAPSAHQNRPSRNPVSRPPNTQVRARRKH ALADGYTERRWTNAPCRAESSFPNCP*SAAPIPDSYDK*PSRSGVLI KACLRARAPTRYPVYRT
3447	A	750	1340	ILHAPAPPFSASASHEQPEWSDKGAQPQRTQSRARSARTNGSGVRILH SLWRIIGIPLLLGYSLVCSRVLLACFWPGSDFWPRSRRKTYGTAPQ CYSFYVALDCGGVSRLVIFVSWRNPQVAPSAHQNRPSRNPVSRPPN TQVRARRKHIALADGYTERRWTNAPCRAESSFPNCP*FAAPIPDSYD

				K*PFRIVS
3448	A	93	699	RASVQQKKLSTDDKGAQPQPRQTQSRARSARTNGSGVRILHSLWRIIGIP LLLGYSLVCSRVLACFWPGSDFWPRSRRKTYGTAPQSCYSFYVALD CGGVSR\RSYLYPGETPRVAPTSAHQNRPSRKPG\TRPNTQRVARR KHYALADGYTER\SATNAPCRAESSFPPELPVPQVPNTGFIQVTFR DCFVNTQPAAASGFW
3449	A	1000	1530	QRYSDNPPNDKGAQPQPRQTQSRARSARTNGSGVRILHSLWRIIGIPLLL GYSLVCSRVLACFWPGSDFWPRSRRKTYGTAPQSCYSFYVALDCGG VSRLVIFVSWRNPQVAPTSAHQNRPSRNPVSRPNTQRVARRKHYAL ADGYTERRWTNAPCRA/VEFPFPNCPWEAQYRIIRK
3450	A	106	375	LGPGKSLLCGYLVAMTDVETTYADFIASGRTGRRNAIHDILVSSASG NSNELALKLAGLDINKTEGEEDAQRSSTEQSGEAGQGEAAKSES
3451	A	232	376	KKGVLSCVRRHSMET*NEKPALLKMSGIKIPSPVHHFVPHKQSEKGA V
3452	A	481	781	IKDKKVSNSQLLCGYLVAMTDVETTYADFIASG\RTGRRNAIHDILV SSASGNSNELALKLAGLDINKT\EGEEDAQRS\STEQSGEAGQGEAAK SESLTPHF
3453	A	15	369	RVGEYDGYEAGPAPCPPRASLCQ/PGPDQGPSPCTQAIAPARKPHPC PWPQGPKKLGELPGLCLQGSPTAGHPCCPPQETGAQGGAPASPWFSQ NNAACGLICFCPPQPRIFLCINSNS
3454	A	201	711	KKMARTKQTARKSTGGKAPRQTAG/LATKAARKSAPSTGGVKKPHRY RPG\TVALREIRR\YQKSTE\LLI\RKLPFOR\LVREIAAGFSKTAL R\FQSARIRCACRRILAKRYLVGLFED\NNLC\AIHAKRVTIHAPKTI Q\LARDDTGEKRALSEGSFYGVLLVKFLLKYFGLIC
3455	A	758	1188	GKLSGRGTGSLLRGDALPRLQKTGCPKAGGNRPAPVQSRRGAVRDE GLLAQTAEGGPRVEEARPPQLPQARGSLPETPPPPAPDA\TPPPPS GSHISPSAEGPSRPPVGAVDSSGAPQPQDPG\PAPAPALLRHRHQ TPRP
3456	A	2	297	ACVPKTCPSYFHCNDGNCIHRWLCDRNDNDCGMSDEKDCPTQPFR CPSWQWQCLGHNICVNLSVVCDDGIFDCPNGTDESPLCSKFPDHSLLA INSF
3457	A	1	1128	MPIENVSGTEIGWRAQRGTIPLQCGGRDSDVNEGEWPAWTWTRGIER MPRLCCHLAEPLPVAGYSGYSFCQDLTAVLTRFPVPLCKQICSHLC LLRPGGYSCACPQGSSEFIEGSTTECDAAIELPINLPPPCRCMHGGNC YFDETDLPKCKCPSGYTGYCEMAFSKGISPGTTAVAVLLTILLIVV IGALAIAGFFHYRRTGSLLPALPKLPSLSSLVKPSSENGNGVTFRSGA DLNMDIGVSGFGPETAIIDRSMAMSEDFVMEMGQPIIFENPMYSARD SAVKVVQPIQGRKHSEWSMLQLPYLQEQDQPKDIRPENNNQNPVLLHS GGGLAAMPGCWPRTFHFCEWCQSKRGLSPFRGLGNTVPEAPQLLYKYL
3458	B	58	1282	MRTLLKNTVIVLLPYKSGKLYGESSTELNVEVLNCTASQFKCASGD KCIGVTNRCDGVFDCSDNSDEAGCPTRPFGMCHSDEFQCCQEDGICIP NFWECDGHPDCLYGSDEHNACVPKTCPSYFHCNDGNCIHRWLCDR DNDGCGMSDEKDCPTQPFRCPSWQWQCLGHNICVNLSVVCDDGIFDCP NGQMSPHFALVAAAVDWLSQDSKWLQDSHIVPDVKLCVVASAYRQSY QSLGNDISLGYRCQPKFSRSIDPTGKAVQTADIRLSARATLWLGSSI EESPVLCSTLRLRLRPLTWTSNRPRTQPCATQQTQNSVGI PSAIRVIYPESVVLNAVIYLPGDPEVSGLPRAFRRFSVEVRLDCGT FKLLLVYCTHPGDIKVNTCKTGALVAFRCFLPX*
3459	A	1	1870	MGKVPMRSEKPAHEVRRASTISTPDLSSIESFFSRGPESTNHTSIKG RPLTAELKNKTNRABEKKKEELAISGVDEDDGGKGIKDTGDLVEMV DLAFRCDRHNDGCDYSDERGCLYQTCQQNQFTCQNGRCISKTFCVDE DNDGCGDSDELMHLCHTPEPTCPPHEFKCDNGRCIEMMKLCNHLDDC LDNSDEKGCGEFIFRASSPGAILILIVAVSTIHAITDPRLGNALPV RRIVQPQYSWTPLTLKLWASRVSNCCQLLSAAKTHHTVQFSILMALP KGHLFSARLTGKCVAVQVIVEGFFAGRDKFVCLNVAFVVPYQFVLSLV RTGTASKSTVGFYRNINISVITGFLIGFLCQSSALDLETFTTVVSHFYF

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				GINECHDPSISGCDHNCTDTLTSFYCSCRPGYKLMSDKRTCVDIDEC TEMPFVCSQKCENVIGSYICKCAPGYLREPDGKTCRQNSNIEPYLIF SNRYYLRLNLTIDGYFYSILILEGLDNVVALDFDRVEKRLYWIDTQRQV IERMFLNKTNKETI INHRLPAAESLAVDWVSSALKGGFVHP/LNGGS QHFTLLVD*VIKWLILISNSVPC*KRRWGLPVFWFGGKREMSWEMMG H*LVEGLCGCCH
3460	B	1	2973	MEKQSIHQQLPYPDQLPTQCSPLTGLNEYPLSGVSI PDESWDKSKH SAAMTLRQVHQHQNFLDHNNTNVEEYSAQMRIGTHCCCTSSSESL LLVASQNKIIADSVTSQVHNIYSLVENGSYIYAVDFDSISGRIFWSD ATQGKTWSAFQNGTDRRVVFDSSIILTETIAIDWVGRNLYWTDYALE TIEVSKIDGSHRTVLISKNLTPRGLALDPRMKLLYFMDSYLDYMDF CDYNGHRRQVIASDLGFEVGP KLLALPPQLVLTESSTCRPGDWPAS PLEPPPTSMHTACDPENHLTSATAITYAMSAVQGRNALHVDVDVSSG FIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGIGENGVRGIAVDW VAETKIERSFLDCTNRTVLVSEGIPTPRGLAVDRSDGYVYVWDDSLD IIARIRINGENSEVIRYGSRYPTPYGITVFENSIIWVDRNLKKIFQA SKEPENTEPPTVIRDNINWLRDVTIFDKQVQPRSPAENVNNPCLENN GGCSHLCFALPGLHTPKCDCAFGLQSDGKNCAISTENFLIFALSNS LRSLHLDPENHSPPFQTINVERTVMSLDYDSVSDRIYFTQNLASGVG QISYATLSSGIHTPTVIASELQMKLLNLHSAGPRQRIERSTLTGVDR EVIVNAAVHAFGLTLYGQYIYWTDLYTQRIYRANKYDGSQGIAMTTN LLSQPRGINTVVKNQKQQCNNPCEQFNGGCSISVHQWKNFLSVRFS KHGWFI SVSKDLMKNDQPFLITVRQHIIFGISLNPEVKSNDAMVPIA GIQNGLDVEFDDAEQYIYWVENPGEIHRVKTGNTNRTVFASISMVGP SMNLALDWISRLYSTNPRQTQSIEVLT LHGDIRYRKTLIANDGTALG VGFPIGITVDPARGICISTVTNTNSCKAETNFETTEAVMEGEGTQHV GNGNAGCVGVGGGDAASQTKSTNTYIVILDSGYCLNPLGLLSRKNY LLS*
3461	A	257	3561	RHKKPFKKSMNPGAG/MLYWSAQGTDSGVPKIASANMDGTSVKTFL TGNLEHLECVTLDIEEQKLYWAVTGRGVIERGNVDGTDRLMLVHQLS HPWGLIAVHDSFLYYTDEQYEVIERVDKATGANKIVLRDNVNLRLGLQ VYHRRITEP/CPN*PKTIKIGHYIKDKPTCSSE/AKWYLPHPGQM*I A/DKPEAQGRSRLTDLEGGNNEIDWSISCDCIYPSQVFDLSAKIE GKVDKRTCCPSSFPKGYGPIAKNSQVYESSANTDSVAVVGGVCFAL WSSRVAGLRRVQREETQLEEFYTNPCKGTNQDSRER/NWP*RRNKY SYP*KWLSAPCSAKVHSAARE*GSCHTLS*WSYQATMFECKNHVC IPPYWKCDGDDDCGDSDEELHLC LDVPCNSPNRFRCDNNRCIYSHE VCNGVDDCGDGTDETEEH\HCRNTKGSYECVADGFTSMSDRPGKRC AAEGSSPLLLLPDNRIRKYNLSSERFSEYLQDEEYIQAVDYDWDPK DIGLNSNNNKRQI/CLSSF*VFC*GSLLVTPNLYNREEQKSECCSC PCLRPWPIHSNNRS/SMLRS/CEDKASTCKRELSIGDDDSYLRPIDG QAIGPSKSSVYRQECQDQNDGQDNDSEENCAPRECTESEFRVNNQ CIPSRWICDHYNDGDNSEDERDCEMRTCHPEYFQCTSGHCVHSELKC DGSADCLDASDEADCRNPYFTFTWYRLSALGPGVCPAGFSDSTFPYTK NASRNSKLKVRFSSTHLQIMLQGIKITHYKVTW/ISLQTKI*TNQ L*KSNLCT/DWRTSKRKVLLRHLHLRLSLLSLLREETQLQF/NS ATEDTFKDTANLVKEDSEGERAHACHFLEFSVDFFPDNCPPWCFA KEVLY/ASLCRCIPIWWKCDGQKDCSDGSDELALCPQRFRCRLGQFQC SDGNCTSPQTLCAHQNC PDGSDERLLC\CANKRCIPESWQCDTFN DCEDNSDEDSSHCASTRCPGQFRCANGRCIPQAWKCDVDNDCGDHS DEPIEECMSSAHLCDNFTEFSCKTNYRCIPKAVCNVDDCRDNDSE QCGGAKGSGSADTTWTL LAVEAAVQKALEGLRFAGVFC
3462	A	1	10725	MAGAPPPASLPCCSLISDCCASNQRDSVGVGPSEPGVGYSLVRRFL SRSEKRNIRVGVTFRSRELPLRFP EHLFFTDWRLGAIIRVRKADG GEMTVIRSGIAYILHLKSYDVNIQTGSNACNQPTHPNGDCSHFCFPV PNFQVRVCGCPYGMRLASNHLTCEGDPTNEPPTQCGFLSFPCKNGR

				<p> VPNYLDCGVDDCHDNSDEQLCGTLNNTCSSSAFTCGHGECIPAHWR CDKRND CVDGSD EHNCPNPTQPASCLDTQYTCDNHQCISKWVCDTD NDCGDSDEKNCILNCTASQFKCASGDKCIGVTNRCDGVFDCSDNSD EAGCPTRPPGMCHSDEFQCCQEDGICIPNFWECGDGHPDCLYGSDEHNA CVPKTCPPSSYFHC DNNGNCIHRALWCDRDND CGDMSDEKDCPTQPFRC PSWQWQCLGHNICVNLSVVC DGI FDCPNGTDESPLCNGNSCSDFNNG CTHECVQEPFGAKCLCPLGFL LANDSKTCEDIDEC DILGSCSQHCYN MRGSFRCS CDTGYMLES DGR TCKVTASES LLLL VASQNKI IADSVTS QVHNIYSLVENGSYI VAVDFDSISGRIFWSDATQGKTWSAFQNGTDR RVVFDSSII LTETIAIDWVGRNLYWTDYALETIEVSKIDGSHRTVLI SKNL TNPRGLALDPRMNEHLLFWSDWGHHPRIERASMDGSMRTVIVQ DKIFWPCGLTIDYPNRLLYFMDSYLDYMDPCDYNGHHRQVIASDLI IRHPYALTLFEDSVYWTD RATTRVMRANKWHGGNQSVMYNIQWPLG IVAVHPSKQPNYDQFLITVRQHII FGISLNPEVKNSDAMVNIQWPLG NGLDVEFD DAEQYIYWVENPGEIHRVKT DGTNR TVFASISMVGPSMN LALDWISRNLYSTNPRTQSIEVLT LHGDIRYRKT LIANDGTALGVGF PIGITVDPARGKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTGNLE HLECVTL D IEEQKLYWAVTGRGVIERGNVDGTD RMILVHQLSHPWGI AVHDSFLYYTDEQYEVIERVDKATGANKIVLRDNVNP NLRGLQVYHRR NAAESSNGCSNMNACQQICLPVPGGLFSCACATGFKLNPDRSCSP YNSFIVVMSLSAIRGFSLELSDHSETMVPVAGQGRNALHVDVDVSSG FIYWCD FSSSVASDN AIRRIKPDGSSLMNIVTHGIGENGVRGIAVDW VAGNLYFTNAFVSETLIEVLRINTTYRRVLLKVTVDMPRHIVDPKN RYLFWADYGQRPK IERSFLDCTNR TVLVSEGI VTPRGLAVDRSDGYV YWVDDSLDI IARIRINGENSEVIRYGSRYPTPYGITVFENSI IWVDR NLKKIFQASKEPENTEPPTVIRDNINWLRDVTIFDKQVQPRSPA EVN NNPCLENNGGCSHLCFALPGLHTPKCDCAFGLTQSDGKNCAISTENF LIFALSNSLRSLHLDPENHSPPFQTINVERTVMSLDYDSVSDRIYFT QNLASGVGQISYATLSSGIHTPTVIASGIGTADGIAFDWI TRRIYYS DYLNQMIN SMAEDGSNR TVIARVPKPRAIVLDP CQGYLYWADWDTHA KIERATLGGNFRVPIVNSSLVMP SGLTLDYEEDLLYWVDASLQRIER STL TGVDREVIVNA AVHAFGLTLYGQYIYWTDLYTQRIYRANKYDGS GQIAMT TNL LSQPRGINTVVKNQKQQC NNPC EQFN GGC SHI CAPGN GAECQCPHEGNWYLAN NRKHCIVDNGERCGASSFTCSNGRCISEEWK CDNDND CGDGSDEMESV CALHTCSPTAFTCANGRCVQYSYRCDYND CGDGSDEAGCLFRDCNATTEFCNNRRCIPREFICNGVDNCHDNNTS DEKNCP THTCSSSEFQCASGRCIPQHWYCDQETDCFDASDEPASC GH SERTCLADEFKCDGGR CIPSEWICDGDND CGDMSDEDKRHQCQNQNC SDSEFLCVNDRPPDRRCIPQSWVCDGDVDCTDGYDENQNCTRTCTSE NEFTCGYGLCIPKIFRCDRHND CGDYSDERGCLYQTCQONQFTCQNG RCISKTFV CDEDNDCGDGSDELMHLCHTPEPTCPPHEFKCDNGR CIE MMKLCNHLDDCLDNSDEKGC GINECHDPSISGCDHNCTDTLTSFYCS CRPGYKLSMDKRTCVDIDECTEMP FVCSQKCENVIYSYICKAPGYL REPDGKTCRQNSNIEPYLIFSNRYYLRNLTIDGYFYSLILEGLDNVV ALDFDRVEKRLYWIDTQRQVIERMFLNKTNKETIINHRLPAAESLAV DWVSRYLWADWGH RAYIGRVGMDGTNKSVIISTKLEWPNGITIDYT NDLLYWADAHLGYIEYSDLEGHHRHTVYD GALPHPF AITIFEDTIYW TDWNTRTVEKG NKYDGSNRQTLVNTTHRPFDIHVYHPYRQPIVSNPC GTNNGGCSHLCLIKPGGKGFTCECPDDFRTLQLSGSTYCMPCSSSTQ FLCANN/EKCLSSPWTID LQSGKGWEFSRPRESSCMSFLGIQC*LL LSR*LLPLVLC*RS AVCSLCRCIP IWWKCDGQKDCSDGSD ELALCPQ RFCRLGQFQCS DGNCTSPQTL CNAHQNC PDGSDEDRLLC\ CANKRCI PESWQCDTFND CEDNSDEDSSH CASRTCRPGQFR CANGRCIPQAWKC DVDNDCGDHSDEPI EECMSSAHLCDNFTEFSCKTNYRCIPK WAVCNG VDDCRDNSDEQGC EERTCHPVGDFRCKNHHCIPLRWQCDGQND CGDN SDEENCAPRECTESEFR CVNQ CIPSRWICDHYNDCGDNSDERDC EM RTCHPEYFQCTSGHCVHSELKCDGSADCLDASDEADCPTRFPD GAYC </p>
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				<p>QATMFECKNHVCIPPYWKCDGDDDCGDGSDEELHLCCLDVPCNSPNRF RCDNNRCIYSHEVCNGVDDCGDGTDETEEHCRKPTPKPCTEYKYKCG NGHCIPHNDVCDADDDCGDWSDELGCNINECEQFGTQPCQHCNRTKGS YECVCADGFTSMSPRGKRCACAEAGSSPLLLLPDNRIRKYNLSSERF SEYLQDEEYIQAVDYDWDPKDIGLSVVYYTVRGEGRFAGIKRAYIP NFESGRNNLVQEVDLKLKYMOPDGIADVWVGRHIYWSDVKNKRIEV AKLDGRYRKWLITDLDQPAIAVNPGLGFMFTDVGKEPKIESAWM NGEDRNILVPEDLGWPTGLSIDYLNNDRIYWSDFKEDVIETIKYDGT DRRVIAKEVPNLCKQICSHLCLLRPGGYSCACPGSSPIEGSTTECD AAIELPINLPCCRCMHGNCYFDETDLPCKCPSGYTGKYCEMAFS KGISPGTTAVAVLLTILLIVVIGALAIAGFFHYRRTGSLLPALPKLP SLSSLVKPSENGNGVTFRSGADLNMDIGVSGFGPETAIIDRSMAMSED FVMEGKQPIIFENPMYSARDSAVKVVQPIQVTVSENVNDKNYGSPI NPSEIVPETNPTSPAADGTQVTKWNLFKRKSQYTNFENPIYAQMEN EQKESVAATPPPSPLPAKPKPPSRDPTPTYSATEDTFKDTANLVK EDSEV</p>
3463	A	3	14105	<p>SWRRCRPGKAFASGAAGAVCYARPPPGEGTARPGTIAEMDRGPAAV ACTLLALVACLAPASGOECDSAHRFCGSGHCIPADWRCDGTOKDCSD DADEIGCAVVTCQQGYFKCQSEGQCIPSSWVCDQDQDCDDGSDERQD CSQSTCSSHQITCSNGQCIPSEYRCDHVRDCPDGADENDCQYPTCEQ LTCDNAGACYNTSQKCDWVKVDCRDSSDEINTEICLHNEFSCGNCECI PRAYVCDHDNDQDGSDEHACNYPTCGGYQFTCPSGRCIYQNWVCDG EDDCKDNGDEDGCEGPHDVHKCSPREWSCEPESGRCSIIYKVCGLIL DCPGREDENNTSTGKYCSMTLCSALNCQYQCHETPYGGACFCPPGYI INHNSRTCVFDDCQIWGICDQKCESRPGRHLCHCEGYILERGQY CKANDSFGEASIIFSNGRDLIGDIHGRSFRILVESQNRGVAVGVAF HYHLQRVFWDTVQNKVFSVDINGLNIQEVNLVSVETPENLAVDWN NKIYLVETKVNRIIDMVNLDGSYRVTLITENLGHPRGIAVDPTVGYLF FSDWESLSGEPKLERAFMDGSNRKDLVKTLGWPAGVTLDMISKRVY WVDSRFDYIETVYTDGIQRKTVVHGGSLIPHPFGVSLFEGQVFTDW TKMAVLKANKFTETNPQVYYQASLRPYGVTVYHSLRQPYATNPCKDN NGGCEQVCVLSHRTDNDGLGFRCKCTFGFQLDTERHCAVQNFLIF SSQVAIRGIPFTLSTQEDVMVPVSGNPSFFVGIDFDAQDSTIFFSDM SKHMIFKQKIDGTGREILAAANRVENVESLAFDWISKNLWYTDSHYKS ISVMRLADKTRRTTVQYLNNPRSVVHPFAGYLFFTDWFPAKIMRA WSDGSHLLPVINTTLGWPNGLAIDWAASRLYWDAYFDKIEHSTFDG LDRRLGHIEQMTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGEMT VIRSGIAYILHLKSYDVNIQTGSNACNQPTHPNGDCSHFCFPVPNFQ RVCGCPYGMRLASNHLTCEGDPTEPPTEQCGLFSFPCKNGRCVPHY YLCDGVDDCHDNDSEQLCGTLNNTCSSSAFTCGHGECPAHWRCDKR NDCVDGSDENHNCPTHAPASCLDTQYTCDNHQICISKNWVCDTDNDGCD GSEKNCNSTETCQPSQFNCNHRCIDLSFVCDGDKDCVDGSDVGC VLNCTASQFKCASGDKCIGVTNRCDGVFDCSDNSDEAGCPTRPFGMC HSDEFQCQEDGICIPNFWECGHPDCLYGSEHNACVPKTCPSYFHC CDNGNCIHRWLCDRDNDCGDMSDEKDCPTQPFRCPSWQWQCLGHNI CVNLSVVCDFIDCPNGTDESPLCNGNSCSDFNNGGCTHECVQEPFGA KCLCPLGFLANDSKTCEDIDECDILGSCSQHCYNMRGSRFCSCDTG YMLESDGRCTCKVTASESLLLLVASQNKIIADSVTSQVHNIYSLVENG SYIVAVDFDSISGRIFWSDATQGKTWSAFQNGTDRRVVFDSSIIILTE TIAIDWVGRNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLAL DPRMNEHLLFWSDWGHHPRIERASMDGSMRTVIVQDKIFWPCGLTID YPNRLLYFMDSYLDYMDFCDYNGHRRQVIASDLIRHPYALTFLFED SVYWTDRASTRVMRANKWHGGNQSVVMYNIQWPLGIVAVHPSKQPNS VNPCAFSRCSHLCLLSSQGPFFYSCVCPSGWSLSPDLLNCLRDDQPF LITVRQHIIFGISLNPEVKSNAMVPIAGIQNGLDVEFDADAEQYIYW VENPGEIHRVKTDTGNRTVFASISMVGPSMNLALDWISRNLYSTNPR TQSEIVLTLHGDIRYRKTLIANDGTALGVGFPIGITVDPARGKLYWS</p>

				DQGTDSGVPAKIASANMDGTSVKTLFTGNLEHLECVTLDIEEQKLYW AVTGRGVIERGNVDGTDRLMILVHQLSHPWGIAVHDSFLYTTDEQYEV IERVDKATGANKIVLRDNPVNLRLGLQVYHRRNAAESSNGCSNNMNAC QQICLPVPGGLFSCACATGFKLNPDRSCSPYNSFIVVSMLSAIRGF SLELSDHSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNA IRRIKPDGSSLMNIVTHGIGENGVRGIAVDWVAGNLYFTNAFVSETL IEVLRINTTYRRVLLKVTVDMPRHIVVDPKNRYLFWADYGQRPKIER SFLDCTNRTVLVSEGIPTPRGLAVDRSDGYVYVWDDSLDIARIRIN GENSEVIRYGSRYPTPYGITVFENSIWVDRNLKKIFQASKEPENTE PPTVIRDNINWLRDVTIFDKQVQPRSPAENVNNPCLENNGGCSHLCF ALPGLHTPKDCAFGTLQSDGKNCAISTENFLIFALSNSLRSLHLDP ENHSPPFQTINVERTVMSLDYDSVSDRIYFTQNLASGVGQISYATLS SGIHTPTVIASGIGTADGIAFDWITRRIYSDYLNQMINSMADGDSN RTVIARVPKPRAIVLDPCQGYLYWADWDTHAKIERATLGGNFRVPIV NSSLVMPGSLTLDYEEDLLYWVDASLQRIERSTLTGVDREVIVNAAV HAFGLTLYGQYIYWTDLYTQRIYRANKYDGGSGQIAMTTNLLSQPRGI NTVVKNQKQCCNNPCEQFNGGCSHICAPGPNGAECQCPHEGNWYLAN NRKHCIVDNGERCGASSFTCSNGRCISEEWKCDNDNDGCGDSDEMES VCALHTCSPTAFTCANGRCVQYSYRCDYNDGCGDSDEAGCLFRDCN ATTEFCNNRRCIPREFICNGVDNCHDNNTSDEKNCPRDTCQSGYTK CHNSNICIPRYLDCGDNDGDNNDENPTYCTTHTCSSSEFQCASGR CIPQTFGICDQETDCFDASDEPSSCGHSERTCLSEFKCDGGRCIPN EWICDGDNDGDMSEDEKQHCQCNQNCSDSEFPVCVNDRPPDRRCIPQ SWPPDGDVDCDGHDEIQNCTRRTCSENEFTCGYGLCIPKIFRCDRH NDCGDYSDERGCYQTCQCNQFTCQNGRCISKTFVCDENDCGDSGD ELMHLCHTPEPTCPPHEFKCDNGRCIEMMKLCNLHDDCLDNDSEKGC GINECHDPSISGCDHNCTDTLTSFYCSCRPGYKLSMDKRTCDVIDEC TEMPFVCSQKCEENVIGSYICKCAPGYLREPDGKTCRQNSNIEPYLIF SNRYRLNLTIDGYFYSLEGLDNVVALDFDRVEKRLYWDTORQV IERMFLNKTNKETIINHRLPAAESLAVDWVSRKLYWLDARLDGLFVS DLNGGHRMLAQHCVDANNTFCFDNPRGLALHPQYGYLYWADWGHRA YIGRVGMDGTNKSIVIISTKLEWPNGITIDYTNDLLYWADAHGYIEY SDLEGHHRHTVYDGAHPHFAITIFEDTIYWTWNTRTVEKGNKYDG SNRQTLVNTTHRPFDIHVYHPYRQPIVSNPCGTNNGGCSHLCLIKPG GKGFTCECPDDFRTLQLSGSTYCMPCSSSTQFLCANNEKCIPIWWKC DGQKDCSDGSDELALCPQRFRLGQFQCSGDNCTSPQTLCAHQNC DGSDEDRLLCENHHCDSEWQCANKRCIPESWQCDSEFNDCEDNSEDE SSHCASRTCRPGQFRCANGRCIPQAWKCDVDNDGCDHSEDEPIECMS SAHLCDNFTEFSCKTNYRCIPKWAVCNGVDDCRDNDSEQGCERTCH PVGDFRCKNHHCIPLRWKCDGQNDGDNSEENCAPRECTESEFRV NQQCIPSRWICDHYNDLWGDNSDERDCEMRTCHPEYFQCTSGHRVHS ELKCDGSADCLDASDEADCPTFRPDGAYCQATMECKNHVCIPPYWK CDGDDDCGDSDEELHLCLDVPCNSPNRFRCDNNRCIYSEVCNGVD DCGDGTDETEHCRKPTPKPCTEYKCGNGHCIPHDNVCDADDDCG DWSDELGCNKGKERTCAENICEQNCQTLNEGGFICSTAGFETNVFD RTSCLDINECEQFGTCQHCNRTKGSYECVCADGFTSMSDRPGKRC AEGSSPLLLLDPDNRIRKYNLSSERFSEYLQDEEYIQAVDYDWDPED IGLSVYYYTVRGEGRFAGIKRAYIPNFESGRNNLVQEVLDLKLKYM QPDGIAVDWVGRHIYWSVDVKNKRIEVAKLDRYRKWLISTDLQDPA IAVNPGLGLMFWTDWGKEPKLESAMNGEDPNILVFEDLGWPTGLSI DYLNDRIYWSDFKEDVIETIKYDGTDRRVIAKEAMNPYSLDIFEDQ LYWISKEKGEVWKQNKFGQKKEKTLVVPWLTQVRIFHQLRYNKS PNLCKQICSHLCLLRPGGYSCACPGSSFIEGSTTECDAAIELPINL PPPCRCMHGGNCYFDETDLPKCKCPSGYTGKYCEMAFSKGISPGTTA VAVLLTILLIVVIGALAIAGFFHYRRTGSLLPALPKLPSLSSLVKPS ENGNGVTFRSGADLNMDIGVSGFGPETAIIDRSMASEDVFMEMGKQP IIFENPMYSARDSAVKVVQPIQVTVSENVDNKNYGSPINPSE\IVPE
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				TNPTSPAADGPQVPKW\NLFRKRSKQT\TNF\ENPFY\AQMGERVKR ESVA\ATPP\PS\PSLPAKP\KPPSRDP\TPYSATEDTFKDTANL VKEDSEV
3464	A	40	380	LWPLGPEPRAGCICRGNLSSTRGTSTRPGATADFGHLHGGLPAGLSS CSAGVPTSTCCAGK*NL*FGLPRGCSCPGFLPSKGTIILDCVKNLKL NGKATPKDSKYVEKLKALF
3465	A	3	450	LPKRNDIFDSLQKAKFDVSGLTTEQMLRKDQKTIYRQGVKVAISAIY MDLEICEVLERSHSPPLKLTTPASSTHPNLHAYLQNGTQVSRKKLLPL LQEALSAYFDSMKIPSGQPETADVSREQVDKELDRASNSLISGLSQD EEDPPPK
3466	A	1	429	YDYIFNYLPHSLPQREAVFPSLTHLAVLAFLVLGPWPTLFDP*SLIC FLGLTTEQMLRKDQKTIYRQGVKVAISAIYMDLEAFLQRSNLLADLH AFCQHS\YDVLVAMTIFFNTHNEPVRQLAIFCPHVALQTTICEVLE RS
3467	A	283	587	FWTPQVCCSCRWRVLPQRSdT\ALEEAV\AEVLDHRPIEPKHCPPC HVSVELVGSCATLVTERILQGAPEILDRQTAALL/HGTIILDCVNMD L*IGMATPKD
3468	A	2	1460	GRAAFVGETSPRPGAPLLDQGRRTLGFI MEDYLOGCRAALQESRPL HVVLGNEACDLSTVSALALAFYLAKTTEAEVFPVPLNIKRSELPL RGDIVFFLQKVHPIESILIFRDEIDLHALYQ\AGQLTLILVDHHILS KSDTAL\EE\AVAEVL\DHRPIEPKHCPP\CHVSVELVG\SCATLV ERI\LOQ\APEILDRQTAALLHGTIILDCVNMDLKIGKATPKDSKYV EKLEALFPDLPKRNDIFDSL\QKAKFDVSGLTTEQMLRKDQKTIYRQ GVKVAISAIYMDLEAFLQRSNLLADLHAFCAHSYDVLVAMTIFFN HNEPVRQLAIFCPHVALQTTICEVLERSHSPPLKLTTPASSTHPNLHA YLQNGTQVSRKKLLPLLQEALSAYFDSMKIPSGQPET\ADVS\REQV DKELDRASNSLISGLSQDEEDPPLPPTPMNSLVDECPLDQGLPKLSA EAVFEKCSQISLSQSTTASLSKK
3469	A	2	230	WQDFYCQ*HIFGAFFTHPDGPSNWAFFSNFVMFCHCLPKCWDYRGES PRPAHFKIFVDQCTVVKKKKIRKIKNKFL
3470	A	134	929	RTAARGCNGIPGAAAWAALPRRRPRRHPSVNP RSRAAGSPRTGRRR TEERPSGSRGLDGRGRGRALPGGRLGGRGRGRAPERVGGRGRGRGTAA PRAAPAARGSRPGPAGTMAAGSITTLPALPEDGGSGAFPPGHFKDPK RLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVSISIKGV VC/SNRYLAMK\EDGRLLASKCVTDECFFFERLESNNYNTYRSRKYT SWYVALKRTGQYKLGSKTGPGQKAILFLPMMSG
3471	A	1	2604	MATFISVQLKKTSEVDLAKPLVKFIQQTYP SGGEEQAQYCRAAEELS KLRRRAVGRPLDKHEGALETLLRYDQICSI EPKFPFSENQICLTFT WKDAFDKGS LFGGSVKLALASLGYEKS CVLFNCAALASQIAAEQNLD NDEGLKIAAKHYQFASGAFLHIKETVLSALSREPTVDISPDTVGTLS LIMLAQAQEVFFLKATRDKMKDAIIAKLANQAADYFGDAFKQCQYKD TLPKEVFPVLAAKHCIMQANA EYHQSILAKQKKFGEEIARLQHAAE LIKTVASRYDEYVNVKDFSDKINRALTA AKKDNDFIYHDRV PDLKDL DPIGKATLVKSTPVNVPISQKFTDLFEKMVPVSVQQSLAAYNQRKAD LVNRSIAQMREATTLANGVLASLNLPA AIEDVSGDTPVQSILTKSRS VIEQGGIQTVDQLIKELPELLQRNREILDESRLLD EEEATDNDLRA KFKERWQRTPSNELYKPLRAEGTNFRTVLDKAVQADGQVKECYQSHR DTIVLLCKPEPELNAAIP SANPAKTMQGS EVNVVLSLLSNLDEVKK EREGLNDLKS VNFDMTSKFLTALAQDGVINEEALS VTELDRVYGGI TTKVQESLKKQEGLLKNIQVSHQEF SKMKQSNNEANLREEVLKNLAT AYDNFVELVANLKEGTFYNELTEILVRFQNKCS DIVFARKTERDEL LKDLQSIAREPSAPS IPTPAYQSLPAGGHAPTPTPAPRTMPPTKP QPPARPPPPVLPANRAP SATAPSPVGAGTAAPAPSQTGPSAPPPQAQ GPPYPTYPGYPGYCQMPMPMGYNPYAYGQYNMPPVYHQSPGQAPY PGPQQPSYFPFPQQSYYPQQ
3472	A	478	697	YLIYQSRFFLFSSIRYCMMPMPMG/YCNPYAYGQYNMPPVYHQSP

				GOAPYPGTOQPSYPPF\QPPQSSYYPQQ
3473	A	21	194	HVSSRLREFLFKHPKRTATLSMRNTSVMKKGIFSAEFLKVFLPSLL LSHLLAIGLG
3474	A	2	767	APLSPGAQLGRGAPTSAPFPFAAEAHPAARRGLRSPQLPSGAMSQNG APGMQEESLQGSWVELHFSNNGNGGSPASVSIYNGDMEKILLDAQH ESGRSSSKS\SHCDSP\SSQTPQDTNRAF\ETDTH\SIGREKQLTV LREDDIERRKEVESILRKNSDWIWDWSSSAGKIFPPKEFLFKTPGSR TATLSMR\NTSVLKKGGIFSAEF\LKVFLPFAALSIAWPIGLGIYI GKASDQPSTSTFGWKEPGSLDLVR
3475	A	1	4220	MLNIVQDSALLEAIGCQMEMGGGNNLKSHSRNTSGISSASGGSTEP TTPDSEPAQALLRDYALNTDSAAGLLIRS IHLVTQRLNSQWRQDMS ISLAALELLSGLAKVKVMVDSGDRKRAISSVCTYIVYQCSRPAPLHS RDLHSMIVAFAFQCLCVWLTEHPDMLDEKDKLKEVLEIVELGISGSKS KNNEQEVKYKGDKEPNPASMVRVKDAEATLTCLVNETLIKYSRLPT INKHSFRYFVLDSVILAMLEQPLGNEQIISHLTICDYHCDPNYPQV HFFFLMVIGISQYVKEACSQTLIAGKGKESGYRICGYKLFVPEPRP VPKNDVGFKYSVKHRPFPEEVDKIPFVKADLSIPDLHEIVTEELEER HEKLRSGMAQQIAYEIHLEQQSEELQKRSFPDPVTDCKPPPPAQEF QTARLFLSHFGFLSLEALKEPANSRLPPHLIALDSTIPGFFDDIGYL DLLPCRPFDTVFI FYMKPGQKTNQEIILKNVESSRTVQPHFLEFLLSL GWSVDVGRHPGWTGHVSTWSINCCDDG\EGSQQEEVISEDIGASI FNGQKKVLYADALTEIAFVVPSPVESLTDLSLESNISDQSDSNMDL MPGILKQPSLTLELFPNHTDNLNSSQRNEHAFLSISRKQWKCLPCES SWMAKPPAQAHTCILVRTKAGPGPGEA AVLDSRQWEAEDRERSSQR LLRFTYGPSFPAPKVPDEASLIPPEMDNECVAQTWFRFLHMLRNAF PVVDAALVLLPVTAARLMIFLLGFCHILWGLEVALLSVPSTDCNPV DLNPAIISSTPKFQEQLNVSGMPQELNQYPCLKHLQP IFFRAMRG ISCLVDAFLGISRPRSDSAPPTPVNRLSMPQSAVSTTPPHNRRHRA VTVNKATMKTSTVRVYITIVMLYKVSTAHASKVQHQTSSSTPLSSPN QTSSEPRPLPAPRRPKVNSILNLFGSWLFDAAFVHCKLHNGINRDS MTAITTQASMEFRKGSQMSTDTMVSNNPMFDASEFPDNYEAGRAEAC GTLCRIFCSKKTGEEILPAYLSRFYMLLIQGLQINDYVCHPVLASVI LNSPPLFCCDLKGIDVVVPYFISALETILPDRELSKFSYVNPTEL RSSINILLSLPLPHFGTVKSEVVLEGKFSNDSSSYDDKPIITFLSL KLRLVNILIGALQTETDPNNTQMILENFPLSELMTEISTGVETTANS STSLRSTTLEKEVPVIFIHPLNTGLFRIKIQATGKFNMVIPLDGM IVSRRALGFLVRQTVINICRRKRLESDSYSPPHVRRKQKITDIVNKY RNKQLEPEFYTSLSFQEGILEPDECLQAWITHSGVNGPLETIMRTIVA MPLPRAADVCPLNCAWELPTLHCVFCLLCPRTTGPPAGPSGQRR
3476	A	3	1676	HASDSFRYFVLDSVILAMLEQPLGNEQNDFPSPVTVLVRGMSGRLA WAQQLCLLPRGAKANQKLFVPEPRPVKNDVGFKYSVKHRPFPEEVD KIPFVKADLSIPDLHEIVTEELEERHRK\LR\SGMAQQIAYEIHLEQ QSEELQKRSFPDPVTDCKPPPPAQEFQTARLFLSHFGFLSLEALKE PANSRLPPHLIALDSTIPGFFDDIGYLDLLPCRPFDTVFI FYMKPGQ KTNQEIILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTW SINCCDDGEGSQQEEVISEDIGASIFNGQKKVLYADALTEIAFV PSPVESLTDLSLESNISDQSDSNMDLMPGILKQPSLTLELFPNHTDN LNSSQRLSPSSRMKLPQGRPVPLGPETR\VS\VVWVERYDDIENF PLSELMTEISTGVETTANSSTSLRSTTLEKEVLVIFIHPLNTGLFRI KIQATGKFNMVIPLDGMIVSRRALGFLVRQTVINICRRKRLESDS YSPPHVRRKQKITDIVNKYRNKQLEPEFYTSLSFQEVGLKNCS
3477	A	288	589	WCSRRRGWYLLLGPHNYWRSSTFLVRCTPSCPGGCCPRYGIYPVRSC PRLPGGVSRYGSIHSG/RWCSWSPSWSPWLTSTVTPRLYVALM*AVVC PVVGKQP
3478	A	1250	1909	GAGPDMVWDTELELALKISKGLQRPKHAHREEREDIGKHESRCVIYF GTAKKWILDKNGRSRVDVISHRLKVSSGLCKTHEIGFDPLALKCPL

				RSRTAPWWPLDRVSFDLHHLVIGNFFVGNRKIFLDYLVYGFHNNRW KLLVQSWSDGCVHRTFGLVKSFASKFCIFITKQRKSSDLALK\QI CANTARVILKLKHFHFVSVMCTFLFTCENGHL
3479	A	3	246	AAAMSALSLLILGLLTAVPPASCQQ/GEPAHMILTVGNKADGVLVGT DGRYSSMAASFRSSEHENAYENVPEEEGKVRSTPM
3480	A	162	530	ELLQPMALSLLILGLLTAVPPASCQQGLGNLQPWMQGLIAAAFLV LVAIAFAVNHFWGAKEEP/ESPAHMILTVGNK\ADGVLVGT\DG\RY SSMAASFRSSEHENAY\ENVPEEEGKVRSTPM
3481	A	4	411	NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLGNDD SDKT/EGTVSGNDSSEVNDTWPLPWWGKQANRPLLSLAGQKSSPF WTFEYYQTFDFVDVTYQVFDRIKGSLLPIPGKNFVRLYIRSIV
3482	A	160	518	MTCNLKLLAGQKSSPFWTFEYYQTFDFVDVTYQVFDRIKGSLLPIPG KNFVRLYIRSNDLYGPFWICATLVFAIAISGNLSNLIHLGEKTYH YVPEFRKVSIAATIIYAYAWLVPLA
3483	A	12	197	SIIFLPTLSSTFSIKIRLKPQDLGNWWQQTALVLGVISLNIHEYFPL QCSSFSLGWGRALS
3484	A	2	321	ARGVYGYSLFYIPTAILWIIPHKAVRW\ILVQ\IALGISGSLAMT FWPAVREDNRRVALATIVTIVLLHMLLSVGCLACFFDAPEMDHLPTT TGTPNQTVAAAKSS
3485	A	187	1280	PLARLNCCLSSLSPLSNLSLSFLIGTSLGCTCSLKHSHKPCQIFF LIIGRRLTGRMAAVDDLQFEFEGNAATSLTANPDATTVNI\EDPGET PKHQPGSPRGSGREEDDELLGNDDSDKTELLAGQKSSPFWTFEYYQ TFDFVDVTYQVFDRIKGSLLPIPGKNFVRLYIRSNDLYGPFWICATL VFAIAISGNLSNLIHLGEKTYHYVPEFRKVSIAATIIYAYAWLVPL ALWGFLMWRNSKVMNIVSYSFLEIVCVYGYSLFYIPTAILWIIPQK AVRWILVMIALGISGSLAMTFWPAVREDNRRVALAL\IVTIVLLHM LLSVGCLAYFFDAPEMDHLPTTTATPNQTVAAAKSS
3486	A	112	563	LDSSHCCSCSTALFRTQTAAAVPRMVIRVYIASS\SGSTAI/RGKR QQDVLGFLEANKIGFRKDIAANGENRKWMRENVENSRRPGTG\YPL PPQIFNESQYRG\DY\DAFFGRPEENN\AVYCLLRGLTAPPGVSKGR QEGAKPKAGQALT
3487	A	105	335	GRLFPKVLVSYSVGYLPLILFCHFLLANCILCLMHFL*FFQSYRF* G*KFGFTQHHCHYIFHKQWPLLWKNFPEH
3488	A	993	1338	QNCLKPHFFFFFETRVSLLLPKREAMGTISTHCNLCPLPGFQGNPAS ASQGR/AGLHGMGPPCR/RGTFVFLIGDRGFLHVGSSWSWNSQPQV IRP\PRPSPKCWGLQGMEATVPSP
3489	A	2	454	PLLPALPGCHALAPSSYIPVAIRALEPPSPYHGQLKMQSIPG\PPQ PRSFLLSSPLDVSQAPRHCTGLPAPSLSSPPWSCPTLFSWFFEAS GVCHHWTSVIAASNSSPIFPELPHPHPLRISAWLFPPWRDHSQDPLC RGATSPVLNS
3490	A	1109	1448	PRLISKCFLLLLFRQSHFVAQAGVQWCDLRSVYHLPPLGRFSCLS LPSSWDYRHLPPCPANFCNFSRDRVSPCCPGWERTPD\PGDPPASAS PKWWEYTL*PPGPDHPKAF
3491	A	14	250	VLSVGLPTGDTGIGLSRKTSPAPVALIHSLSLKQAH*LTLSRTGN IHAIYYRGVLKYCNFICLGFMLRYQLVSPSF
3492	A	1	1065	MGSVPLIKRPKRASLSLPPHEVSNANDDPLESEKFNPNKLTYLAV HSTALGN SPLALPLKPPILPAVKCTRIVVVMCISPMANDVERLSVCF TGHLCIFFGEMSIQVERIVDKRKNKKGKTEYLVRWKGYDSEDDTWE EQHLVNCEEYIHDENRRHTEKQKESTLTRTNRTPSPNNARKQISRSTN SNFSKTS PKALVIGKDHEKNSQLFAASQKFRKNTAPSLSSRKNDL AKSGIKILVPKSPVKSRTAVDGFQSESPEKLDPEQQQEDTVAPEVA AEKPVGALLGPGAERARMGSRPRIHPLVPQVPGPVTAAMATGLAVNG KGECLGSCSGSVVPIEGSGPSLEIRP
3493	A	90	1937	AGGNQRTQSPRKNFMAFQASHRPAGWKSRRKNWQYEGPTQKFLKRN NVSAPDGPSDPSISASSEQSGAQPPGLQVERIVDKRKNKKGKTEYL VRWKGYDSEDDTWEPEQHLVNCEEYIHDENRRHTEKQKESTLTRTNR

				TSPNNARKQISRSTNSNFSKTS PKALVIGKD HESKNSQLFAASQKFR KNTAPSLSSRKNDLAKSGIKILVPKSPVKSRTAVDGFQSESPEKLD PVEQQQEDTVAPEVAAEKPVGALLGPGAERARMGSRPRIHPLVPQVP GPVTAAMATGLAVNGKGTSPFMDALTANGTTNIQTSVTGVTASKRKF IDDRDQPFDKRLRFSVRQTESAYRYRDIVVRKQDGFTHILLSTKSS ENNSLNP\EVLREVQSALSTAAANDSKV\VLPRAVGSVF\CCGLNFN YFKPR\LPNARKRESIKMAEAI RNFNVTFIQFKKPIIVAVNGPAIG\ LGASILPLCDVVWANAKAWFQTPYTTFG\QSQEGCSPVMFPKIMGGS ICILDAVLGDRNLTAQ\EACGKGLVSRVFWPGTSPRKVMVRIKELAS CNPVVLEESKALVRCNMKMELEQANERECEVLKKIWG\SAQGDGTRM LKVLCRGKIE
3494	A	2	572	WCLQHD/LGHASIFKKSWWNHVAQKFVMGQ/LKGFSAHWWNFRHFQH HAKPNI FHKDPDVTVPVFLLGESSVEYGKKRRYLPYNQOHLFFL IGPPLTLVNFEVENLAYMLVCMQWAVSGVADPGHTAAVAGGASG DSTCP* RQTGCT\DLLWAASFYARFFLSYLPFYGVPGVLLFFVAVRY GREWR
3495	A	25	430	YKNSFPPIALGKCAMLTFPLPLSHQAQSQGHRAAEYTCEGRSPFP VGSPLPWGQAAMRAGGWGRTAECFSFGMESRPG*RVSGRGAGGQPRP SPGMSLGGPVPPAPSSPLLPPAGRCNPRTERTNLPTRSWA
3496	A	821	1412	GSARASPGQPGKPLVRVDHTDEHPQGDPRAPGLQLSAGSHLQR GALTF\HQLVQRAPQLPDRAPPLPQDAETQ\LPQGPCAC\QVAVCQ\ ARPQLR\SEALP\HRAGGHRQVPEESLVTSCWTPTSISEGNTQAGRE GLRAPATKPSPRDRIPPTPPLTSLGVPCLPWSYCCPLPLGLTCVFS SPMALALGLMGQG
3497	A	32	616	VLQCSHGCFSSQSSGG\LTDEAASSCCSDADPSTKDFLLQQTMLRV KDPKSLDFYT\RVLGMT\LIQKCDPIM\KFSLYFLAYEDKNDIPK \EKDEK\IAWAV\SRKATLELTQQFGALKDDATQSYHNGNSDPRGFG HIGIAVP\DVYSACK\RFEELGVKFVKPDDGKMKGL\AFIQDPDGY WIEILNPNKMATLM
3498	A	77	403	CSIRCSFQCPACRWPSLSHAHPLQLTLCVSSFPQVNIDHETRELTR MNLQTATATCFDAAQKTRTLMERDSYPRFLKSPAYRDLAAQASAAS ATLSSCSLDEPSHT
3499	A	18	753	TQPQLTSTCYRAFASWRTRSLLPATILPTTCCPAPAAMCRTLAAFP TTCLERAKEFKTLGIFPHKS\ELGFDGTGSGKFEWGSKHSKGD LKT SQKDVLGWRESF\DLLSSKNG\VAAFHAFKTEFSEENLE\FWL\A CEEFFKI\RSATKLASRAH\QIFEEFICSEAPKEVNIDHETRELTRM NLQTATATCFDAAQKTRTLMEKD/SPYPRFLKSPAYRDL\AAQASA ASATLSSCS\LDEPSHT
3500	A	28	342	PGSTHASADAWHPKNI/SSVNALSPGPHCAQTEV/IVSPAPRCLCH RRGPRPSCCPNPVPSLTSLTRFPSLCRATLKNRKA CLNPASPIVK KII EKMLNSDKSN
3501	A	1	274	MARATLSAAPSNNRLLRVALLLLLVAAARRAAGASVVTCLRCQCLQ TLQGIHLKNIQSVN\ATLKNKGKACLNPASPMVQKII EKILNNP
3502	A	1	893	MSSREVTPPGKDVARSLRSGSGSDPRRTALGSRSSASSQAVISVSLRA AGSRSRSDSGQKENIPQLAGVTQDSQTRTSLVSAPTPLHPRGGAIA FLPNSGSIWSSGNFPGPLRAFQPQPCIKGVRSSRRATEPGPQAAPC QLSSSHSRNRLSPMARATLSAAPSNNRLLRVALLLLLVAAARRA AGAPLATELRCQCLQTLQGIHLKNIQSVKVKSPGPHCAQTEVM*VSP IAAAATAGVPDSPAAPNPVLSPTSCLTRFPSLCRATLKNRKA CLNP ASPMVKKII EKMLKK
3503	A	1	407	ATEPGPQAPPRQLFRSSHSRQTRLLSPMARAALSAAPSNNRLLRVALL LLLLLVAAARRAAGASVATELRCQCLQTLQGIHPKNIQSVNVKSPGP HCAQNEVHKHTQEMGGKACLNP\ASPIIKKII EKMLNSDKSN
3504	A	3	406	GPDAGWGDRIPLIILVQIFGLLVAADGPMFPLGRAARVCRRWQEAS QPALWHTVTLSSPLVGRPAKGSVKA EKLLASLEWLMNRFSQLQRL TLIHWKSQLVGECCPRLTFLKLSGCHGVTADALVMLAKAC

3505	A	2	347	AARVCRRWQEAASQPALWHTVTLSSPLVGRPAKGGVKAEEKLLASLE WLMPNRCWVGRTRVGTLVQLCLRCRPRFSQLQRLTLIHWSQVHPVL KVRAPGCDCTSPATLWDWSVL
3506	A	2	1333	VYKPRPFRSLGLPRAPSVVMAAPASRQVRRRARAAPRPRSAEDWWWD RLAPRSGSYHLLQSDSMLLVLSEPGPARPRAQRASRRTPRQPPRG SAAAKPKAGLRSEAAAAAPAPAPAPTPTPEEGPDAGWGDRIPLEILVQ IFGLLVAADGPMFPLGRAARVCRRWQEAASQPALWHTVTLSSPLVGR PAKGG\ VKAEKKLLASLEWLMPNRFSQLQRLTLIHWSQVHPVLKLV GECCPRLTFLKLSGCHGVTADALVMLAKACQQLHSLDLQHSMVESTA VVSFLEEAGSRMRKLWLTYSSTTATILGDLGSCCPQLQVLEVSTGI NRNSIPLQLPVEALQKGCPCQLPGPCPQVLRLLNLMWLKPPGGRGVA PGPGFPSLEELCLASSTCNFVSNEVLGRLLHGSPNLRLLDLRGCA TPAGLQDLPCRQGSWVVR
3507	A	47	891	KQPFVWPAGGERLSGARPKKEARLLRWCPMSFKRNRSD\RFYSTRC CG\CCHVRTGTIILGTWYMVNLLMAILLTVEVTHPN SMP\AVNIQY E\VI\GNYS\SERMADNAC/VFFFAVSVLVKYNPVPMLVYGSNFLY PSGVGWIPFF\CYRLFDFVLS\CLVAISSLTYPRIKEYL\DLPDF \PDKDDLRL\DS\SCLLFIVLVFFALFIIFKAYLINCWNCYKYIN NRN/VCPEIAVYPAFEAPPQ\YVLPTYEMGREKWPEKEPHPLLTWP EGNSGLWTINP
3508	A	246	559	MPVAVMAES/AFSFKLLDQCENQELEAPGGIATPPVYGQLLALYLL HN/GQRIWQDFFPGIYTTINAHQWSETVQPIEALRDATRRRAFALV SQAYTSIIADDDFA
3509	A	2	250	IIADDDFAAFVGLPVEEAVKGILEQGWQADSTTRMVLPRKPVAGALDV SFNKFIPLEPAPVPPPIPNEQQLARLTDYVAFLEN
3510	A	2	119	LKNSVKYLLNKCVRNELRAVITLSYNKQLQIFRGLSHRE
3511	A	197	921	GTWVGLAVRTVQRRGPAKMPVAVMAESAF\SPFKLLDQCENQELEA P\GGIA\TPKVYQQLLALYLLHNDMN\NARYLWKRIIPPAIKSANSEL GG\IWSVGQRIWQ\RDFFPGIYTTIN\AHQWSET\VQPIYKGHFRDAT R/RDRAFAPGLLQAVYFQSIRPMIFAFAVG\LPV\EEAVKGIL\EQ W\QA\DSSTRNGSCPGKPVCRGPWDVFPFNKFISLYSEP\APV\PI PNEQQLARLTDYVAFLEN
3512	A	3	356	HEVYSGGDDGLLRGWDTRVPGKFLFTSKSYDEHILLWDTRNMKQPLA DTPVQGGVWRIKWHPPFHHLLLAACMHSGFKILNCQKAMEERQEATV LTSHTLPDSL VGADWSWLLFRS
3513	A	1	179	SSVVEFGACTGISTASRSARMAWGCEREGDHAPRSSLWESCPASVRS VSSSVPRSSRG
3514	A	63	386	LRTLISCHLVLMFLHTGDDGLLRGWDTRVPGKFLFTSKR*PPK GQHSVPTPAPAFPGSPALPFPGWVCVLDTGSEAAASACRHTMGVCSIQ SSPHREHILATGR
3515	A	1	147	GLANTPGQGVWRIKGHPFHHLLLAACMHSGFKILNCQKAMGCGSL RA
3516	A	450	1154	KSHVLEPLSSLALEEQLALS LDWSTGKTGRAGDQPLKIISSDSTGQ LHLLMVNETRPRLOKVASWQAHQFEAW/TCCFQLPWHPEIVYSGDD GLLRGWDTRVPGTFLFTS/IKTHHGCVASIQSKPSSGAHPWPRESYD ETHPTV\DTRNMKQPLADTPVQGGVWRIKWHPPFHHLLLAACMHSGF KILNCQKAMEERQEATVLTSHTLPDLSVYGADWSWLLFRSLQRAPLV VLS
3517	A	73	168	PIQAGLSLLKTAGKKGPEGSPPVFYSPLNPGA
3518	A	322	673	RLWASPAAPGKKKEMGNSMKSTPAPAERPLPNPEGLDSDFLAVLSY PSPDINPPIFRRGEKLRVISDERGWKA\ISLSTGRESYI PAICVAR SYHGWLRLRGP\KNMAEELLQLPD
3519	A	624	1580	KAATSENKIICCEWRTSQAALMLHRLWASPAAPGKKKEMGNSMKSTP APAERPLPNPEGLDSDFLAVLSYDPSPDISPPIFRRGEKLRVISDEG GWKAISL\STGRESYIPG\ICVARV\YHGL/WLFEGLGRDKAEELL QLPDTKVGSFMI\RESETKKGFYSLSVRHRQVKT\YRIFRLPNNWYY

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				ISPRLTFQCL\EDL\VNHYSEVADGLCCVLTTPCL\TQSTA\APAV\ RACSSPVTLRQKTVDWRRVSRLOEDPEGTENPLGVVESLPSYGLRES IASYLSLTSEDISSFDRKKKSIISLMYGGSKRKSSFFSSPPYFED
3520	A	24	688	VDHPPYKRTEKVRQSRSPKSQDIYLG\LLVKLYRFSGPEEPNSNIQT RVVLK\RLFMSRT\NRP\PLS\LSRMIREDEAFLAGKKKNAVVVGP QKLIMCGVQKGTPLKVCALGGTQAGPHKRI\LRARGORSITFDQLA LD/SPLRGCTVLL\SGPSKG\REVYRHFGKAPGNP\HSHTKPYVRS KGRKFE\RARG\RRASRGYKKLTLDPTLLYKKIFADSEKKKK
3521	A	109	446	EDEKVERVPSPDHRRRSYRDLKPRRSPTLRYRRSRSPIRRSP KRRSPFPRRERHRSKS\SRHRSRSDRRHRSRSKSPGHHRSHRHS HSKSPERSKSKSHKISRRE
3522	A	195	391	PGVAGARHPLLGAAPKGR\EVLAVGFHGSAAQVWVSKSHPQFIPT DQEIIGDRALKGTCRLPLS
3523	A	112	492	AHSRTPARPENRAAASAPRKPRRAMSSPPEGKLETKAGHPPAVKAGG MRIVQKHPTGDTKEEKDKDDQEWESPPPKPTVVISGVIARGDKDF PPAAQV\AHQKPHASMDKHPSPTQHIQPRK
3524	A	3	982	GTRVGVAWSVRLLGPGAGLRGGVVLKVSPSPCRGGRVPVRAEGA RGRGPRNKVPGASSGAAGAARLTAPLLAKAMASKLLRAVIL\GPPG LGKGAPVCQRIANFGLQ\HLS\SGHFLRENIKA\STEVGEMANQVY REKVFLVPDHVITRLMMSELENRRGQHWLL\DGFPRTLQAEALDKI CEVDLVISLNIFFETLKDGLN\RRWIHP\PSG\RVYNL\DFNPPHVH GIDDVTEPLVQGEDDKP\EAVAL\RLRQYKDVAKPVIEL\YKS\RG VLBHQSFGTET\NKMWP\YVY\TLFSNKITPIQSKESILTALQWEEPW NDVGHSFQ
3525	A	19	445	LYFRRRKQQLCADLCTQMLEKSPYDQAAWILKARALTEMVYIDEIDV DQEGIAEMMLDENAIQVPRPGTSLKLPGTNQTGGPSQAVRPITQAG RPITGFLRPSTQSGRPGTMEQAIPTPTAYTARPITSSSGRFVRLGT A
3526	A	1	623	QAAWILKARALTEMVYIDEIDVDQEGIAEMMLDENAIQVPRPGTSL KLPGTNQTGGPSQAVRP\TSHSEKPTITGFLRPSTQSGRPGTMEQAIR TPRTAYTARPITSSSGRFVRLGTASMLTSPDGPFIN*SRNLTKYSQ KPKMAKALPEYIFHHENDVKTALELAALSTEHSQYKDWVWKVQIEKR YYRLGMYREAEKQLISAMQ
3527	A	1	1509	MKAIECKSRTVKDWHNHQKLGEKNKTDSPQPSEGNTANTLILDFW PLEMIACCWETFPQRLTAELFMNPTHRWHGYKNQSVGALRAPLGQGP SRRGLPGRVGRRLFTPRPPLSWSAGPSLAAPAAAMSEMEPLLLAWS YFRRRKQQLCADLCTQMLEKSPYDQEPDPELPHVQAAILKARALTE MVIYIDEIDVDQEGIAEMMLDENAI/PSSTPITQAGRPITGFLRPST QSGRPGTMEQAIPTPTAYTARPITSSSGRFVRLGT\LGMYREAEKQ FKSALKQQEMVDTFLYLAKVYVSLDQPVLTALNLFKQGLDKFPGEVTL LCGIARIYEEMNNMSSAAEYKEVLKQDNTHVEAIACIGSNHFYSQ PEIALRFYRRLQMGYINGQLFNNLGLCCFYAQYDMTLTSFERALS LAENEEEAADVWYNLGHVAVGIGDTNLAHQCFRLALVNNNNHAEAYN NLAVLGDAEG/RHVEQARALLQTASSIS\PHMYEPHF
3528	C	179	289	MHRRLVASPXSVYVRQSVHMLVCFPMASDKXLNKYL*
3529	A	3	206	SWSGSRDVTGALLVAAAVASEAVGSLRVAEGGPNTLLQVCRGSKGT SATCPFRFPPLWSLLGTGR
3530	A	1	857	MPRAEPRATLGEQEKAGLPLGAWRLYLLRHFRKQTELRRSGSRDVTG ALLVAAAVASEAVGSLRVAEGGPNTLLQVLR\SW\PWCNKELKTME ERKVRRSPKSFSAHCTQVVNVQKMSIPVSK\ST\GFSNPASQVNF TSRPKVKKEVMK\EKTKPQGLEEGQRHSSQLPIQHSFLT\DVSRCSR KMERGLLSL\LNDFHSWKTFKHFGN\ECSI\EQMEHVSSELQEKLAR LNLELYGELEELPEDKEKTASDS\NLDRLSDLEELNSSIQLHLA\ DAQDVNTFR
3531	A	1	174	MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSSEVPGVYCLCVLQ HLGKIDISGK

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3532	A	1	190	MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVL\FQKPDQGIIVPLQYPV
3533	A	3	210	CPRVHQAMDAAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVL*V*YVCCEYDTPDCLWYLVMAA
3534	A	1	386	GISLAQFSSSACPRVHQAMDAAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWSA/EAFQKPDQGIIVPLQYPVEKKSSARSTQGTGIREDPDVCLKAP
3535	A	224	751	LVPGCCSSGISLAQFSSSACPRVHQAMDAAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWSAETAPG\VKRYFRMKKSHFQHFQKQDQ\GIVIPLO\YPVEKKSSARSTQGTGIREDEP\VCLNAPLIKISPLRPLFSITFNIC
3536	A	3	199	SIRAEMRSV\ALAVLALLSLSGLEAIQRTPKIQVYITSSSREWKVKFPPELLCVWVSSTPTLKLTY
3537	A	134	405	HLYPASRAGKGLVSWQQGEPGLGWPQLSLQVRSPGPCSSCDLHGHGVLGKREVELVPLVEDAGDAHSEPRAPEDHRLQEAPHACQEVHS
3538	A	415	533	CSQEKSGDLRGCDVPPGPRHDLEHVCCGLDGAEGRSAGP
3539	A	1	3349	MDQPEAPCSTGPRLAWARELLAALAEELSSEQQLKRFHKLRLDVGPGRSIPWGRLERAVDAVLAELAQFYGPEPALEVARCTLKRADARDVAQQLQERLQRLGLSGTLLSVSEYKKKYREHVLQKHARVKERNARSVKITKRFTKLLIAPESAAPPEALGPAEEPEPGRARRSDTHTFNRLFRDEEGRRLTVVLQGPAGIGKTMAAKKILYDWAAGKLYQGQVDFAFPMPCGELLERPGTRSLADLILDQCPDRGAPVPMQLAQPQRLLFILDGADLPLALGGPEAAPCTDPFEAASGARVLGGLLSKALLPTALLVTTAAAPGRLQGRCLSPQCAEVGRGFSKDKKKYFYKFFRDERRAERAYRFVKENETLFCALCFVPFCWIVCTVLRQQLELGRDLRSTSKTTTSVYLLFITSVLSSAPVADGPRLOGLDLRNLCLAREGVLGRRAQFAEKELEQLELRGSKVQTLFSLKKEPLGVLETEVTYQFIDQSFQFLAALSYLEDDGGVPRTAAGGVGTLLRGDAQPHSHLVLTTRFLFGLLSAERMRDIERHFGCMVSERVKQEAALRWVQGGQGGCPGVAPEVTEGAKGLEDTEEPPEEEEEGEEPNYPLELLYCLYETQEDAFVRQALCRFPALALQVRVFCRMDVAVLSYCVRCCPAGQALRLISCRVAAQEKKKSLGKRLQAR\LGGSWLGTQLAPEVPFRPPCCDICPTPPDPRLQKGAFARVPLNIAPIQPLPRGLASVERMNVTVLAGAGPGDPKTHAMTDPLCHLSSLTLSHCKLPDAVCRDLSEALRAAPALTELGLLHNRLSEAGLRMLSEGLAWPQCRVQTVRVQLPDPQRGLQYLVGMLRQSPALTTLDLSGCQLPAPMVTYLCAVLQHQCGGLQTLSSLSPSDPTSSFSGRCREPGRRGLGLESRWPRSAPEPSGRQGEDPGGGGRGRREEAREGTPGPAPPTAAPGRSSSGSRLELCSLRALRAGNARPPDATHAAAASGDRGEPGPRPRVHVPPPGPAQRPPPPPRDRPRLPATARALGAGTADLPGGAAAGRLLLPFGPGVEQRDTGSHAGARRPGGAAAQAQQLHGGRRRGPHHVCCPLSAQ
3540	A	3	261	AIHLYPEILPLGNEKSTTGDGRPELDNLSDEYLSCLRKLQHCREELNQSQQLPPRRQCGRWLPVLMVVIAAALAVFLANKDNLM
3541	A	3	431	DAWADAWADAWALRIQQREQLQARLQQFFRRRNLELEEKGAQHPOAREQGPSRRPGQVTVLKEPLSCARRISSPREQVTGTSSEVFPQHPPPSGICRDLSDHLSSQAGGLPPQDTPIKKPKHHRGTQTKAEGPTIKND
3542	A	1	859	ALGKQKCEEWSKY/EALK/ED/WRNLGAQHRE\LESQHLVLSKLQGADSRDLQMNQALRSQNEHQQLQAKIECLQADRDLCSLYTQDLQDLKRSEAEKLTIVTRVQQLQGLLQNSQLQLEQEKLLTK/KRSANLLPQILRYCSFSYLPBGSGMDYMTSWSPSQFWEFC*VRDVWELFKD*SLALRTLQVLVSLLS*DQALPVWSPKSFNEVEPEGTGKEKDWDLRDQLQKKTLLQQAKEKECRELHSELNLSDEYLSCLRKLQHCREELNQSQQLPPRRQCGRWLP
3543	A	392	2016	AKNRNRCLEVIMISPDPRPSPGLARGAESYEAKCERRQEIRSRRCRPNVTTCRQVGKTLRIQQREQLQARLQQFFRRRNLELEEKGAQHPPQAREQGPSRRPGQVTGTSSEVFPQHPPPSGICRDLSDHLSSQAGGLPP

				QDTPIKKPPKHHRGTQTKAEGPTIKNDASQQTNYGVAVLDKBIIQLS DYLKEALQRELVLKQKMWILQDLLSTLIQASDSSWKGQLNEDKLKKGK LRSLENQLYTCTQKYSFWMKKVLLMEDQKNSYEQKAKESLQKVLB EKMNAEQQLQSTQRSALALAEQKCEEWSQYEALEDWRTLTGTOHREL ESQLHVLQSKLQGADSRDLQMNQALRFLNEHQQLQAKIECLQGGDRD LCSLDTQDLQDLKRSEAEKLTIVTRVQQLQGLLQNSLQLEQEK LTKKDQALPVWSFKSPNEVEPEGTGKEKDWDLRDQLQKTLQLOAK EKECRELHSELDNLSDEYLSCLRKLQHCREELNQSQQLPPRR\QCG\ KGLPVLMMVVIAPALAVFLANKNNLMI
3544	A	35	219	DTEVKPQSALPQASALTIWVSQQGVLSATILYEILLGKATLYAVLV SALVLMAMVKKRDF
3545	A	293	479	GRPEPPVHRCALHALFLSTESYQAGVLSATILYEILLGKATLYAALVS ALVLMAMVKKRDSRG
3546	A	1	968	VKLPCPDPMGTSLLCWMALCLLGADHADTGVSQNPРНITKRGQN VTFRCDPISEHNRLYWYRQTLGQGPFLTYFQNEAQLEKSRLLSDRF SAERPFGSFTLEIQRTSQGDSAMYLCASSLAGLNQPPHFGDGRLS ILEDLNKVPPEVAVFEPSEAEISHTQKATLVCLATG\FPPDHVELS WWVNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFW\QNP RN\HFRQVQFYGLSENDEWTQDRAKPVTOIVSAEAWGRADCGFTSV \SYQGVLS\ATILYEILLGKATLYAVLVSAVLMAMVKKRDF
3547	A	278	1283	GGIGEIKQRPSCDGRCLDPSLSVLMNISLEGSVFSAVISQKPSRDI CHRGTSLTIQSQVDSQVTMMFWYRQPGQSLTLIATANQSEATYES GFVIDKFPISRPNLTPSTLTVSNMSPEDSSIYLCSSVEEQGFVGAET QYFG\PGTRLLVLEDLKNVFPPEVA/VLFEPSEAEISHTQKATLVCL AICFYLDHVELSWWVNGKEAHSGVSTDPQLKEQPALNDSRYCLSSR LRVSA\TFWQNPРНHFRQVQFYGLSENDEWTQDRAKPVTOIVSAEA WGRADCGFTSGK\SYQGVLSATILYEILLGKATLYAVLVSAVLMAM VKKRDSRG
3548	A	151	286	FLKDLSSSTPMASNTASIAQARKLVEQLKMEANIDRIKVSAAAAD
3549	A	28	177	GVFLKDLSSSTPMASNTASIAQARKLVEQLKMEANIDRIKVSAAAAD LMA
3550	A	422	671	RIYPALRMPSINTASIAQARKLVEQLFMF\ANIDRIKVSAAAADLMA YCEAHAKE\DP\LLTPVP\ASENPFKE\KKFFCAHPLSL
3551	B	62	299	MFSLLKKNVAMWSWDVECDTCAICRVQVMDGIGVRNWSEALNLIY ASEMGFDLDMGSQTSLSPLAHWLLNNLGWMNLX*
3552	A	1	602	ADVEDGETCALASHSGSSGSGGDKMFSLLKKNVAMWSWDVECD TCAICRVQVMDGIGVRNWSEALNLINASEMGFDCRSGSTALAVPSV SLASHQPCLDHR*QPIGSIQSSLF*RNSQVS*GRK*KVASYELLKE GFCVNACLRCAENKQEDCVVVWGECNHSFHNCMSLWVKQNNRCPL CQQDWVVRIGK
3553	A	2	428	SGGSTPEPLGSAFPKPTSSAVGSVGAAMADVEDGETCALASHSGSS GSKSGGDKMFSLLKKNVAMWSWDVECDTCAICRVQVMDACFRCAE NKQEDFFVVLGECNH\SFHNCCHVPCGSKQNNRCPLCQ\QDWVV\QR IGK
3554	A	114	1139	EETSGHCVVGPAAKRFSAGCFPRFPRPVPRALLIAPGPSVSARLTV GCDDMSNKEGSGGFRKRKHDFPHNQRREGKDVNSSSPVMLAFKSFQ QELDARHDKYERLVKLSRDITVESKRTIFLL\HRITSAP\DMEDILT ESEIKLDGVRQKIFQVAQELSGEDMHQFHRAITTLQEQYVEAVSFQH FIKTRSLISMDEINKQLIFTEDNGKENKTPSSDAQDKQFGTWRLRV TPVDYLLGVADLTGELMRMCINSVNGDIDTPFEVSQFLRQVYDGFS FIGNTGPYEVSKKLYTLKQSLAKVENACYALKVRGSEIPKHMALADV SVKTEMIDQEEGIS
3555	A	3	378	QAQPSLEMQNDAGEFVDLYVPRKCSASNRIIGAKDHASIQMNVAEVD KVTGRFNGQFKTYAICGAIRRMVSVSLGFAHHFGTSWTLPCALECVM VPEQICWQSSLSQLDWAGRLPLLEGGRGVL
3556	A	2	299	LLNSRPRRRQAQPSLEMQNDAGEFVDLYVPRKCSASNRIIGAKDHA

				SIQMNVAEVDKVTGRFNGQFKTYAICGAI\RRMGESHDSFLRMAKAD GIVSK
3557	A	1	392	RRYLCRVTSCLSLSRVWWPARRSPAFEMQNGRRRSSDLYRARGK LSASNRIIG\AKDHASIQMN\VAEVDKVTGRFNGQFKTYAICGAI\R RMGESDDSI\RLAKADGIVFKELFDWREITDVGFCHK
3558	A	1	417	FRDIVNENGEIEIQDEEEDGYDDD\EMTGTGMKES*NSPWVMAG/HG GSNPQANRQTSDDSSAKMSTPADKVLKRFENKINLDKLNVTDSVIYK ATEKF/DTKGIKYVLDPTTRMILFKMLTRGIITDIDGCISTGREANV
3559	A	139	1914	AVPFHRAAASGGALQSWTTGGLLSRVVPGQFDDADSSDSENRLDK TVKEKDDILFEDLQDNVNENGEIEDEE/WKEGYDDD\EMTGTGMK ELENPRVMSGIGRKQPTGKSTD\PDSSAKMSTPADKVLKRFENKI NLDKLNVTDSVINKVTEKSRQKEADMYRIKDKADRATVEQVLDPRTR MILFKMVTRGIITEINGCISTGKEANGYHASTANGESRAIKIYKTSI LVFKDRDKYVSGEFRFRHGYCRGNPRKMVKTWAEKEMRNLIIRLNHSR /GYHCPEPIMLRHGLAMSFIGKDDMPATNFGKMFQLSSEKARELYL QVIQYMRMYQDARLVHADLSEFN\IMYHGGGV\YIID\VSQSVEHD HPHALEFLRKDCANVNDFFMRHSVAVMTVRELFEFVTDPILPHHEN\ LDAYLSKAMEIASQRTKERTV/SSQDHVDEEVFKRS\YIPRNL\DEV KNYERDMDIIMKLKEEDMAMNAQQDNILYQTVTGLKKDLSGVQKVP LLENQVEERTCSDSEDIGSSECSDDTDSEEQGDHARPKKHTTDPIDK KERKK\EVKEAQREKRKNKIPKHVKKRKEKTAKTKKK
3560	A	129	567	SYKSRLARKS\TGGKAP\RK\QLAYKKPASQECGPLLGLKKPHRYR \PGTVALREIRR\YQKSTE\LMIRK\LRFOR\LVREIAQDF\KTDLR FQERSNQVALQ\EA\RRAYLVWPFLKDTNLVCLSMKRPVIMPKRHS SSARRHHVENVL
3561	A	3	256	MDHEFVAKGHLFRKGIMKIMVYKIFRILVPGNTDSTEALSLSYLVEL SVVAPAGQDMVSDDMKNFAEQLKPLVHLEKIDPKRLM
3562	A	3	205	KIMVYKIFRILVPGNTDSTEALSLSYLVELSVVAPAGQDMVSDDMKN FAEQLKPLVHLEKIDPKRLM
3563	A	66	852	PECWYLIVAQKLLSARVDIIPGFSRRHYSLEKVPVPLYTGGSESSC VVFNLDTMEAPPVTMPVTGGTINMMEYLLQGSVLDHSLESILHR\L RGLCDNMEPETFLDHVMVFLKGGQASPFVLRARRSMDRAGAPWHLR YLGQPEMGDKNRHALVRNCVDIATSENLTDFLMEMGFRMDHEFVAKG HLFRKGIMKIMVYKIFRILVPGNTDSTEALSLSYLVELSVVAPAGQD MVSDDMKNFAEQLKPLVHLEKIDPKRLM
3564	A	194	338	GKVPGGDCPLVWGQCCHFCMHHCILKWLHAQQVQQHCPMCRQEWKFK E
3565	A	197	522	GSAAMKVKIKCWNGVAH\WLWVANDENCIGICRMFNGCCPGCECSPS MLSERPRLQGAPATDCPAGCGGPVLPTCFQHALHPQVGLHAQQVQQA LAPMLPPRIGKFKE
3566	A	1	6521	MLRKRKWLGVVAHCNPSTLGGQGHDPKQPVRRLLSAPGSRIAGQW VLDLSKSPHLLKGENDKNSLSQKAFLYVAHVLDSESGVLVTMTTE TGPDSVKKAEAPQQPEAAAAVTPVTPAGHGHPEANSNEKHPSQ QDTRPAEQSLDMEEKDYSEADGLSERTTPSKAQKSPQKIAKKYKSAI CRVTLLDASEYECEVEKHGRGQVLFDLVCEHLNLEKDYFGLTFCD DSQKNWLDPSKEIKQIRSEWLTVFGEVGPWNFAFTVKFYPPDPAQ LTEDITRYLCLQLRADIITGRLPCSFVTHALLGSYAVQAEGLDYDA EEHVGNVYSELRFAPNQTRELEERIMELHKTIRGMPGEAEIHFLN AKKLSMYGVDLHAKDSEGIDIMLGVCANGLLIYRDLRINRFAWPK ILKISYKRSNFYIKIRPGEYEQFESTIGFKLPNHRSAKRLWKVCIEH HTFFRLVSPPEPPKGFVLMGSKFRYSGRTOAQTRQASALIDRPAPFF ERSSSKRYTMSRSLDGAEFSPASVSENHDAGPDGDKRDEGESGGQ RSEAEEGEVRTPTKIKELKFLDKPEDVLLKHQASINELKRTLKEPNS KLIHRDRDWERERRLPSSPASPSKGTPEKANESQRTQDISQRDLVP EPGAAAGLEVFTQKSLAASPEGSEHWVFIEREYTRPEELGLLKVTM QQEERQAGLAGILANGRLSKVDVLVDKFKVEVATEEMVGNRRANTQQ

				QGKMIASPEDFESVGEEGPWIRESPGGAALASGRTLAEKLLLEGSELR ADTREATIRNRCMSDQPEGQTELKRGLEEPHTCGRPTAPGTRPAEV DVLSPASDKGGLQSFLLDPAHAEEARAELSNETDTSFAERSFYLYNEE KDSEDQVLPPPLEERKGRDLAPPGEPRPTLNSLDLRVSAASSRSK DEAHMTSPKEGAGTPKNHGGPGDLKGSPAGQTFAGWEDAQWGVGE FPHLTASAAREEGTPVSGDLLGKAEESPTTEELKKHPPHRGQGVHPDP QACALPRAIPLNVRKPKVPDRGNFPKRGVVPVPTQKGGAELKDREAS AFLHMEV I I PLPASPGHSEDLA ALEEASPSPTSHGSGEPSELREPFL RHHVLSKASPEPKDQVGVFVVPATGGERRPPPIITSRKPRVVPPEAEG RIPLGFGFSPGKRREMTSFQAGDQEGSLEDISKTSVANKIRIFETHG AETRMSEGEARSLPNDVSSEAPVGQAEQQRSTLSDLGFAQLQPPGD FASPKATHSTVIPLATRHFRDTSASYQEAHTELEPVSPNSGCETTL AEATGTGVTGRNKSGDAVREEKRSTNLAANTPGKGRLRFASPSGPQ RAGLREGSEEKVKPPRPAPESDTGDEDDQDQERDVTFLKDNHLAIER KCSSITVSSSTSLEAEVDFTVIGDYHGSFEDFSRSLPELDRDKSDS DTEGLLSRDLNKGAPSQDDESGGIEDSPDRGACSTPDMPQFEPVKT ETMTVSSLAIRKKIEPEAVLQTRVSAMDNTQVDGSASVGREFIATTP SITTETISTMTENSLKSGKAAAMIPGPQTVATEIRSLSPIIGKQVL TSTYGATAETLSTSTTHVTKTVMKGGFSETRIEKRIIITGDEDDVDQD QALALAIKEAKLQHPDMLVTKAVVYRETDPSPEERDKKPKLRET NNKRQPCIRRNLOARAILPATQGSAGPLPPSLQSDAKAGELPVRFR TGTWGEALFIKEKGFFWSPPTGPMAAVQMDPELAKRLFFEGATVVIL NMPKGTEFGIDYNSWEVGPKFRGVKMIIPPGIHLHYSSVDKANPKEV GPRMGFFL\SLHQRLTVLRWSTLREE/VLDLSPAPESEVEAMRANL QELDQFLGPYPYATLKKWT\SLTNFISEATVEKLQENRQICAFSDV LPVLSMKHTKDRVGQNLPRCGIECKSYQEGLARLPKMPRAGTEIRF SELPTQMPPEGATPAEITKHSMDLSYALETVLNKQFPSSQDVLGEL QFAFVCFLLGNVYEAFAHWRLLNLLCRSEAAMMKHTLYINLISIL YHQLGEIPADFFVDIVSQDNFLTSTLQKGFLIDISED FIEVFLRGT ERFSKANLLDESIAVDATLRKKAKEKFAHLTKKFRWDFAAEPEDC APVVVELPEGIEMG
3567	A	1	1232	GCTGTWGEALFIKEKGFFWSPATGPMAAVQMDPELAKRLFFEGATVV ILNMPKGTEFGIDYNSWEVGPKLRGVKMIIPPGIHLHYSSVDKANPK EVGPRMGFFLSLHQRLTVLRWSTLREEVDLSPAPESEVEAMRANLQ ELDQFLGPYPYATLKKWISLTNFISEATVKKLQENRQICAFSDVLP VLSMKHTKDRVGQNLPRCGIECKSYQEGLARLPKMPRAGTEIRFSE LPTQMPPEGATPAEITKHSMDLSYALETVLNKQFPSSQDVLGELQF AFVCFLLGNVYEAFAHWRLLNLLCRSEAAMKK/HATRLWINLISIL HHQLGEIPADFFVDIVSQHNFLTSTLQVFFSSACSIAVDATLRKKA KFQAHLTKKFRWDFAEPEDCAPVVEELPEGIEMG
3568	A	2	166	FKLYKLFIKFLPVLENGGVVQVGELLPCCKICGRTFPPVALVSRLILY LYGFTDL
3569	A	56	1072	ARGGGAMEGLEENGVVQVGELLPCCKICGRTF\FPVALKKHGPICQK TATKKRKTFDSSRQRAEGTDIPTVKPLKPRPEPPKKPSNWRRKHEEF IATIRAAGLDQALKEG\GKL\PPPPP\PS\YDPGFIIQW\CPY\CQ RKIPMENAADRHINFCKEQAARISNKRRTSTDTKGKPTSRTQVYKPP ALKKSNSPGTASSGSSRPQPSGAG\KTVVGVP/SQGVSSSSSSSLG /NTKLQTLSPSHKGIAAPHAGANVKPRNSTPPSFA\NRP\APGVLTN K\RKTYTESYIARPDGDCASSLNGGNIKGIEGHPGNFPKF\CHCEG TKYPVEWAKFCCECGIRRMIL
3570	A	2	413	PRVRGILPSCSVVVSLLLLLLLLRLGEPWGRMVC\EKCEKKLGTVI TPDTW\KDGARNT\TEN\GGRKLNNENKALTSKK\ARFDPYKGNKFST CRICK\SSV\HQPGSH\YCQ\GCAYKKGICAMCGKK\VLDTKNYKQT SV
3571	A	32	469	PTCLHLLPYATVPNFPTFSCFLSPPNCSNLCLLPSSKVTSTFSGIF SAMPHTTLLQFPISFSFPSETSLAWPSFISLSAFWSQLFNNCLGSA

				KLSCLLSPPNCSNLCLLSSSSKASSTFSSITTRLESLLRGLSQDVSG KYKT
3572	A	659	1149	EVTACRQPSVAFSTSLALALTALLEEPPSLLLHCESPLLGWASSCG GCAGSPSSAGPAGIVLK/SLAGPQLPPCRVGLGTCSLPYLSLPPAVG SPMARASLMSAAPCSMARVPSTTQGLLSRTFPQCGQMAQDWQAAPPAS PVQDPLEEASWAPESGDLNFYV
3573	C	361	501	MLFLRYAPLVGGSFICIWSHPLQFFLTSTIKVNFVETLFCFQSFKDIF*
3574	A	124	579	EPLPGLAKAGAGSLSCSVRPCAAGASPTSATPCSIAPSPIDHPRAEE CGRMVQDWAAPPAPRCGIHWVKPAGLLSLLMSMIRINMIVKLLVF VILLVT*FTVKVCLYIFQGLCCGLLFCKILHGSPSHHRPKDLWHHCD LDVRHEVKGDH
3575	A	2765	3139	YSLKSGSVMPPALFFWLRIALAMQALFWFHMNFKVVSNSLKKVIGS FMGMALNL*ITLGSMIAFTILILPTHEHGMFFHLFVSSFISLSSGL* FSLKRSFTSLVSWIPRYFILFEAIVNGSSL
3576	A	265	665	GRASGVVRSRWPVCDLAGFRGEAADLHGVCYSRLRSPAGFTQWIOHQ GSRWSCLPVPRRAPALL\ALGWSMG\WAPPQPLAWVLSPLPGAGSA DWLLQVRGPPSPRPPGTPAGPPAPCAALVPARVSPSTLPS
3577	A	82	361	LRSPAGFTQWIRTGAAGGAACQFRAVRPALLSPWVVDGTGRRGAGGG AYRGGSGRTGAHGTGGGSGMAGCRSRAVPRRKAATRPCEVQKRQHN VNYLFPVVETKAQTVKWFVLA*ASPCSVGSCAARASISAAPCSTAP SPIDHPRAEECWAHGTLAGSSTCSPGADPLGEASWAPES
3578	A	806	934	KILSSKFPFSFLPSYVCTSSFP*THPSIISTSSSSSHSVPTN
3579	A	1034	1393	AVTLTGKVCSTPEASETTNPPGGTNNRRASLRAATLTVKVRSTFP RGAASFFKSVRPRTHQFRTQYSPRMSKIRDCSRSCSFISFLASWRI ICLL*VLISLCAW*RYRLFVWPLPSS
3580	A	529	750	REFRVGVASADPAFGAAGRPCPQGG*GA*HTGQWLRRVYVWPQQCQP TGVALDFSPGLSCLPAGQSGSPAARHA
3581	A	2	343	HAVFFISIRSFMMFFKLVLVSNSSKLFSTFLVSLHWVRTCSFSSEE FVITHFLKPTSVNSSNSFSVQFCSLAGEEL*SFGGEEAFWFLEFSAP LHWFFLIFMDLSTFGLCCC
3582	A	289	422	WIPHRGCRWSCLPVPVPCARTPQPLGGGWDWARTHQTHCKLDLS
3583	A	189	309	WLGQMEIQNHVPKIQMELCGQHSAAVSLKAGGRALQE
3584	A	587	802	LKTFHTAVFVRFGPWLDPDTGFCSSLSFQFSFLISLDTLPYRKGVICL LEALDDLLFFLVETWYHQEAVSAL
3585	A	76	1740	SLTAASSFQPOLKQSSHLSPSGWDYRLRMTQNKCLKCSKANVYTE VPDGGGWAVAVSFFFVEVFTYGIKTFGVFFNDLMSDFNESNSRIS WIISICVFLTFSAPLATVLSNR\LGHRLVV\MLGGLLVSTGMVAAS FSQEVSHMYVAIGIISGLGYCFSFLPTVTILSQYFGTRRSIVTAVA\ ST\GECFAVFAFAPAIMALKERIGWRYSLLFV\LLQLNIVIFGALL RPIFIRGPASPKIVIQENRKEAQYMLENEKTRTSIDSIDSGVELTTS PKNVPTHNTLELEPKAD\MQQVLVKTSPRPSEKKAPLLDFSILKEKS FICYALFGLFATLGFFAPSLYIIPLGISLGIDQDRAAFLSTMAIAE VFGRIGAGFVLNREPIRKIYIELICVILLTVSLPFAFTFATEFWGLMS CSIFFGFMVGTIGGLTFHCLLKMSWALQKMSSAAGVYIFIQSIAGL AGPPLAGLLVDQSKIYSRAFYSACAAGMALAAVCLALVRPCKMGLCQR HHSGETKVSVSHRGKTLQDIPEDFLEMDLAKNEHRVHVQMEPV
3586	A	1	2472	GFVFLLLLAPLSRLEFHKSRGLKNVFEGLEAEFCYKVLHDGGEEL EWVRPDAETTTTHQGRVSQEKHQALGCKWPKLCGDALCVILSAPSPID HPKAEECRRRARDWQAAPPAAPVRDPLGEASWAPESGQQMKEAAELG VSCMGPDLEKLTLYEVKLRLOGCKAAQRPLGCTLLAIQGTLYQRIFS PLTQPELVNGKGWHLTQESLSQNGSLEFLTSEPHSPNPNEGSSRRQS LHTNANNMAFASEQFPNLPSCSGSRGFPGRARVLHLDQCNCQRLTAG PAQLQGSRAANRRKALVSPSSSVAREDDGFAEEMVFTYGIKTFGVFF NDLMSDFNESNSRISWIISICVFLTFSAPLATVLSNRFGHRLVVML GGLLVSTGMVAASFSQEVSHMYVAIGIISAIMALKERIGWRYSLLFV GLLQLNIVIFGALLRPIFIRGPASPKIVIQENRKEAQYMLENEKTRT

				SIDSIDSGVELTTSPKNVPTHNTNLELEPKADMQQVLVKTSPRPSEKK APLLDFSILKEKSFICYALFGLFATLGFFAPSLYIIPLGISLGLIDQD RAAFLSTMAIAEVFGRIGAGFVLNREPIRKIYIELICVILLTVSLF AFTFATEFWGLMSCSIFFGFMVGTIGG\LTFFHCLLRMMSWAL/QKMS SAAGVYIFIQSIAGLAGPPLAGLLVDQSKIYSRAFYSACAAGMALAAV CLALVRPCKMGLCQHHSGETKVVSHRGKTLQDIPEDFLEMDLAKNE HRVHVQMEPVVRRRFAAAGPAGLGAAGSDAFAFPAREGPERRAGYSGP AAACFDFSTAAPKREQRGPLSLVGLEM
3587	A	323	1303	STLYLPAMDNTNQEIEIPDLLALGTSAWSSTLAALPEPFSPLHCGSPF LGWSRPELAPSACREVWREKPEWELGLRTVLAGQCEFRVGVSGDST RSSWPPLLAPGNEGLSTRASSCGGCTGSPSRAGPPVLCSISCQALAA FPRGRARGLQAMPPEPPRLRGLLCSPEPPRLVPPAPGHPVPLTTQ GLRSTGTHKRDWQAAPPAAPVRDPLGEASWAPESANLVGKWRTFVSS SGTANAPISTLSKQTTGLYQSAGCGWGQNLGAKYRA/LCRPVKSD*H GRQTKDTGVRLSGKGLSNNP*LFRVGTVGSHRPHFPTYMDGLASGV
3588	A	1	3552	MCELDILHDSLYQFCPELHLKRLNSLTACHALLDCKTLTLTELGRN LPTKARTKHNIKRIDRLGNRHLHKERLAVYRWHA SFICSGNTMPIV LVDWSDIREQKRLMVLASVALHGRSVTLYEKAFFLSEQCCKKAHDQ FLADLASILPSNTTPLIVSDAGFKVPWYKSVEKLGWYWSRVRGKVQ YADLGAENWKPI SNLHDMSSSHSKTLGYKRLTKSNPISCQILLYKSR SKGRKNQRSTRTHCHHPSPKIYSASAKEPWVLA TNLPVEIRTPKQLV NIYSKRMQIEETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIALMLQ LTCWLAGVHAQKQGWDKHFQANTVRNRNKEVEVNDLSGLISDVVMSP IPLTSLLCGNPDEIRSFPSLCPECTEGPIDLVFVIDGSKSLGEENFE VVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMK KAVAHMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVF TDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASEPTNKH LFYAEDFSTMDIEISEKLKKGICEGINYCALNKPGEHCVNMEESYY CRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCEG FLINEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCEGHVAAAM GRRVQSVLGEEDAPEKRFALLSDPGDLTAHELDSCALGDHGCEHSCV SSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSY TCECLEGFRLAEDGKRCRKSSCENKRADLVFIIDSSRSVNTHDYAKV KEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSKTFKRRKSEVERA VKMRHLSTGTMGTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTD GRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVF LVANFSQIETLTSVFQKKLCTILASGTNSNRQLPSAFAPPLLLAICF RFRSRSSGSARRALHCGKSFLSRSPAILAAVGRKMVAAKTKKSL SINSRLQLVMKSGKYVLGYKQTLKMIRQGKAKLVILANNC PALRKSE IEYYAMLAKTGVHHYSGNNIELGTACGKYRVCTLAIIDPGDSDIIR SMPEQTGEK
3589	A	375	646	KKSLLSINSRLQL\VMKSGKYVLG\YKQTLKMIRQGKAKLVILANNC PALSGNNIELGTACGKYRVCTLAIIDPGDSDIIR\SMPEQTGEK
3590	A	75	335	LRILKFLSCSLSLLGWGPSPSLRQEDGGRKRRRKSLESINLRLQLV M\KSGKLLPGGTSQTLKMI\RQGKAK\LVILANN/CGPALRKSE\IE YYCYVWLKTGC/HHPLTVGNNI\ELGATA\CGKITRYVLHTGLFIDP G*LLTSFRKACPEQTC*KMVAAKEDEKSRWSRSTLGSNSLWKS GKLL PGGTSQTLKMIQTRQSEMWSFSLTTGPSFEET
3591	A	1	2580	MGSHHLVVVLIESPQTESQIVSDSHASKRIKYLGIHLTRDVKDLFKE NYKPLLNEIKEDTNKWKNI PCSWVGRINIMKMAILPKVVYRFNAIPI KLPMFTFFTELEKTTLKFIWNQKTAHIAKSILRQKNKAGGIMLPDFKL YYKATVTKTAWYWYQNRDIDQWNRTEPSEIMPHIYNYLI FDKPEKNK QWGKDSL FNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRP KTIKITLEENLGITIQHIGTGKDFMSKTPKAMATKAKTDKWDLIKLS FCTAKETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELQQIYKKKT NNPIKWKVDMNRHFSKEDIYAAKKHMKKCSPLAIREMQIKTMYRY

				HLTPVRMAI IKKSGNNSKLPFEP SRNKRVMPEPCAHTILSSLARPAS KMHSPPLSMEPSAGPGGSQNFNPEEAEDRPTLNFEGETWALTGPD ARYFNYTREARGENSLVSGGCRPLAAGRARASTSGWAAKRVGTLQGG PLTWAMPAPISPPPMVTCLTIIFLAEEAVDEEDTERMNCLVTKAM VWQRRRQRGDPGREDARGGQPRKARLWGRGPTRPCS PRAPGVPTPQ GGGGASSPALPIPGGCNVPALSGYTRAGSQLSAAGARVSAGLRPAEQ RDLAAGVLWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYKRG ILSCHRLYHEHTDECDVEVQAGGQQRASFRELAPPVAAVVL PATCTL KMGSQSVSPYQKRLCNFLVMGELFPLPSPLQFLDQVIKTPM TSQKTF ESLVDFSKALGKHPVSKVAAATGHTVVLVDQTEDILAKSKKGIEES LRKVAKKKFAENPK
3592	A	1	1386	APVTENNGSPFGSQNELFPEPCFLLDKTEILTPNLGMALGLNDCQGA VTCEIRGSLQIFGLRNLCDDDVPHIRSSNKVPVQPSHAVHPLTPL ITYSDEHFS PGSHPSHIPSDVNSKQMSRHPPAPDIPTFYPLSPGGV GQITPPLGWFFNEQLIFFKNEFRRIEYLP LLVSGQVRQGPVYPITG GFRQPYPSSLSVDTSMSRCQRESRVGALRCAPAGPATPSGDGLSLLG KRCLQTN SWPPDCMGMTVRKADITRRVCLIQNMPGVGFSSHMI PGPP GPHTTGIPHPAIVTPQVKQEHPTDSDLMHVKPQHEQRKEQEPKRPH IKKPLN AFMLYMKEMRANVVAECTLKESAAINQILGRRRDQYLSLCL PPRHIIHMSIIVIE MWVSGTPVFSAPRLHTVTQLLSGQFCSAGGRL IKALGKVRHSWSGDTQPAARAALTEPCTAEAVAQMERLF
3593	A	2	1419	RPPGIRAPRQLHPAAGRFPDASARPRFRPTVLLHDPFQLSFPPPLS YPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDP ELCATDEMI PFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNESEIIPASNGH EVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKGPSYSSSYGYIMM PNMNNDPYMSNGSLSPPIPRTSNKVPVQPSHAVHPLTPLITYSDEH FSPGSHPSHIPSDVNSKQMSRHPPAPDIPTFYPLSPGGVGQITPPL GWQGPVYPITGGFRQPYPSSLSGDTSMSRFSHP\MIPGPPGP\HTI GIP\HPAIVT\ PQV\KQDHPHH\SSDLMHVKPQPE\QRKEQEPKRPP TKK\PLNAFMLYMKEMRANVVAECTLKESAAINQILGRRWHALSREE QAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKREKLQESASGTG PRMTAAYI
3594	A	59	435	STCPAPQSARVQWCNLSLQPPPTPTPRSSNSPASASQIAG\ITGV RHHTQLIFV\FLVGDGGFHCVGSGWVSNCWPSGWRPLWPHLFLGFHK DLEVVGFLVFASISFRSWRWDLKNSSVLTHFFK
3595	A	54	442	NHFQHTLLWPKGFS LRSTNLTTTNLGFSHISGHWSWAHACSPCPH ISSQPGPCPASIIYRPDSPHLPCCPELNIDLHLDVTWSVTWECYCSI IPRPTVAHGA KTSKQPPSWKGNALGVMEKTFYK
3596	A	360	1023	GQGRLP ERGYLA EAGVYRICGRQSRHEDGTHRGAQVIEQRRKWLPAA LGFQPIILQLCGKRVP\APSRAS TGQPQASRAWSGPL/PHPQCGSDI RLRVRAEYCEHGPAL EQGVASRRPQALARQLDVFQQA TAVLRSRDLG SVVCDIKFSELSYLD AFWGDYLSGALLQALRGVFLTEALREAVGREA VRLLSVDEADYEAGRRRLLLMEEEGGRRPTEAS
3597	A	3	370	QMYCVFN RNEDACRY/GS/AIGVLAFLASAFFLVDDAYFPQISNATD RKYLVIGDLLFSG\VLASLAYQRYKAGVDDFIQNYVDPTPDNTAYA SYPGASVDNYQQPPTQNAETTEGYQPPPVY
3598	A	1	1356	MGRGRGDLQPSGLGRPRTPAAPRAGREPGAARVRIDRGADAAAAARP RLLCEPVPVPGPGCRELGPA PLARAYWKRAPERRKARRLEPGAALGRGQ GRARCSGAPGCRALLGHTGRVPPPGTRPVLRAPRASQRRSPQAVVKG MKLGFAQGGGHQASSGSSGSSNELGHHQPYQVLP SRQVFALIVFSCI YGE GYSNAHESKQMYCVFN RNEDACRYGSAIGVLAFLASAFFLVDA YFPQISNATDRKYLVI GDL LFSALWTF LWFEGFCFLNNQWAVNKP KD VLVGADSGSEPPKRGSKVNP GARRLSSGCPSDRPELIRPRCIRAEA RNSTSRKHIQRNIHERRRTHDTPEQQKNTATTGTAQRFNLPQFNCP LIGPPLALRGSP LHEIGIRTSKGFFSSLLNGNHFEYLSLT LGELPWS RNCIGYGRNPLYHYMPTGRLQRRIEQRST

3599	A	3	706	GGGSGDGDMEAGAYGAAGAGGSFDLRRFLTQPPVVARAVVL\VFAL IVFSCIYGEYSNAHESKQMYCVFNRNEDACRYGSAI\GVLAFLASA F\FLVVDAYFPQISNATDRKYLVIIGDLLFSALWTFWVFGCFLTNO WAVTK\PKTVLVGADSVRAAITFSFFSIFSWGVLASLG\YQRYKAGV DDFIQNYVDPTDPNTAYASYPGASVDNYQQPPF\TQNAETTEGYQP PPV
3600	A	1	166	VIPQIQKVCEVVDGFIYVANAEAHK\VQDTEAETLTGFLNGIEWILE EVESKRAR
3601	A	1	1193	DSVVEFQAMAGSEPRSTRTPPP\FS\WGRLEAAILSGWKTFWQA LSTERVARTTSLEEVDAAANTLRLPIDVQLYILSFLSPHDLCLQG\ ST\NHYWNETVRDS\ILW\RYFLSRDLPSWASVDWKSPLDLEISKKP ISDVTGALFDYLAHYRMCCPYTRRASESSRPYMGADTSFLHSLIIQ NEPRYALFGPGLEELNTSLVLSLMSSEELCPTAGLPQRQIDGIGSGV NFQLNNQHKFNILILYSTTRKERDRAREEHTSAVNKMFSSRHNEGDDQ QGSRYSVIPQIQKVCEVVDGFIYVANAEAHKRHEWQDEFSHIMAMTD PAFGSSGRPLLVLSCISQGDVKRMPFCFYLAHELHLNLLNHPWLQ\D TEAETLTGFLNGIEWILEEVESKRAR
3602	A	1	171	RILMAINGKVFVDVTKGRKFYGPVKYHHVHGKLLTAGEEPA\VYSDEEE PKDESARKND
3603	A	3	253	LSLQEFGTSTFAGRDASGLATFCLDKEALKDEYDDLSDLTAAQOETL SDWESQFTFK/LLKEGEEPT\VYSDEEPPKDESARKND
3604	A	3	701	PARHSLAQREEKVASSGSLPSAAQPLLSEIMAAEDVVATGADPSD\L ESGGLLHEIFTSPNLNLLGL\CIFLLYKIVRGDQPA\SGSDDDDE PPPLPRLKRRDFTP\AE\LRRFDGVQDPAPYSWAINGKVFVDV\KG\ RKFLTGPPEGYPYGVFAGRKCIQALPTFLLDKEA\LKDE\YDD\LSDL T\AAQOE\TSDWESQFTFKYHHVHGKLLKEGEEPTVYSDEEPPKDES ARKND
3605	A	3	678	KRLPKMAEVQVLVL\DGRAHSSLG\RLA\AIVAK\QVLLGRK\VVVV \RCEGI\NISGNF\YR\NKLKYLGFPPSGMNTNPSR\GPYHFG\AP SRILLAGTVRGM\LPHKTKAEAKAA\LDRL\KVFDGIP\PPYGQES GMVVP\AALKVVR\LPTRKFCLIWGR\APEVG\WKYQAVTATLEE \KRKREKPRFHYRKKENSIMRL\RKQAREETWRKKIDKYTEVLKTHG LLV
3606	A	114	353	ALSSRGVMAEYGTLLQDLTNITLEDLEQLKSACKEDIPSEKSEET TGSAWFSFLESHNKLDKDNLFHVVPTQTVAL
3607	A	104	342	ALSSRGDNLSYIEHIFEISRRPDLLTMVVDYRTRVLKISEEDELDTK LTRIPSAKKYKDIIRQPSEEEI IKLAPPPKA
3608	A	211	241	NFNGRGGLAAGRRKKPDWLDSTLNS*PSH
3609	A	37	116	RPTRPPTRPDLRLKPPFTRYPGPLGL
3610	A	104	516	ALSSRGVMAEYGTLLQDLTNITLEDLEQLKSAFKE\DIPEKSEET TGSAWFSFLESHNKLDKDNLSYIEHIFEISRRPDLLTMVVDYRTRV LKISEEDELDTKLTRIPSAKKYKDIIRLPSEEEI IKL/APPPKA
3611	A	569	838	PTVLWEPPSFPPPPQGIPIHSG/PDTLTGRRRASPSGLCYSENGGL TEEGSTRPPAH/SPGATVSSPPPPPPSSSLPCCLGNRHFFDDR
3612	A	268	356	EFFILTFKNNIFIYRYNRISREWTQKYAM
3613	A	489	605	QLQVCYCT*RPYSGTRCGVSNVQLLLCSLLSHLCCSAS
3614	A	391	561	AYTERSEEARRQAHTMALKRINKELSDLARDPPAQCSAGPVGDDMFH WQATIMGPND
3615	A	367	855	GARRQAHTMALK\RINKELSDLARDPPAQCSA\GPVG\DDMFH\WKA TINGDLMDKPIFKGGVFLTIHF\PTDYPFKTP\KVAF\TTRIYHPN INSNG\SICLDILRSQWSPALTISKVLLSI\CSLL\CDPNP\D\DP LVE\IARV\YKTDKDRKYNRISREWTQKYAM
3616	A	1002	1480	MLLLKTTERFEVSVCMCTYV\SNLGKKQRSVSFLASGLMRVSTGPE LRLHHSFVLTGDVGRRICRLLVGLFTKGDTSKRV\HPFSPPG\CFL LCDLAR\VGSSPKINRVPHFTRTQTSTQRSCTVFVWQRCSLVGPFOV

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				TVFTM\YFHHSLSRSISRFSSG
3617	A	223	415	MEPAAPSQKPSRSGSGLPRIPLLAATPLHTRRQPGPRHRTAEIIVG ALFGTANLTANGAVGGE
3618	A	1	858	MQNKLDSLLKATDLIREQPHLNPAVPHLQKQERLPGLSDKAAAPL AVRFAVPKSCCKTGLETGIQLQIHPLHAKGPGRASTAPPQPEVTHRA DYFFRRPPVARPRLSPAGSIHAKSVGSGSCRAKGGCRTRSSRTWNNR GRLRDPGASLGPRMYSHGIELACQKQKEFVKSSVACKWNLAEEAQQKL GSLALHNSESLDQEHAKAQTAVSELRQREEEWRQKEEALVQREKMCCL WSTDAISKDVFNKSFINQDKRKDTEDEDKSESFMQKYEQKIRHFGFG YDAL
3619	A	144	1339	DPEQPDMEQPWPPPGPWSLPRAEGEAEESDFDVPSSPRCPQLPGG GAQMYSHGIELACQKQKEFVKSSVACKWNLAEEAQQKLGLSLALHNSES LDQEHAKAQTSSIRTEGNGKKNWRQKEEAL\ RQREKMCFLWDAISK DVFNKSFINQDKRKDTEDEDKSESFMQKYEQKIRHFGMLSRWDDSOR FLSDHPYLVCEETAKYLILWCFHLEAEKKGALMEQIAHQAVVMQFIM EMAKNCNVDPGRCFRLFFQKAKAEEEGYFEAFKNELEAFKSRVRLYS QSQSFPQMTVQNHVPHSGVGSIGLLESPLQNPDPYLQYSISTALCSLN SVVHKEDDEPKMMGHCI I WVKTAEAKCYFVTGKGGTWAIFLDTFMGV LALYFCSVFDGRERVLCFCFVNF
3620	A	2	486	ESGQVKLRPVSSASRGLRPAKPRRTMLKAKILFVGPCESGKTVLTN FLTESSDITEYSPTQGVRFEPWCW PALMKDAHGVAIVFDADIPSHRKE LEMWDSFCFCQPSLQDTQCMLIAHHKPSGDDKGSLSLSPPLNKLKL VHSNLEDDPEEIRMEFIKYL
3621	A	1	1080	MRSHFSALGWSMGLSALEQGVVLVGEARAAQEPMEWVGSGIAGCRS RALPRGKAAKARFESCWPALMKDAHGVIIVFNADIPSHRKEMEMWYS CFVQPPSLQDTQCMLIAHHKPSGDDKGSLSLSSGGGNNRRQGRSCPR GWTLGVAAGAAAAAQKEARGLHVGSTWAPATPLGNLSPAAPYSGDL DSNHCPEEVVEASPVLMSPGSPSKDLYLHFSFSQSGKTVLANFLTESS DITEYSPTQGVRIEFENPHVTSNNKGTGCEFELWDCGGDAKYVSFK ESHFIKWFKNQLPKPGAVAHTCNSSTLGGQGGAMATPGTLRAAPEP AFEFQKTIISMQVKVAKRLVCI TRNLNLAFLI
3622	A	48	653	RAASRGLRPAKPRRTMLKAKILFVGPCESGKTVLANFLTESSDITE YSPTQGVRIEFENPHVTSNNKGTGCEFELWDCGGDAKFESCWPALM KDAHGVIIVFNA\ ESQATGRKWRWGI PAFVQPPSLQDTQC\ ILIAHH KPGSGDDKGSLSLSPPLNKLKL VHSNLEDDPEEIRMEFIKYLKSIIN SMSES RDREEMS IMT
3623	A	44	421	SICLPPVAPWLRPVHRQLGEANE EFALRVQQLVAKELGQTGTRLTPA DKAEHMKRQRHPRLRPQSAQSSFPSPGSPDPVQLATLAQRVKEVLP HVPLGVIQRDLAKTGCVDLTITNLLEGAVAF
3624	A	20	422	LGIHVFLVSCALPDSVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRV LISNHVTPFDHNI VNLTTCTSTPLLRFCSTRLPPTPLLLFPPEEA TNGREGLLRFSWPFSIQDVVQPLTLQVQRPLVSVTVSDA
3625	A	1	346	LRPQSAQSSFPSPGSPDPVQLATLAQRVKEVLP HVPLGVIQRDLAK TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKF/ PRQESLQE RKQALY EYARRRFTERRAQEAY
3626	A	162	461	LVAKELGQTGTRLTPADKAEHMKRQRHPRLRPQSAQSSFPSPGSP DVQLATLAQRVKEVLP HVPLGVIQRDLGMGKGGPTLGDGHREEKWV KEESK
3627	A	39	260	DCKPVARPSTKAKTDQSGPFLSLLPHRYLSLSLTLRSSSPESMTCWM EGREKEKSASQ*VTTTFRASMSSYA
3628	A	1	2160	FRPGAPEAAVMELSSWGPRLFD SHRLPGDCFLLLVLLLYAPVGFC LLVLRFLGIIHVFLVSCALPDSVLRRFVVRTMCAVLGLVARQEDSGL RDHSVRVLI SNHVTPFDHNI VNLTTCTSTVSESEADSATVRFPGAQL KAPLSPLAFPMEDTEALPLTPILYPTCQFFFFIFLNI FLLAFSSPGS QPLLNKSPQAFV\ CWSRGFMEMNGRGE\ LVE\ SLKRFCSTRLPPTP LLLFPKKATNGREGLLRFSWPFSIQDVVQPLTLQVQRPLVS/VGE

				CVLNRESLGLGEI SHPWPLRPHLMPSQTVSDASWVSELLWSLFV PFTVYQLVAKELGQTGTRLTPA\DKAEHMKRQRHPLRPQSAQSSFP PSPGSPDVQ/IWATLAQRVKEVLPH/VGPLGVIQRDLGMGKGGPTL GDGHRBEEKWVKEETKTGCVDLTITNLLGAVAFMPEDITKGTQSLP TASASKFPSSGPVTPQPTALTFAKSSWARQESLQERKQALYFYARRT FPQVTRSHIISTALEDPCLSKISTTCORGNLSLRSCQRATMTSQPLRL AEEYGPSPGESELA VNPFDGLPFSSRYEYELLKQRQALPIWAARFTFL EQLESNPTGVVLVSGEPGSGKSTQIPQWCAEFALARGFQKGQVTVTQ PYPLAARSLALRVADMDLTGHEVGYISIPQEDCTGPNLTLLRFCWDR LLLQEVASTRGPGKLGRAGTR
3629	A	1	789	MGFRHVQGAGLKLTTSSDLPALASQVQCKLVVPASAERHISPLQRL IAFSLRPDPGLAGDRASLGVPPLCGYRIGNPRRS PKRTRHCARTAAVS CSAYSKCLYQFRPNVGHSA STPKAMCQTTAAGEGAHADEGYTQRVV GARRGTPQRYTGAETKNRAFRSYPKMETSWPRGGSTPPVALDAQV ERECALGSGAQGHKSLAVRVVLIFCINEHYPTLTLYRLPFVLP LRS GGTPTSWRALFFPSSSDSNCKLCGGTSS
3630	A	1706	2082	ILLFFSFFLRWSFALVTQAGVQWRDLGSLQPPPPGFKRFSCLSPPSS WDYRCPLPRLANF\LVETGFHHVGQAGLKLTTSGDPPTLASQSVGIT GRSHRARPNLILTGYCRIISVLSLMILNPII
3631	C	44	340	MKCSQPXRCHFQSD FQKCAPCPRAQTHWLEPPGRVQTISSMRNAQKG FADSIRLWRLPASGVGVVVSPEGAGDP SHLLDPGHSAPYSPAPRQL SRVP*
3632	C	2037	2426	MKCSQPXRCHFQSD FQKCAPCPRAQTHWLEPPGRVQTISSMRNAQKG FADSIRLWRLPASGVGVVVSPPITQTEVAPEGMYLVGSSSGTLGGCR ALTQVFLSLSSLGVCACACACLCFSLWAHQDVSS*
3633	A	184	9818	IEEPRDTRLQVCSGVIHCLDKFKMRKHRHPLVAVFCLFLSGFPTT HAQQQADVKNGAAADIIFLVDSSWTIGEEHFQLVREFLYDVVKSIA VGENDHFALVQFNGNPHTFLLNTYRTKQEVLSHISNMSYIGGTNQ TGKGLEIYIM\QSHLTKAAGSRAGDGVQVIVVLTGHSKDGALPSA ELKSADVNVFAIGVEDADEGALKEIASEPLNMHMFNLNFTSLHDIV GNLVSCVHSSVSPERAGDTETLKDITAQDSADIIFLIDGSMNTGSVN FAVILDFLVNLLEKLPIGTQQIRVGVVQFSDEPRTMFSLDTYSTKAQ VLGAVKALGFAGGELANIGLALDFVVENHFTRAGGSRVEEGVPQVLV LISAGPSSDEIRYGVVALKQASVFSFGLGAQAASRAELQHIATDDNL VFTVPEFRSFGDLQEKLLPYIVGVAQRHIVLKPPTIVTQVIEVNKR D IVFLVDGSSALGLANFNAI RDFIAKVIQRLEIGQDLIQVAVAYADT VRPEFYFNTHPTKREVITAVRKMKPLDGSALYTGSDLFVRNNLFTS SAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSSIMAFAGNKG ADQAELEEIAFDSSLVFI PAEFRAAPLQGMPLGLLAPLRTLSTGPEV HSNKRDIIFLLDGSANVGKTNFPYVRDFVMNLVNSLDIGNDNIRVGL VQFSDTPVTEFSLNTYQTKSDILGHLRQLQLQGGSGLNTGSALSYVY ANHFTAGGSRIREHVPQLLLLL TAGQSEDSYLAANALTRAGILTF CVGASQANKAELEQIAFNPSLVYLMDDFSSLPALPQQLIQPLTTYVS GGVEEVPLAQPESKRDILFLFDGSANLVGQFPVVRDFLYKI IDELNV KPEGTRIAVAQYSDDVKVESRFDEHQSKPEILNLVKRMKIKTGKALN LGYALDYAQRIFYVKSAGSRIEDGVLQFLVLLVAGRSSDRVDGPASN LKQSGVVPFIFQAKNADPAELEQIVLSPAFILAAESLPKIGDLHPQI VNLLKSVHNGAPAPVSGEKDVVFLLDGSEGVRSGLLKEFVQRVVE SLDVGQDRVRVAVVQYSDRTRPEFYLN SYMNKQDVVNVRQLTLLGG PTPNTGAALFVLRNVLVSSAGSRITEGVPQLLIVLTADRSGDDVRN PSVVVKRGGAVPIGIGIGNADITEMQTISFIPDFAVAIPTFRQLGTV QQVISERVTLTREELSRLQPVLPPLSPGVGGRDVFVFLIDGSQSA GPEFQYVRTLIERLDYLDVGFDTRVAVIQFSDDPKAEFLNNAHSS KDEVQNAVQRLRPKGRQINVGNALEYVSRNIFKRPLGSRIEEGVPQ FLVLISSGKSDDEVVPAVELKQFGVAPFTIARNADQEEVLKISLSP EYVFSVSTFRELP SLEQKLLTPIITLTSEIQIKLLASTRYPPPAVES

				DAADIVFLIDSSEGVPRDGFHIRDVFSRIVRRLNIGPSKVRVGVVQ FSNDVFPEFYLKTYRSQAPVLDAIRRLRLRGGSPLNTGKALEFVARN LFVKSAGSRIEDGVPQHLVVLVGGKSQDDVSRFAQVIRSSGIVSLGV GDRNIDRTELQTIITNDPRLVFTVREFRELPNIEERIMNSFGPSAATP APPGVDTPPPSRPEKKADIVFLLDGSINFRRDSFQEVLRVSEIVD TVYEDGDSIQVGLVQYNSDPTDEFFLKDFSTKRQIIDAINKVVKGG RHANTKVGLEHLRVNHVPEAGSRLDQRPVQIAFVITGGKSVEDAQD VSLALTQRGVKVFAVGVRNIDSEEVGKIASNSATAFRVGNVQELSEL SEQVLETLDAMHETLCPGVTDAAKACNLDVILGFDGSRDQNVFVAQ KGFESKVDAILNRISQMRVSCSGGRSPTVRVSVVANTPFG\PEEAF DFDEYQPEMLEKFRNMR\SQHPY\VLTEDTLKVYLNKFRQSSPDSVK VVIHFTDGDADGLADLHRASENLRQEGVRALILVGLERVNLERLMH LEFGRGFMYDRPLRLNL\LALG\YDQADQLDNIAEKACCGVPCKCSG QRGDRGPISIGPKGIPGEDGYRGYPGDEGGP\GERGPPGVNGTQGF QGCPCQRGVKGSRGFPGEKGEVGEIGLDGLDGEDGDKGLPGSSGEKG NPGRRGDKGPRGENGERGDVILGGPGLSY/GQDSQERGPGETGDL GPMGVPGRDGVPGGPGETGKNGGFRRGPPGAKGNKGGPGQPGFEGE QGTRGAQGPAGPAGPPGLIGEQQGISGPRGSGGAAGAPGERGRTGPLG RKGEPI\GEPGPKGGIGNRGPRGETGDDGRDGVGSEGRGK\GERGF PGYPGPKGNPGEPGLNGTTGPKGIRRRGNSGPPGIVGQKGRP\GY GPAGPKGNRGDSIDQCALIQSIKDKCPCCYGPLECPVFPTELAFALD TSEGVNQDTFGRMRDVVLSIVNDLTIAESNCPRGARVAVVTYNNEVT TEIRFADSKRKSVLDDKIKNLQVALTSKQOSLETAMSFVARNTFKRV RNGFLMRKVAVFFSNTPTRASQPLREAVLKLSDAGITPLFLTRQEDR QLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDICNIDPS CGFGSWRPSFRDRRAAGSDVDIDMAFILDSEATTTLFQFNMKKYIA YLVRQLDMSDPKKG\SOHFARVAVVQHAPSESVDNAMPVVKVEFSL TDYGSKEKLVDFLSRGMTOQLQGTALGSAIEYTIENVFESAPNPRDL KIVVLMLTGEVPEQQLEEAQRVILQAKCKGYFFVVLGIGRKVNIKEV YTFASEPNDVFFKLVDKSTELNEEPLMRFGRLLPFSVSSENAFYLS PDIRKQCDW\FQGDQPTKNLVKFGHKQVNVN\NNVTSSPTSNP\VT TK\PVTTTKPVTTTTPVTITINH\PFVKPAA\AKSPAPAK PVA\AKPVATKTATVRPPVAVKPATAAKPVA\AKPAVRPPAAAAAK PVATKPEVPRPQAAKPAATKPAATTKPMVKMSREVDFEITENSALH WERPEPPGPYFYDLTVTSAHDQSLVLKQNLTVTDRVIGLLAGQTYH VAVVCYLRSQVKAIYHGSFSTKKSQPPPPQP\ARSAS\SSTINLMV\ STEP\LALTETDICKLPKDEGT/CARDFILKWYDPNT\KSCA\RFW YGGCGGNENKFGSQKECEKVCAPVLAKPGVISVMGT
3634	A	65	244	SRRRGVSAPTSFYGRDRRMFPAQEEADRTVFVGNLEARVREEILYE LFLQCCSFLTMK
3635	A	65	262	SRRRGVSAPTSFYGRDRRMFPAQEEADRTVFVGNLEARVREEILYE LFLQVLCPREMGILSISP
3636	A	2	649	GKSRRMFPAQEEADRTVFVGNLEARVREEILYELFLQFLI\AGPLTK VTICKDREGKPKSFGFVCFKHPEVSVAIALLINGIRLYGRPINVQYR FGSSRSSEBANQSFESCVKINSHNYRNEEMVVGSSFPMPQYFPINNT SLPQEYFLFQKMRHVYNPVLQLPYHEMTAPLPNSASVSSSLNHVPD LEAGPSSYKWITHQQPSDSDLLSDDSSTS
3637	A	312	805	GPQAGSSPEILLPEDNSLIRWAGAGCHTQDSATTVTASWAPLCAGAG REEDGTPCVCLGRSARPKLVFGRPLRTSAALRPGACIPHGLLCYPRE PVDFRPGSGRAWPPRSPSP/CQDPRPSRSAPGSEPGW/CPDPPAPPR LVTLGRASPHLTLPRRAAPPPCRWRP
3638	A	2	1581	HGDVSPRCLFKEGSAAQLQTLELAGSLHLSAPSGSAKATKVESLQSR IYIHLVLVMAVTACLEQLLRGCQLQYGRRGQSCPLLDRDSGRQEHAR APSPTTTSARETHVPGHSCSRPAAALHPAIPALLGAQETPCPCRLKV PAPEVAVHMSASAPAAEGEGTPTQPASEK\DEMPGPRESEEEEEED ED\DEEEEEEEKEKSLIVEGKREKKKVERLTMQVSSSLQREPFTIAQG

				KGQKLCEIERIHFFLSKKKTDELRLNLHKLKLYNRPGTVSSLK\KNVGQ FSGFPFEKGSVQYKKKEEMLKKFRNAMLKSI CEVLDLERSGVNSELV KRILNFMHPKRSGKPLPKFKKSCSKGSKDRNSSGMASKAKRTKCP EILSDESSSDEDEKKNKEESSDEDEKSEEEPSKKTVKRE\KPKQRA TSKSKSVKSANVKKADSSTTKKNQNSSKKESESEDSSDEPLIKKL KKPPTDEELKETIKKLLASANLEEVMTKQICKKVYENPTYDLT\ER KDFIKTTVKELIS
3639	B	199	286	XSELESALQMEPAAFQALYSAEKPKEDEHLVFFCQMGRGLQAHAA GPESWIHWGSQLRWSL*
3640	A	754	1082	GMVIIICCLGAPRTQPFQAQLPNLSAKLLAFPSTLSTPPVSELESALQ M\DQPAFQALYSAEKPKEDEHLVFFCQMGRGLQATQLARSLGYTG ARNYAGAYREWLEKES
3641	A	113	737	AGPDSFCNFVSPSSTSTAWILVLAQFLLSPTLLPSRMLTVALLAL LCASASGNAIQARSSSYSGEYSGGGKRFSGNQLDGPITALRVRV NTYYIVGLQVRYGKWSYDYGGRNGDLEEIFLHPGESVIQVSGKYKW YLKEAGYLVPTKGP\FLSFGKSKGP\SFNAVPLHPNTVVRFISGRSG SLIDAIGLHWGCFTHTSCSRC
3642	A	1724	1819	AFVSLGLMCFGALIGLCACICRSLYPTIATG
3643	A	1	894	RGESRVLWSELEGEAGGAGWASSLNARMDNRFATAFVIACVLSLIS TIYMEG\SIGTDFWYEURSPQENSSDLNKS I WDEFISDEADATYN \DALF\RYNGTVGFLRRVSPYKTLHWVLAHHERTESFDVVTK\CV SFTL\TEQFMEKF\VDPGK/HTNSRGLDLLRTYL\WRCQFLLPF\VS LGFDVLWGALIGLCA\CICRSLYPSIATGILHLLAGLCTLGVSVCYV AGIELLHQLELDPDNVSGEFG\WSFCLACVSAPLQFM\ASALFIWAA HTNRKE\YTLMK\AYRVGMSKKPACF
3644	A	323	898	IVVHLVPTTQRSKGKIMELVERSUVARVEVGHGFLERGLPIAAN DMKKSPEIISGRMTFGKNADLDNALSASPGGSLQCTRDQEILQVI RAGTGPDKNQGNLSLVQWTFVLVLPREYGEIEASKVIPAGQNLNRTH PNETSVWKCHKEAGSLWNI PFAGLPAASVMEKRWFFPAAEVQALTGG QQQ
3645	A	816	1171	LFKHFWGPVANWGLPIAANDMKKSPGDYSVGRMTF\ALC\CYS\LT FMEILPYKVQPSGTWASCFACHGTNEVRPSFIQEGRLIPNTRMDLK RASGINQWGKGKNKVFEGDSLCPGCC
3646	A	205	369	SSQPPTLLPAGIDVEQVSVINFDLPVDKDGPNPDNETYLHRIGRTR FGKRGLAV
3647	A	3	452	CSGAGAEPANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALAVDE QEAAAE/SGAVVKTNANAECTDEEEKEDRAAQSLNKLIRSNLVDNT NQVEVLQORDPNSPLYSGKSFEELRLKPQLLQGVYAMGNQPSKIQEN ALPLMLAEPY
3648	A	1	186	WFPVPIAEPANLWSRFLVPSLECTSTSVPPAPGTMATDSWALAV DEQEAAAEVSWLQP
3649	A	2	261	SSANNISILGAFRSVTKWLS*THPL*FFCQCLCLSPTYELALQTGKV IEQMCKFYPELKLAYAVRGNKCEYGRRLNSEQGRGLGV
3650	A	1	2613	MPSQTRKTASWLAELSKEGHQVALLSGEMMVEQRAAVIERFREGKE KVLVTTNVCARGVKLQFTVVRVTALKVVRRELLVPLGGLLVLLASRL EAVDLCAVSSGSYSYMTSSASEFLLSLTLPAGAPQIVHSQVEBQQ LLAAGSSVVSCLLEACP LGPGNVLQHCHLLVKPERVGTGLGGMATLP YLDGSGALDGTNRVCLVPGYAGLQRLSKERLSGKSCACRRCMGDAGAS DWFDSHFDGNI SPVWTRENMDLPPDVQRWWMGFFVPRMKPKGSSWS TAPSIWAKVLFLLQLLKKLGYRMNQAPTGVFEQDVGSRTTHHFMYP ESAKNLPANVSFVLVPPFKVLDLLWIASALSTGQIRFSCIQGLSGSVF KKRSCPSICGHKASREWNEHIAVRTLFWRQGAGTYLNVWPSEFFKRT GVRAIINYPTQGPSLKEDTGVLAAANTNSRGYHVIKSMKSVLALTLH TKMLCRQGDRLQPQFKSHNTNEVLEKLFQIVPGENPYRFRDPPPCR RCAVVGNSGNLRGSGYGQDVGHNFI MRLPFCLQGLTVEYGISPALP ONLIAQSQSGTGKTAFLAMLRSRVEPSDRYPQCLCLSPTYELALQT

				GKVIEQMGKFYPELKLAYAVRGNKSGYWGPMTFLPSRILPLPSTLGP VSTRSVGEEALTRECQSQKCVSAARTSRMELTAVSTKSYNIRISDYH PIFHISRIIRTIRRTLSRYSPPFLEIPQFPNLHLHTIPMYAVLRIHRV TIWVAITKYRYPNYLNPNEWIPFHTSRLRLPNTLYTPVHIAVSN SPFVSHFLKPSTVHIRFADPNLSPLSFTIPFRHSNTFRIPLPNKQ FQVTISVPVSESGAMTSLHLERNFQ
3651	A	3	550	LCSSR/DEKFKALCNLPG/AITMAQAMIFCHTRKTA\SWLAAELSKE GHQVALLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGEQRTCP WSARLGVPGPIRARNPCIQGSRMVSGRWGLVTLFSLRRDCLDFPEV VRTHTCQVRWLMPAIPROENCLNPGDRGCSEPRMCYSTPSWVTE
3652	A	1	1571	CRGAGAEPANPRSPRSLVPSLEYTSTSVPPAPGTMATDSWA\LA VEQEAASLSNLHLKEEKIKPDTNGA\VVKTNANAECTDEEEKEDRA AQSLNLKILRSNLVDNTNQVEVLQORDPNSPLYSVKSFEEWL\KPQL SQGVYAMGFNRPSKIQENALPLMLAEPQNLIAQSQSGTGKTSPLV LA\MLSR\VEPIRPDTPQCLCLFPT\YEAGGFKQKGKVIEQMGKFYPE LKLAYAVRGKLERGQKISEQIVIGTPGT/VGLNW\CFQLKFIDPKK IKVFLVDEADVMIAATQGHQDQSIRIQMLPRNCQMLLSATFEDSVW KFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSRDEKFQALCNLYG AITIAQAMIF\CHTRKTASWLAAEL\SKEGHQVVMLSGEMMVEQRAA VIERFREGKEKVLVT/TPNLCSRgidVDQVSVINFDLPVDKD\GNP DNET\YLH\RIGRTARFGK\RGLA\VMVDSK\HSMNIL\NRIQ\EH F\NKKIER\LDTDDLDEIEEN
3653	A	3	421	QNTIDNMSLLGPKVLLFLAAFIITSDWIPLGVNSQRGDDVTQATPET FTEDPNLVNDPATDETVLAVLADIAPSTDDLECWDEKFTCTRLYSVH RPAKQCIHQLCFTGLRRMYIVNKEICSLGLWKEHEAMKEELCRSK
3654	A	209	436	RLLCIFLLYLSFPPIPSILHLCCFYLDLLIFLYWASSEWDEKFTCT RLYSVHRPQKQCIHQLCFTSLRRMYIVN
3655	A	126	775	APAKVRTAQEDRDTFSSQRTWKEQNTIDNMALLGPKGLLFLAAFIIT T\SDWIPLGV\NSQ\RGDDVTQ\ATPETFTEDP\NLVNDP\ATDET LAVLADIAPSTDDL\ASLSEKNTTA\ECW\DEKFT\CTRLYSCASGP VNQMHFIQLCFHPVLR\RMYIVQPREI\CSSVLVCKGTPKPMKDEL \RQMAGLPPLGRL\RRPQLLPDFPPCENVDLQRPNGL
3656	A	3	220	SRSAAHCCHGGTKMAALAYNLGKREINHSCMMHKYKISEAKNCLVDK HIAFIGDSRIRQLFYSFVKIINPQF
3657	A	525	1625	GAPRCWPRWPCCCSQRATSPPAATEAMIPCEYLLSSGRFLGEKVWQP HSCMMHKYKISEAKNCLVDKHI\AFIG\DSRIRQLFYSFVKIINPQF KEEGNKDFLWHPEVNGSMKQCIKVTEDSIAKPHVIVAGAAATWSIKI HNGSSEALSQYKMNITSIAPLLEKLAKTSDVYVWLQDPVYEDLLSEN RKMITNEKIDAYNEAAVSILNSSTRNSKSNVCMFVSVKLIAQETIME SLDGLHLPRESSRETKLAACFFTLIIIGYLIFYIIHRNAHRKNKPC LESGEKKNIINTPVSSLEILLQSFCKLGLIMAYFYMCDRANLFMKE NKFYTHSSFFIPIIYILVLGVFYNNENTKEKKYPSKKKHE
3658	A	190	892	SLPRRLESFGRLLAMAARGVIAPVGES/LCRYAEVPCSPSAKRPDADV DQORLVRSLIAGVQGVAAALAFAG\RYAL\RIWKPLE\QVITETAKGR FQTPSFSSYYK\GGFDQK\MS\RREA\GLILGVSP\SAGKAK\IRT\ AHR\RMILESPQIKGGSP\YVAAKINEAKD\LLETPTPTMLKDHT EGKKNEGTSKKKSPAKYSKTWSFLIFYMGFHSLIFRPLSCITNM LIVLLFIIF
3659	A	32	763	ARGNLNHHPGAAVVAPCVRLVPCSLVLALS/LRPSP/RVLHTATKQ KNSCQHLEEDVD\QTKWRTDTPSMDKILMEEVKLEEQLKEAVEEDKQ ALADTEGSEQSSQKLVEEGNMYSIQGFCKDSLEVADVLEKATQCVPE EEIKDNNPHLKNLSLWDHLVAGKEGQDSQSFYIMSMEKLSSTKLVA PPKIGDRCTQHREKNKKLSLPLSPQPRCLTPLSLMQQEAPGERFSP ILYFCHVLITVW
3660	C	162	425	MVGPSLHAGXXVYIPRFLYIRSWLPCIFFSGGVTVGNIGRQLAMGV PEKPIVIESSKPXILESXGRFLEENLXLVDYXKGLSFFLK*

3661	A	89	308	PMPRSLGLGITIAFLATLITQFLVYNGVYQYTSPDFLYIRSWLPCI FFSGGVTVGNIGRQLAMGVPEKPHSD
3662	A	2	454	GRVGGRVGLSLTLAALSLGLWWTFRSRSGLGLGITIAFLATLITQF LGYNGVYQYTSPDFLYIRSWLPCIFFSGGVTVGNIGRQLAMLIPFCE ELNLKTTWLFHKTRSNIYRVFLKSPIVIESSKPPILRARKILEENLTV DYDQDYLFS
3663	A	570	1418	PMPRLHDHFWSCSAHSARRRGPPRAIAAGLAAKVGEMIIVFVSGPS LMAVLSASDADPAPRGRSAVKSGPYPGSPYNTWHHSLMQKSLVLF VGEVLALVLNLLQIQNVTLFPEEVIATIFSSAWVPP\CCGTAPAD VGLLYPCIDSHLGEPHKFKERMGOVSMRCIAVFVGINHASAKLDFAN NVQLSLTLAALSLGLWWTFRSRSGLGLG\ITIAFLATL\ITQFLVY NGVYQYTSPDFLYIRSWLPC\IFFSGSVT\VGNIG\RQLGYGVFLEK PHSD
3664	A	195	462	RIFSMTSGRLRWCTWRPATALWSASLRGTSSMHPSPRSISLP/PV HVHTHNSGKEVLGLQVQSRSGTGPAQSGAVQGGNWCIF
3665	A	12102	12327	RIFSMTSGRLRWCTWRPATALWSASLRGTSSMHPSPRSISLPLSM MLSPLPSNTRGLSPTALFRPHSLSPQM
3666	A	535	992	RIFSMTSGRLRWCTWRPATALWSA\SLRLGTSSMHP\SPRSI\SLP LS\MMLS\PLPS\NTRGLSPTALVRSP\NSEHATSCP\RLHLWRCRA PLRSPSPGLRPLGATPGVPSHVHT\HNSGKEVLGLQVQSRSGTGPA CSQAGSGAVQGGNWCIF
3667	A	164	280	CGQVHMANWKQTEEVSPPSALLVVAGPMPLLPRTPLSS
3668	A	3	2142	GRMLDGLFSEGPDSPRELQDEESGSLWVQKSKLLVIEVKTISCHY RRRAPSRQPMDFQASHWARGFQNRTCGPRPGSPQPPRRPWAYRVLO EATNWRAGPLAEVRAREQEKRKAASQEREAKETERKRRKAGGARRSP PGRPRPEPRNAPRVAQLAGLPAPLRPERLAPVGRAPRPSAQPSQDPG SAWAGPWGRRPGPPSYEAHLLLRGSAGTAPRRRWDPRPPYVAPPSY EGPHRTLGTGRPGNSQVPTSSAPAATPARTDGGRTKKRLDPRIYRD VLGAWGLRQGGGLGSGPGCGAARARPEPGKGVVEKSLGLAAADLNS GSDSHPOAKATGSAGTEIAPAGSATAAPCAPHPAPRSRHHLKGSREG KEGEQIWFPKCWIWIPSPKKQPPRHSQTLPRPWAPGGTGWRESLGLGEG AGPETLEGWKATRRRAHTLPRSSQGLSRGE\GVFVIDATCVVIRSQYV PTPRTQVQVQLLPSGVTRVVGDSPPSQSKPGKEEGEGATVFPSPCKRL SSSRLLHQPGGGRGGEAEGGRPGDSTLEERTFRILGLPAPEVNLRDA PTQPGSPEHQALGPAASGAQGRAEGSEVAVVQRRAGRGWARTPGPYA GALREAVSRIRRHAPDSDTDEAEELSVHSGSSDGSDEAPGASWRN ERTLPEVGNSSPEEDGKTAELSDSVGEILDVISQTEEVLFVGRDIRG TQQGNRKRQ
3669	A	76	419	AFIPAMAEIQQKLQGEVEKYQQLQKDLKSKMSGRQKLEAQLTENNI VKEVRDWDLWGEEGPVLAMVLITYVPSLHQELALLDGSNNVFKLLGP VLVKQELGEARATVGKRLDY
3670	A	71	350	AFIPAMAEIQQKLQGEVEKYQQLQKDLKSKMSGRQKLEAQLTENNI VKE\KRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAGAPGKA
3671	A	334	1191	GLLPHLGPVRQRLPRLSLSTLACGLTRGPHFPFLLPQIHIHLTRIVGI GGTFDVSCLPFLSSPDLSKMSGRQKLEAQLTEYNIKEVRDWDLWG EEGPVLAMVLITYVPSLHQELALLDGSNNVFKLLGPVLVKQELGEAR ATVGKRLDYITAEM*VFIPPPCAAPCDASEPLE*RC*TIAEQLSIVA PSPVPPTLSFPF*PPFFSLPWISRFSTYLFLAFSTLHSESY*FLPF CLSPLSLLSKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAGAGA PGKA
3672	A	210	617	AFIPAMAEIQQKLQGEVEKYQQLQKDLKSKMSGRQKLEAQLTENN IVKEELALL\DGSNV\VFKL\LGPPVLVKQELGEARATVGKRLDYITA EIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAGAPGKA
3673	A	3	266	GARGEKTYGAGVALEAGDSDSGSRGGLSHHRAKLSLQQLPTPPPL HELNNAANSQSSREEPPEVVESATQKSLLDHRTVTSGS
3674	A	31	500	ARVTAASAAVAKRVRWDGFDSCGYSLTTILLVQPTKRP\EGRTY

				ADYES\VNECMEG\VCKMYEEHLK\RMNP\NGPSI\THNTTSQFLDF ID\DLADLSCLVYRA\DTQTY\QPYN\KOWIKDEDPTVLLSSGKAQQ AREIIIVGSHWGGWGGAWDTGV
3675	A	1	653	MLQQDSNDDTKDVSFLDAEEETTNRPRKVIRHPVASFFHLFFRVSA IIVCLLCELLSSSFITCMVTIILLSCDFWAVKNITGRMLVGLRWVNH VDEGKSHWVFESRKESQENETVSEAESGIFWLGLVACPVLWVILA FSARFSFR/VKKWLAVVIVGVVLQGANLYGYLRCKVPSVRIESLDTQ LGIQNWRIGWYEGKAHTSGVRSVGNRRSE
3676	A	399	659	VQPVDICIPERNAAGPDGGEKFLWDLQCSHSL*HVGSKPSHPLFRG RSDSCVI*SKDPSSGHTTSEDTR*IPRPCWECGPPLPV
3677	A	291	948	RGSWKQGWRRAMLQQDSNDDTEDVSFLDAEEETTNRPRKAKFSIPV \ASFFHLFFRVSAIIVCLLCELLSSSFITCMVTIILL\SC\DFWAV KKVP\GYLL\VGLRWVNHIDEDGKSHWVFESRKES\QENKTVSRLG NSRIF\WLGLIACPVLWVIFAFSALFSF\RVKWWGGWVIMGVVLQ\G ANLY\GYIRCKVRSRKHLSMATFILLESSLRQNTWR
3678	A	1	134	KNKDNVKFKVRCRYLYTLVITDKEKAELKQSLPPGLAVKELK
3679	A	162	437	RRGLFPAGPGPRQEPSRASSPMPSERLRNKID\FLLT\ARRKDAKS\ VKIKKNKDNV\KFKV\RCSRYLLHPWSSPDKEKAEL\KQSLPPRFK K
3680	A	60	216	ISLTGEELWHLRSTSLGIASPPMHEVPFLEVGDGDRTKTQVFPLTNL RRAC
3681	A	505	795	NVVECLFKDALPQLSADRFLASSILLGDLGVEEV\HFSVSNLTGEEL WHLLRSTSLGIASPPMHEVPFLEVGDGDRTKTQVFPLTNLHVRAHASA HAS
3682	A	685	1484	LRLTFPEFSHTKVRTMSLFPSPPLLLLSMVAASYSETVTCEDAQKTC PAVIACSSPGINGFPKGDKGRDGTGKEGEPGQGLRGLQGPGLGPP GNPGPSGSPGPKGQKDPGKSPDGDS\QAASERKALQTEMARIKKW LTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRN\AAEN GAIQNLIKEEAFLGMPDEKTEGQFVDLTGNRLT\YTNWNEGEP\NNA GS\DEDCVL\LLKNG\QWNSPC\STSHLAVCEFFI
3683	A	427	751	CLSPSNPPCWGFLEDAFVVRGLLDLYEASQESAWLEWALRLQDTQD RLFWDSQGGGYFCSEAELGAGLPLRLKDDQDGAEPSANSVSPQPAQV PITDPCELRKLHP
3684	A	31	560	EFVPHSEKMLYDQAQLAVAYLYAFQLSGDEFYSDVAKGILQYVARSL SHRSGGFYSAEDADSPPERGQRPKEGAYYVWTVKEVQQLPEPVLGA TEPLTSGQLLMKHXYCLTEAGNISPSQDPKGETCRARMLLDRPVLWE LTAARFGLDV/EKAVRTLLNTGLEKLFQARKHRPKP
3685	A	3	399	KCVCLLTAFSEMRMRVPALPEMVRALSAQQQTLKQIVI/VWRPSGQ RTPKALVQCVMHSVYIPNKVLILADGDPSSFLSRQLPFLSTLRLLEDQ ATAYVCENQACSVPIITDPCELRKLHPLTCPYPLGWGR
3686	A	2	2238	NVAAMLGARAWLVRLVLLPRAGAGLAASRRGSSSRDKDRSATVSSSV PMPAGGKGSHPSTPQRPVNRLLIHEKSPYLLQHAYNPVDWYPWGQEA FDKARKENKPIFLSVGYSTCHWCHMMEESFQNEEIGRLLSEDFVSV KVDREERPDVDKVYMTFVQATSSGGGWPMNVWLTPLN\QPCVGGTYF PPEDGLTRVGFRVLLRIREQWKQNKNTLLENSQRVTTALLARSEIS VGDRQLPPSAATVNNRCFQQLDEGYDEEYGGFAEAPKFPTPVILSFL FSYWLSHRLTQDGSRAQQMALHTLKMMANGGIRDHVGQGFHRYSTDR QWHVPHFEKMLYDQAQLAVAYSQAFQLSGDEFYSDVAKGILQYVARSL SHRSGGFYSAEDADSPPERGQRPKEGAYYVWTVKEVQQLPEPVLG ATEPLTSGQLLMKHXYGLTEAGNISPSQACELADKGHSPQDPKGELOQ QNVLTVRYSELTAARFGLDVEAVRTLLNSGLEKLFQARKHRPKPHL DSKMLAAWNGLMVSGYAVTGAVLGPRQ\LINYATNGAKFLKRHMFDV ASGRDLADLLHR/HLGGLWSTATPPCWGFLEDAFVVRGLLDLYBAS QESAWLEWALRLQDTQDRLFWDSSQGGGYFCSEA\DWGAGLPLRLKDA QDEAEPANSVSAHNLLRLHGFTGHKDWMDKCVCLLTAFSEMRMRVP VALPEMVRALSAQQQTLKQIVICGDRQAKDTKALGAVRPLCLHS

3687	A	5	188	NTFYWERSWFFQAHILPKCKWFLQSGSRIVSFSWMVGSRSILPWIP CFGLLDLQMEVVTL
3688	A	132	342	GFTSFISRLSCLSFCLLLET/CPVTCWCWEAPRCNQKCTDPAARRPD PQTCASQDRLRCACTCHQPLASR
3689	C	4	204	MCFQRKSYFHIQTLYCPLICISALRYSTGPAPAMWKHTAPVQKDWL TPLPITLISSPNFLTINL*
3690	C	57	209	MEVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGRLLF GPL*
3691	A	363	424	KEPDLEPPWILIGELPSVWI
3692	A	2	264	KFSLIKLRKENFPTARICRLVYPLYPLKIFIPKALNFCREVGPICP PPKK\GSFPKIPKVAENRPPLRKKIIPSQPALNWGP RPV
3693	A	1	237	SVIFVFYSMFQDACELDVIEISLFVNRCFSVQLIHFLICKLIPHGCH QLSQVIFLNGACCFIKASRSISDDIFRICAI
3694	A	230	946	RERDGGGELSRCGIPHAVNSFLQFPADLQKLTNSLRTIDLSNNKIE SLPPLLIGKFTLLKSLSLNNNKLTVLPDEICNLKKL\ETLSLNNNHL REL PSTFGQLSALKTLSLGNQLGALPPQLCSLRNLVDVKDSLKN\QI \EGIPDSVGELQVIDLNLNQSQISQISGEFTNSCWPRLKILCL\EKN CLELSMLPQSILSDSQICLLAVEGNLFEIKKLRELEGYDKYMERFTA TKKKFA
3695	A	2	201	GRVGSQSCRQQQGDTRRRRLSSYPWRRRRQRWRRRR\TSSRRKPQFL RQRQRPRQARRRWRATRFA
3696	A	31	445	EKAVVTSAASSLVYTVYTAQAPAPRSFHPFCSTWSAKEPNTTAGEGGS TNECQCLSA/CPGANCPGLGTLKSPQNCPSSSLPRPLPACRGSYES VWARLLQSVHAIGQRRRESWSPKLYWVHPPQEVVGAFTFLFLV
3697	A	73	404	AYSRTSSLSTMNQTAILICCLIFLTLSGIQGVPLSRTVRCCTCISIS NQPVNPRSLEKLEIIPASQF\CPR\VEIIATMKKKGEKRCCLNPESKA IKNLLKAVSKERSKRSP
3698	A	507	1212	GHRPTWLAFFLLNGVCCSCPLRALFPGILDVRVQQAQKMLSSIKCV L\VGDSAVGKTFVL\VRFTSRTLREGYSPPVYENTGVDVFM\GIQI SLG\LWDTAANDAFRSIRPLSYQQADVLMCYSVANHNSFLNLK\NK WIGEIRSNLPCTPVLVVAT\QTDQR\EMGPHKASCVNALLEG\KKLAQ DVR\ARGYLECSALS\NRGVQQVFECV/RETAVNQARRNRRLRFL\ SI\NECKIF
3699	C	250	495	MSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPG KKGTPWEGGLFKLRMLFKDDYPSSXPKCKFEPLF
3700	A	226	854	RVPGLTNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMN WECAIPGKKGTPWEGGLFKLRMLFKDEYPSSPPCKKFGPPLFPNCV TSGASCL\SFLEEDKDWRAITIKQILLGIQELLNEPNIQDPAQAEA YTIYCQNRVEYEKRVRAQAKKFAPSCRSSLEPSRTWAVLLLSLRPQV SISVLRHFLCVYMAFCLCCCLE
3701	A	813	1637	TCQGIALSRLAQEY\KAW\RKDHPFG\YNAVPTKNPDGTMNLM\NWE CAIPGKKGTPW\EGGLFKLRMLFKDDYPS\SPPK\CKFEP\PLFSPR IVYPSGAKCACPSLEE\QDRTWRPSPFTIQTRFLLRNYRNFLKWNPN I\QDPSFQAEA\YTIY\CQNRV/ESYEKRVSTKPRKFCAPHKQRPC GNRQKRDWFGQELVYNIFCKSKVCSHTMTSHLGGVGRAPSSHCPPR GVRSRIRLNCVSIQGSFLRCFCIFGLLCKTRLFILILMSSISTAV KL
3702	B	236	362	KQEQIPICQGGKDAAVLQGSQPSLAGIRTTLRDPSKKWPKGX*
3703	A	1	808	TPPFLAMAPALLIPAALASFILAFGTGVEFVRFTSLRPLLGGIPES GGPDARQGW\LAALQDRSILAPLAWDLGLLLLFVQHSLSMAAERVKA WTSRYFGVLQRSLYVACTALALQVMRYWEPKPGPVLWEARAEPWA TWVPLLCFVLHVISWLLIFS\IFLVFDYAEMLGKQVYYHVLGLGEP LALKSPRALRFLSHLRHPVCVELLTVLWVVPTLGTDRLLLAFLLTLY LGLAHGLDQDRLRYLR\AQLRKLHLLSRPQDGEAE
3704	A	221	1728	GQAGCSDTMGSCCCLNRDSVPDNHPTKFKVTNVDDGVELGSGVME

				LTQSELVHLHRREAVRWPYLCLRRYGYDSNLSFSFESGRRCQTGHGI FAFKCSRAEEIFNLLQDLMQCNSINVMEEPVITRNSHPAELDLPRA PQPPN\ALGYNV\SSFSNGCPGEGPRFSAPQRLSTSSLRHPSLGEES THALIAPDEQSHTYVNTPASEDDHRRGRHCLQPLPEGQAPFLPQARG PDQORDPQVFLQPGQVKFVLGPTPARRHMKVCQGLCPSLHDPHHNN NEAPSECPAQPKCTYENVVTGGLWRGAGWRLSPEEPGWNGLAHRRAL LHYENLPPLPPVWESQAQQLGGEAGDDGDSRDGLTPSSNGFPDGEED ETPLQKPTSTRAAIRSHGSFPVPLTRRRGSPRVFNDFRFPGEPPR QLNYIQ\VKLKGWGGDRPKGP\QNPSSPQAPMPTTHPARSSDSYAVI DLKKTVAMSNLQRALPRDDGTARKTRHNSTDLP
3705	A	1143	1849	PAILSPNLDLNFVSRASVPTLAPSAPSASSPARIPAATROGRRSP RIPPAPSNEASAPGRPRVPGAA\PPRFPKPTIQASGADRAVDCGIL KLQKS\PARLARPRWRPRPSKRFWSAAGSVEEQPKPPKAP/PAKSPE QSPQLSVLPLATITPQAYGASFEMKMLKTRRGGRSRWHFFPNVPIQ APSLKWGFQTSDAASAEVHVDRSLASHKMGPRRPRSPWAPPFWN PRH
3706	A	130	360	SLPKKKPNPDLHGFVGKPYQTFKEKIPASSSSNKF/PQDIYEASITL/ IPKPDQDFRKKENCSSVSLIIFPEIINKILEN
3707	A	46	292	DQASSNGVMTIARNPDTLRFLPDEARSLPPPCLTDPRLLYIGFLG YCSGLIDNV\IRRRPIATADKKTYGEIFEKFHPIR
3708	A	269	476	STCLGLPRCWNRYRREQPRLVYM*FVHLYYF
3709	A	448	894	DQASSNGVMTIARNPEPLRFLPDEARSLPPPCLTDPRLLYIGFLG YCSGLIDNVIRRRPI\ATAG\LH\RQLLYINGLFFLLGYLVK\RED YLYAVRDREMFGIYGNLHPEDFFLKEDK\KTYGEIFLKNSHPHTLKV LQKCLAPSFH
3710	A	629	790	SLRGEQLRPWAPGDLVSMSFRDLRSKAAPRPCDLRVFQRFAPARRV PCVGDP
3711	A	2	323	KSGSNDSDSDIDIQEDDESSELEERRLPKPQTAMEMLMQGRPGKRIV GTMQGGSDDDNEDSESEIDMEDDDDEDDDEDESISLSPTKPNRRV RKSEPLDESND
3712	A	3628	3908	ASSSLHKSACQSHPRCPSLHTVAAAPAEDRLLPFLSGTDSPPAASS PPPALCRCLAAPAVPSGQSSSRLAQRVLGVGGPLVPVPALPAPGG
3713	A	70	1296	GGEQLRPWAPGDLVSMSFRDLRNFTMMRALGYPRHISMENFRTPNF GLVSEVLLWLVRREYEPQTDIPPDVDTEQDRVFFIKAIQAFMATKAHI KLNTKKLYQADGYAVKELLKITSVLYNAMKTKMGESIVKEDVNK\ FKFDLGSK\IAD\LKAARQLAS\EITSGASLY/DLSLGMEVE\LRE MRTEAIARPLEINETEKVMRIAIKEILTQVQKTKDLLNNVASDEANL EAKIEKRKLELERNRKRLETLOSVRPCFMDEYEKTEELQK\QYDTY LEKFQNLTYLEQQLEDHHRMEQERFEEAKNTL/CAVIQNKLEEEKR LLKSGSN\DDSDIDIQED\DES\DSELEERRLPK\P\QTAMEM\LMQ GRPGKRIVGTMPG\GSDDDNVSPPLPSVVLCTGLAVPIDGSG
3714	A	1	948	MDKKDQVYLSQVVSAAIGPKRNVSLSKSVTLTFQHVKMTPTKKVF CVYWKSTGQSQWSRDGCFLIHVNKSHTCNCNCSHLSSFAVLMALTSQ EEDPVLTVITYVGLSVSLLCLLLAALTFLCKAIRNTSTSLHLQLSL CLFLAHLFLVIGIDRTEPKVLCIIAGALHYLYLAFTWMLLEGVHL FLTARNLTVVNYSSINRLMKWIMFPVGYGPAVTVAIISAASWPHLYG TADRMLAFKATAQLFILGCTWCLGLLQVGPAQVMAYLFTIINSLOQ FFIFLVYCLLSQQAQKHFTPMEVPRQNHRCLOQN
3715	A	644	2036	AIETQAITDNCSEERKTFNINVQMNSMDIRCSDIQGDTQGPSVIAF ISYSSLGNIINATFFEEMDKKDQVYLSQVVSAAIGPKRNVSLSKSV TLTFQHVKMTPTSTKKVFCVYWKSTGAG/CSQWSRDGCFLIHVNKSH MCNCSHLSSFAVLMALTSQEEDPVLTVITYVGLSVSLLCLL\LAALT FLLCKAIQNTSTSLHLQLSLCLFLAHLFLVAIDQTHKVLCSIIAG TLHYLYLATLTWMLLEALYLFALTARNLTVVNYSSINRFMKKLMFPVG YGVPAVTVAISAASRPHLYGTADRCWLHLDQGMWSFLGPVCAIFSA NLVLFILVFILKRLSSLNSEVSTIQNTRMLAFKATAQLFILGCTW

				CLGLLQVGPAQVMAYLFTIINSLOGF\FIFL\VYCL\LSAQVQKQ YQKWFREIVKSKSESETYTLSSKMGPDSPKSEGDVFPRTSEKIL
3716	A	1	451	FFFFFVRQDLALSPRLCNGIIFAHCNLCPLDSSDPP\TSAFQVAR TTGRNYAQLI\LYFFVETEFAMLTRAGLNLSSRGPLASASQSVGD YR\NSHHAQLIFCIGRDR\VSLW\CPEWSQTPEFKRSACLPKCWDY RGEPHPVPSAL
3717	A	1	5898	MAFVATQGATVVDQTTLMKKYLQFVAALTDVNTQHIIPRFLTLQDG EVQFLQEKPAQQLRKLVLLEIHRIPITNEHLRPHTKNVLSVMFRFLET ENEENVLICLRIIIEHLKQFRPPITQENRYFENPQVIPENTVPPPEM VGMITTIIVKVNPEREDSETRTLYKLNHNVAEFVPLIMNTIAIQV SAQARQHKLYNKELYADFAAQIKTLSFLAYIIRIYQELVTKYSQQM VKGMLQLLSNCPAETAHLRKELLIAAKHILTTELNRQFPCMDKLF ESILIGSGYTARETLRPLAYSTLADLVHHVRQHLPLSDLSLAVQLFA KNIDDESPLSSIQTMSCKLLNLVDCIRSKSEQESGNGRDVLMRMLE VFLKFTIARYQLSAIFKKCKPQSELGAVEAALPGVPTAPAAPGPA PSPAPVPAPPPPPPPPPATPVTPAPVPPFEKQGEKDEKQTFQVT DCRSVLKTLVCGVKTITWGITSCKAPGEAQFIPNKQLQPKETQIYIK LVKYAMQALDIYQVQIAGNGQTYIRVANCQTVRMKEEVELEHFAV FTMMNPLTFKEIFQTTVPYMERISKNYALQIVANSFLANPTTSALF ATILVEYLLDRLPEMGSNVELSNLYLKLFLVFGSVSLFAAENBQML KPHLHKIVNSSMELAQTAKEPYNYFLLLRALFRSIGGGLNMLQSG KQHMKDLFVELCLTVPVRLSSLLPYLPMLMDPLVLSALNGSQTLSVG LRTLELCVDNLQPDFLYDHIQPVRAELMQALWRTLNRNADSLSHVAY RVLGKFGGSNRKMLKESQKLHYVVTEVQGPSITVEFSDCKASLQPM EKAJETALDCLKSANTEPYRRQAWEVKCFVLVAMMSLEDNKHALYQ LLAHPNFTEKTIPNVIISHRYKAQDTPARKTFEQALTGAFFMSAVIKD LRPSALPFVASLIRHYTMVAVAQCGPFLPCYQVGSQPSTAMPHSE ENGSKGMDPLVLIDAIACMAYEEKELCKIGEVALAVIFDVASIILG SKERACQLPLFSYIVERLCACCYEQAWYAKLGGVSIKFLMERLPLT WVLQNOQTFLKALLFVMDLTGEVSNGAVAMAKTTLEQLMRCATPL KDEERAEEIVAAQESFHHVTHDLVREVTSPNSTVRKQAMHSLQVLA QVTGKSVTVIMEPHKEVLQDMVPPKKHLLRHQPANAQIGLMEGNTFC TTLOPRLFTMDLNVVEHKVFYTESREKIIAALFKALNSTNSELQEAG EACMRKFLEGATIEVDQIHTHMRPLLMMLGDYRSLTLNVNRLTSVT RLFPNSFNDKFCQMMQHLRKWMEVVVITHKGGQSDGNEMKISAI INLFHLIPAAPQTLVKPLLEVVMKTERAMLI EAGSPFREPLIKFLTR HPSQTVELFMMEATLNDPQWSRMFMSFLKHKDARPLRDVLAANPNRF ITLLLPGGAQTAVRPGSPSTSTMRLDLQFQAIKIIISIVKNDSDSWLA SQHSLVSQLRRVWVSENFQERHRKENMAATNWKEPKLLAYCLLNYCK RNYGDIELLFQLLRAFTGRFLCNMTFLKEYMEEEEIPKNYSIAQKRAL FFRFVDFNDPNFGDELKAKVLQHILNPAFLYSFEKGEQELGPPNP EGDNPESTITSVFITKVLDEKQADMLDSLRIYLLQYATLLVEHAPHH IHDNNKNRNSKLRRMLTFAWPCLLSKACVDPACKYSGHLLLAHIIAK FAIHKKIVLQVFHSLKHAHAMEARAIVRQAMAILTPAVPARMEDGHQ MLTHWTRKIIVEEGHTVPQLVHILHLIVQHFKVYYPVRHHLVQHMVS AMQRLGFTPSVTIEQRR LAVDLSEVVIKWELQRIKDQKQSVSKTKRL CVFKPDSDMDPNSSGEGVNSVSSSIKRGLSVDSAQEVKRFRTATGAI SAVFGRSQSLPGADSLAKPIDKQHTDTVVNFLIRVACQ
3718	A	1	333	VYYPVRHHLVQHVMVSAMQRLGFTPSVTIEQRR LAVDLSEVVIKWELQ RIKDQKQSVSKTKRLCVFKPDSDMDPNSSGEGVNSVSSSIKRGLSVD SAQEVKRFRTATGAISA
3719	A	1	5699	VNDNTNTAGSPGEVLSRRVCVNLKLTALRPDMWPKSELKLQWFDKLLM TVEQPNQVNYGNICTGLEVL SFLITVLQSPAILSSFKPLQRGIAACM TCGNTKVLRAVHSLLSRLMSIFPTEPSTSSVASKYEELECLYAAVGK VIYEGLTNYEKATNANPSQLFGDQGSWVTLAPGTL MILKSACSNNPS YIDRLISVFMRS LQKVMREHLNPQAASGSTSEATSGTSELVMLSLELV

				KTRLAVMSMEMRKNFIQAILTSLIEKSPDAKILRAVVKIVEEWVKN SPMAANQTPTLREKSILLVKMMTYIEKRFPEDELENAQFLDLVNVY RDETLGSELTALEPAFLSGLRCAQPLIRAKFFEVDNSMKRRVYE RLLYVTC SQNWEAMGNHFWIKQCIEVTS AVQVVLVHLPVNETRSPR TMSPETAGTEGGLVLFDEKKGLLLAVCEKSTPIGTSCQGAMLP SITN VINLADSHDRAAFAMVTHVKQEPRERENSESKEEDVEIDIELAPGDQ TSTPKTKELSEK\DIGNQLHMLTNRHDKFLDTLREVKTGALLSAFVQ LCHISTTLAEKTWVQLFPRLWKILSDRQQHALAGEISPFLCSGSHQV QRDCQPSALNCFVEAMSQCVPPIPIRPCVLKYLKGTNHLWFRSTLML EHQAFEKGLSLQIKPKQTTEFYEQESITPPQOEILDSLAELYSLLQE EDMWAGLWQKRCKYSETATAIAYEQHGFFEQAQESYEKAMD KAKKEH ERSNASPAIFPEYQLWEDHWIRCSKELNQWEALTEYGQSKGHINPYL VLECAWRVSNWTAMKEALVQEVSCPKEMAWKVNMYRGYLAICHPEE QQLSFIERLVEMASSLAIREWRRRLPHVSVHVTPLLOSLLCWSHQAA QQIIELQEAAQINAGLQPTNLGRNNSLHDMKTVVKTWRNRLPIVSDD LSHWSSIFMWRQHYYQAIVTAYENSSQHDPSSNNAMLG VHASASAI QYGKIARKQGLVNVALDILSRIHTIPTVPIVDCFQKIRQQVKCYLQL AGVMGKNECMQVRTGHLKNEARSEEANKAFSAVQMHVDLVKAWAMW GDYLENIFVKERQLHLGVSAITCYLHACRHQNESKSRKYLA KVLWLL SFDDDKNTLADAVDKYCIGVPPIQWLAWIPQLLTCLVSGEKL LNL ISQVGRVYPQAVYFPRTLYTLTKIEQ RERYKSALRALASVGFALT ALCVLLSDSGQQQPSSVGNQSHSASDPGPIRATAPMWRC SRIMHMQR ELHPTLLSSLEGIVDQMVWFRENWHEEVLRQLQQGLAKCYSVAF EKS GAVSDAKITPHTLNFVKLVSTFGVGLNVSNVSTMFSSAASESLAR RAQATAQDPVFQKLKGQFTTGHTL RTPALGPALVWVQHATAAVSSTR QPASLGQLTNKWGRPQPSSLPQRWDQ RALCGPGPCFAAVLVGFVLTS SRPDFDFSVPGSMKLHNLISK LKKWIKILEAKTKQLPKFFLIEE KCR FLSNFSAQTAEVGNSWGSFCMPKPT\HYYIKIARFMPRVEIVQKHNT AARLYIRGHNGKIYPYLVMDACL/TQSSRREERV LQLLSAGTPV WEKRKETT KRLHFFTVP RVVAVSPQMR LVEDNPSSLVBEIYKQRC A KKGIEHDNPISRYDRLATVQARGTQASHQVLRDILKEVQSNMVP RS MLKEWALHTFPNATDYWTFRKMTIQLALIGFAEFVLHLNRLNPEML QIAQDTGKLVNAYFRFDINDATGDL DANRPVPFRLTPNISEFLT TIG VSGPLTASMIAVARCFAQPNFKVDGILKT VLRDEI IAWHKKTQEDTS SPLSAAGQPNMDSQQLVSLVQKAVTAIMTRLHNL AQFEGGESKVNT LVAAANS LDNLCRMDPAWH PWL
3720	A	109	11749	ARRGERRLVELMDPIILFSGEANQPKRKMAFVATQGATEVDQT TLMKK YLQFVAALTDVNTPDETKLMMHEVSENFENG TSSPQYSTFLEHIIP RVLTFLODGEVQFLQEKPAQQLRKLVL EIIHRIPTNEHLRPHTKNVL SVMFRFLETENEENVLICLR IIIELHKQFRPPITQEIHHFLDFVKQI YKELPKVVNRYFENPQVIPENTVPPPEMVGMITTI AVKVNPEREDSE TRTHSII PRGSLSLKVLAE LPIIVVL MYQLYKLNIHNVAEFVPLIM NTIAIQVSAQARQHKL NLYADFI AAQIKTLSFLAYIIRIYQELV TKYSQQMVKGMLQLLSNCPAETAHLRKELLIAAKHILTTEL RNQFIP CMDKLFDESILIGSGYTARETLRPLAYSTLADLVHVRQH LPLSDLS LAVQLFAKNIDDES LPS SIQTMSC KLLLNLVDCIRSKSEQESGN GRD VLMRMLEVFVLKFHTIARYQLSAIFKKCKPQSELGAVEAALPGVPTA PAAPGPAPSPAPVPAPPPPPPPPPPPATPVP PAPVPPEKQGEKD KED KQTFQVTD CRSLVKT LVCVGVTITWGITSC KAPGEAQFI PNKQLQPK ETQIYIKLVKYAMQALDIYQVQIAGNGQTYIRVANCQTVRMKEEKEV LEHFAGVFTMMNPLTFKEIFQTTVPY MVERISKNYALQIVANSFLAN PTTSALFATILVEYLLDRLPEMG SNVELSNLYLKLFLVFGSVSLFA AENEQMLKPHLHKIVNSSMELAQTAKEPYNYFLLLRALFRS IGGGSH DLYQEFLPLLPNLLQGLNMLQSG LHKQHMKDLFVELCLTVPVRLSS LLPYLPMLMDPLVSALNGSQT LVSQGLRTLELCVDNLQPDFLYDHIQ PVRAELMQALWRTL RNPADSI SHVAYRVLGKFGGSNRKMLKESQKLH YVTEVQGPSITVEFSDCKASLQ LPM EKAIETALDCLKS ANTEPYR

				<p> RQAWEVKCFVLVAMMSLEDNKHLYQLLAHPNFTEKTI PNVI ISHRY KAQDTPARKTFEQALTGAFMSAVIKDLRPSALPFVASLIRHYTMVAV AQQCGPFLPCYQVGSQPSTAMFHSEENGSKGMDPLVLIDAIAICMA YEEKELCKIGEVALAVIFDVASIILGSKERACQLPLFSYIVERLCAC CYEQAWYAKLGGVVSIFLMEERLPLTWVLQNNQOTFLKALLFVMMDLT GEVSNAGAVAMAKTTLEQLLMRCATPLKDEERAEEIVAAQEKSFHHT HDLVREVTSPNSTVRKQAMHSLQVLAQVTGKSVTVIMEPHKEVLQDM VPPKKHLLRHQPANAQIGLMEGNTFCTTLQPRFLTMDLNVVEHKVYF TELLNLCEAEDSALTKLPCYKSLPSLVPLRIAALNALAACNYLPQSR EKIIAALFKALNSTNSELQEAGEACMRKFLEGATIEVDQIHTHMRPL LMMLGDYRSLTLNVVNRLLTSVTRLFPNSFNDDKCDQMMQHLLRWMEV VVITHKGGQSRSDGNEMKICSAIINLFHLIPAAPQTLVKPLLEVVMKT ERAMLIEAGSPFREPLIKFLTRHPSQTVELFMMEATLNDPQWSRMFM SFLKHKDARPLRDVLAANPNRFITLLLPGGAQTAVRPGSPSTSTMRL DLQFOAIKIIISIVKNDSDWLASQHSLSVQLRRVWVSENFQERHRKE NMAATNWKEPKLLAYCLLNYCKRNYGDIELLFQLLRAFTGRFLCNMT FLKEYMEEEEIPKNYSIAQKRALFFRFVDFNDPNFGDELKAKVLQHIL NPAFLYSFEKGEQQLLGPENPEGDNPEISITSVFITKVLDPKQADM LDSLRIYLLQYATLLVEHAPHHIDHNNKNRNSKLRLMTFAWPCLLS KACVDPACKYSGHLLLAHIAKFAIHKKIVLQVFHSLKKAHAMEARA IVRQAMAILTPAVPARMEDGHQMLTHWTRKIIIVEEGHTVAPQLVHILH LIVQHFKVYYPVRHHLVQHMVSAMQRLGFTPSVTIEQRR LAVDLSEV VIKWELQRIKQPDSDMDPNSSGEGVNSVSSSIKRGLSVDSAEVK RFRTATGAISAVFGRSQSLPGADSLAKPIDKQHTDTVVNFLIRVAC QVNDNTNTAGSPGEVLSRRVCVNLKLTALRPDMWPKSELKLQWFDKLL MTVEQPNQVNYGNICTGLEVL SFLTTLVLSQSPAILSSFKPLQRGIAAC MTCGNTKVLRAVHSLLSRLMSIFPTEPSTSSVASKYEELCLYAAVG KVIYEGLTNYEKATNANPSQLFGTLMILKSACSNNPSYIDRLISVFM RSLQKMOVREHLNPQAASGSTEATSGTSELVMSLELVKTRLAVMSME MRKNFIQAILTSLEKSPDAKILRAVVKIVEEWVKNNSPMAANQTPT LREKSILLVKMMTYIEKRFPEDELENAQFLDLVNYVYRDETLSGSEL TAKLEPAFLSGLRCAQPLIRAKFFEVDNSMKRRVYERLLYVTCSON WEAMGNHFWIKQCIELLLAVCEKSTPIGTSCQGAMLP SITNVINLAD SHDRAAFAMVTHVKQEPRERENSESKEEDVEIDIELAPGDQSTPKT KELSEKDIGNQLHMLTNRHDKFLDTLREVKTGALLSAFVQLCHISTT LAEKTWVQLFPRLWKILSDRQQHALAGEISPFCLSGSHQVQRDCQPS ALNCFVEAMSQCVPPIPIRCPVLKYL GKTHNLWFRSTLMLEHQAFEK GLSLQIKPKQTTEFYEQESITPPQOEILDLSLAELYSLLQEEDMWAGL WQKRCKYSETATAIAYEQHGFFEQAQESYEKAMD KAKKEHERSNASP AIFPEYQLWEDHWIRCSKELNQWEALTEYGQSKGHINPYLVLECAWR VSNWTAMKEALVQVEVSCPKEMAWKVNMYRGYLAICHPEEQLSFIE RLVEMASSLAIREWRRLPHVVSHVHTPLLQAAQOIIEQLQEAQINAG LQPTNLGRNNSLHDMKT VVKTRNRLPIVSDDL SHWSSIFMWRQHYY QAIVTAYENSSQHDPSSNNAMLGVHASASAI IQYGKIARKQGLVNVA LDILSRIHTIPTVPIVDCFQKIRQVVKCYLQLAGVMGKNECMQGLEV IESTNLKYFTKEMTAEFYALKGMFLAQINKSEEANKAFSAVQMHDV LVKAWAMWGDYLENIFVKERQLHLGVSAITCYLHACRHQNESKSRKY LAKVLWLLSFDDDKNTLADAVDKYCIGVPIQWLAWIPQLLTCLVGS EGKLLNLISQVGRVYPQAVYFPIRTLYLTLKIEQ RERYKSDPGPIR ATAPMWRCSRIMHMRELHPTLLSSLEGIVDQMVWFRENWHEEVLRO LQQGLAKCYSVAFKSGAVSDAKITPHTLNFVKKLVSTFGVGLENV NVSTMFSSAASESLARRAQATAQDPVFPQKLKGQFTTDFDFSVPGSMK LHNLISKLLKWKILEAKTKQLPLFFL\IEEYCRFLSNFSSQTAEDV IPGEFLMP\KPTHYIKIARFMPRVEIVQKH\NSAARRL\YIRGHNG \KIYPYLRSWNDALPSQSSRRARRRVVWQLLRLLYPFLEKIKETTKR HLFFTVP RVVAVSPQMRLVEDNPSSLSLVEIYKQRC AKKGIEHDNPI SRYYDRLATVQARGTQASHQVLRDILKEVQSNMVP RSMLKEWALHTF </p>
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				PNATDYWTFRKMFTIQLALIGFAEFVLHLNRLNPEMLQIAQDTGKLN VAYFRFDINDATGDLNANRPVPFRLTPNISEFLTITIGVSGPLTASMI AVARCFAPNFKVDGILKTVLRDEIIAWHKKTQEDTSSPLSAGQPE NMDSQQILVSLVQKAVTAIMTRLHNLAQFEGGESKVNTLVAAANSL\ D NLCRMDFAWHPWACDCGRHGTRECEGRSGL
3721	A	106	11708	EANQPKRKMAFVATQGATVVDQTTLMKKYLQFVAALTDVNTPDETKL KMMQEVSENFENVTSPPQYSTFLEHII PRFLTFLQDGEVQFLQEKPA QQLRKLVLLEIIHRIPTNEHLRPHTKNVLSVMFRFLETENEENVLICL RIIEELHKQFRPPITQEIHHFLDFVKQIYKELPKVVMRYFENPQVIP ENTVPPPEMVGMITTIAVKVNPEREDSETRTHSIIPRGSLSLKVLAEL LPIIIVVLMYQLYKLNHNVAEFVPLIMNTIAIQVSAQARQHKLYNK ELYADFIAAQIKTSLFLAYIIRIYQELVTKYSSQQMVKGMLQLLSNCP AETAHLRKELLIAAKHILTTTELNRQFIPCMDKLFDESILIGSGYTAR ETLRPLAYSTLADLVHVRQHLPLSDLSLAVQLFAKNIDDESPLSSI QTMSCKLLLNLDVCIRSKSEQESGNGRDVLMRMLEVFVLKFHTIARY QLSAIFKCKKPQSELGAVEAALPGVPTAPAAPGPAPSPAPVPAPPPP PPPPPPATPVTPAPVPPFEKQGEKDKEDKQTFQVTDCLSLVKTLCVCG VKTITWGITSCAPGEAQFIPNKQLQPKETQIYIKLVKYAMQALDIY QVQIAGNGQTYIRVANCQTVRMKEEKEVLEHFAGVFTMMNPLTFKEI FQTTVPYMVDRISKNYALQIVANSFLANPTTSALFATILVEYLLDRL PEMGSNVELSNLYLKLFLVFGSVSLFAAENEQMLKPHLHKIVNSSM ELAQTAKPEPYNFLLLRALFRS IGGGSHDLLYQEFPLPLNLLQGLN MLQSGLHKQHMKDLFVELCLTVPVRLSSLLPYLPLMDPLVSALNGS QTLVSQGLRTLELCVDNLQPDFLYDHIQPVRAELMQALWRTLNRNAD SISHVAYRVLGKFGGSNRKMLKESQKLHYVVTEVQGPSITVEFSDCK ASLQLPMEKAIETALDCLKSANTEPYRRQAWEVKICFLVAMMSLED NKHALYQLLAHPNFTEKTIPNVIISHRYKAQDTPARKTFEQALTGAF MSAVIKDLRPSALPFVASLIRHYTMVAVAQQCGPFLPCYQVGSQPS TAMFHSEENGSKGMDPLVLIDAIACMAYEEKELCKIGEVALAVIFD VASIILGSKERACQLPLFSYIVERLCACCYEQAWYAKLGGVVSIFL MERLPLTWVLQNNQOTFLKALLFVMDLTGEVSNAGAVAMAKTTLEQLL MRCATPLKDEERAEEIVAAQEKSFHHVTHDLVREVTSPNSTVRKQAM HSLQVLAQVTGKSVTIVMEPHKEVLQDMVPPKKHLLRHQPANAQIGL MEGNTFCTTLQPRFLTMDLNVVEHKVFYTELLNLCEAEDSALTKLPC YKSLPSLVPLRIAALNALAACNYLPQSREKIIAALFKALNSTNSELQ EAGEACMRKFLEGATIEVDQIHTMRPLMLMGDYRSLTLNVNRLT SVTRLFPNSFNDKFCDDMMQHLRKWMEVVVITHKGGQRSDGNESISE CGRCPLSPFCQFEEMKICSAIINLFHLIPAAPQTLVKPLLEVVMKTE RAMLIEAGSPFREPLIKFLTRHPSQTVELFMMEATLNDPQWSRMFMS FLKHKDARPLRDVLAANPNRFITLLPGGAQTAVRPGSPSTSTMRLD LQFQAIKIIISIVKNDSDWLASQHSLSVSQLRRVWVSENFQERHRKEN MAATNWKEPKLLAYCLLNYCKRNYGDIELLFQLLRAFTGRFLCNMTF LKEYMEEIIPKNYSIAQKRALFFRVDFNDPNFGDELKAKVLQHILN PAFLYSFEKGEQEQLLGPNNPEGDNPESITSVFITKVLDPKQADML DSLRIYLLQYATLLVEHAPHHIIHDNNKNRNSKLRRLMTFAWPCLLSK ACVDPACKYSGHLLLAHIIAKFAIHKKIVLQVFHSLKKAHAMEARAI VRQAMAILTPAVPARMEDGHQMLTHWTRKIIVEEGHTVPQLVHILHL IVQHFKVYYPVRHHLVQHVMVSAMQRLGFTPSVTIEQRRLAVDLSEVV IKWELQRIKQQPDSDMDPNSSGEGVNSVSSSIKRGSLVSDAQEVKR FRTATGAISAVFGRSQSLPGADSLAKPIDKQHTDVTVNFLIRVACQ VNDNTNTAGSPGEVLSRRVCNLLKTALRPDMWPKSELKLQWFDKLLM TVEQPNQVNYGNICTGLEVL SFLLTVLQSPAILSSFKPLQRGIAACM TCGNTKVLRAVHSLLSRLMSIFPTEPSTSSVASKYEELECLYAAVGK VIYEGLTNYEKATNANPSQLFGTLMILKSACSNPNPSYIDRLISVFMR SLQKMVREHLNPQAASGSTAATSGTSELVMSLELVKTRLAVMSMEM RKNFIQAILTSLIEKSPDAKILRAVVKIVEEWVKNNSPMAANQTPTL REKSILLVKMMTYIEKRFPEDELENAQFLDLVNYVYRDETLSGSELT

				AKLEPAFLSGLRCAQPLIRAKFFEVDNSMKRRVYERLLYVTCSQNW EAMGNHFWIKQCIELLAVCEKSTPIGTSCQGAMLPSITNVINLADS HDRAAFAMVTHVKQEPRERENSESKEEDVEIDIELAPGDTSTPKTK ELSEKDIGNQLHMLTNRHDKFLDTLREVKTGALLSAFVQLCHISTTL AEKTWVQLFPRWLKILSDRQQHALAGEISPFLCSGSHQVQRDCQPSA LNCFVEAMSQCVPPIPIRPCVLKYLKGKTHNLWFRSTLMLEHQAFEKG LSLQIKPKQTTEFYEQESITPPQOEILDSLAELYSLLQEEDMWAGLW QKRCYSETATAIAYEQHGFFEQAQESYEKAMDKAKKEHERSNASPA IFPEYQLWEDHWIRCSKELNQWEALTEYGQSKGHINPYLVLECAWRV SNWTAMKEALVQEVSCPKEMAWKVNMYRGLAICHPEEQQLSFIER LVEMASSLAIREWRRLPHVVSHTVHTPLLQAAQIIELQEAAQINAGL QPTNLGRNNSLHDMKTVVKTWRNRLPIVSDDLSHWSSIFMWRQHYYQ GKPTWSGMHSSSIVTAYENSSQHDPSNNAMLGVHASASAIQYVKI ARKQGLVNLVALDILSRIHTIPTVPIVDCFQKIRQQVKCYLQLAGVMG KNECMQGLEVIESTNLKYFTKEMTAEFYALKGMFLAQINKSEEANKA FSAAVQMHDVLVKAWAMWGDYLENIFVKERQLHLGVSAITCYLHACR HQNESKSRKYLAKVLWLLSFDDDKNTLADAVDKYICIGVPPIQWLAWI PQLLTCLVGSEGLLLNLISQVGRVYPQAVYFPRTLYLTLKIEQRE RYKSDPGPIRATAPMWRCRIMHMQRRLHPTLLSSLEGIVDQMVWER ENWHEVLRLQLQQGLAKCYSVAFEKSGAVSDAKITPHTLNFVKLLVS TFGVGLENVSNVSTMFSSAASESLARRAQATAQDPVFKLKGQFTTD FDFSVPGSMKLNLSKLLKWKILEAKTKQLPKFFLIEEKCRLSN FSAQTAEVEIPGEFLMPKPTHYIYIKIARFMPRVEIVQKHNTAARRLY IRGHNGKIYPYLVMDACLTESRREERVQLLRLNLCLEKRRKETTK RHLFFTVPVVAVSPQMRLVEDNPSSLSLVEIYKQRCACKGIEHDNP ISRYYDRLATVQARGTQASHQVLRDILKEVQSNMVPMSMLKEWALHT FPNATDYWTFRKMTIQLALIGFAEFVLHNLRLNPEMLQIAQDTGKL NVAYFRFDINDATGDLNANRPVPFRLTPNISEFLTITIGVSGPLTASM IAVARCFAQPNFKVDGILKTVLRDEI IAWHKKQTQEDTSSPLSAAGQP ENMDSQQLVSLVQKAVTAIMTRLHNLAQFEGGESKVNTLVAAANSLD NLCRMDFAWHPWL
3722	A	2	581	RRFERRMPRPHEVYTPPLVLQPLSLVSPWKSSQHIF\RVLNT\NID\ GRRKNSPLPITAHLRVWARRYAHVVLRKADIDLTK\RAGELT\EDE\ VERVIT/ISMQNPRQYKDPKTGFQEODKDKVDWKITARVLAQVWWT TSSRERPGSRLEERFRAHKKGL\RHFLGGLSCSEGAHPRPTWPAVG RHRGASAGARR
3723	A	6	297	GIRPRKREQAASEDADKGPKEPLEYGKAKLSFQSCCEGKAFQRHDHL ARHRSHL\HLKDKARPFQCRYCVKSFTQNYDLLRHERLHMRRSKQA LNSY
3724	A	201	405	TANVRCLQAQPSAMACPLDQAIGLLVAIFHKYSGREGDKHTLSKKEL KELIQKELTIGSKLQDAEIA
3725	C	78	422	MASCPHAGGPAIPCPVQPLDPDWGHLWRSPAGGIVRSSSAVPAPSPA LSHGMPPGSGHWLLVAIFHKYSGREGDKHTLSKKELKELIQKELTIG SKLQDAEIA RXMEDLDRNKDQ
3726	A	591	966	EVLVTMALTRPSAASSKPQSSPWQCPLDSSHWPPSVAHLPTSYSGR E\GDKHTLSK\RELKELIQKGAPPLASKLQDA\EIARL\MEDL\DRN KDQ\EVNFPRKYVTFPGGAFAFESTIEGLKRVEK
3727	A	3	1274	GGSSVIFYGLICMYTLWWMMLRA\SLKKYSFESIREESSYSDIPDVKN DFAFMLHLIDQYDPLYSKRFVFLSEVSENKLRQLNLNNEWTLDKLR QRLTKNAQDKLELHFLMLSGIPDVTVDLVEVLKLELIPDVTIPPS IAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLW IYSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKL PQVVTDVGVHLQKLSINNEGTKLILWYNHAIYIPIQIGNLTNLERLY LNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIGLLQNLQNLAI TANRIETLPPPELFQCRKLRLHLGNVQLSLPSRVGELTNLTQIELR GNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQ

				A
3728	A	165	828	KEKARGRPKPLLLPITSATTAMGLTISSLF SRLFGKKQMRILMVGL D\AAGKA\TILYKL\KLGEIVTTIP\TIGFGV\KTIGYRNICFHS MLGGPDRIPLWKHYFQ\NT\QGLIFVV\DSNDRERIQEVADELHKM LLVDEL RDP\VLLLFANKQD\LPNAM\AISEMTDKLWLQSLRNRTWY VQATCATQGTGLYEGLDWLSNELSKQLNEIGYLTQGPWFG
3729	A	191	1574	GVSQRDLTRLFGFSSPQLKKKLDAWLSEDMNYARFITAASARRNPS PIRTMTDILSRGPKSMISLAGGLPNPNMFPFKTAVITVENGKTIQFG EEMMKRAL\QYSPSAGIPELLSW\LKQLQIKLHNPPTIHYPPSQGQM DLCVTSGSQQLCKVFEMIINPGDNVLLDEPAYSGTLQSLHPLGCNI INVASDESGIVPDSLRLILSRW\KPEDAKNPQKNTPKFLYCYCFQMG NPTGNSLTSEKKIYELARKYDFLIIEDDPYFYLQFNKFRVPTFLS MDVDGRVIRADSPSKIISGLRIGFLTGPKPLIERVILHIQVSTLHP STFNQLMISQLLHEWGEEGFMAHVDRVIDFYSNQDAILAAADKWLT GLAEWHVPAAGMFLWIKVKGINDVK\ELIERKRPLKMGVL\MLP\GN AFLRRIAQLPSPYLRASFSSASP\EQMDVAF\QVLAQLIKESL
3730	A	2	454	RSFFFFCEVGSWVGSMRVVMARLLSEGEQCPTACAAFAQPGGRP RRGLAGVGEQPGQCSWVNYRCTLFLVSLLGTDLARGGNSATGP\T APADSKQLSCKTFI AVL SLSKEAGFCNVVQGWVSTSWGSSSPSPVQF FPKLLEFTGQ
3731	A	379	640	DGVSLCYPGWNTVAQSQTLVGSISWAQVIL\QTQPPRVAVAPGRTTV YRDRVSLCCPGWSGLIVLGLKPPRVLGITGMGSPQPRPGI
3732	A	373	598	YPCPPE/RCAQRHGQACLPSLERKCVISLPPSPHQTFAGPKGLGH GDALSLGIWQPOTPSCEPTQTPKQSNQLVN
3733	A	2	445	GRVGGKPTTSSSEACFCGSRSGTELSAVGVCSDADCQEYAKIACS KTHPCGHPCGGVKNEEHCLPCLHGCDKSATSLKQDADDMCMICFTEA LSALDCSHIFHLQCCRRVLENRWLGPRITFGFISCPICKNKINHIVL KDLLDP
3734	A	151	487	SPRGHYQLLLSGRALADRYRRIYTAALNDRDQGGGSAGHPAS/RSEN LENTV IIPDIKLHNSPFAFNIYCNVRHCVLEWQKKEISLAAASKNSV QSGESDSDEEEESKEPPIN
3735	A	1	176	NPSAFNIYCNVRHCVLEWQKKEISLAAASKNSVQSGESDSDEEEESK EPPIKLPKVSH
3736	A	1	6570	VCAHIVQAIRMEATRVREWEHAISSKENANSQPNDEDASSDAYCFE LLSMVLALSGSNVGRQYLAQQLTLLQDLFSLHTASPRVQRQVTSLL RRVLPEVTPSRLAS IIGVKS LPPADISDIHSTEGDWNKLGILDMF LGCIAKALTVQLKAGTTITGTAGTTVGKGVTTVTLPMIFNSSYLRR GESHWMMKGSTPTQISEI I I KLIKDMAAGHLSEAWSRVTKNAIETI IALTKMEEEF RSPWLALASLCVLDQDHVDR LSSGRWMGKDGQKQOM PMCDNHDDGETAAI ILCNVCGNLCTDCDRFLHLHRRRTKTHQRQVFKE EEEAIKVDLHEGCGRTKLFWLMALADSKTMKAMVEFREHTGKPTTSS SEACRFCGSRSGTELSAVGVCSDADCQEYAKIACSKTHPCGHPCGG VKNEEHCLPCLHGCDKSATSLKQDADDMCMICFTEALSAAPAIQNKI NHIVLKDLLDP I KELYEDVRRKALMRLEYEGLHKSEAITTPGVRFYN DPAGYAMNRYAYYVCYKCRKAYFGGEARCD AEAGRDDYDPRELICG ACSDVSRAQVWEYLHYQLSIPNLKSKMLQAALTEQWRLEAFKFAKPE KNLKRHTKGPERRRELQEKEPEPQRWSRVGALRGTSASDAGGARGAA AAGARSGPGAPHVRAAGPAAA AVPGARGGVWGKPPPAAKIESGVV VHADTLEAEVEGLLDLRRSRLQMKRGGRRSDRNSSEEGTAEKSKLRL TTNEHSQTCDWGNLLQDI ILQVFKYLP LLDRAHASQVCRNWNQV FHM PDLWRCFEFELNQPATSYLKATHPELIKQIIKRHSNHLQYVSFKVDS SKESAEEACDILSQLVNC SLKTLGLISTARPSFMDLPKSHFISALT VFVNSKSLSSLKIDDPVDDPSLKVLVANNSDTLKLKMS SCPHVSP AGILCVADQCHGLRELALNYHLLSDELLALSSEKHVRLEHLRIDVV SENPQTHFHTIQKSSWDAFIRHSPKVNLMYFFLYEBEEDFPFRYE IPATHLYFGRSVSKDVLGRVGMTCPRLVELVVCANGLRPLDEELIRI

				<p>AERCKNLSAIGLGECEVSCSAFVEFVKMCGGRLSQLSIMEEVLIPDQ KYSLEQIHWEVSKHLASTSEKSELSSKHSRSLKPDGRMSRTTADQKK PRGTELSASESLILKSDAAKLRSDSHSRSLSPNHNTLQTLKSDGRM PSSSRAESPGPGSRLSSPKPKTLPANRSPSPGASSPRSSSPHDKNLP QKSTAPVKTLDPPRERSKSDSYTLDPDLRKKKMPLTEPLRGRSTS PKPKSVPKDSTDSPGSENRAPSPHVVQENLHSEVVEVCTSSTLKTNLS LTDSTCDDSSGFGVGVKVSNNKVHFIIGKAPLKDEQEMRASPKISRK CANRLTRPTLEQSSFLFKGDGSKPLEPAKQAMSPSVAECARAVFASF LWHEGIVHDAMACSSFLKFHPELSKEHAPIRSSLSNQPTTEKDTKL KNRHSLEISSALNMFNIAPHGPDISKMGSIKNKNVLSMLKEPPLHEK FLKKKECEKENKSKKEKKKEKAEVRPRGNLFGEMAQLAVGGPEKD TICELCGESHYPVPVYHMRQAHPGCGRYAGGQGYNSIGHFCGGWAGN CGDGGIGGSTWYLVCDRCREKYLREKQAAAREKAAEGRESAPVAPP PCSPDLAPQPHIPQHLRSCVQSRSLPPPAAPARPLAADSALAHSPG ALARWRWGPRKRVVMMAVISKEHVQSTDTTRMSSCSNHIEMRQ GWAGNHSGVSGDFLDVLAERAGVKRGQCSSGGQPSVIIIFHPPSVVG TLGSAASAKFLGLSSTKCREALAIIVSHAGAPMANAATQTKPLHIG NAAKHGIEAFLAMLGLQGNKQVLDLEAGFGAFYANYSPKVLPSIAS YSWLLDQQDVAFKRFPAHLSTHWADAAASVRKHLVAERALLPTDYI KRIVLRIPNVQYVNRFPVSEHEARHSFQYVACAMLLDGGITVPSFH ECQINRPQDGATFTDRSDTFYGHWRKPLSQEDLEEKFRANASKMLSW DTVESLIKIVKNLEDEDCSVLTTLLKGPSPEGLAVAQGGORDILED HQLQMDESLFWGMPNSHGKSLTTLRPTSYAEAQDCHREWSHGCMASL QLFSHPSPGTRHESEDTVVDIQPSQAFR</p>
3737	A	114	14222	<p>AAPVAAPGALFMPVPDGSVAAAGLGLGLPAADSPGHYQLLLSGRALA DRYRRIYTAALNDRDQGGGSAGHPASRNKKILNKKLKRKQKSKSV KTRSKSENLENTVIIPDIKLHNSPSAFNIYCNVRHCVLEWQKKEISL AAASKNSVQSGESDSDEEESKEPPIKLPKIEVGLCEVFELIKETR FSHPSLCLRSLOALLNVLQGGQPEVLQSEPPEVLESFQLLLEITVR STGMNDSTGQSLTALSCACLFSLVASWGETGRTLQAIASAILTNNGSH ACQTIQVPTILNSLQRSVQAVLVGKIQIQDWFNSNGIKKAALMHKNPL KEISVDEDDQCLLQNDGFFLYLLCKDGLYKIGSGYSGTVRGHIYNST SRIRNRKEKKSGLGYAQGYLLYRDVNNHSMATAIRISPETLEQDGTVM LPDCHTEGQNILFTDGEYINQIAASRDDGFVVRIFATSTEPVLQOEL QLKLARKCLHACRISLFDLEKDLHIISTGFDEESAILGAGREFALMK TANGKIYYTGKYQSLGIKQGGPSAGKWELPITKSPKIVHFSVGHG SHALLVAEDGSIFFTGSAKGEDGESIKSRRQSKPYKPKKIKMEGK I\VVYTACNNGSSSVISKDGLYMF GKDAIYSDSSSVVTDLKGHFVT QVAMGKAHACVLMKNGEVWTFGVNNKGQCERDTGAMNQGKGFGVES MASAMDEALEEELDEKDEKYMCPGPMHKWLEQCMVCTVCGDCTGY GASCVSSGRPDRVPGGICGCGSGESGCAVCGCKACARELDGQEARQ RGILDAVKEMIPDLDLLAVPVPVGNIEEHLQLRQEEKRQVRIRRHRL EEGRGPLVFAGPIFMNHRQALARLRSHPAHVHKRDKHKDGSGERG EKDASKITTYPPGSVRFDCELRAVQVSCGFHHSVVLMEGNDVYTFGY GQHGQLGHGVDVNSRGCPVLVQALPGPSTQVTAGSNHTAVLLMDGQVF TFGSFSKGQLGRPILDVPYWNAPAPMPNIGSKYGRKATWIGASGDQ TFLRIDEALINSHVLATSEIFASKHIIGLVPASISEPPPFKCLLINK VDGSKCTFNDSEQEDLQGFVCLDPYDVIWFRFPNTRELWCYNAV ADARLPSAADMQRCSILSPELALPTGSRALTTRSHAALHILGCLDT LAAMQDLKMGVASTEETQAVMKVSKEDYSVVRNFESHGGGWGYS HSVEAIRFSADTDILLGGLGLFGGRGEYTAKIKLPELGPDDGDHETD GDLLAETDVLAYDCAAREKYAMMFDEPVLQAGWYVAVARVSGPSS DCGSHGQASITTDGVVFQFKSSKSNNGTDVNAGQIPQLLYRLPTS DGSASKGKQQTSEPVHILKRSFARTVSVECFESLLSILHWSWTTVL GVEELRGLKGFOFTATLLDLERLRFVGTCLRLRLRVYTCEIYPVSAT GKAVVEETSKLAECIGKTRTLRLKILSEPLDHCMVKLDNDPQGYLSQ PLSLLEAVLQECHNTFTACFHSFYPTPALQWACLCDLLNCLDQDIE</p>

				<p> ANFKTSSSRLLAAVMSALCHTSVKLTSIFPIAYDGEVLLRSIVKQVS TENDSTLVHRFPPLLVAHMEKLSQSEENISGMTSPREVLEKMLVIVVL PVRNSLRRENELFSSHLVSNTCGLLASIVSELTAALGSEVDGLNSL HSVKASANRFTKTSQGRSWNTGNGSPDAICFSVDKPGIVVVGFSVYG GGGIHEYELEVLVDDSEHAGDSTSHRWTSLELVKGTYYTDDSPSDI AEIRLDKVPLKENVKYAVRLRNYGSRTANGDGGMTTVQCPDGVTF FSTCSLSSNGTNQTRGQIPQILYRSEFDGLQSQLLSKANEEDKNC SRALSUVSTVVRASKDLLHRALAVDADDIPELLSSSSSFLSMLLPLII AYIGPVAAAIPKVAVEVFGLVQQLLPSVAILNQKYAPAFNPNQSTD STTGNQPEQGLSACTTSSHYAVIESEHPYKPAACVMHYKVTFPECVRW MTIEFDPQCGTAQSEDVLRLLIPVRTVQNSGYGPKLTSVHENLNSWI ELKKFSGSSGWPTMVLVLPNEALFSLETASDYVKDDKASFYGFMC AIGYEFSPGPDEGVIQLEKELANLGGVCAAALMKDLALPIGNELEE DLEILEEAALQVCKTHSGILGKGLALSHSPTILEALEGNLPLQIQSN EQSFLLDFIACVPGSSGRLARWLQPDYADPQKTSILNKKDDIRCG WPTTITVQTKDQYGDVHVPMKVEVKAVPVSKKMSLQDQAKKPQ RIPGSPAVTAASSNTDMTYGGLASPKLDVSYEPMIVKEARYIAITMM KVYENYSFEELR\FASPTPKRPSNMLIRVNNDGTYCANWTPGAIGL YTLHVTIDGIEIDAGLEVVKVDPKGMIPPGTQLVKPKSEPQPNKVR KFVAKDSAGLRI\RSHPQLQ\SEQIGTSEKSMETITFIDEIHNDGDC V\WLRLNDETIKKYVPMNGYTEAWCLSFNQHLGKSLLPVDESKTN TDDFFKDINSCCPQEATMQEQDMPFLRGGPGMYKVVKTGPSGHNIRS CPNLRGIPIGMLVLGNKVKAVGEVTNSEGTWVQLDQNSMVEFCESDE GEAWSLARDRGGNQYLRHEDEQALLDQNSQTTPPPSPFSVQAFNKGAS CSAQGFYDGLGNSKGDGRNISTSSKPASTSGKSELSSKHSRSLKPDG RMSRTTADQKKPRGTESLSASESLILKSDAAKLRSDSHSRSLSPNHN TLQTLKSDGRMPSSSRAESPGPGSRLSSPKPKTLPANRSSPSGASSP RSSSPHDKNLPQKSTAPVKTCLDPPRERSKSDSYTLDPDTLRKKMP LTEPLRGRSTSPKPKSVPKDSTDSPGSENRAPSPHVVQIGKAPLKDEQE VCTSSLTKTNSLTDCDDSEFKSVDEGSNKVHFSIGKAPLKDEQE MRASPKISRKCANRHRTPKKEKSSFLFKGDGSKPLEPAQAMSPSVA ECARAVFASFLWHEGIVHDAMACSSFLKFHPELSKEHAPIRSSLSNSQ QPTEEKETKLKNRHSLEISYSVQMIPLMNVFNI/AHPHGPRYILRWG SINKNKVLSYALRNPLHEKCEDGKTET\TFEMS\MHNTMKS\KSPL PLTLQHLVAFWEDISLATIKAASQNMIFSPGSCAVLKKKECEKGRN KKSKEKKEKKEKAEVPRGNLFGEMAQLAVGGPEKDTICELCGESH YPVTYHMRQAHPGCGRYAGGQGYNSIGHFCGGWAGNCGDGGIGGSTW YLVCDCREKYLREKQAAAREKVKQSRKPMQVKTPTALPTMEAHQV IK\AQCQSFLLSLSSAAEPSILCYHPAKPFQSQLPSVKEGISEDLPV KMPCLYLQTLARHHHENFVGYQDDNLFQDEMRYLRSTSVPPAPYISVT PDASPNVFEEPESNMKSMPPSLETSPITDIDLAKRTVFQRSYSVVAS EYDKQHSILPARVKAIPRRRVNSGDETEVGSSLLRHPSPELSRLISAH SSLSKGERNFQWPVLAFFVIQHHDLEGLEIAMKQALRKSACRVFAMEA FNWLLCNVIQTTLSDHILWHFVASLTPAPVEPEEEEEDEENKTSKENS EQEKDTRVCEHPLSDIYAGERAHPLPHTFHRLLOTISDLMMSLPSG SSLQOMALRCWSLKFQSDHQLHQSNNVFHHINNILSKSDDGDSEES FSISIQSGFEAMSQELCIVMCLKDLTSIVDIKTSSRPAMIGSLTDGS TETFWESGDEDKNKTNITINCVKG/ISLPRYVSCFTVDIS\RDGL\ NKVTSMTFLTGKAVQD/LCPRIKQ\VDLDSRHIGWVTSELPGGDNIH IKIELKGPENTLRVRQVKVLGW\KDGESTKIAGQIS\ASVAPARGNC EAGDSCRVFRLITSQVFGKLISGDAEPTPEQEEKALLSSPEGEKVY NATSDADLKEHMGIIFSSKLTNLQKQVCAHIVQAIRMEATRVREE WEHAISSKENANSQPNDEDASSDAYCFELLSMVLALSGSNVGRQYLA QQLTLLQDLFSLHTASPRVQRQVTSLLRRVLPEVTPSRLASIIIGVK SLPPADISDIIHSTEKGDWNKLGILDMFLGCIAKALTQVKAKGTTI TGTAGTTVGKGVTTVTLPMIFNSSYLRRGESHWMMKSTPTQISEII IKLIKDMAAGHLSEAWSRVTKNAIAETIIALTKEEEFRSPVRCIAT </p>
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				TRLWLALASLCVLDQDHVDRLLSSGRWMGKDGQKQMPMCDNHDDGET AAIILCNVCNGLCTDCDRFLHLHRRRTKTHQRQVFKEEEEAIKVDLHE GCGR\TKLFWLMGTGQILKTMEGQWVGFPRTTQGGKPTTSSSKACRFC GSRSGTELSAVGSVCSDAHCOEYAKIACSKTHPCGHPGGVKNKHC LPCLHGCDKSATSLKQDAHDMCMICFTEALSAPAIQLDCSHIFHLQ CCRRVLENRWLGPRITFGFISCPICKNKINHIVLKDLLDPIKELYED VRRK\ALMRLEYEGLHKSEAITTP/GVVRFYNDPAGYAMNRYAYYVC YKCRKAYFGGEARCDAEAGRDDYDPRELICGACSDVSRAQMCPKHG \TDFL\EYKCRYCCSVAVFFCFGTTHF\CNACHDDFQRMSTSIKPEEL PHCP\AGPKAKQL\EGTECPHVVHPPT\GKE\FALGCGVCRNAHTF KTTQILCLQREKLPSSTEDGGEV
3738	A	373	662	CRKNSCYQAQNFNLRIPFSTTKLINLFHF*NDSQKST*/SDSHLARS SQFCSLN*NY*I*TAKSHDVVCTRQHFPPLSSESYIWHVKEKKYNPTA AAI
3739	A	29	658	LSVASLSFLPNASAEDTMSRLSRSLWAATCLGVLCVLSADKNTTQH PNVTTLAPISNVTSAVPTSLPLVTPPETCEGRNSCVSCFNVSUVN TT\CFW\IDCKDESYCSHNST\VSD\CQVGNTTDFCSVST\ATPVPT ANS\TAKTHSSSPPLLQLPRQLLHQGTNNNTVNS\TSQPVKSTFDA ASFIGGIVLVLEIRCHTRNYIPDLKK
3740	A	1	183	KKGLSPEQDIKFSGHVSWSVGKTSMEVKMQMFQ\PAFVNPLIPESPEE EELFRQGECTLICL
3741	A	185	1548	LNQGPQNPKKQGNFHIHETSSSIHANHVRDKLREIV\KASTNWRDHV KAMEERKLHLSFLAKSQDGLPPRRMKDSYIEVLLPLGSEPELREKYL TVQNTVRFGRILEDLDSLGRFLFCYMHNKIHSKMSPLSIVTALVDK IDMCKKSLSPEQDIKFSGHVSWSVGKTSMEVKMQMFQHLHGDEFPCVLD ATFVMVARDSENKGPAFVNPLIPESPEEEELFRQGEELNKGRIAFSS TSL\KMAPSAEERTTIHEMFLSTL\DPKTIISFRSRVLPNSGSGVWE NSKLKEFWEI/CAHPSGSRNIFNRILVGFLMRKAYELAWATACS\FG \GSRPFVGAADD\IMF\QNPVEVG\SLLF\LSSQVCFTQNNYI\QVR VH\SEVALPLQEKPAIQPHMPSFHFHRFHVGKKEASPL\FPPKTYG ESPCCTLDG\QRAFTPMSSGP\ATLEKGPTLVEPLRTPTIC
3742	A	352	1692	RRGVSGARVRVAFQNERGSKWAARGGARDAGGRGRSGLWKGPKLMR RAPAAERLLELGFPPRCGRQEPFFPLGVTRGWGRWPIQKRREGARPV PFSERSQEDGRGPAARSSGTLWRIRTRLSLCRDPEPPPPPLCLLRVSL LCALRAGGRGSRWGEDGARLLLLPPARAAGNGEAEPSSGPPSYAGRML ESSGCKALKEGVLEKRSDDLQWLKWKCCILTEEGLLIIPPKQ\LOH QQQQQQQQQQQQQPGQGA\EPSQPSGPA\VASLEPPVKLK\ELLF SNMKTVDVCVERKGY\MYFTVMAEGKEIDFRCPQDQGWNAEITLQM VQYKNRQAILAVKSTRQKQHLVQQPPSPQPPQPPQPPQPPQPPQPP QPPQPSQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP HQIPHPHPQPHSQPHGHRLLRST\SNSA
3743	A	2	286	TALQRHSEPSKLTFFVGE LAHGRFSK/MGTALGVYHGLPASHMELA QELMETCYQMNRMQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL LP
3744	A	1	287	RHEDLPEISSRMTQRHIOGRGPHLQIRPPSQDTNHSRLKPEQVSV GRPEGGFVVPGTGVTETAQGAALPGLVKPQVSPIQSGGAAVTPE A
3745	A	1	339	RPLLAFRLEEEQKMRPEIAGLKPANPPVLPAPQKADTDPENLPG\MG *PSGQPRVQLCPGS*SLRCPQSKGLEGLP*LQRPEAPGLALVFTSWT QGSSWPPRRGLGLDGKSV
3746	A	2	991	LEFRELSRLTGDKKFQEAVEKVTOHIGLSGKKDGLVPMFINTHSGL FTHLGVFTLGRADSYEYLLKQWIIQGGKQETQLLEDYVEAIEGVRT HLLRHSEPSKLTFFVGE LAHGRFSKMDHLVCFLPGTLALGVYHGLPA SHMELAQELMETCYQMNRMQMETGLSPEIVHFNLYPQPGRRDVEVKPA DRHNLRLPETVESLFYLYRVTDGRKYQDWGWEILQSFSTRFTRVSTCP RPAWSRPPGHRHGWAVGLRLAPLLVAVTWVREGRACRSLGVATLQL

3747	A	1	2296	GGPGIPIPTELHCGGTQSTWRGWAPLIFISQGLSREGLCCGPSIPPV FRVDGAAMAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPP PPPPPHRDFISVTLFSGESYDNSKSWRRRSCWKWKQLSRLQRNMIL F\LLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRP\EFAGLKPAN PPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQ\DLK DGTQEEATKRQEAPVDPRPEGDP\QRTVISWRGAVIEPEQGTLP RAEVPTKPPLPARTQGTVPVH\LNYRQKGVIDVLLHAWKGYR\KFAW GHDDLKPVSRFSSEWFLGLTLIDALDTMWILGLRKEFEARKWVSK KLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLM PAFRTPSKIPIYSDVNIGTGVHPPRWTSDSTVAEVTSIQLEFRELSR LTGDKKFQEAWEKVTOHIGLSGKKDG\LVPLFHQLPTVGLFTHLG\ VFTLGARADSYEYLLKQWIIQGGKQETQLLEDYVEAIEGVRTHLLRH SEPSKLTFFVGEALHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMEL AQELMETCYQMNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL LRPETVESLFYLYRVGTDRKYQDWGWEILQSFSRFRTRVPSSGGYSSIN NVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTE AHPLPIWTPGLGWMAAGVGTSGGQRHLGSAVAFSKGPRRHRQPPSGP GSELGLGFLLVSAIIRTP
3748	A	2	183	KMTEPGASPEDLWVKVEYAYS DNSLDPDPAGDCDWRPAPIEKPALLT GSWKPGEQPTRGP
3749	A	1	3816	MARTVVLITGCSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRW EAARALACPPGSLETQLQDVDRS KSVAAARERVTEGRVDVLVCNAGL GLLGPLEALGEDAVASVLDVNVVGTVMRLQAF LPMKRRGSGRVLVT GSVGGMLMGLPFNDVYCASKFALEGLCESLAVLLLPFGVHLSLSIECG PVHTAFMEKVLGSPEEVLDRTDIHTFHRFYQYLAHSKQVFREAAQNP EEVAEVFLTALRAPKPTLRYFTTERFLPLLRMLDDPSGSNYVTAMH REVFGDVPKAEAGAEAGGGAGPGAEDAEAGRSARPRKQAHQRIWVVR EPPTAARYTQGLSFSICEMGTWTDLSSSLPCENPRTERRGSDRHQGF THSQSLRDQPHPISRTPMPLEISRESRAEAKSRRLTFLRFRSSELR FLRLGSMVAFRSGLLVLTTPPLASLAPRLASILTSAARLVNHTLYVHL QPGMSLEGPAQPQYSPVQATFEVLDPITHLYAGADVHRHLDVRIILLT NIRTKSTFLPPLPTSQNLAHPPPEVVLTDFTLDGSQYNPVKQQLVR YATSCYSCCPRLASVLLYSDYGIGEVPEPLDVLPLSTIRPASPVAG SPKQPVRGYRGA VGGTFDRLHNAHKVLLSVACILAEQQLVVG VADK DLLKSKLLPELLOPYTERVEHLSEFLVDIKPSLTDFDVIPLDPYGA GSDPSLEFLVVSEETYRGGM INFRLENDLEELALYQIQLLKDLRH TENEE DKVSSSSFRQMLGNLLRPPYERPELPTCLYVIGLTGISGSG KSSIAQRLKGLGAFVIDSDHLGHRAYAPGGPAYQPVVEAFGTDILHK DGIINRKVLGSRVFGNKKQLKILTDIMWPIIAKLAREEMDRAVAEGK RVCVIDAAVLEAGWQNLVHEVWTA VIPETEAVRRIVERDGLSEAAA QSRLQSQMSGQQLVEQSHVVLSTLWEPHITQRQSLQPGGVGRCGWGL LCPVPDTPASSAGPVEYAYS DNSLDPGLFVESTRKGSVVS RANSIGS TSASSVPNTDDESDYHQEAYKESYKDRRRRAHTQAEQKRRDAIKRG YDDLQTIPTCQEQDFSIGSQKLSKAIVLQKSMARESTGGDGAKRGC EEASASYPPMARPWCGDCHGIVGVWAIDYIQFLHKEKKKQEEVSTL RKDV TALKIMKVNYEQIVKAHRDNPHEGEDQVSDQVKFN VFGIMDS LFQSFNASISVASFQELSACVFSWIEEHCKPQTLREIVIGVLHQLKN QLY
3750	A	2	94	ARVTEPGASPEDPWVKVEYAYS DNSLDPGE
3751	A	16	689	PSPGACHEETWVKVEYAYRDHSLDPGLFVESTRKGSVVS RANSIGST SASSVPNTDDESDYHQEAYKESYKDRRRRAHTQAEQKRRDAIKRG\ YDDLQTIPTCQEQDFSIGSQKLSKAIVLQKSMARESTGGDGAKRGC L*KQSLLPTHGSALVR*LP*DSWGLG*GEQSOPYLLG*EYFCTCPF FLAPT LAIDYIQFLHKEKKKQEEVSTLRKDVTRLKIM
3752	A	2	981	IEALEPPVD PVDPRVRKMTPEGASPEDPWVKVEYAYS DNSLDPGLFV ESTRKGSVVS RANSIGSTSASSVPNTDDESDYHQEAYKESYKDRRR

				RAHTQAEQKRRDAIKRGYDDLQTIPTCQQQDFSIGSHKLSKAIVLQ KTIDYIQFLHKEKKKQEEVSTLRKDVLTALKIMKVNYEQIVKAHQGQ PHKKGRTEFSDQSRFQRVSKGIMDSL\QSFNAS\ISVA\SFQELSA CVFSWIEEHCKPS\QTLREIVIGVLHQLKNQLYLTGSWKPGRTANKR PLNLYVATELLGPGDWTTTPTHTGQLDIYLVFGFSQPHFIFSGAAVFL
3753	C	150	584	MHPSCCPCICKPFSTLVKSHVTASASSVPDSTCLRRGQSQCEVVLWQ DRVSFQARELKAVINSAVQTSSCFIRHLPRSVSSAIAEGVTSVAIIS SSSPSAGGALLWSAPFFETQQTAVAPPASLETGLFHLQPHLLHTAGS FG**
3754	A	292	483	LGSLLSLSFLFCTPVELGPLVFCSGEDEAADENPESQEMLEEQLVLM LTREVMDLITVCCVSKK
3755	A	84	316	GGKLINIKYLFYTSY*FLSFPWHFLLAASRAQQGEVMRLACRLDPKT SFQAGEWLKYQLSTFLD\AGSVNWKFFSLL
3756	A	423	1186	LPKDPLNILEEENHIKDALSRIIVVEMIKREWPHWPDMLIELDTLSK QGKTDTSQESKAQANCRVGVAALNTLAGYIDWVSMHITAENCKLLE ILCLLLNEQELQLGAAECLLIIVSRKTCQEAEGAVRPSLTGKAWNGG GDGTSEPGAEGWAYRSPLHSPNLRAAALSPDSGCWQALCSLLTCSW MLQNQKMKLSFVLGSWSIQMERGNALVVLRSLLWPGLTFYHAPRTKN YGYVYVGTGEKNMDLPFML
3757	A	222	435	PCFLALAVCCVSKKGADHSSAPPADGDDEEMMATEVTPSAMAELTDL GKCLMKHEDVCTALLITAFH\SLAW
3758	A	1	936	MAEPFTKALDMLDAEKSAIILGLPQPLLELNDSPVFKTVLERMQRFPS TLYEN/CECPWVGLFI*CTEHYEALVSPILGPLFTYLH\CGEDEAAD ENPESQEMLEEQLVRLTREVMDLITVCCVSKKGADHSSAPPADGDD EEMMATEVTPSAMAELTDLGKCLMKHEVLSGTLLADAVTWLFTSVLK GLQMHGQHDGCMASLVHLAFQIYEALRPRYLEIRAVMEQIPEIQKDS LDQFDCKLLNPSLQKVADKRRKDQFKRLIAGCIGKPLGEQFRKEVHI KNLPSLFKKTKPMLETEVLDNDGGGLATIFEP
3759	A	30	3498	VAIVRHFGQLILEHVVKFRWNGMSRLEKVYLKNSVMELIANGTLNIL EEENHIKDALSRIIVVEMIKREWPHWPDMLIELDTLSKQGETQTELV MFILLRLAEDVVTFTQLPPQRRRDIQQTLTQNMERIFSLLNTLQEN VNKYQQVKTDTSQESKAQANCRVGVAALNTLAGYIDWVSMHITAEN CKLLEILCLLLNEQELQLGAAECLLIIVSRKGLKLEDRKPLMVLFGDV AMHYILSAAQTADGGGLVEKHVFLKRLCQVLCALGNQLCALLGADS DVETPSNFGKYLESFLAFTTHPSQFLRSSTQMTWGALFRHEILSRDP LLLAIIIPKYLRASMTNLVKMGFSPKTDSPSCEYSRFDSDSDFNAP FNSSRAQQGEVMRLACRLDPKTSFQAGEWLKYQLSTFLDAGSVNSC SAVGTGEGSLCSVSPSFVQWEAMTLFLESVITQMFTLNREEIPVN DGIELLQMVLFNFDTKDPLILSCV\LTNVSAFPF\VTYRPEFLPQVF SKLFSSVTFTETVEESKAPRTRAVRNVRRHACSSIIKMCRDYPQLVLP NFDMLYNHVKQLLSNELLLTQMEKCALMEALVLISTQFKNYERQKVF LEELMAPVASIWLSDMHRV\LSDVNAFVAYVGTQKSCDPGLEDCQ GLNRARMSFCVYSILGVVKRTCWPTDLQEAAGGFVGYTSSGNPIF RNPCTEQILKLLDNLALIRTHNTLYAPEMLAKMAEPFTKAL\DMLD AEKSAIILGLPQPLL\ELNDSPVFKTVL\ERNAFLSSYPMLMENCCHI LGEGQGSPMQQDFYTVEDLATQLLSSAF\VLNNIPDYRLRPMRLRVF VKPLVLFPCPEHYEALVSPILGPLFTYLHMRSLQKWQVINQRSLLCG EDEAADENPESQEMLEEQLVRLTREVMDLITVCCVSKKGADHSSAP PADGDDEEMMATEVTPSAMAELTDLGKCLMKHEDVCTALLITAFNSL A\WKD\TLSCQRTT/SQKFCLPLLQTKLSGTLLADAVTWLFTSVLK GLQMHGAARTGCMASPGPIWPFQIYEALRPR\Y\LEIRAVMEQIP\E IQKDSLDQFDCKLLNPSLQKVADKRRKDQFKRLIAGCIGKPLGEQFR KEVHIKNLPSLFKKTKPMLETEVLD\NDGGG\LATIFEP
3760	A	1	168	PLKRSDDGNCNDRPTRPPTRPDPTTVFTSNLQTRMVHLTPVERVCRYC PVG\QKPG

3761	B	54	1731	XKLSRECEIKYTGFRDRPHEERQARFQACRDGRSEIAFVATGTNLS LQFFPASWQGEQRQTPSREYVDLEREAGKVYLKAPMILNGVCVIWKG WIDLQRLDGMGCLEFDEERAQQEDALAQQAFEEARRRTREFEDRDRS HREEMEVHELEKSKRALETQMEEMKTQLEEELEDELQASEDAKLRLLEV NMQALKGQFERDLQARDEQNEEKRRQLQRLHEYETELEDERNERAL AAAANKKLEGLDLQADSAIKGREEAIKQLRKLQAQMKDFQREL EDARASRDEIFATAKENEKKAKSLEADLMQLQEDLAAAERARKQADL EKEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEEEQGNMEAM SDRVRKATQQAQELSNEATERSTAQKNESARQQLERQNKELRSKLH EMEGAVKSKFKSTIAALEAKIAQLEEVEQEAREKQAATKSLKQKDK KLKEILLQVEDERKMAEQYKEQAEKGNARVKQLKRQLEEAEEESQRI NANRRKLQRELDEATESNEAMGREVNALKSKLRGPPPPQETSQ*
3762	A	1	2448	PRVVPDQRSKFENEEFFRKLRSRECEIKYTGFRDRPHEERQARFQAC RDGRSEIAFVATGTNLSLQFFPASWQGEQRQTPSREYVDLEREAGKV YLKAPMILNGVCVIWKGWIDLQRLDGMGCLEFDEERAQQEDALAQQA FEEARRRTREFEDRDRSHREEMENEVESVTGMLNEAEGKAIKLAKDV ASLSSQLQDTQELLQEETRQKLNVS TKLRQLEEEERNSLQDQLDEEME AKQNLERHISTLNIQLSDSKKKLQDFASTVEALEEGKKRFQKEIENL TQQYEEKAAAYDKLEKTKNRLQQELDDLVDLDNQRQLVSNLEKKQR KFDQLLAEKNISSKYADERDRAEAAREKETKALS LARALEEAELEA KEELERTNKMLKAEMEDLVSSKDDVGKNVHELEKSKRALETQMEEMK TQLEEELEDELQASEDAKLRLLEVNMQALKGQFERDLQARDEQNEEKRR QLQRLHEYETELEDERNERALAAAANKKLEGLDLQADSAIKG REEAIKQLRKLQAQMKDFQRELEDARASRDEIFATAKENEKKAKSLE ADLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRR LEARIAQLEEELEEEQGNMEAMSDRVRKATQQAQELSNEATERSTA QKNESARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLE EQVEQEAREKQAATKSLKQKDKKLKEILLQVEDERKMAEQYKEQAEK GNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESNEAMGREV NALKSKLRGPPPPQETSQ
3763	A	1	2655	PRVVPDQRSKFENEEFFRKLRSRECEIKYTGFRDRPHEERQARFQAC RDGRSEIAFVATGTNLSLQFFPASWQGEQRQTPSREYVDLEREAGKV YLKAPMILNGVCVIWKGWIDLQRLDGMGCLEFDEERAQQEDALAQQA FEEARRRTREFEDRDRSHREEMAKANLDKNKQTLKENADLAGELR VLGQAKQEVHEHKKKKLEAQVQELQSKCSDGERARAE LNDKVHKLQNE VESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEETRQKLNVS TKLRQLEEEERNSLQDQLDEEMEAQNLERHISTLNIQLSDSKKKLQD FASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLEKTKNRLQQEL DDLVDLDNQRQLVSNLEKKQRKFDQLLAEKNISSKYADERDRAEA EAREKETKALS LARALEEAELEAKEELERTNKMLKAEMEDLVSSKDDV GKNVHELEKSKRALETQMEEMKTQLEEELEDELQASEDAKLRLLEVNMQ ALKGQFERDLQARDEQNEEKRRQLQRLHEYETELEDERNERALAAA AKKKLEGLDLQADSAIKGREEAIKQLRKLQAQMKDFQRELEDA RASRDEIFATAKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKE ELAEELASSLSGRNALQDEKRRLEARIAQLEEELEEEQGNMEAMSDR VRKATQQAQELSNEATERSTAQKNESARQQLERQNKELRSKLHEME GAVKSKFKSTIAALEAKIAQLEEVEQEAREKQAATKSLKQKDKKLK EILLQVEDERKMAEQYKEQAEKGNARVKQLKRQLEEAEEESQRINAN RRKLQRELDEATESNEAMGREVNALKSKLRGPPPPQETSQ
3764	A	1	928	MRLHRLHARPSAVACGLLLLLLQGHYEAPAEGLCCRPVITVIASGSS WLSMCGVLGQGGALSPPKGPQTSMMRKPAFCFDGSKLGFGKESKNMA GYQGVISWDTKGEKGGKMPRVVPDQRSKFENEEFFRKLRSRECEIKYT GFRDRPHEERQARFQACRDGRSEIAFVATGTNLSLQFFPASWQGD QRQTPIREYVDLEREAGTVYLKAPMILNGVCAIWKGWIDLQRLHGMG CLEFDEERAQQEDALTQQAFFEEARRMTREFEDRDRSHRQEMEARSQ LLAVTGKK\QLDPRPGSNLGGGDDLKLR

3765	A	1	234	METSSLRITPDLLNARATERESPKVGPIIGVLPRPPGTLASICGGLV MLLPEITGIALPETVDDVEKLGRHCPKFNP
3766	A	1	1697	LRAAGGGRTMPSPFDEALQVRGEFGRFQRRVFLLLCLTGVTFAFLVVG VVFLGTQPDHYWCRGPSAAALAERCWSPREEWNRTAPASRGPEPPE RRGRCQRYLLEAANDSASATSALSCADPLAAFNNRSAPLVPCRGGWR YAQAHSITVSEFDLVCVNAWMLDLTQAILNLGFLTGAFTLGYAADRY GRIVIIYLLSCLGVGTGVVAFAPNFPVFIIFRFLQGVFF\SLTWMT CYVIVTEIVGSKQRRIVGIVIQMFFTLGIIILPGIAYFIPNWQGIQL AITLPSFLFLLYWEVPESPRWLI TRKKGDKALQILRRIACKNGKYL SSNYSEITVTDEEASNPSFLDLVTRTPQMRKCTLILMFAWFTSAVVYQ GLVMRLGIIGGNLYIDFFISGVVELPGALLILTIERLGRRLPFAAS NIVAGVACLVTAFLEPIAWLRTTVATLGRLGITMAFEIVYLVNSEL YPTTLRNFGVSLCSSLCDFGGIIAPFLLFRLAAVWLELPLIIFGILA SICGGLVMLLPETKGIAPETVDDVEKLGSPHSCCKGRNKKTPVSRS HL
3767	A	103	370	IGVPGAISSSASGRLAVALGTILSFSFSISEFFRFLRVVGQVDLSG DVVYCTYPLFIPLSALSLEDYSPETKVFK*LKTKHDSHMTGN
3768	A	97	1639	CPLQWICAINNISRQIYLTNDPEAVAIKLNQTALQAGTPIITSFGKKQ ESSCPSQNLKNSEMEENDKIVPKATASLPEAEELIAPGTPIQFDIV LPATEFLDQNRGSRRTNPFGETEDESFPPEAQDQQQEVNEILSGKCC LPDSSLQQMFIIVRFLGSMVAKTDSTTEVIYEAMQVLAARAIHNIFR MTESHLMVTSQSLRAPGGGGCGRSFSRLKCSCLPALKRAAGLPAQR LSSAKGQTASSSESLTLVVPDGETPPSRNRQTPHTGEFQLASGHQHQ RPKVDKSTKMRKKQHRKAENSKNQNASPPKDHNSLPAREQNWTENE FEEFTERGFRSDRENGTKLENTLQDIIQENFHNLARQANIQIQEIQR TPQRYSSRRATPRHIIIRFTKVEMKEKMLRAAREKGQVVTHKGKSIR LTADLSAETLQVRREWGPIFNNLKEKNFQPRISYPAKLSFISKGEIK F\FTDKQMLKDVVTTTRPAL\KELLKEALNMRKNQYQPLQKHTKM
3769	A	159	277	WDNEWNLVLTSTPMLSQASLCVYRYNRIAREWTQKYAM
3770	A	1	474	HPPPTMALKRIHKELNDLARDPPAQCSAGPVGDDMFHW\QA\TIMGP NDGPL/YQGGVFFLTIPFPQQITPFPK\PKVAFTTRIYHP\NINHNG \SICLDILRSQWSPALTISKVLLS\ICSLLCDPNPDDPLVPEIARIY KT\DRE\KYNRIAR\EWTQKYAM
3771	A	153	291	LKQLGGLFTFSNVQTYFPLSIFSFTSFCLSIHPCLFLKPIDGTH
3772	A	1	336	MGRWWLMPVIPALWEAEAGGSPESPFLCAQQPLSRNRQPLSPSSS VFVPPQSPSFLCAQPPTQNMILVSHIGGIMLLESGELEVANISERRD QPTLTQDLATLLKCPGIIQ
3773	A	1	2336	MVRSWLTATSASQVQAILLPQPPKTQLNFTVAIDFTASNGETRMSEK VGGNPLQPTSLHYMSPYQLSAYAMALKAVGEIIQDYDSDKLFPAYGF GAKLPPEGRIHQFPLNNNDEDPNCAGIEGVLESYFQSLRTVQLYGP TYFAPVINQVASNSWSSVTLGTDSEPAVEVPQYVGIILLVEGFTIKK PMAMCHRRMGVRPAVPLLTQRGSGEGKDSGTPHSLHTKAQLPSPHV LRHQGQVLRQHSKLVGKALSTTGKALRTLPTAKVFISLP*GPWHR R*AGRDSCSAGR*AAEDSLRLFHSSVSHHWKP*SQWLL*SSAVSWEA EAGELLEPGRRRLQ
3774	A	1015	1292	AGRAWWRMPYNPQHFGRRPRVDHLRSGVQDQPGQ\HGETP\SLKGP KIGWAWWRTVPVIP\ATWEAEP\GELLEPRRQRLQVSQDRTTALQPGQ E
3775	A	183	511	SQHFGRLRWADCLRSIGIQDQPGQHGETLSLLKIQ\KLARSGGTCLQS QLLARLRQENHFSLGGEGCSEPRSGHCTPAWARV/GHSVLKTNEQKN SSTLHTKSHWIFQFPGH
3776	A	238	362	LKRQANTFPILS*TKNTHNVAFLGKTCFLYFT*ECNITLP
3777	A	276	503	RCSPCSEENKPVFLPFT*KRSIKTTVLS*GCGEIRTHIWEWNAVKL WLTRIFGQVQWLTVPVIPTPWEAKVGRIT
3778	A	131	518	CSMVPSASGQVRSHYVDWRMWRDVKRRKMAYEYADERLRINSLRKN TILPKILQDVADEEIAA\LPR\DSCPVRIRNRCVMTSRPRG\VKRRW

				RLSRIVFRHLADHGQLSGIQRATCLNSIQLFLYFFFK
3779	A	60	363	RAEQVCEAKCLRGAPRGENPEEKETARIGPEKOPTSSPLIMANIHQE NEEMEQPMQNGEEDRPLGGGEGHQPAGNRRGQARRLAPNFRWAI PNR QIHDGM
3780	A	2	616	ERTEKSDRAVRSGAPHADGSREAVFCACIWRWRVGGRRSCCTGRPS WGASSAVTRGPHVTRSCRATQPSLQSSLASGYQLPAALSSARSAGFP GKSGAGSATAK\SSGAPRGENPEEKETARIGPGKTKKMEQPYARME EEDR/HLWGGGEGPPSPARKIERG\KARPTCPLNFRMGYPNRPESM DGDGWMEMDMGKYSMGR
3781	A	2	888	RQRQRPRAGPAGRTGGQKAPGARVPPGPAMEGASFGAGRAGAALDPV SFARRPQTLLRVASWVFSIAVFGPIVNEGIVNTDSGPRLRCVFNGNA GACRFVALGLGAFLACAAFLLLDVRFQQISSVRDRRRRAVLLDLGFS GLWSFLWFVGFCFLTQWQRTAPGPF\TTHAGDAARAAIAFNFFSIL SWVALTVKALQRFRLGTDMSLFATEQLSTGASQAYPGYPVSGVEGT ETYQSPPTETLDTSPKGYQVPAYYRLAGTDQGSKATPPTQAPGSPG PPLGPSSSVPRTE
3782	A	1	1944	MADRTKELESIPDSRNRGSIMGNSRDFADFGTTIKQDFRLLGQTSVD RLLQLSQQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQL ARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGN QLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQWTL VPNWNTTQPLSGDILLIYKGFRCFRNHHQTGFSLAGANQRGPLAATL SGPGGEGQSAVARLTGEKKNHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAGYLSEGLVTKWYRSPRLLSPNNYTKAIDMWAAGCILAEMLT GRMLFAERDRASASSLLTIACLLLTQKPSSVAYQMAPLLLYLVLPQC HLISSPIIPHTEAVGTVMASLSTIGPTSFWLDFAFGTTIKQDFRL LGQTSVDRLLQLSQQAVKGNQLLPVSLVKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQ QAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSR ESGQNFADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADSLMQLARQVSR/HGKRAGYLSEGLV TKWYRSPRLLSPNNYTKAIDMWAAGCILAEMLTGRMLFA/GAG*SLC ILLAHHCPLAINKAALLCGLPDGPSSSLSCPPV/RSTSSHLPSPTL RLLAPTSWPPSPQLVPHHSGWILPISEPPS/QQDFRLLGQTSVDRLL QLSQQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLPVSLVKRKTTLAPN TQTASPRALADSLMQLARQVSRLESGQWTLVPNWNTTQPLSGDILLI YKGFRCFRNHHQTGFSLAGANQRGPLAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAGYLSEGLVTKWY RSPRLLSPNNYTKAIDMWAAGCILAEMLTGRMLFAERDRASASSLL TIACLLLTQKPSSVAYQMAPLLLYLVLPQC HLISSPIIPHTEAVGT VMASLSTIGPTSFWLDFAFGTTIKQDFRLLGQTSVDRLLQLSQQA VKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLPVSLVKR KTTLAPNTQTASPRALADSLMQLARQVSRLESGQNFADFGTTIKQDF RLLGQTSVDRLLQLSQQAVKGNQLLPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQ
3783	A	1	578	MGVEGRYPVSLSSDLEWRPDRCQDASEVQDRPRAGSAPLAEDVQVDP RKDSHSSSERFLEQSHSSMERAFEADYGRSCDYKVGSPSYLDKLLWR DNKPHHYSEPKLILDL SHWKQAAGAPPTATGLADTGAREDEPASLFL ENPQGVKSTQG\AQNTPARPPTTPSAAWLPRPP\PPGPTLADSCSVT KWGQV
3784	A	861	2636	GARGRPLAETWPFLTAPVLPGLQITEPTMAEKGDCIASVYGYDLGG RFVDFQPLGFGVNLVLSAVDSRACRKVAVKKIALSDARSMKHALRE IKIIRRLDHDNIVKVYEVLPKGTDLQGE LFKFSVAYIVQYMETDL

				ARLLEQGTLAEEHAKLFMYQLLRGLKYIHSANVLHRDLKPANIFIST EDLVLKIGDF\GLAKESLNQ\HYS\HKGYLEGLVTKWYRSPRLLLS PNNYTKAIDMWAAGCILAEMLTGRMLFAGAHELEQMLILETIPVIR EEDKDELLRVMPFSFVSSTWEVKRPLRKLLEPVNSEAIDFLEKILTFN PMDRLTAEMGLQHPYMSPYSCPEDEPTSQHPFRIEDEIDDIV\LMAA NQSQLSNWDTCSSRYPVSLSSDLEWRPDRCQDASEVQRDPRAGSAPL AENVQKDPKRDHSSSERFLEQSHSSMERAFEADYGRSCDYKVGSPS YLDKLLWRDNKPHHYSEPKLILDLSHWKQAAGAPPTATG\LADTGAR EDEPASLFLE\IAQWVKSTQG\AQSTP\TRPPTTPSAACLP RPP\PP GPGGRR\RQPPVRPGRVHLRPEALHQARGPAGQ
3785	A	3	495	GGIPRVFLYELLPEPFFLECNSTSPDPHKGLVLLPKTECDVREVE LMRCLRLRQSSLEPVAFRLPRVRKEFFQDDVFPD TAVIWEPVLSAEA WLQGANQPWLLSLQPPDMSPGAPRDWVWGGSGMGVGERDRRRLKF HSCWHAESSGLWEGGVAVSISL
3786	A	3	1356	GYKLLPCLSRSTAATGHKWIHPRLVAKDCRSHKLHLSSVPVRI*SRV LQAEAQK*CQDTQDGGLLPRVPASKNHGPGPFHGP/GPSPGLGQAPS ALKHLLQPPNPLAAKVSASCSYMKLRPWPADPWQCWA/SDVAPSTLL PSYDPDTGLVLLTGKGDTRVFLYELLPEPFFLECNSTSPDPHKGL VLLPKTECDVREVELMRCLRLRQSSLEPVAFRLPRVRKEFFQDDVFP DTAVIWEPVLSAEAWLQGANQPWLLSLQPPDMSPVSAQPREAPARR APSSAQYLEEKSDQKKEELNAMVAKLGNREDPLPQDSFEGVDEDE WAKYLAQIIVMGVQVVGRAFARALRQEFAASRAAADARAGHRSAA ASNLSGLSLQEAQQILNVSKLSPPEVQKNYEHFKVNDKSVGGSFYL QSKVVRAKERLDEELKIQAQEDREKQMPHT
3787	A	1	2016	MLLAGSAGAAGLCLVPLLDPSGLLVLAGKGFSSQQTGLSSDSFQGE RQLCYEVVPPQPALSPVTQC VLESVLRGAALVPRQALAVMSCEVLR VLQLSDTAIVPIGYHVPRKAVEFHEDLFPDTAGCVPATDPHSWWAGD NQVQKVSLNPACRPHPSFTSCLVPPAEPLPDTAQPAVMPETVPGDAD ASPGALTLQHWHRDQPQFEVAAEPAGSKFRHAQGTVLHRDSHITNL KGLNLTTPGESDGFCAKLRVAVPLLSGGQVAVLELRKPGRLPDTA LPTLQNGAAVTDLAWDPFDPHRLAVAGEDARIRLWRVPAEGLEEVLT TPETVLTGHTKICSLRFHPLASHGL\ASPSYDLTVRIWDLQAGADR LKLQGHQDQIFSLAWSPDGQQLATVCKDGRVRVYRPRSGPEPLQEGP GPKGGRGA\ALSGYVMVAVCWCLALTAKVSASCSYMKLRPWPADPWQ CWA/SDVAPSTLLPSYDPDTGLVLLTGKGDTRVFLYELLPEPFFLE CNSFTSPDPHKGLVLLPKTECDVREVELMRCLRLRQSSLEPVAFRLP RI\RKEFFQDDVFPD TAVIWEPVLSAEAWLQGANQPWLLSLQPPDM SPVSAQPREAPARRAPSSAQYLEEKSDQKKEELNAMVAKLGNRE\ DPLPQDS\FEGVDENEWD
3788	A	1	167	ILTQCGGFQPTLDKPFSSRASEIALAKAKQVINTPTSSSFNATTVLS AFLLEKS
3789	A	1	1685	NTIHDTIELYLSRCWVCAVSAIARARAALPNIIVGEKGGAGSARSS PRRAAECAQIPQPRRSPAVQAEPARRSRFPFTLQGAFASSAIIGAG IGGTSAAYYLRQKFGKDVKIDLFEREVGGRLATMMVQGEYEAGGS VIHPLNLHMKRFVKDLGLSAVQASG\GLLGIYNGETL\VFEEFNWFI INVIKLVWRYGFQSLRMHMWVEDVVDKFMRIYRYQSHDYAFSSVEKL LHALGGDDFLGMLNRTLLET\QKPGCSEKLLNEMIGPVMRVNYGQS TDINAFVVGAGSLSCSDSGLWAVEGGNKLVCSSGLLQASKSNLISGSVM YIEEKTCTKYTGNTKMYEVVYQIGTETRSDFY\DIVLVATPLNRKM SNITFLNF\DPPI\EEF\HQYYQHIVTTLVKGELNTSIFSSRPIDKF GLNTVLTDDNSDLFINSIGIVPSVREKEDPEPSTDGTIVWKIFSQET LTAKAQLKFLSYDYAVKKPWLAYPHYK/PPPEKPLLSFSHDLRY \LNGIECAASA\MEMSAIAA\HNAALLAYHRWNGHTDMIDQ\DGLEYE KLKTEL
3790	A	52	264	QSFAPGPPFFIPPPWGGRAGGFPGPGMG/PPPGPPGGTSSSSKIPKF GRPRGGPPFPPLPKRVRPGDFFYP

3791	A	627	1524	SHGENCKCPSTGDYRKLIYHLKGCQGLRNKGSSPFTSIVSAAKVCGA ASESPSVKSLCLLVADQDFSFKAGQWVDFPIPGVSVVGGFSICSSPR LLEQERVIELAVKYTNHPPALVWHNTCTLDCEVAVRVGGEFFDPPQ ADASRNVLVIAGGVGINPLLSILRHAA\DLLREQANKRNGYEIGTIK TILQCKKYPALLFKKNILDLVNEFPEKIASLHVTKTDYTNPMRNS KPYITEGRITEKEIRDHISKETLFYICGPPMTDFFSKQLENNHVPK EHICFEEVVVGGRRQRQKK
3792	A	331	758	WKRSLKYLWLLRSHNSHPSSSLTPSLSPSAEAEEDGDLQCLCVKTTS QVRPRHITSLEVIKAGPHCPTAQL/IVSPRTASVSAPAPCLLCPSLP LLMPFANPRTESHVSSLFPARATLKNRGIKICLDLQALLYKKIIKEHL ES
3793	A	3	402	HEETOPEFPPIALSTEILLEALPQHELRSRVL/AORPGLLFLGLLLL PLVVAFR\RAEAEEDGDLQCLCVKTTSQVRPRHIHQPR*SKAGP\H CPTCPT**PR*KNRGIWLGWTQAPLLQKG*FKETFWESLAN
3794	A	2	146	QTTANLLKIQCHIIAPPEALTFLPTWPLEYTQNRKKKGKVGKGT A
3795	A	3	1034	SEFPARTPRRCPRSPGPAMGLTVSALFSRIFGKKQMPILMVGLDAA GK/TSHILYKLKLGEIVTTIPTIGFNVETVEYKNICFTVWDVGGQ\D KIRPLWRHYFQNTQGLIFVVDSD\REVRQESA\D\ELQKMLQEDEL RDAVLLVFS\NKQDMPNAMP\VSELT\DKLG\LQHLRS\RTWYV\QA HLLPTQGTGFVTMVDWL\SHELFKALNQPWGRPLDARKSRCVQSPT MSQNSPTPRGKCFPPPTPSLPHSPQASASAPCSCLVLSVVGAVEPL LSGHRGVPLFLPAGTYGRGFAGPRPPSSRGAGIWSFFFPCFGCTL GGQVGRGKVRAFGWCYNVALDLE
3796	A	1536	1838	GLPQQTLLKRIQQVLKCCCLAFYLFLLFFFLRWSLALLPILE\CSGVI SAHCNLRPLGLGDSLASASRVAGM\TTGTCHHAQLIFCIFSRRDGVSV LARTVWIS
3797	A	2	740	GRVGQSTSKVPKEGLLSLHLLCSTAHYQKTAEMKSIYFVAGLFVMLV QGSWQSRSLQDTE\EKSRFSASQ\ADPLSDPDQMNEKRRHSQGTFTS DYSKYL\DSRRAQDF\LQW\LMNTKRNRRNNIAKRHDEFERHAEGTFT SDVSSYLEGQAAKEFIAWLVKGRGRDFFPGEGRPLLKNLAGRHA\DG SFSDEMNTILDNLP\AR\DFINWL\IRTKI\TDREITYITYSEIIFT NITLLAHVGCLEMFKSW
3798	C	204	272	MEAPQVPPCPAGPLIYTKVPCFL
3799	A	1	350	GVLSPPVKSMIDLNPIDKRISKGAQPTCHDFNQFTAATETISLLVGF SAGQVQYLDPIKKDTSKLFNEEVIAAPRAPNFSAFSPHTHYMPLGCSC LRNSVGLRGAGPGRDGEWGDSS
3800	A	1	397	QRPI*PTKPIQQRVSKGHQ\TRH\DFQF\LAHETISRLVGFSAQ QV\QYLDLIKK\DPKLFNEERLIDTKVTYLKWLPESESFLASHA SGHLYLYNVSHPCASAPPQYSLLKQGEFVSVAAYNDLFL
3801	A	1	2066	MAAGGAEGSGPGAAMGDCAEIKSQFRTREGFYKLLPGDGAARRSGP ASAQTPVPPQPPQPPGPASASGPGAAGPASSPPAGPGPALPAV RLSLVRLGEPDSAGAGEPPATPAGLGSGGDRVCNFGRELYFYPGCC RRGSQRWHTPLTPFLPPLKSIDLKPIDKRIYKGTQPTCHDFNQFTA ATETISLLVGFSAQVQYLDLIKKDTSKLFNEERLIDTKVTYLKWL PESESFLASHASGHLYLYNVSHPCASAPPQYSLLKQ\AWGFSFYAA KSKAPRNPLAKWAVGEGPLNEFAFSPDGRHLACVSQDGLRVFHFDS MLLRGLMKSIFYGGLLCVCWSPDGRYVVTGGEDDLVTWVSFTEGRVVA RGHGHKSWNNAFAFDSLYTTRAEAAATAAGADGERSGEEEEPEAA GTGSAGGAPLSPLPKAGSITYRFGSAGQDTQFCLWDLTEDVLYPHPP LARTRTLPGTPTGTPPAASSSRGGEPPGGLPRSLSRNSLPHPAGG GKAGGPGVAAEPGTPFSIGRFATLTQERRDRGAKEHKRYHSLGNI SRGGSGSGSGGKPSGVPVRSRLDPAKVLGTALCPRIHEVPILLEPL VCKKIAQERLTVLLFLEDCCIITACQEGLICWPRPGKAFTEETEAO TGEGSWPRSPSKSVVEGISSQPGNSPSGTVV
3802	A	1	1155	MGGTTLAWSMARDSAGLVAGNLDLSEKHDP RPPLHPPGPTAVLAG

				DGSFRNPALGKPLTKSQATWMTLSYDAARRAGGGGDPGGPEPGWV DPRTWLSFQGGPPGGPGIGPGVGPSEVWGIPPCPPPYEFCGGMAYCG PQVGVLVPQGGLETSQPEGEAGVGVESNSDGASPEPCTVTPGAVKL EKEKLEQNPEEARKVFSQTTICRFEALQLSFKNMCKLRPLLQKWVEE ADNNENLQEICKAETLVQARKRKRTSIENRVRGNLENLFLQCPKPTL QQISHIAQQLGLEKDVRVWFCNRRQKGRSSSDYAQREDFEAAGSP FSGGPVSFPLAPGPHFGTPGYGSPHFTALYSSVFPPEGEAFPPVSVT TLGSPMHSN
3803	A	285	1444	LLISPGPRLGAPSFPMAGHLASDFAFSPPPGGGGDPGGPEPGWVDP RTWLSF\QRPPGGPGIGPGVGPSEVWGIPPCPP\PYEFCGGMAYCG PQVGVLVPQGGLETSQPEGEAGVGVESNS\DGASPEP\CTVTPGA\ VKLEKEKLEQNPEK\SQDIKALQKELEQFAKL\LKQKRITLGYTQAD VGLTLGVLFQKVFSTTTICRFEALQLSFKNMCKLRPLLQKWVEEADN NENLQEICKAETLVQARKRKRTSIENRVRGNLENLFLQCPETPHWQQ I\SHIAQQLGLKKHVVRVWFCN\RRQKKG\RSSSDFA\QREDFE AAGSPF\SGGP\VSFP\LPPGPHFGTPGYGSPHFTA\LYSSVFPF\ EGEAFPPVSVTILG\SPMHSN
3804	A	1	824	MVPDERYITQEGHKLETGAPRPPATVTNAVSWRSEGIKYRKNEVFLD VIESVNLLQLEVTFPAGEKRFETETPTVSLTLSCGNRLIVARATPP PFLEQLSQSKRSEAAIRAEIVFANRKCCTPATEALESVMEAYEQVQK GPLKL\KGFAELGVTKRK\KKK\KDKDKAKLLEAMGT\SKKN\EEEE RRGLDKRTPAQAAFEKMQEKRVLCRNYRGDMDSEVEHFMPILMEK EEEGMLSPILAHGGVRFMWIKHNNLYRIPLGLVLPDGDSCVGV
3805	A	3	475	AATESTGMVAYYQVQKGPLKLGVAKLGVTK/RVRPEGPRDSVFIP KPFLGTPGPDPTTRLLMFFSRKKKKDKDKAK\LLEAMGTSKKNEE EKRRGL\DKRTPAQADFEKMQEKQMERILMKA\SKPHRQVEDFNR HL\DTLTEHY\DI PKV\TWTK
3806	A	3	225	GQTSQHHVALRTTQHWWALGQHRVALHTVEYYLALKRKEMDTGC\KW MELEYIVLSGISQSQEDMHCMIPFVSGP
3807	A	874	1444	CQARPMPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLALFGLHALAQAFVTGPATKRFGEKQAI IAGMGPNALGYVLLAFATRG\WMAFPIMILLASGGIGMPALQAMWLA E*ITDTRANVKRLLLQNVCDLSNNMGLRFPFCVKSCGTPTSVLTKR WH
3808	B	1	1917	MIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAHGGRRAGRLA GVPTRGWMAFPIMILLASGASGCRVAGHAVQAALRAQGLLKEAEHVE SQAETVLTPEDECQLLGYLDKGKRRKEKAGSLQWAYMAIARLGGFM DSKRTGIASWGALCAGAAVLFVKTDLSGALNELQDEARLSWLATTG VPCAAVLDVVTEAGRDWLLLGEPVPGDILLSSHLAPAEKVSIMADAMR RLHTLDPATCFPDHQAQKHRIERARTRMEAGLKDLMRDQDLIKRQDE DRSHDEQDDARRSPAAWWRAYSATAATTDNSGRPVLVFKTDLSGALN ELQDEARLSWLATTGVPCAAVLDVVTEAGRDWLLLGEPVPGDILLSS HLAPAEKVSIMADAMRLHTLDPATCFPDHQAQKHRIERARTRMEAGL VDQDDLDEEHQGLAPAEFLARLKARMPDGEDLVVTHGDAACRISWWK MAAFLDSSTVAGWDIALATRDIAEELGGEWADRFLVLYVLLSGTLGF EMTDQATPNLPSRDFDSTAIFYERLGFIVFRDAGWMILQRGDLMLE FFAHPGLDPLASWFSCCLRLDDLAIFYRQCKSVGIQETS SGYPRIHA PELQEWGGTMAALVRI FVKEPYFCGVT*
3809	A	1057	1905	ALEVHLVLPQPDLPVLGGQRLQPRARAQSEVHLIPVSSFRWARGM TIVAALMTVFFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFG ILHALAQAFVTGPATKRFGEKQAI IAGMAADALGYVLLAFATRGWMA FPIMILLASGGIGMPALQAMQPLAEHIHRVRHLQPHAAHLGQRWVL ATGAHDRAPVVEDPVSRMNHRYASEREATAAAKRLRPEQQHEWSSV SVFRKVLLEKLNELDADEQADICESLHDHADELYRSCLARFGDDGEN L
3810	A	1	2928	MTMWVLHCAFTYFVSAWSKHGYAHAVTAKILYAGRIVAGITGATGAV

				AGAYIADITDGEDRARHFGGLMSACFGVGMVAGPVAGGLGAISLHAP FLAAAVLNGNLNLLGCFMQESHKGERRRPMPLRAFNPVSSFRWARGM TIVAALMTVFFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFG ILHALAQAFVTGPATKRFGEKQAI IAGMAADALGYVLLAFATRGWMA FPIMILLASGGIGMPALQAMLSRQVDDDHQGGQLQGSALAALTSLSII GPLIVTAIYAASASTWNGLAWIAFAKSFTLPQALRAQGLLKEAEHVE SQAETVLTPEDECQLLGYLDKGRKRKEKAGSPAAWVERLFGYDWAQ QTIGCSDAAVFRLSAQGRPVLFVKTDLSGALNELQDEAARLSWLATT GVPCAALVDVVTAGRDWLLGEVPGQDLLSSHLAPAEKVSIMADAM RRLHTLDPATCPFDHQAKHRIERARTRMEAGLVDQDDLDEEHQGLAP AELFARLKARMPDGEDLVVTHGDACLPMIMVENGRFSGFIDCGR LGV ADRYQDIALATRDIAEELGGEWADRFLVLYVLLSGTLGFEMTDQATP NLPSRDFDSTAIFYERLFGFIVFRDAGWMILQRGDLMLEFFAHPLGLD PLASWFSCCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQEWGG TMAALVRIFVKEPYFCE TLVKVDAEDQLGARVGYIELDLNSGKILE SFRPEERFPMSTFKVLLCGAVLSRVDAGQEQLGRRIRHYSQNDLVEY SPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFL HNMGDHSVTRLDWEPELNEAIPNDERDTTPAAMATTLRKLLTGELL TLASRQQLIDWMEADKVAGPLLSALPAGWFIADKSGAGGRSLWKNA SNAFLRLFLAFCWPFAMFFPALSPDSVDNRITAFE
3811	A	630	1159	GAPWGQVPAALWVIFG\EDRFRWSATMIGLSLAVFGILHALAQAFVT GPATKRFGEKQAI IAGMAADALGYVLLAFATRGWMAFPIMILLASGG IGMPALQAMLSRQVDDDHQGGQLQGSALAALTSLSIIIGPLIVTAIYAA SASTWNGLAWIVGAALYLVLCPA\LRRGAWSRATST
3812	A	1	3525	MNMNIKKIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSH ITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVNHFTIDYRTGR LQPAIPQSLPEALRLAADLAEQKQRLQKMLMDAPKVEFAERVATAR KVLIGNYAKVLGLGQNYLFTWLRDNGILIA TGERRNVPKQEYISRGY FTLKETVIDTSNGSRISFTTRITGKGQQWLMKRLLDADVVRTTSIVM LAKVTFLSCITMSDFTPSGYELACFVTHSGLSRSAGHILSQCANLAA TTSEYFIHKPHRLIAETGYSQSTVVRAFREAVNKGILSVEIVIGDH RERRANLYRFTPSPLAFAQQAKNALIESKLKISSAATKVKA VLAKTL ALFNFLSTPPCQNDTPSPCQDDVAIKNKKSQVKKTKRSVSGGAGTTS LKKLTSWIAKAKAKADNLRLSKKRTQKHEFKQKVEAAARKYAYLKNK RSPDIGGISNFDNLPHCMTVNEALNAVLAKNKONEQWGA VAGAYIAD ITDGEDRARHFGGLMSACFGVGMVAGPVAGGLGAISLHAPFLAAAVL NGLNLLGCFMQESHKGERRGEEEDMSFFSTLKTALSLKEKLAATG VLVLICALVGAGFAWERHQLKQAI EKIGSLDQAVKERDKSIMDLNQT IETMNKAEQHFHSQEVKNESEQAKYADROMERKAEVQKQLVAAGNVR QRIPADTQRLRESISEFNADADKGIFMSDKVTVKQTINKATSIYKI EQITVGKPGSEYRRAFELADQLGLKHPDCIEHVFTPYADEQC THVL TEEDFFSTEEREGVDR CIGVICSSVSDELFPNVPEYGGIGYQFLYEG DELCYEHDIIESKAKELTVNSNNTVQPVALMRLGVFVPKPSKSKGES KEIDATKAFSQLEIAKAEGYDDIKITGPRLDMDTDFKTWIGVIYAFS KYGLSSNTIQLSFQEFKACGFPSKRLDAKLRLTIHESLGR LRNKG I AFKRGKDAKGGYQTGLLKVGRFDADLDLIELEADSKLWELFQLDYRV LLQHHLRALPKKEAAQAIYTFIESLPQNPLPLSFARIRERLALQSA VGEQNR I IKKAEQLKTIGYLDCSI EKKGRESFVIVHSRNP KLKLE
3813	A	1	1606	MLMKAHKGVLGEQEKVPRRLMKVLKGVPGEQEKVLWEAREEGVSSRW TGSPMGCEQVRVWVGDEQAMEPLGLADGKLWRTFMGAADAERKEGRGM KVAPAPAVVKKQEAKKVVNPLFEKRPKNFGVGQDIQPKRDLTRFVKW PRYIKLQHQRALYKRLKVPPAINQFTQALDRQTATQ LLELAHKYRP ETKQEKQRLLAQAEKTAGKGDISTKRLPVLQAGVNWEDKSALAKL VEGIRTNYNERYNEIHHHWGGNVLG PESVARI AKLKKADGSLRLDFT VCKKAWIVSHPVSRKLPQQKQNRKKRQEVQAWGSGPCLSLVVGSE

				PATGGSSCSETSGFGKSCVKETNPQPMATPTLEQGEAAHAIEIP PACSHGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVT GPATKRFGEKQAI IAGMAADALGYVLLAFATRGMWMAFPIMILLASGG IGMPALQAMLSRQ\LTSSIIGPLIVTAIYAASASTWNGLAWIVGAALY LVCLPALRRGAWSRATST
3814	A	1701	1904	VPGLLRDIVHSDSIASHYGVLLALYALMQFLCAPVLGALSDFRGRPP VLLASLLGAMSAVLAPGCCF
3815	A	1	427	MAKMKNQIIPSVGEKLEQQKPSYDARAFVTGPATKRFGEKQAI IAGM ATDALGYVLLAFATRGMWMAFPIMILLASGGIGMPALQAMLSRQ\LTSS IIGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAWSRATS T
3816	A	1	1629	MKSNNALIVILGTVTLDVAVGIGLVMPVLPGLLRDIVHSDSIASHYGV LLALYALMQFLCAPVLGALSDFRGRPPVLLASLLGATIDYAIMATTP VLWILYAGRIVAGITGATGAVAGAYIADITDGEDRARHFGLMSACFG VGMVAGPVAGGLLGAISLHAPFLAAAVLNGNLNLLGCFLMQESHKGE RRPMPPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWV IFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI I GMAADALGYVLLAFATRGMWMAFPIMILLASGGIGMPALQAMLSRQVD DDHQQLQGSALAALTSLSIIGPLIVTAIYAASASTWNGLAWIVGAA LYLVCLPALRRERSVAAGRFLVRIAATCRANRAMSSSTTPHSRTAS SIENFGIQSLFHLLICDLSTPTASAVFSVPSIAILLSNALSIRRASL RLFARTICSYMQIETKEMVIFLRDDGISLQYPDGQCAGYIDGNMLI FMGQSCLEFPTKIIILHDQRTTNFTHK
3817	A	1	1013	MMGLRNSYDVKERLKHQVRGGKAPKAVNSGKLLPFPRLKELAGVEGM GNCYLGRTQPGTRMQWSPMKLSVELRAGQSRLLRESKGEIPEPRCA AVGGKEPEAKPPKVPMPPLRAFNPVSSFRWARGMTIVAALMTVFFI MQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTG PATKRFGEKQAI IAGMAADALGYVLLAFATRGMWMAFPIMILLASGGI GMPALQAMLSRQVDDDHQQLQ\SLAALTSLSIIGPLIVTAI\YA ASASTWNGLAWI*PGMFIISNPYREHPLSFHRYHYHPEQKSPLHGGI SDQTGKNRP
3818	A	1	2634	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGMA ADALGYVLLAFATRGMWMAFPIMILLASGGIGMPALQAMLSRQVDDDH QGQLQGSALAALTSLSIIGPLIVTAIYAASASTWNGMLLATLWNTYI CINEALALTLSDFSLVPPHPYRQLFTLTTFHNRACSSSVTRIVSILS RFIGIITPMNRNPPYTEASVTKEKTALNMARFIRSQTLTLEKLNE LDADEQADICESLHDHADELYRSCARFGDDGNSYDHDYAKLACLQV EGRGGGTFAHELLAVEYAGWISPAFRLKVNQTFIDYRTGRQLQPAIPQ SLPEALRLAADLAEQQRLEQKMLMDAPKVEFAERVATASGVLIIGNY AKVLGLGQNYLFTWLRDNGILITGERRNVPKQEYISRGYFTLKETV IDTSNGSRISFTTRITGKGQQWLMKRLLDARNRDYKQWKQDFFHDS YNRQSAGHILSQCANLAATTSEYFIHKPHRLIAAETGYSQSTVVRAF REAVNKGILSVEIVIGDHRERRANLYRFTPSFLAFAQQAKNALIESK LKISSAATKDDVAIKNKKSQVKKTKRSVSGGAGTSLKCLTSWIAKA KAKADNRLRLSKKRTQKHEFKQKVEAAARKYAYLKNKRSPDIGGISNF DNLPHCMTILYAGRIVAGITGATGAVAGAYIADITDGEDRARHFGLM SACFGVGMVAGPVAGGLLGAISLHAPFLAAAVLNGNLNLLGCFLMQE SHKGERRGELLKIVVLPGDHVGQEITAEAIKVLKAI SDVRSNVKFD ENHLIGGAIDLQGGGKPRCVSKSLMLHCTR
3819	A	1328	2536	RSQAPCMKSNNALIVILGTVTLDVAVGIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQFLCAPVLGALSDFRGRPPVLLASLLGATIDYA IMATTPVLWILYAGRIVAGITGATGAVAGAYIADITDGEDRARHFGL MSACFGVGMVAGPVAGGLLGAISLHAPFLAAAVLNGNLNLLGCFLMQ ESHKGERRMPPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVP AALWVIFGEDRFRWSATMIGLSLAVFGMLHALAQAFVTGPATKRFGE

10262

				KQAI IAGMAADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAM LSRQVDDDHQGLQGS LAALTSLSITGPLIVTAIYAASASTWNGLA WIVGAALYLVCPLALRRGAWSRATST
3820	A	1	1594	MSAAPCSTVPSPIDHPRAEECGHTARDWQVAPPAAQSHDDDEEEED EKEEEEEEEELL LAGSPYSPTVPCFPLECPCLENGSRQKQDKHTPGF KHKFQHAF FFSPLATITHSFWVAEHSRLRLEGKQGAQISPHLQVGP LVWQGYLWQNR EAGSSRDSHLNMPGMAAGHSHSGTLFSDQGLWEQC QLLKSTSVFARCHPLVDPEPFVALCEKTLCECAGGLECACPALLEYA RTCAQEGMVLYGWDHSACSPVCPAGMEYRQCVSPCARTCQSLHINE MCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPGTSLSRD CNTCICRNSQWICSNEECPDREGHNSRQREVALSAQVGCNHVTPALV SGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPAT KRFGEKQAI IAGMAADALGYVLLAFATRGMMAFPIMILLASGGIGMP ALQAMLSRQ\LT SIIGPLIVTAIYAASASTWNGLAWIVGAALYLVCPL ALRRGAWSRATST
3821	A	3	995	TSPTATGPALVCYRASLVALREEDTRSQEYVFPFRGNRDFAHVKKMG LGLLAMDVPEELGGAGLDYLAIAIAMEEISRGCASTGVIMSVNNSLY LGPILKFGSKEQKQAWVTPFTSGDKIGCFALSGTRAFNPVSSFRWAR GMTIVAALMTVFFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAV FGILHALAQAFVTGPATKRFGEKQAI IAGMAADALGYVLLAFATRGM MAFPIMILLASGGIGMPALQAMLSRQVDDDHQGLQGS LAALTSLS IIGPLIVTAIYAASASTWNGLAWIVGAALYLVCPLA\LR RGAWSRAT ST
3822	A	1	619	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGMA ADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQVDDDH QGQLQGS LAALTSLSIIGPLIVTAIYAASASTWNGLAWIVGAALYL VCLPA\LR RGAWSRATST
3823	A	1	565	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGMA ADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQ\LT SI IGPLIVTAIYAASASTWNGLAWIVGAALYLVCPLALRRGAWSRATST
3824	A	1	934	MTMWVLHCAFTYFVSAWSKHGYAHAVTAKILYAGRIVAGITGATGAV AGAYIADITDGEDRARHFGLMSACFGVGMVAGPVAGLLGAI SLHAP FLAAAVLNGLNLLGCFMQESHKGERRPMP LRAFNPVSSFRWARGM TIVAALMTVFFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFG ILHALAQAFVTGPATKRFGEKQAI IAGMAADALGYVLLAFATRGMMA FPIMILLASGGIGMPALQAMLSRQ\LT SIIGPLIVTAIYAASASTWN GLAWIVGAALYLVCPLALRRGAWSRATST
3825	A	657	7035	LRTCWHSDCQNTAADHSAQSGRRHRKPCNRCAPGSQNWAVPLLPDI SCRTGCAVRKDRLIAGPIQ*N/LKTAVVGRQPYLT KLCLMLGCLGRM RWRCSTGWLRLRTSSVQCS*RISNRMSCTGSMLTTWL*MKLQQVNGL GQGLIQSAGKDCDVQGLEHDMEEINARWNTLNKKVAQRI AQLEALL HCGKFQDALEPLLSWLADTEELIANQKPPSAEYKVVKAQIQEQKLLQ RLDDRKATVDMLQAEKGRI AQSAELADREKITGOLESLESRWTELL SKAAARQKQLEDILVLAKQPHETAEPISDFLSVTEKKLANSEPVGTQ TAKIQQQIIRHKALEEDIENHATDVHQAVKIGQSLSSLTSPAEQGV SEKIDSLQARYSEIQDRCCRKAALLDQALSNAFLGEDEVEVLNWL EVEDKLSSVFVKDFQDVLHRQHADHLALNEEIVNRKNVDAQKNG QALLKQTTGEEVLLIQEKLDGIKTRYADITVTSSKALRTLEQARQLA TKFQSTYEELTGWLREVEEELATSGQSPTGEQIPQFQQRQKELKE VMEHRLVLDTVNEVSRALLELVPRAREGLDKLVSDANEQYKLVSDT IGQRVDEIDAAIQRSQQYEQAADAELAWVAETKRKLMLALGPRIREQD QTTAQLQVQKAFSIDIIRHKDSMDELFSHRSEIFGTCGEEQKTVLQE KTESLIQQYE AISLLNSERYARLERAQVLVNQFWETYEELSPWIEET RALIAQLPSPAIDHEQLRQQQEEMRQLRESIAEHKPHIDKLLKIGPQ

				<p>LKELNPEEGEMVEEKYQKAENMYAQIKEEVRQRALALDEAVSQSTQF HDKIEPMLETLENLSSRLRMPPLIPAEVDKIRECISDNKSATVELEK LQPSFEALKRRGEELIGRSQGADKDLAAKEIQDKLDQMVFFWEDIKA RAEEREIKFLDVLELAEKFWYDMAALLTTIKDQDIVHDLSPGIDP SIIKQQVEAAETIKEETDGLHEEELFIRILGADLIFACGETEKPEVR KSIDEMNNAWENLNKTWKERLEKLEDAMQAAVQYQDTLQAMFDWLDN TVIKLCTMPPVGTDLNLTVDQLNEMKEFKVEVYQQQIEMEKLNHQGE LMLKKATDETDRIIREPLTELKHLWENLGEKIAHRQHKLEGALLAL GQFQHALEELMSWLTHTEELLDAQRPISGDPKVIEWELAKHHVLKND VLAHQATVETVKNAGNELLESSAGDDASSLSRLEAMNQCWESVLQK TEEREQQQLQSTLQQAQGFHSEIEDFLLELTRMESQLSASKPTGGLPE TAREQLDTHMELYSQLKAKEETYNQLLDKGRMLLSRDDSGSGSKTE QSVALLEQKWHVVSXKMEERKSKLEELNLALETFQEFINWLT AEQSLNIASPPSLILNTVLSQIEEHKVFANEVNAHRDQIIEILDQTN QLKFLSQKQDVVLIKNLLSVQSRWEKVVQRSIERGRSLDDARKRAK QFHEAWKKLIDWLEDAESHLDSELEISNDPDKIKLQLSKHKEFQKTL GGKQPVYDTTIRTGRALKEKTLLPEDSQKLDNFLGEVRDKWDTVCGK SVERQHKLEEALLFSGQFMDALQALVDWLYKVEPQLAEDQPVHGDLD LVMNLMDAHKVFQKELGKRTGTQVQLKRSGRELIENSRDDTTWVKGQ LQELSTRWDTVCKLSVSKQSRLEQALKQAEVFRDVTVMHLEWLSEAE QTLRFRGALPDDTEALQSLIDTHKEFMKKVEEKRVVDVNSAVAMGEVI LAVCHPDCITTIKHWITIRARFEEVLTWAKQHQRLETALSELVAN AELLEELLAWIQWAETTLIQRDQEPQPONIDRVKALIAEHQTFMEEM TRKQPDVDRVTKYKRKNIEPTHAPFIEKSRSGGRKSLSQPTPPMP ILSQSEAKNPRINQLSARWQQVWLLALERQRKLNDAALDPSIVSPKCR RPGGRQAYPLVNSGGSKRQIAKNRGATQAFAKENNQKAYKETYGVSH ITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVDNSIDSWKNA GRVFKDSKFDANDPILKDQTQEWSGSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYYQGEESLFNK AYYGGGTNFFRKESQKLQSSAKKRDAELANGALGIIELNNDYTLKKV MKPLITSNTVTDEIERANVFKMNGKWYLFDTSRGSKMTIDGINSNDI YMLGYVSHSLTGPKPLNKTGLVLQMGGLDPNDVTFYSHFAVPQAKG NNVVITSYMTNRGFFEDKKATFAPSFLMNIKGNKTSVVKNSILEQQG LTVN</p>
3826	A	140	2298	<p>LFPRLLSFLTTPPHCSFSICFVICSRRTLILKGSSSLITG/CTQFRLSE TKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQR MPDFLPLPAGALSLISKVTDRANDSMEQGAETSQGALGTLANVTS LANLSESLNNGDTSEIQPEDQSASEITRAFDTLAKALNTTSSSSPS LADGIDTSGGGSIHVISRDQSTPIIEVEGPLLSDTHVTFKSIREDRN GRSQKTVHTEGDMNMNIKKIVKQATVLTFTTALLAGGATQAFAKENN QKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQK VGDNSIDSWKNAGRVFKDSKFDANDPILKDQTQEWSGSATFTSDGK IRLFYTDYSGKHYGKQSLTTAQVNVSKSDDTLKINGVEDHKTIFDGD GKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTE NGYQGEESLFNKAYYGGGTNFFRKESQKLQSSAKKRDAELANGALGI IELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGKWYLFDTSRGS KMTIDGINSNDIYMLGYVSNLTGPKPLNKTGLVLQMGGLDPNDVTF TYSHFAVPQAKGNNVVITSYMTNRGFFEDKKATFAPSFLMNIKGNKT SVVKNSILEQQQLTVN</p>
3827	A	1	2604	<p>MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAIAGMA ADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDH QGQLQSSLAALTSLSIIGPLIVTAIYAASASTWNGNRACSSSVTRI</p>

				VSILSRFIGIITPMNRNPPYTEASVTKQEK TALNMARFIRSQTLTLLEKLNEBDADEQADICESLHDHADELYRSCLARFGDDGNSYDHDYAKLACLQVEGRGGGTF AHELLAVEYAGWISPAFRLKVNQTFIDYRTGRLOPAIPQSLPEALRLAADLAEQKQRLQEQMLMDAPKVEFAERVATASGVLIGNYAKVLGLGQNYLFTWLRDNGILIATGERRNVPKQEYISRGYFTLKETVIDTSNGSRISFTTRITGKGQQWLMKRLLDARNRDYKQWKQDFFHDSYNRQSAGHILSQCANLAATTSEYFIHKPHRLIAAETGYSQSTVVRAPREAVNKGILSVEIVIGDHRERRANLYRFTPSFLAFAQQAKNALIESKLIKISSAATKVAVLAKTLALFNFLSTPPCQNDTPSPCQDDVAIKNKKSQVKKTKRSVSGGAGTTSLLKLT SWIAKAKAKADNLRSLSKRTQKHEFKQKVEAAARKYAYLKNKRSPDIGGISNFDNLPHCM TVNEALNAVLAKNKDNEQWGAVAGAYIADITDGEDRARHFGLMSACFGVGMVAGPVAGGLLGAISLHAPFLAAAVLNGLNLLGCFLMQESHKGERRGELLKIVVLPGDHVGQEITAEAIKVLKAISDVRSNVKFD FENHLIGGAAILDQGGGGKPRCVSKSLMLHCTR
3828	C	1	2076	MNMNIKKIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQNGADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDN SIDSWKNA GRVFKDSKDFDANDPILKDQQTQEWSGSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQSIREDNRNGRSQKT VHTERDMIMNIKKIVKQATVLTFTTALLAGGATHAFAKENNQKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQNGADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDN SIDSWKNAGR VFKDSKDFDANDPILKDQQTQEWSGSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQ QSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGK WYLF TDSRGSKMTIDGINSNDIYMLGYVSNSLTGPYKPLNKTGLVLQMG LDPNDVTFTYSHFAVPQAKGNV VITSYMTNRGFFEDK KATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN*
3829	A	1	3603	MKLMETLNQCINAGHEMTKAIAIAQFNDDSP EARKITRRWRIGEAADLVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVF GTRLRRAEDVFPVPVIGVA AHKGGVYKTSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIPSC LALHRIETELMGKFDEGKLPTDPHMLRLAIETVAHDYDVIVID SAPNLGIGTINVVCAADVLI VTPAELFDYTSALQFFDMLRDL LKNVDLKGFE PDAAEIIAKFLGLDKRNFKATRG SATLHHWQQLAQP HLG GILDPRPGVVTKG FRTL DVDLDEVYCLNDFEEDTATSTP VQHP ETSGERSQARVTVSGSRSYSPRPQASPEEMQEP PAATEEEEEEEEEEE GSVLCAERVGQMTKTYNDIDAVTR LLEEVASR FVWLALARAAGEAGV HFLCPVGKALQDIPASLLPGSVWND SHICLGPGLPNELICPWSPKLIRGFSYNL GCGPQMKGQRLPHRLNAGIPSN SHGLENLHEVLVLCVWQAGVAQEETWHSASQLLLFQLKLVLKGAK ECACTASEHLYWG PLGSVNGSPQGGQRTPI SRNISWQALDTHLEI LLLTICAAGT LMSFLFSDLWVLMEAMESRRRPKEGRQVSKVLKPEIWP FQNTTRTPGPVGS PHVTTCQDDAAPPFLETQQRDSESPKTGIIRGSSCLLQRSNGLIPKALGAGGATQAFAKENNQKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQNGADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDN SIDSWKNAGR VFKDSKDFDANDPILKDQQTQEWSGSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDLKINGVEDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQ QSAKKRDAELANGALGIIELNNDYTLKKVMKPLITSNTVTDEIERANVFKMNGK WYLF TDSRGSKMTIDGINSNDIYMLGYVSNSLTGPYKPLNKTGLVLQMG LDPNDVTFTYSHFAVPQAKGNV VITSYMTNRGFFEDK KATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN

3830	A	2455	3151	DRRCPIFCLLPFGIRFILLFGSSSLQRGPFIIILFFFFLIFFFFFIILL SILGSFFFFLLSPVLLLLHHFFLSLFPACLLHLLLLLLQVLGAQLG RCLHA/SSPTWCRGRGR/VLAGSRGPGAETEGPWTAEGGRGNLARW RRRRRQRQRPLGKGLWKRRQRAGWGGGGSGAETRAAAVRRAGG RAVQAVAGALGRGSSIPGSPPPHQQAADQPCRPREGNPLIRRLP
3831	A	1	2376	MKLMETLNQCINAGHEMTKAIATAQFNDDSPARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQVRGYTIEQINHMDDVF GTRLRRAEDVFPPVIGVAAHKGGVYKTSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIIPSCALHRIETELMGKFDEGKLPTDPHMLRLAIETVAHDY D*FVQLYNQHVAQPVL/GISISGCSRPAFSASLIA*EETPTKSAAS PILQRRVIFLASGLSSLNCAMATAFVIS
3832	A	1289	3109	ETPYVSLYAFWLFSAKA*VAPPSGFSPTVVSDDSWLGLSVPYTLIA RT/PELIFVVRQQVLDVERGAAACG*FLPRLVG*VPDLDAVGLYSTA PII*GAIPGQGG*G\LRMSEAQGVPAAGSSGLSTTVRLTWACLLPSLF STSSV*QPQCSWRAARMVSLLPFSLSFTMCSLSWICFRNFIQVQVM G*VPVTLNNSSTDSPARTFWSSGNWMI*GGIAAFGGVLAGAFFTVA S/PLSS*HGRKRALGPPGFHLWGLGVLTGWSIIHGDLAALRLASVI LGYTLV*ASVLRQCLLDGDG\QSEPSWERMNNLVLMVFPFSVQMMV AGGSEDTWHWSSSFLPSAT*TSCSFCLKAGAVPWLSDLSLSVVPWA PLLQFTSFLTSLSSSLADFRFSSGLALPMGFRVSAGLALPIGFRV SAGLALPTGFKGPEGCALLRGLELSTALAFRVSAALLPFSAGNFFLP PSTERKSGVAGFGGTFSGTGVLVFPFLARTERKSTCWGLCTFLSSS DTVFGFTCRCLARKSICSAGISFRSSSDRVFVLTFFPRRSRKSSCS TSCWRIASSVCCLVSTRLFSTPRTSSPSSSSSQPCPLAQGPGLRDP
3833	A	1	2968	MTIVAALMTVFFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEKQAI IAGMAADALGYVLLAFATRGWM AFPIMILLASGGIGMPALQAMLSRQPNFDHWTADRHGDLCLRGHME RVGMDCRRRPIPCLPFRVASRCMEPHGLDMNGSRRHLANGFTTTPRIG ANQFLRRTVNAQTNPWQNIASIAISSRTRRISGVSWSWRSGNAE VSALHHYVPDLHRRMLLATLWNTYICINEALATLSDFSVPHPYR QLFTLTTFHNRACSSSVTRIVSILSRFIGIITPMNRNPPYTEASVTK QEKALNMARFIRSQTLTLEKLNELDADEQADICESLHDHADELYR SCLARFGDDGENSDTCSSRRRSQLVCKRMPGADKPLNQTFIDYRTGR LQPAIPQSLPEALRLAADLAEQQRLEQKMLMDAPKVEFAERVATAS GVLIGNYAKVLGLGQNYLFTWLRDNGILIAATGERNVPKQEYISRGY FTLKETVIDTSNGSRISFTTRITGKGQQWLMKRLLDAGVLVPVAATL TDVVRTTSIVMLAKVTFLSCITMSDFTFSGYELACFVTHSGLSRG HILSQCANLAATTSEYFIHKPHRLIAAETGYSQSTVVRAFREAVNKG ILSVEIVIGDHRERGANLDRVTPSFLALAAQAKSALTESKLKISSAA TKILYAGRIVAGITGATGAVAGAYIADITDGEDRARHFGLMSACFGV GMVAGPVAGGLLGAISLHAPFLAAAVLNGNLNLLGCFLMQESHKGER RPMPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIF GEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAG MAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQ\LT SIIGPLIVTAIYAASASTWNGLAWIVGAALYLVLCPALRRGAWSRAT ST
3834	A	1	563	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQAI IAGMA ADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQ\LT SIIGPLIVTAIYAASASTWNGLAWIVGAALYLVLCPALRRGAWSRATST
3835	A	850	1280	PGCIRCKCVAVDGDPCKMSNNALIVILGTVTLDVAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYALMQFLCAPVLGALSDFRGRPVLLA SLLGATIDVSCPCSRLFLTTDVLPLPMFIKKLGANVAFLLSSKKPLF VM
3836	A	3	3971	VCTGSSTRHIVTFDQGNFKLTGSCSYVLFQNKEDLEVI LHNACSP

				GARQGCMSIEVKHSALSVELHSDMEAFRFLVHGHPYSITTACFLVK LCKVKLCFLVKLFFILEELPTNIKVTVNGRLVSVPVVGGNMEVNVYG AIMHEVRFNHLGHIFTFTFPQNNFQLQLSPKTFASKTYGLCGICDEN GANDFMLRDGTVTDDWKTLLVQEWTVQRPQGTCQPILEEQLVPDSSH CQVLLPLFAECHKVLAPATFYAICQODSCHQEYQCEVIASYAHLCR TNGVCVDWRTPDFCAMSCPPSLVYNHCEHGCPRHCDGNVSSCGDHPS EGCFCPPDKVMLEGSCVPEEACTQCIGEDGVQHGFLEAWVPDHQPCQ ICTCLSGRKVNCTTQPCPTAKAPTCGLCEVARLRQADQCCPEYECV CDPVSCDLPPVPHCERGLQPTLTNPGECPNFTCACRKEECKRVSP SCPPHRLPTLRKTQCCDEYECACNCVNSTVSCPLGYLASTATNDGCG TTTTCLPDKVCVHRSTIYPVGQFWEEGCDVCTCTDMEDAVMGLRVAQ CSQKPCEDSCRSNTVPYKLLGKCQVTSWGSPLNHVGEQYVDRVFLY GRLALREWRLDPSHPECASRASLTFCMKASAVEGACHLPVSSGDAWSP ENPCLINECVRVKEEVFIQQRNVSCPQLEVPVPCPSGFLSCKTSACC PSCRCERMEACMLNGTVIGPGKTMIDVCTTCRCMVQVGVISGFKLE CRKTTCNCPCLGYKEENNTGECCGRCLPTACTIQLRGGQIMTLKRDE TLQDQCDTHFCKVNERGEYFWEKRVGTGCPPFDEHKCLAEGGKIMKIP GTCCDTCEEPECNDITARLQYVKVGSCKSEVEVDIHYCQGGKASKAM YSIDINDVQDQSCCSPTRTEPMQVALHCTNGSVVYHEVLNAMECKC SPRKCSKGDGTGIFLKWSCIPAEEKGLQTSAGAVEADIPLLPSPRRLL SPQAGSRGGQGPKHGQQCLKMPGPRAPGLQGGSNRDPGQPCGGESTR SSSVINNYLDANEPVSLERLSRMHFHDSQRKVDYVLAYHYRKRGVH LAQGFPGHSLAIVSNETGKEPHAGGPGDIELGPLDALEERKEQRE EFEHNLMEAGLELEKDLEVWQSLDVWHNLNLCSTESKGDILGQVPAA LWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGTPATKRFGEKQ AIIAGMAADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLS RQ\LTSSIIGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGA WSRATST
3837	A	1838	4062	KRHKKPFKKSTNPGAGFFEKINKIDRLLARLIKKKREKNQIDAINKD KGDITTDPTTEMQTTVREYYKHLVYNKPENLEEMDKFLDYTLPRLNQ EELESLNKPITGSEIEAIINSLPTKKSPGPDGFTAIFYQRYKEELL FLLKLFQSIEKEGILPNSFYEASIIILIPKGRDITTKENFRPISLMN IDANILNNILANQIQQHIKKLIHHDEVGFIPGMQGWFNIRKSINLIP HVNRTKDKNHMVISVDAEKAFDKIQQHFMKLTLNKLIDGTYLKIIIR PIFDKPTADIIILNRQKLEALPLKTGTRQRCSLSPLLFNIVLEVLARA IRQEKEIKIGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLIGNF SKVSEYTNVQKSQSFLYTNNRQTESQIMSELPFTIASKRIKYLGIQ LTREVKDFFKENYKPLLDEIKENTNKWKNI PWSWVGRIDIVKMAILP KQMPDVNVSWDGEQPKQLPFIDISVAVATDKGLLTPIIKDAAAKGIQ EIASVRSNIVLQCARPMPPLRAFNPVSSFRWARGMTIVAALMTVFF IMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVT GTPATKRFGEKQAIAGMAADALGYVLLAFATRGMMAFPIMILLASGG IGMPALQAMLSRQVDDDHQGLQGLSLAALTSLTSSIIGPLIVTAIYAA SASTWNGLAWIVGAALYLVCLPA\LRRGAWSRATST
3838	A	346	777	GELYFQVCGQFWRNRCGVVMKKMYILLFLSGEFCRCL*YSLMVVCISV GSVVISPLSFFIVSI*FFSLFFFISLASSLSILLILSKNQLLDSLIF
3839	A	1	564	MPLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAALWVIFGE DRFRWSATMIGLSLAVFGILHALAQAFVTGTPATKRFGEKQAIAGMA ADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQPNFDH WTADRHGDLCLRGHEMERVGMDCRRRPIPCLPFRVASRCMEPGHLDL NGSRRHLANGFTTPRIGANQFLRRTVNAQTNPWQNIASAISSSRT RRISGSVGSWPRSGNAEVSALHHYVVDLHRRMLLATLWNTYICINEA LALTLSDFSLVPPHPYRQLFTLTTFHNRACSSSVTRIVSILSRFIGI ITPMNRNPPYTEASVTKEKTALNMARFIRSQTLTLEKLNLDADE QADICESLHDHADELYRSCLARFGDDGLGGGQSCRTVLRERVRIEIA STHIALQHAIVTGDVAGMDDIPQEARQYRHNQAYAYSIQGDGAEDDD

				ERIFRTLKEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVDWA TIIRGKFQTVYRDIIERVKSSDCDVSSEVLKFHVIRTPSTSQAPC MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIVHSDSIASHYGV LLALYALMQFLCAPVLGALSDRFGRRPVLLASLLGATIDYAIMATTP VLWICLAGLPQFFNLPAQLFVLNFSIPFGIPFYDGGGRVIKHLITLAT ASQNGHSLFLPVLNESLAIKDWHRLGYAGTAGPLAGYRPFQRHQS WRAVALYALMQFLCAPVLGALFDRFAAAKSCNFATWSHYRLRDHATT PVLWICLAGLPQFFNLPAQLFVLNFSIRFGIPFYDGGGRVIKHLITLA TASQNGHSLFLPVLNGSKALEYSNGIFDCQSPTSPFMGSLRALHLVE DLRGLLEMMETDEKEGLRCQIPDSTAETLVEWLQSQMTNRRILNSSR TKKINIMFIPYFKIHCLHSALGVAETEKETAELDLAGASSRPKDSQ RNSPFIQPPSPDSKKSRSRIGIMKLPGNLGPYGGHRRSNQRAYTSRPF LFISSNIGSSMSMRQPGSPGCRMCSEAAKRSYWRSKTRYMFLIALWP CLYRQCYFSVNRALWPRRTFSSVFQRFVDFQRFVGINTRFNFELIGT DGYLVLRWLITLDTKADVVDVGAVAGAYIADIPDGEDRARHFLMSA CFGVGMVAGPVAGGLLGAISLHAPFLAAAVLNGLNLLGCFLMQESH KGERRPMLRAFNPVSSFRWARGMTIVAALMTVFFIMQLVGQVPAAL WVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGEKQA IAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSR Q\LTISIIGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAW SRATST
3840	A	3	1049	GSLQGCAASCARAFLRTCCARSESGLAVRGTKGVAFGENPRAAGTCS QSPFFPVAPPPGVRLWVLCPRFTGAPLLRRTTALNVRAGDEGPRRL LRAPRVPSRPSAPLAPAPASTPARRLPVPMQAPGRGPLGLRLMPG RRGALREPGGCGSCLGVALALLLLLLPACCPVRAQNDTEPIVLEGKC LVVCDSSPSADGAVTSSLGISVRSGSAKVAFSATRSTNHEPSEMSNR TMTIYIDQVFSNIGHHFDLASSIFVAPRKGIIYSFSFHVVKVYNRQTI QVSL\LNQYPVISAWAGYQDVTGEAASNGVLLMEREDKVHLKLER GNLMGGWKYSTFSGFLVFPL
3841	A	1	401	KGASSPVQVPGPVAASTEALLQEAQCSGLSWVVALPQVKQEKADTQD EWTPGTAVLTSPVLVPGCPSKAVDPGLPSVKQEPDPDEEDKEENKDD SASKLAPEEEITEIFSLGGPRFRDTAV*LPRSKDLKKPR
3842	C	108	293	MNMACLGCFVVALIILPFSNPAPPPLKSNFLYSGSWECKMHQLSTLS LPFPLTSSRSSKYS*
3843	A	1	1490	MIREQKIYHKYLAQRREEEKAQEKEFDRILEEDKAKKLAEKDKELRL EKEARRQLVDEVMCTRLQVQEKSYVKKLLAAHPTGDRIRSKVELT RYLGPACDLTLDFDKQGILCYPAKHPVAVASKRKKPSRPAKTRK RQVGPQSSEVRKEAPRDETKADTDAPASFPAPGCCENCGISFSGDG TQRQLKTLCKDCRAQRIAFNREQRMFKQPYTNRRQNRKCGACAACL RRMDCGRCDFCCDKPKFGGSNQKRQKCRWRQCLQFAMKRLLPVSWSE SEDGAGSPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQPDHTQAPT KQEAGGGFVLPPPGLDLVFLREGASSPVQVPGPVAASTEALLQEAQC SGLSWVVALPQVKQEKADTQDEWTPGTAVLTSPVLVPGCPSKAVDPG LPSVKQEPDPDEEDKEENKDDSAKLAPEEEAGGAGTPV/VTSVDSI YPERQL*VSSWSYLHSCGTERYPCGSI
3844	A	1	1758	MAEDWLDCPALGPGWKREVFRRKSGATCGRSDTYYSPTGDRIRSKV ELTRYLGPACDLTLDFDKQGILCYPAKHPVAVASKRKKPSRPAK TRKRQVGPQSSEVRKEAPRDETKADTDAPASFPAPGCCENCGISFS GDGTQRQLKTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDC GACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGCGVCRGCQTQE DCGHCPICLRPPRGLRRQWKVQRRCLRGKHARRKGGCDSKMAARR RPGAQPLPPPPPSQSPEPTEPQPYT/IPPAEPQVRGLCSLPTAEWMW PLR\FCCDKPKFGGSNQKRQKCRWRQCLQFAMKRLLPVSWSEADGA GSPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQPDHTQAPTKQEAG GGFVLPPPGLDLVFLREGASSPVQVPGPVAASTEALLQAVDPGLPSV KQEPDPDEEDKEENKDDSAKLAPEEEAGGAGTPVITEIFSLGGTRF

				RD TAVWLPSLQGRHSGREDGCKVWETEDTVEPTSTSWNPRGWP GTHV SLSPPPASMMWVSCRRSWCPSSQS
3845	A	1	1647	MAEDWLDCPALGPGWKRRREVFRKSGATCGRSDTYYSPTGDRIRSKV ELTRYLGPACDLTLFDFKQGILCYPAPKAHPVAVASKRKKPSRPAK TRKRQVGPQSSEVRKEAPRDETKADTD TAPASFPAPGCCENC GISFS GDGTQRQRLKTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDC GACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGCGVCRGCQTQE DCGHCPICLRPPRPLRRQWKCVQRRCLRGKHARRKGGCDSKMAARR RPGAQPLPPPPPSQSPEPTEPHPRALAPSPPAEFIYYCVDEDELQRL LPSVWSESEDGAGSPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQ DHTQAPTQKEAGGGFVLPPPGTDLVFLREGASSPVQVPGPVAASTE LLQEAQCSGLSWVVALPQVKQEKADTQDEWTPGTAVLTSPVLVPGCP SKAVDPGLPSVKQEPDPDEEDKEENKDD SASKLAPEEEAGGAGTPVI TEIFSLGGTRFRD TAVWLPRSKDLKKPGARKQ
3846	A	1	1821	MAEDWLDCPALGPGWKRRREVFRKSGATCGRSDTYYSPTGDRIRSKV ELTRYLGPACDLTLFDFKQGILCYPAPKAHPVAVASKRKKPSRPAK TRKRQVGPQSSEVRKEAPRDETKADTD TAPASFPAPGCCENC GISF SGDGTQRQRLKTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTE CGACSTCLLQLPHDVASGLFCKCERRRCLRIV\ERSRGCG\VCGRGQ \TQED/CLGHCPICLRPPRPLRRQWKCVQRRCLRGKHARRKGGCDS KMAARRRPGAQPLPPPPPSQSPEPTEPHPRALAPSPPAEFIYYCVDE DELQPYTNRRQNRKCGACAACLRNGCGRCD FCCDKPKFGGSNQKRQ KCRWRQCLQFAMKRLLPVWSESEDGAGSPPPYRRRKRPSSARRHHL GPTLKPTLATRTAQPDHTQAPTQKEAGGGFVLPPPGTDLVFLREGAS SPVQVPGPVAASTEALLQEAQCSGLSWVVALPQVKQEKADTQDEWTP GTAVLTSPVLVPGCPSKAVDPGLPSVKQEPDPDEEDKEENKDD SASK LAPEEEAGGAGTPVITEIFSLGGTRFRD TAVWLPRSKDLKKPGARKQ
3847	A	1	1723	MAEDWLDCPALGPGWKRRREVFRKSGATCGRSDTYYSPTGDRIRSKV ELTRYLGPACDLTLFDFKQGILCYPAPKAHPVAVASKRKKPSRPAK TRKRQVGPQSSEVRKEAPRDETKADTD TAPASFPAPGCCENC GISFS GDGTQRQRLKTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDC GACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGCGVCRGCQTQE DCGHCPICLRPPRPLRRQWKCVQRRCLRH LAHRLRRRHQRCQRRTP LAVAPPTGKHARRKGGCDSKMAARRRPGAQPLPPPPPSQSPEPTEPH PRALAPSPPAEFIYYCVDEDELKRLLPVWSESEDGAGSPPPYRRRK RPSSARRHHLGPTLKPTLATRTAQPDHTQAPTQKEAGGGFVLPPPGT DLVFLREGASSPVQVPGPVAASTEALLQEAQCSGLSWVVALPQVKQ KADTQDEWTPGTAVLTSPVLVPGCPSKAVDPGLPSVKQEPDPDEEDK EENKDD SASKLAPEEEAGGAGTPVITEIFSLGGTRFRD TAVWLPRSK DLKKPGARKQ
3848	A	1	1950	MAEDWLDCPALGPGWKRRREVFRKSGATCGRSDTYYSPTGDRIRSKV ELTRYLGPACDLTLFDFKQGILCYPAPKAHPVAVASKRKKPSRPAK TRKRQVGPQSSEVRKEAPRDETKADTD TAPASFPAPGCCENC GISFS GDGTQRQRLKTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDC GACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGCGVCRGCQTQE DCGHCPICLRPPRPLRRQWKCVQRRCLRH LAHRLRRRHQRCQRRTP LAVAPPTGKHARRKGGCDSKMAARRRPGAQPLPPPPPSQSPEPTEPH PRALAPSPPAEFIYYCVDEDELQPYTNRRQNRKCGACAACLRMDCG RCD FCCDKPKFGGSNQKRQKCRWRQCLQFAMKRLLPVWSESEDGAG SPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQPDHTQAPTQKEAGG GFVLPPPGH*TL CFLREG\ASSPVQVPGPVAASTEALLQEAQCSGLS WVVALPQVKQEKADTQDEWTPGTAVLTSPVLVPGCPSKAVDPGLPSV KQEPDPDEEDKEENKDD SASKLAPEEEAGGAGTPVITEIFSLGGTRF RD TAVWLPSLQGRHSGREDGCKVWETEDTVEPTSTSWN
3849	A	2	1682	LC DTPPGRGGGGGRGGGRGLQEGPSFMGPRGLEWRKIPAWLPNWLL LLPVASMAED\WLYCPALGPGWKRRREVFRKSRATCGRLNTYYQSPTG

				DRILSKVELTRYLGP\ACDLTLFDFKQGIL\CYPSPQRPIPLGGLPG KKRKKP\SRPAKT\RKRQVGPQSGEVRKEAPRDETKADTDAPASFP APGCCENCGISFSGDTQRQLKTLCKDCRAQRIAFNREQRMFKRVG CGECAACQVTEDCGACSTCLLQLPHDVASGLFCKCERRRCLRIVERS RGCVCRCGCTQEDCGHCPICLRPPRPLRRQWKVCVORRCLRGKHAR RKGCCDSKMAARRRPGAQPLPPPPPSQSPEPTEPHPRALAPSPPAEF IYYCVDEDELKRLLPVWSESEDGAGSPPPYRRRKRPSSARRHHLGP TLKPTLATRTAQPDHTQAPTKQEAGGGFVLPPPGTDLVFLREGASSP VQVPGPVAASTEALLQAVDPGLPSVKQEPDPDEEDKEENKDDASAKL APEEEAGGAGTPVITEIFSLGGTRFRDRTAVWLPKSKDLKKPGARKQ
3850	A	1	393	SPLNKVQLINELNEREVLGVANKVSWHSEYKDSAWIFLGGLPYDLT \KGDIIICVFSQ\QRSTIVAVDNFNIGIKIGRTIRVDHVSNYRAPKDS EEIDDVTRQLQEKGCARTPSPSLSESSEDEKPTKKP
3851	A	1	135	ARTPSPSLSESSEDEKPTKKHKKGKALRLKRRFVWVLSALPCIH
3852	A	18	238	SPPPPFSLAEREPEEMNPLTKVKLINELNEREVLGVADKVSWHSEY KDSAWIFLGGLPYELTEGDIICVFSQ
3853	A	254	1424	SPLTRVKLINELNEREVLGVADKVFHSEYKDSAWIFLGGLPYELT EGDIICVFSQYGEIVNINLVRDKKTGKSGKGCFLCYEDQRSTILAVD NFNGIKINGRTIRVDHVSNYRAPKDSSEIDDVTRQLQEKGCARTPS PSLSESSEDEKPTKKHKKAPQONATVFGDKVFEEVTQDGNLYLVQPLDI SKVTDIQVGFSEALSWRPRQWLLHAAAKVLLMHIPHFLAYKKEKKK KKKEKEKADREVQAEQPSSSSPRRKTVKEKDDTGPKKHSSKNSERAQ KSEPREGQKLPKSRTAYSGGAEDLERELKKEPKHEHKSSSRREARE EKTRIDRGRSSDAHSSWYNGRSEGRSYRSRSDKSHRHKRARRS RERESSNPDRWRH
3854	A	8	1015	FLSAEREPEEMNPLTKVKLINELNEREVLGVADKVSWHSEYKDSA\ WISLG\GLPYELTEG\DIICVFSQYGEIVNINLVRD\KKTGKS\KGF CFLCYEDQRSTILAVDNFNIGIKIGRTIRVDHVS\NYRAPKDSID DVTRQLQEKGSGARPPSPSLSESSEDEKPTKKHKKDKK\EKKKKKE KEKADREVQAEQPSSSSPRRKTVKEKDDTGPKKHSSKNSERAQKSEP REGQKLPKSRTAYSGGAEDLERELKKEPKHEHKSSSRREAREEKTR IRDRGRSSDAHSSWYWRW\EGRSYRSRSDKSHRHKRARRSRER E\SSNPDRWRH
3855	A	299	374	PRANKHFFLLFFSMLQEKEREFOEV
3856	A	1	993	MRDLFGTRLRRAEDVFPVIGVAAHKGGVYKTSVSVHLAQDLALKGL RVLLVEGNPDQGTASMYHGWVDPDLHIHAEDTLLPFYLGEKDDVTYAI KPTCWPGLDIIIPSCALHRIETELMGKFDEGKLPTDPLMLRLAIET VAHDYDVIVIDSAPNLGIGTINVCAADVLIIVPTPAELFDYTSALQF FDMRLDLLKNVDLKGFEPPDLKKSFKSPEPRLFTPEEFFRIFNRSID AFKDFVVASETSDCVVSSSTLSPEKVLRASWKRSDNSLKSLSPTQIR LGEVLTPVMSAFWEAEVWNSGDSDDMALDFDCTSSEVDAESTNRKVL RP
3857	A	3009	3583	LFCLFFHILQPSHCWISSEMVVQLS\DSLTDLLDKFSNISEGLSNYSI IDKLVNIVDDLVECVKENS SKDLKKSFKSPEPRLFTPEEFFRIFNRS IDAFKDFVVASETSDCVVSSSTLSPEKGKAKNPPGDSSLHWAAMALPA LFSLIIGFAFGALYWKQRQPSLTRAVENTIQINEEDNEISMLQEKERE FOEV
3858	A	2	989	TPAPAEAEQKGSQCPSGSTAQSWSAMDIIVPLLQLLVLLTLPLHLM ALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGLTG\P PGKVALLELCGCTGGNFQFYPPGCRVTCLDPNPHFEKFLTKSMAENR HLQYERFVAPGEDMRQLADGSMDVVVCTLVLCSVQSPRKVLQEVRR VLRPGGVLFWEHVAEPYGSWAFMWQVFEPTWKHIGEGCCLTQKTW KDLEK\AQFSENQORERQAPSLKGPTLWAPPSLERGCKKFFPRDGEQE TGALQPDKGAYRSLRESGPTGAGLRNRSQSVLPTGLQGHLPKPS L
3859	A	880	1196	SPTTRRGTPGTCLKPTACAGAA*PGCSARRTCASAAPLSTCPSSCA

10270

				APPPAPAAVSTPRPTSPSPWAAPASPSRRRTQTASTPASTNRPASS CWAPTTRPLAP
3860	A	305	631	IEKISLEPKNRPSPQIPNLVGP/RLFLVPGDFQSQVFNFLPFKPSSG PHPAAGKGQPFSSFLPAWRSTGPERATPGPGRPAACSALEAPSLRGPS GYSAQEPPRRPISARI
3861	A	2	205	QLPDPAIEDQGGEYVQPMLSKYAAVCVRCPGYGTGRGPAKKPSAHSQS QASSSPEWIPELLPCPDAAA
3862	A	1	627	DRVDEIRAANRDEFYSRPSKLADFWGNNNEILSGLDMEEGKEGGTWT GISTRGKLAALTNYLQPLDWQARGR/GTAKGDVICYYGNRGEPPDI VLTPGTYGLSNALLETPWRKLCFGKQLFLEAVERSQUALPKDVLIASL PDVLNNEEA*VGRSCWG/DPSVPPPGQRRERQALLPREAHGSGQAGSP AAGKLMIDLSSLPVPLSQLRFPT
3863	A	2	336	PRHSPEATGAAVPANASVLLGGPQSVPTCSPCTSQAGPAPRRWGLDL DAGSRGVPEGRWIRKRS DARAARSFGAAPGAGRQEVAAASERQRAQPT GHRHAARRPAPRCAAQW
3864	A	68	354	TRLRAGHRGTNGHHFSPSCRQLPDPAIEDQGGEYVQPMLSK\YAAV\ WCAC/AGYGTNRNTIILVDADGHVTFTERSMMDKDLSHWETRTYEFT LQS
3865	A	1	2364	MTCLRTGTEGAQGGVGRGTQAGGPGGAPSLTPEAAGAARREDTSGPS VPLSFPAARCPKVPGLPPLGLLESFGGCRALAARRQASRGAGTAAG SGRARLECSVDARTGPARNRPRASPPALTRPVRKADRAGDANLRP APSDSKFSHWSRDPARHGNRRRLGGCAEMTACHWASGMSVPADDRPP RGGAAAPHLPEPLRRRWQGTDRSLPADLREHPPTIQPRAGTGRAGA PSPDSGRVASATTSSQVSFFSACYSLRAARRSLLSTSNCILHASRE REFCCYPHFTVGKQPQRGSHLLEHSRLTLGPGGSLILTPGPRSGET MEGAESPKAAGSGSAQTPAQPEALAQPRGRGARRWQPPSDSAPSQR DAGMRAAPPLAARNPGERAGFGLGGTGLAAVARGRGTRKSAAVAEA TSRPVSAEPPCTTMCIIFFKFDPRPVSKNAYRVLGAQPVLMPPKLLC AGRLILAA\NRDE\FYS\RPSKLAD\WWGNNNEILSGLGH/EEGRAR KEGTWAGAFSTRGQAGQHFTNYL\QPQLDWQARGRGELVTHFLTDDV DSLSYLKKVSMEGHLYNGFNLIAADLSTGKG\DVICYYGNRGEPPDI VLTPGTYGLSNALLETPWWKLCFGKQLFLEAVERSQUALPKDVLIASL LLDVLNNEEAQLPDPAIEDQGGEYVQPMLSKYAAVCVRCPGYGTTRYC STVGAPPPIPCPTSHARGPAKKPSAHSQSQASSSPEWIPELLPCPDA AAGTNTIILVDADGHVTFTERSMMDKDLSHWETRTYEFTLQS
3866	A	136	230	FITSLGHRCLIKISKISKIA*NTFVSHLM
3867	A	109	1114	LEFFKMSGVVPTAPEQPAGEMENQTKPPDPRPDAPPEYNHFLPRPP GTAVPPPTGYPSGLPMGYYSPOQPSTFPLYQPVGGIHPVRYQPGKYP MPNQSVPI TWMPGPTPMANCPPGLEYLVLQDLQ\IHVLQHFEPLEMMT CFETNNRYDIKNNSDQMVVVTEDTDDFTRNAYRTLRFVLRVTDCM GREIMTMQRPFRCTCCCFCCPSARQELVQCFFGVITGFVAEHWNL RAVYSIQNEKKENVMRVRGPCSTYGCSDSVFEVKS LDGISNIGSII RKWNGMLSAMADADHFDIHFPLDL DVKMKAMIFGACFLIDFMYFERS PPQRSR
3868	A	980	1498	VSLINLQVLRQSLEQVTETFTSYFKPSCQ/PPTSPIRAMKWTELRLFL SCLPAGRQHYLLPATPPCSVRGVHGKPTVPPAAPSPSTAQSHQPAS HPLSSPTFLFEPIDAGTHASLFSRDRHLFPFTCHIRRPQPCLSP HCSQGSRTGRAVTAALRMAAAAAMTGNQSPTRI
3869	A	94	484	AAAALAAASLLLRREDPGPGAGSPMAETEALSKLREDFRMQNKS VFI LGASGETGR\VLLKEILE\QGLFSKVTILIG\RRKLTDEEAYKNVNQ EVGGLLKSLLDDYASAFQGH\LGFC\CLGYHQEGKAGGG
3870	A	302	1187	TALVPRDKDWQSPDTLKTGICRCYFSPMAETEALSKLREDFRMQNKS \VFILGATVETGRVLLKEILEQGLFSKVTILIGRRKLTDEEAYKNVN QEVVD FEKLLDDYASAF\QGHVGFCCLG\TTRGKAGAEG\FV\RVDR DYV\LKSAELEKAGGCKHFNLLSSKGADKSSNFLYLQVKGEVEAKVE ELKF\DRYSVFRPGVLLCDRQESRPGEWLVRKFFGSLP\DSWA\RGH

				SVPVVTVVRAMLN\NVVRPRDKQMELEN\KAHGPGGKRHGSSQGH DHTGRNGFYLFNLNTHDQIG
3871	A	71	335	PTRSTSSGSYMKRRSGSCSP/MISDTSVVLSDMNSRSSRAVVVKIE TRDGKLVSSESDVLPK*TAAAPPSLPLLRCPRAWEGGRYAW
3872	A	35	450	DIEECESMH*DDIRKHTEMENEFALIKKDMDEAYKNKVELESHLEGL TEEISFLTQLYEEEEIRELHVPDLGHICGAVH*QQLPGHEQHHR*GQ GTVRGDRQPQPG*G*EHEIKYEELQTLAWKHGMTRGAQRLRSR
3873	A	2121	2371	LENQSPRHVYSLSLKSKNDVMLL/DTAIFCPEATSEALDVVTSWAS EAGTEELAFGFGVLVSLSYCKLSTSLSVASSFVGGDWL
3874	A	29	3977	AEVAHARWERCFFSPTPFLWGCFRDRLLPGRACFRAGRLKRGSYN CSQLWLCVEKALAMDRSGFGEISSPVIREAEVTRTARKQSAQKRVLL QASQDENFGNTTPRNQVIP\RTPSSFRQPF\KSRSLLRQPDISCI LGTGGKSPRLTQSSGFFGNLSMVTNLDDSNWAAAFSSQRS/GLFTNT EPHSITEDVTISAVMLREDDPGEAASMSMFSDFLQSFLLKSSSTVFD LVEEYENICGSQVNILSKIIVSRATPGLQKFSKTASMLWLLQQEMVTW RLLASLYRVTKQSKVSNSSGPRAFSSSHSYMCGPSACISSSSFSRMS SSFRGSLGGDFGRASGRGGITPVTVNQSLSPNLLEVDPNIQAVCTQ VKEQIKTLNKFASFIDKLYTLGQEKLELVELDNMQGLTEVDFKNKY EDDIKHTEMENEFVLIKDMDEAYKNKVELESHLEGLTEEISFLRQ LYEEEEIRELQSQISDTSVVLSDNSRSLDMNSIIAETBISKMNRI RLQDEIEGLKGQASLEAAIADAEQHGEALAVKDANTKLSKLEAVNAS EKTVEALFQRDSLVRQSQLVVDWLESIAKDEIGEFSNIEFYAKSV YWENTLHTLKQRQLTSYVGSVRPLVTELDPAIRQKMPDLDDRED EVRLLKYLFTLIRAGMTEEKSSVLVTIVTRQITSQLSGVKRPYYAH GFRGGLSPREVIHRIKHLAHTPVLAAQCRGSKSAYLGREEARTSFLV LKNAGKPVGLVPDLSLSIIVDFLLNISFPTSIRATWRENQFLKRC PEKWSQTVSAVGVPVPTVKPSDFVEGSVAQIRSAKFLRYVLRNER TADRRDFVSPRLSLHSPVSLKRTYRETGSDSASLHPGEINSLVAHTK PVWWSLHTDVRERYHVGSESKQEDLFPWGLKEENCAGNRTWSLQWE EYKGSYSVKLDGPGQLQRITLMAEEPSASSEGLPAFAGSHLRAWRQ EPGAYGDTGDGAHQHEAPKRAIFACEGSGPISQVIASSVDDTICG PIRLEKKFSVTSEKYPFSLKASGNHLSGSLQGHILAIRVYLSPLV YKEENRGTRGAHAIGPTANKTCNSSHKPKPLGKEILYSHSKETGMK FLQTPVPWAWGRVEEAEVWDQFQEQRGIVSRIKQTRKPSALRDLGY IVHIDRNISSLHKDSWAHSMTWEQQKI IKTEDRDDKLSGLPCETLKE TFPDHPIGRRLAALIDVHILIPETCEYVTLHGKRGLAGIERAEDLNV LFLEKGDGCPDGKDNPCPFMYRYGFQSAVRAVLDDLRNPPLKFLHRQ KL
3875	A	597	1088	GCQRQVVPWRPPLQRAQDMAWQLLEYQELMNIKLALDIEIATYRK LLEGEESQLDSGMQNMSIHTKTTGGYAGGLSSAYGDLTDPGLSYSLG SSFGSGAGSSFSRTSSSRRAVVVKIETRDGKLVSSESDVLPK*TAA AAPPSLPLLRCPRAWEGGRYAG
3876	A	1537	1827	PTTSLDWLAGYVFLSSQLCGQCHTPSWTTTALACIFQCCFCQRGQS HGSSRTSPELSECPGEMVKMTKSKTFQAYLPNCHRTYSCIHCRAHL ANH
3877	A	109	696	PGPGPDGRGCGPRGPRSGRYVFLSSQLCGQCHTPSWTTTALACIFQC CFCQRGQOSHGSSRTSPELSECPGEMVKMTKSKTFQAYLPNCHRT\ YS\CIHCR\AHWPNHDELISKSFQGSQGRAYLFNSVVNVGCGPAED\ RVLL\TGLHAVADIYC\ENCK\TTLGWKYEHAFAESSQKYKEGKFI\I ELAHMIKDNGWE
3878	A	1	2474	MPGYSALSINKPMLETTQMSITRGMGKLLVVRGTEKAGPAVPGMEG PRSSTHVPLVPLLVLLLLLAPARQAAAQRCPCQACICDNSRRHVACRY QNLTEVPDAIPELTQRLDLQGNLLKVI PAAAFQGVPHLTHLDRHCB VELVAEGAFRGLGRLLLLNLASNHLRELPOEALDGLGSLRRLELEGN ALEELRPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRLRLSH NALSVLAPALAGLPALRRLSLHHNELQALPGPVLSQARGLARLELG

				HNPLTYAGEEDGLALPGLRELLDGGALQALGPRAFAHCPRLHTLDL RGNQLDTLPPLQGGPQLRRRLRLQGNPLWCGCQARPLLEWLARARVRS DGACQGPRLRGEALDALRPWDLRCPGDAAQEEEELEERAVAGPRAP PRGPPRGPGEEERAVAPCPACVCVPESRHSSCEGCGLOAVPRGFPSD TQLLDLRRNHFPSPRAAFPGLGHLVSLHLQHCGIAELEAGALAGLG RLIYLYLSDNQLAGLSAAALEGAPRLGYLYLERNRFLQVPGAALRAL PSLFSHLQDNAVDR LAPGDLGRTRALRWGL/HLSGNRITEVSLGAL GPARELEKLHLDRNQLREVPTGALEGLPALLEQLSGNPLRALRDGA FQPVGRSLQHLFLNSSGLEQVGTGHLAGLVQEAQAQHRQRAFTQQAF ASPLVPGLGPGQLSLHLQKNQLRALPALPSLSQLELIDLSSNPFHCD CQLPLHRWLTGLNLRVGATCATPPNARGQVRKAAA VFCPCPGWAA RKAKRTPASRPSARRTPIQRKTVWTR
3879	A	1	531	ETPSSEPMEEEDDDLELFGGYDSFRSYNSSVGSSESSSYLESSEAE NEDREAGEL/HDLPAFAQPWDSLLGWQWF*ASCL/LRCVSVWVQG KPSSPRPRGSAASPAPGATPPTPRKPVSWLGYRENHRPKPKSCTRL PGLPKLEPSSTLKGQDSWQMGHQDQTLWSWASTGGSS
3880	A	143	606	NKYTDYQCQLLKKSKGVDDKKGKTASSLPEGSQSISREHLPAQSWLPWA CLLLWLPALL/HDEMQRKQLPGLRSRAHSARQVRW/PCREAAAGCR MRQASHLKSPEGKFHGHFLNTRVGRAGGNPHRPGKKWLLPSSVYVCN TEHCLWGAWCPKPNG
3881	A	253	514	ECBLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLSDAILTSSSID AMDDSAFSGPYKFPPTPPLESFNLCFYTSQVVPVPIILGFY
3882	A	950	1612	IIPILASVTQPKQPAWKGTGYKGPQVSI SITEKVKSMQYDKQGIA DTW\QVVGTVTCKCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTS LDSAILTSSSIDAMDDSAFSGPYKFPPTPPLESFNLCFYTSQSVIDD QPSKLLNDGIGELMGFNWSNRSCGQVGSNQYAYCMPYAADQRTWRR GAWTSKYRNKNALYTFVKRFSHLRKQREKNPYP
3883	C	110	199	MDSSIRGSLARLCKGLQACCYMFNWAPOV*
3884	A	3161	4765	SAFLRNENWSGNRFEPLESKEKGKSDSDSQIGRMEERLGRLLPADWG VGGTAEGGGGAACRRCLRCWAPGQLPGTLRPPWTSRRVTASSATT TRAPRCKVLWALRSAAAAATGAAWYASLPDVQCLENCCFIYFVEFFG YLRRGELQNEAVFMWTAELNIATLCFKALENSNYGVRVAVSKLLGT VMATALMPKQATVMRQNVKRATFDEVLELMATGFLRGSSGFLKSGGE MLKVGGSVNREVRVGVTOAYVVFVTTLGGQWLEFSFATFLSHVLDLV SHPRATQTHVEAVYSRRCVSFI LRATVGSLLGEKAQIAAAKEICQAI GKQMKAVEAVVNDTSGENKSGAADIAASQHVMSVLCALQELGSLVQSLN ATASPLIQEASIGL\LEIVTSVLLHP\TMAARLAAWCLRCVAVALP FQLTPFLDRCAERLNNLKTSP EAVSGYSFAMAALLGGVHQCPLGIPH AKGKMVVSIAEDLLRTAAQNSRSLQRTQAGWLLLGALMTLGPSVVR YHLPKMLLLWRNVFPRSLKELEAEKARGDSFTWQVTLERAGALCAM RSFVAHCPELLEDVIRKLMTPIECAMTMMSHI PSVMKAHGAHLKAS AAMVRLRLYDILALLPPKTYEGSFNALLRELVAEFTLTDNSANTTTS LLRSLCHYDDSVLLGSLWQETDHKSIEDQLQPNASGSGALEHDPSS IYLRIPAGEAVPGPLPLGVSVIDASVALFGVVFPHVSYKHRLQMLDH FAECVKQAKGVRQAVQLNIFTAVLSALKGLAENKSTLGPEEVRKSA LTLVMGPDLNPNPILRCAAGEALGRMAQVVG EATFIARMAQYSFDKL KSARDVVSRTGHSALGCLHRYVGGIGSGQHLKTSVSILLALA QDGT SPEVQTWSLHSLALIVDSSGPMYRGYVEPTLSLVLTLTLTVPPSHTE VHQCLGRCLGAIITTVGP ELQNGATTSTIRSSCLVGCAITQDHSDS LVQAAAISCLQQLHMFAPRHVNLSLVP SLCVHLCSSHLLLRRAVA CLRQLAQREAAEVCEYAMSLAKNTGDKESSANVSFPAPGVSSRTDI HCRHQGVNITETGLEGLLFGMLDRETDRKLCSDIHD TLGHMLSSLAV EKLSHWMLCKDVLAASSDMSTATLLSSGKDEEA EKDEMDDTMTFT TLGEEDKSKPFVAPRWATR VFAADCLCRI INLCENADQAHFDLALAR SAKLNPNTDILLVHLSDLIRMAFMAATDHSNQLRMAGLQAEEDIK KFASVPEPEFPGHVILEQYQANVGAALRPAFSQDTPSDI IAKACQVC

				STWIGSGVVSDLNDLRRVHNLVSSSLDKVQAGKGSSSQLYRESATM EKLAVLKAWAEVYVAMNIKEAESKPKRAIKNTDDDDDDCGTIDEL PPDSLITLVQPELPTLSRLWLAALKDYALLTLPAEFSSQLPPDARSD EEVLSVSRGNRRWRGIAEBEERNRGKKQSSSLVVIEREDDRVLGATGN NEEVNSVTGTGPEEPY
3885	A	1	687	ARGDASEFSKNPHIGSFVGNQVTIRKADGSLVHISITPYPAILHEYV SSSKWEDAVRLCRFVKEQTMWACLAAMAAANRDMTTAEIAYAAIGEI DKVQYINSIKNLPSESKMAHILLSSGNIQEABIVLLQAGLCYQAIQ ININL\YHWERALELAVQHKTHVDTVLAIRYQKFLETFGLOETNKRYL HYAKGLPIYWEKSKATIEMEITQEREHFLRSQSSKSIGLKP
3886	B	146	326	MDESAPFLCRTLGRVDSDDPGLIPGCASGPLAVPESEQKVHERKSLH WDLGTLVSLVRAQX*
3887	A	575	828	CYPKVGRKPIKGEGEAPGAREKKNFAAEKRGLIPHGRKCLPISPTG TRGPWCP\CSSSGCASADTCTPRGALGAQKPIRESNF
3888	A	3	267	AMVGGGGVGGGLENANPLIYQSRGERPVTAGEEDEQVPDSIDAREI FDLIRS*AWPLTPQPAYWYPPGSSCQGCYRCFLESITMRN
3889	A	1	942	MVIYPLDKHFTSPCRSKLWGRRTPGPMCPLRPGSGLYVSARYWLARP SAAVVPSSQRLLLQRPSCSRVRAARAATAVLAPQAENPQGVSLARL RRHATPPSRSPPEVRGLERKRTPARISGGGSAMVGGGGVGGGLENAN PLIYQSRGERPVTAGEEDEQVPDSIDAREIFDIRRCWARAEELNVVE QVRVQVSHFRGERVVPESQKGFCAAGAGVLYAHEHRRVSDPESTVAV AFTPTIPHCSMATLIGLSIKVKLLRSLPQRFKMDVHITPGTHASEHA VNKQLADKERVAAALENTHLLLEVNNQCLSARS
3890	A	3	471	AMVGGGGVGGGLENANPLIYQSRGERPVTAGEEDEQVPDSIDAREI FDIRRCWARAGSGGLRWGEQ*YRAAGGAASQQGVPPGRGF*VGKGAES LFLHFPQ\LIRFLNDP\EHSLTLEELNVVEQVRVQVSDPESTVAVAF TPTISHWSMGTIGVC
3891	A	2	604	ARSHRISGGGSAMVGGGGVGGGLENANPLIYQRFGE\RPVTAGEED EQVPDSIDAREVF\DLIRSHQMTPEHP\LTLEELNVV\EQVR\QVVS DP\ESTVAVGFPPKPTHSGTCRHGPPLIGLS\IKVK\LLRSLPSAFSR WDVAHLLPGDPLPQEHAVEQATLQIKEAGWATALGRTHHLLLEVNN\Q CLSSPAPGTWAFVPLSLA
3892	A	73	204	DICYFQLTRLEQHDTTNVADQHDVLCRWLGTEEARALRRNKHRR
3893	A	1	846	QGANMPRYAQL\VMGPAGIVKSTYCATMVQHCEALNRSVQVVNLDPA AQHFNYSVMADIRELIEVDDVMEDDSLRFGPNGLVFCMEYFANNFD WLENCLGHVEDDYILF\DCPGQIGVVTLTWPV\MKQLVPA\LEQWEP RVCGVFLVDSQFMV\DSRFISGHL\AALSA\MISLEIPQVNMIMTK MDLLSKKAKKEIEKFLDPDMSLLEDSTSDLRKAKNSRKLDLKAIMW DLIGWTYSLVRIF/IPYDQSDEESMNIVLQHI\GFAIQYG\EDLEFK RNPKEREE
3894	A	225	405	EFLHMAPGEVTITVRLIRSFHEHRNFKPVVYHGVNLDQTVKEFIVFLK QDALKIIHQAHK
3895	A	1	403	REQEFLHMAPGEVTITVR\LIRSLHR\NFKPVVYHGVNLDQTVKEF IVFLKQDIPLRTNLPPFRNYKYDALKIIHQAHKSKTNELVLSLEDD ERLLLLKEDSTLKAAGIASETEIGIF\REEDYRNYKANPISSW
3896	A	1	1319	MDYGLLCGQQLVPQVEPVIQRGHESLVHHILLYQCSNNFNDSVLESG HECYHPNMPDAFLTCTETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHY VLLEVHYDNPTYEEVLDAEKYKYKVLASDEGLLTGHNMAVGFTWWKG LIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGH CTLECLEEAEAEKPSGIHVFAVLLHAHLAAGRIRLRHFRKGKEMKL LAYDDDFDFNFQEFQYLKEEQITLPGDNLITECRYNTKDRAEMTWGG LSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT WPFIIKSPKQYKNLSFMDAM\NKFKWTKEGLSFNKLVL\SLPVNR CSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSSSSLHRDFSIN LLVCLLLLSCTL\STKSL
3897	A	1	394	GEEPRGRASSVAGWVGAFRAPFIEAAVAGLGAGSGKRRRGWKMPVHS

				RGDKKETNHHDEMEVDYAENEGSSSEDEDETESSSVSEGDSDSEMDDDE DCERRRMECLDEMSNLEKQFTDLKDQAKSCCYMIQSR
3898	A	1	150	SEKLLLYDVTQVQSELEEKIRRLIEDRHSIDITSVYMLQDLIDEDWTT IRK
3899	A	708	911	SLPNLDNAAICLYPAPPPEHDNHFEMDDDCERRRMECLDEMSNLEK QFTDLKDHLGFLSSSLPGCHH
3900	A	1	1349	MAAGQRRSSLSRLGSGFINCDPECQLSCLVGLVQKEEVIRAAEGWK RAAPAGLRPTNYNSRQASEGRVVIAGNQSYQSRASPRPLARWKASAN GRAPIAEPAAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEV DYAENEGSSSEDEDETESSSVSEGDSDSEMDDDCERRRMECLDEMSN LEKQFTDLKDQLYKERLSQVDAKLQEVIV\ ERAPEH\ LEPAGN\ LQE NMQIRTKVAGIYRELCLSVKNKYECEIQASRQHCESEKLLLYDVTQ SELEEKIRRLIEDRHSIDITSELWNDELQSRKKRKPFPWPKKKPGV VSGPYIVYMLQDLIDEDWTTIKNAMATLGPHRVKTDPPVKLEKHLH SAISEEGRLYYDGEWYIRGQTICIDKKDECPTSAVITTINHDEVWPK RPDGSKSPLYISQLQKGKYSIITFIIMI
3901	A	38	384	QRGRVISPLTRTGGAGSKTGRLEEQLLASMQSRERHGMSEFLQEHF NPQRRYNPSSHVLGACAGAVAAAATPLDVCKTLLNTQESLALNSH ITGHITGMASAFRTVYQVGGV
3902	A	252	528	IWILSITGWLLSPFPSSLMALLVVQORMQMYNSPYHRVTDVCRAVWQ NEGAGAFYRSYTTQLTMNVFPQAIHFMTYEFLEQEHFNPQRRYNP
3903	A	777	1719	LLTLTFPRCSVAQPLPFTGGTSVSWALLALHVAVVFLEFAGAAGCVA TLLHDAAMNPAEVVKQRMQMYNSPYHRVTDVCRAVWQNEGAGAFYRS YPTQLDHDVPP\QAIHFMDLWNSCRSTLTPKRSYNPDS\HFFSGLCA GAVAAAATPL\DVCKTLLNTPGVLGFEFELTHYRTY\QGMASAFRTVY QVGGVTAYFRGVQA\RVYQIP\STAIAWSVYEFFKYLIHLKGQEEW RAGKVKLALNESPGVQDDTDASWSHSLSPGMLPPQVELKGKEKGLSP TDFGVLNTSSCQPLPPPPFLPGPKHVQQSTPOHL
3904	A	1	1788	MLQQGAILEAETKPSPDTKYTSALIFNFPASTADLGKTKRPAVEEKE TPNKTRAQSLFLLAKERRQDPFRPGLSALPLVKMAAIGGAHSEGRR LPCRPRPFTRSPPRPSRLDALQVQRDQSDGAALFGQPLQGRAGLSE PCQTERGKKPQQRQLSNRLQTAFRRGPLGSGFQLRWSCRGGVNAAR SPPGSAQRSRSREPLLGPRWPGSRGWIQLCESLKKIAKGWVSQDPSP RQLKECGQSASTSPRTPYSQDLLQHPKLEVAADPRTRGTREPAALV ERLEMLSGAGSVVDAVPLLVVRRRRRRRRRHSQAQALAAAAAAASE PLDCQMRLCASLGVFSTAPSSSACRADITDCVSGLAGGEMVPRRVLA DQLTEEQIAEFKEAFSLFDKDG\ DGTITTKEL\ GTVMRSLGQTQTEG \EL\QDMINEVYADNGTIDFPVFLTMMARKMKDTSDEEII\RESFR V\FAKDNGYISAAELRHVMTNLGEKTT\ DLE\ VDEMIREA\ DIDGD GQVNYEEFVQMMTGKMEDLTFQLPFSPPLEESNWNLLTLLQKKEKK KKVHLHFHSCFLYSKTECQKYL LVHTHQNLHVLVGGPVP
3905	A	1	351	GPPRPPTPPLPKPIRGATARPPRSRF*PRSDIPPLSRVLVARPPRSP PLGKPLWIMGRPRPPIAPLARAPMGRPNRAWMLLLPRRCFKLFEGNR RQCSSRGCHHGSGRRAGDRPNLS
3906	A	3	345	SCRCRRKAGKGRPGEQTDPRTPROPTSNNELSSHTTAYASNQPP*LT RAPPPSTQVRPVPGPAGAVVAVPGGALASVSFDSRDSKTAAQSSSE VGALPPHQDVTICAVRAAT
3907	A	3	388	RPLQTKGRKGQAGFGRSPARLPEPWWQPREH/WASVSFDSRDSKMA AQSA PKVVLKSTTKMSLNERFTNMLKNKQPTPVNIRASMQQQQQLAS ARNRRLAQOMENRPSVQAALKLKQKSLKQRLGKSN
3908	A	565	719	GRDVTPRSKPAPRWTSRSSPNGLKKRWCSRSWRSWERGPR*SSALG KSNIQARL/WPTHGPGQGSNRRTRPTPYSREALPREGLRGGRATEN PT*GRDVTPRSKPAPRWTSRSSPNGLKKRWCSRSWRSWERGPRAWSY GSWRNRW
3909	A	299	557	ADGSADLDSQRSSNELSSHTTAYASNQ/LHLANPSPSTSQLRFRPV PAVAVPGAVGGSPREEHLASVSFDSRDSKMAAQVSSEKLC

10275

3910	A	1	420	KLCTMVAPKLRSMYAVYGALAVMGTMGPWYLLLLLGHCVGLYVASL LGQPWLCGLGLASLASFKMDPLISWQVSQVEPVRREGELWHIRAQA GLSVVAIMAVDIFFFHYILTIPSDLKFANRLPDSALAGLAYSNLV
3911	A	2	438	HPSCARGILEDPGLTKYPASVCYHAGRLGTSRSVTSLGHTLVECAL TRPSPSPHRTSPKVEESNSKLESERKLQEERHRTVVLEQHLEKIR LEPGKASSQRAAPMTKTAPLLDVCCVRGLGCDGHNGPLVPAAAAWS LCGP
3912	A	10	250	PAQVQLLPAMNFWAIIMYNLVSLSLKFTELVARRRLLLTGFPQTTL ILFVTYCGVQLVKERERTLALEEEQKQDKEKPE
3913	A	2824	3156	SNIEGVKLSRQKAWTADYNFCLGGNCHFSGFYFSDSCYSSYRRCRT CCDFCNSGRNCSGFWFGLCCTILCSDF*SSFLISRSTWTPGLAIIIP TRRLIT*TLISWSTV
3914	A	1	70	LVKERERTLALEEEQKQDKEKPE
3915	A	42	140	TACFLSPLFRTFNFWPPLMFPPSASLMFKFTF
3916	A	4594	4848	HIYCE*SLYLFRE*DLDDGDLDLECELARLRDLVYDLE
3917	B	565	1161	MYHGWVPLHHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIIPSC ALHRIETELMGKFDEGKLPTDPHMLRLAIETVAHDYDVIVIDSA LGIGTINVCAADVLIPTPAELFDYTSALQFFDMLRDLKKNVDLKG FEPDVRILLTKYSNSNGSQSPWMEEQIRDAWGSMLKKNVRETDE VKGDLHALLVRL*
3918	A	3	226	LSVLFCCFGVESNFNFYVYSCCVFMATSQTDFICMHTYSLIEMIV HYNLEFF*ISKMATIAVLGLRLDIYHV
3919	A	1469	2806	CGSPPFATSSFFALSGHVLFAKLCTMVAPKLRSMYAVYGALAVMG MGPWYLLLLLGHCVGLYVASLLGQPWLCGLGLASLASFKMDPLIS WQSGFVTGTFDLQEVLFHGGSSFTVLRCTSFALSCAHPDRHYS LADL LKYNFYLPFFFFGPIMTFDRFHAQVSQVEPVRREGELWHI RAQAGLS VVAIMAVDIFFFHYILTIPSDLKFANRLPDSALAGL AYSNLVYDWV KAAVLFGVNTVACLDHLDPPQPPKCITALYVFAE THFDRGINDWL\ CKYVYNHIGGEHSAVIPELAATVATFAI\TTL WLGPDCDIVLWSFLN CFBPQTLKL\WVPKTGQKWGPPKHEIEG LLCQVQMSRRV\RALFGAH ELSWPIIMYN\LVSLNSL\KFTE\LV ARRLLLTGFPQTTLILFVTY CGVQLVKERERTLALEEEQK\QD KKKPE
3920	B	54	316	TIWDGEETVYCFKERSRAALKACYRGNRYPTPDEKRRLATLTGL SLT QVSNWFKNRRQRDRTGAGGGAPCKRKLPPGQPCVWQPHRDG*
3921	A	1	2219	MATLPAEPSAGPAAGGEAVAAAAATEEEEEEARQLLQTLQAAEG EAA AAAGAGAGAAAAGAECPGSPGVPGSPPEAASEPPTGLRFS PEQVACV CEA\LLQAGHAGRLSRFLGALPPAERLRGSDPVLRA RALVAFQRGEY AELYRLLESRPFAAHHAFLQDLYLRARYHEAER ARALGAVDKYR LRKKFPLPKTIWDGEETVYCFKERSRAALKACY RGNRYPTPDEKRRL ATLTGLSLTQVSNWFKNRRQRDRTGAGGG APCKSES DGNPTTEDESS RSPEDLGERAAPVSAEAAAQGSIF LAGTGPPAPCPASSS ILVNGSFL AASGSPAVLLNGGPVIIN GLALGEASSLGPLLLTGGGGAPPPQSPQ GASETKTSLVLDPQ TGEVRLEEAQSEAPETKGAQVAAPGPALGEEVL GPLAQVVP GPPTAATFPLPPGPVPAVAAPQVPLSPPPGYPTGLSPT SPLLNLPQVVPTSQVVTLPQAVGPLQLLAAGPGSPVKVAAA AGPANV HLINSVGVTALQLPSATAPGNFLANPVSGSPIVTG VALQQGKIIL TATFPTSMVLSQVLPAPGLALPLKPETAISV PEGGLPVAPSPALPE AHALGTLAQPPPPAAATTSSTSLPFS PDSPLLPNFPAPPPEGLML SPAAVPVWSAGLELSAGTEGL LEAEKGLGTQAPHTVLRLPDPDP EGL LLGATAGGEVDEGLE AEAKVLTQLQSVPEEPL
3922	A	185	479	VSDTLWLAGLAAGRWAGGCQTLGLQGVVQGLGLLINGPRAGA APLS LGNLHPPSAARWHP* AASHTGTGQSLVGIVEPHNPTSS GG*RPGTA GRSQ
3923	A	74	593	RGWVMWVDEFQPALVLSPIYERQLNLDASVQHLEDGDGKRKR SSSPR SINKKAKALDNSLPKSLAASSPPPCSQPSQCPEEK PQGVKPHEGPR GPLSASGVPGPQWPQGQGG/WWGAAGRVA EPRTESREPVSGAGTSSR

3924	A	1	284	SPSPT\GFRQPPHPSARPSRAAPGQRGWAGDRR AAAAEAKSVCRRLDYITQSLQQQGVQAEINITVTKDFRRVENAYHMEA EKLRLRRGGV*L*SQLPGRLLKQKKRSNLGGRAYSEPRSHHCTSAWVTK
3925	A	2	795	AKIAMSLQKTPPTRVFFVELVPWADRSRENNLASGRETLPGLRHPLSS TQAQTATREVQVSGTSEVSAGPDRAQVVVRVSSTKEAAAEAKKSVCR RLDYITQSLQQQGVQAEINITVTKDFRRVENAYHMEAEEVCITFTFEGK MQNICNFLVEKLDS\LLSSAHPSSI\NTPGSVENLRRQACLVAVENA WRKAQEVCLNVLGQTLGKPLLIKEEETKEWEGQIDDHQSSRLSSSLTV QQKIKSATIHAASKVFITFEVKGKEKRKKHL
3926	A	1	1810	EHDLHYAKLGTRATGGGGRGPSGHNVFLDEGGTPLLAESLVYQIFLS LGLADLLAAGLVCRQWQAVSRDEFLWREQFYRYQVARDVPRHPAAM SWYEEFQRLYDTVPCVEVQTLREHTDQVLHLSFSHSGYQFASCSKDC TVNIWSNDLTISLLHSADMRPYNWSYTQFSQFNKDDSLLLASGVFLG PHNSSSGEIAVISLDSFALLSRVRNKPYPVFGCWLTTETSLISGNLHR IGDITSCSVLWLNNAFQDVESENVNVKRLFKIQNLNASTVRTVMVA DCSRFDSPLLLEAGDPATSPCRIFDLGSDNEE\GWLCSPPAHAKEG LRHFLDRVLEGRAQPQLSERMLETKVAELLAQGHTKPPER SATGAKS KYLIFTTGCLTYSHPHQIGIKQILPHQMTTAGPVLG\EGRGSD\AFFD RRLDH\VIDIHG\HIIG\MGL\SPDNRYLYVNSRAWPNG\SVVA\DP MQP\PPIAEEIDL\LVFDL\KTMREVRRLRAHRAYPNDECCFFIFL \DVS\RDF\VASGAE\DRHG\YI\WDRHYNI\CLARLRHEDVVNSV FSPQGARRCCFTAKGHAT\IKSW\RSRPTMGVLQ\APRPRPRTFFSW LASQRR
3927	A	1	2936	MALMFTGHLLFLALLMFAFSTFEESVSNYSEWAVFTDDIDQFKTQKV QDFRPNQKLKKSMLHPSLYFDAGEIQAMRQKSRASHLHLFRAIRSAV TVMLSNPTYLLPPPKHADFAAKWNEIYGNLPLALYCLLCPEDKVA PEFVLEYMDRMVGYKDWLVENAPGDEVPIGHSLTGFATAFDLYNLL DNHRRQKYLEKIWVITEEMYEYSKVRSWGKQLLHNHQTATNMIALLTG ALVTGVDKGSKANIWKQAVVDVMEKTMFLLNHIVDGSLEGVAYGSY TAKSVTQYVFLAQRHFNINNLDNNWLKMHFWFYATLLPGFQRTVGI ADSNYNWFYGPESQLVFLDKFILKNGAGNWLAAQIRKHRPKDGPMPV STAQRWSTLHTEYIWDYDQLTQPPADYGTAKIHTFPNWGVVITYGAG LPNTQTNTFVSFKSGKLGGRAVDIVHFQPYSWIDGWSFNPGHEHP DQNSFTFAPNGQVFVSEALYGPKL\THLNNVLVFAPSPSSQCNKPWE GQLGECAQWLKWTGEEVGDAAGEIITASQHGEMVVFVSGEAVSAYSSA MRLKSVMYRALLLLNSQTLVVDHIERQEDSPINSVSAFFHNLDIDFK YIPYKFMNRYNGAMMDVWDAHYKMFWDHGHGNSPMASIQEAEQAAEF KKRWTQFVNVTQFMESTITRIAYVFYGPYINVSSCRFIDSSNPGLOI SLNVNNTHEVVSIVTDYHNLKTRFNYLGFGGFASVADQGGQITRFLG TQAIVKPVVRHDRIIFPGFKFNIAVGLILCISLVILTFQWRFYLSFR KLMRWILILVIALWFIELLDVWSTCSQPICAKWTRTEAGSKSLSS EGHHMDLPDVTITSLPGSGAEILKQLFFNSDFLYIRVPTAYIDIPE TELEIDSFVDACEWKVSDIRSGHFRLLRGWLQSLVQDTKLHLQNIHL HEPNRGKLAQYFAMNKDKKRKFKRRESLPEQRSQMKRRL
3928	A	2	513	SSVVEFSRPRGGTSQSDISTLSTFPSSPDLEVSETAMEVDTPAEQFL QPSTSSSTMSAQAHSTSSPTESPHSTPLLSSPDSEQRQSVEASGHHTH HQSDNNNEKLSPKPGTGEPVLSLHYSTEGTTTSTIKLNFTEWSSIA SSSRGIGSHCKSEGQESFRPTEFSAPTR
3929	A	1	399	EGETAMEVDTPAEQFLQPSTSSSTMSAQAHSTSSPTESPHSTPLLSSP DSEQRQSVEASGHHTHHQSDSPSSVNVKQLGSMLEQDQDNNNEKLS PKPGTGEPVLSLHYSTEGTTTSTIKLNFTEWSSIASSF
3930	A	1	1812	NRRTRPGCGVVTTCYRREFIQRLKLEAALNVHDGCVNTICWNDTGEYI LSGSDDTKLVISNPYSRKVLTTIRSGHRANIFSAKFLPCTNDKQIVS CSGDGVIFYTNVE\QDA\ETNRQC\QFTCHYGTTYEIMTVPNDPYTF LSCGEDGTVRWFDTRIKTSCTKEDCKDDILINCRRRAATSVAI CPPIP YYLAVG\CSDSSVR\IYDR\RMLGHKELQGNV\AGRG\TTGIGLPRF

				ISLPHLNNKSCRVTSLCYSEDGQEILVSYSSDYIYLFDPKDDTAREL KTPSAE\ERREELRQPPVKRLRLRGDWSDTGPRARPE\SERERDGE ESPMCPM\QRMS\DMLSRWFEASEVAQSNRGRGRSRPRGGTSQSD ISTLPTVPSSPDLEVSETAMEVDTPAEQLQPSTSSSTMSAQAHST\S SPKESPHSYSCFYFLPDS\DQRQSVESAGHHTHHQSEFLRGPEIAL RKRLQQLRLKAEQQRQQLAAHTQQQPSTSDQSSHEGSSQDPHASD SPSSVVKQLGSM SLDEQQDNNNEKLSPKPGTGEPVLSLHYSTEGTT TSTIKLNFTEWSSIASSSRGIGSHCKSEGQEEFVQPSSVQPPEGD S
3931	A	1	1878	MVSAHCAHLHAPTAAATLTGGRRSLGTAGRAPPGGLGTRDHAPAG RRVSGGEGSRKAAAAALAAVAAAPGPVRRCSSQSCFSSSGSSHYSAR TSPVRVRPRRSLSSRSAAGNRAEATESAMEKTLETVPLERKKREKEQ FRKLFIGGLSFETTEESLRNYEYQWGKLTDCVVMRDPASKRSRGFGF VTFSSMAEVDAAAMAARPHSIDGRVVEPKRAVAREESGKPGAHVTVKK LFVGGIKEDTEHHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTF DDHDPVDKIVLQKYHTINGHNAEVRKALSRQEMQEVQSSRSRGRGDGY GSGRGFGDGYNGYGGGPGGNGFGGSPGYGGGRGGYGGGPGYGNQGG GYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGSRNM GPYGGAEASQVIINKAFLGSFSGVSGMKQMKKQNGKSKKVEEAEP EEFVVEKVLDRRVVNGKVEYFLKWKGFDTADNTEPENLDCPELIE AFLNSQKAGKEKDGTKRKSLSDSEDDSKSKKRDAAADKPRGFARGL DPERIIGATDSSGELMFLMKWKDSDEADLVLAKEANMKCPQIVIAFY EERLTHWSCPEDAEQ
3932	A	2	202	RNYGGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGG NYGPGGSGGSGGYGGRSRY
3933	A	9	111	SRQAWHEASNYGPMKSGNFGGI\RNMGGPYGGGNL
3934	A	297	613	QWGLRFMNGVLSGGLSVQTASPPSASRRHFP SLGVGDGELSHGGRC AGVKVGRGGGNSYSLSKARCFGGHGVSSASVSAGSRSS*ARLRSFPS PSLTGTGFGR
3935	A	14	1276	KSGGTALAAVAAAPGPVRRCSSQSCFSSSGSSHYSARTSPVRVRPRR SLSSRSAAGNRAEATESAMEKTLETVPLERKKREKEQFRKLFIGGLS FETTEESLRNYEYQWGKLTDCV\VMRDLAS\KRSRGFCFVTFSIHGL EVDAAIAS\RPH\SINGEVVEQKRAVAREESGKPGAHVTVKKLFVGG IKEDTEHHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDP VDKIVLQKYHTINGHNAEVRKALSRQEMQEVQSSRSRGRGNFGGDS RGGGNGFGPGGSGNFRGGSDGYGSGRGFGDGYNGYGGGPGGNGFGGS PGYGGGRGGYGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNY NQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY
3936	A	827	2064	QORRVPCGAPRRVVSRAAAVLTTAPGRVRFVVRGDLSHLARLREI GLKRLSPRWREKKKQFRKLFIGGLSFETTEESLRNYEYQWGKLTDCV VMRDPASKRSRGFGFVTLSSMAEVDAAAMAARPHSIDGRVVEPKRAV REESGKPGAHVTVKKLLVGGIKEDTEHHHLRDYFEEYGKIDT\IEI ITDRQSGKKRGFGFVTFDDHDPVD\KLDLRKYHTINGHNAEVRKALSR QEMQEVQSSRSRGRGNFGGDSRGGGNGFGPGGSGNFRGGSDGYGSG RGFGDGYNGYGGGPGGNGFGGSPGYGGGRGGYGGGPGYGNQGGGYG GGYDNYGGGNYGSGNYNDFGNYNQQSS\YGPMKSGNFGCWR\NMGG P\YGGGNYGP\GGSGGSG\YGGRSPIKLKLPICHGASLV
3937	A	36	320	GPGRWVVVDEVMTMWLELEQYPVSFLKQPFEIGHLDLPKGTYGICVN MCPGNKSC/PRGKRCQSNCGHVCKVVPETSKSQPLRCSQGMTHWS SL
3938	A	3	715	LCGGVIDVNDHAPVETMSAFTSPIPENAPETVVALFSVSDLDSENG KISCSIQEDLPFLKSSVGNFYTLTETPLDRESRAEYNTITVTDL GTPRLTTHLNMTVLVSDNNSPALHIGSVSATDRDSGTNAQVYSLLP PQDPLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSP ALSSEALVRVVLDANDDSFVLYPLQNGSAPCTELVPRAAEPGYLV TK

3939	A	1	519	LLKATELGFGVWAHNGEDNGEPPRSATATLHVLLVDGFSQPYLPLP EAAPAQAQAEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRA ASVGRCSVPEGPPFGHLVDVRGAETLSQSYQYEVCLTGGPGTSEFKF LKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ
3940	A	1	967	MGHMLMIDKLVALGGLYYAIQRHYATKCSVLKNDQILVIGLFMIQNV IYRKHFANPLSALFLOQGIELFAAIAEIHITVAERNHAITQIRLEA QTIFDSLKEWHNAIRKSLDYALQAFEFVRGATDRGFALSSSEALVR VLVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGD SGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLLSERDVAKHRLV LVKDNGEPPRSATATLQVLLVDGFSQPYLPLPRAAPAQAQADSLTVY LVVALASVSSLFLLSVLLFVAVR\LCRRSRAAPVGRCSV
3941	A	1	2785	RILSVDDFVELNVSSLVAVAEGIGYRDLDSNMKKLGRHPNRQVLAF ILMVFLSQVRLEPIRYSVLEETESGSFVAHLAKDLGLGIGELASRSA RVLSDDDKQRLQLDRQTGDLRLREKLDREELCGPIEPCVLHLQVVLE MPVQFFQGELLIQDINDHSPFPEREVLLKILENSQGTFLPLLIAE DLVDGNSGLQKYTISPNSHFHILTRNHSEGKKYPDLVQDKPLDREEQ PEFSLTLVALDGGSPPRSGTVMVRILIMDINDNAPEFVHTPYGVQVL ENSPLDSPIVRVLARDIDAGNFGSVSYGLFQASDEIKQTFSSINEVTG EILLKKKLD FEKIKSYHVEIEATDGGGLSGKGTVVIEVDVNDNPPE LIISLSTSSIPENAPETVVSIFRIRDRDSGENGKMICSIPDNLPFIL KPTLKNFYTLVTERPLDRE\TSAEYNITIAVTDLGTPLKTQONITV QVSDVNDNAPFTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQV TYSLLPPQDPHLPLASL\VSINTDNHGLF\AL\RLSDY\EALQAFRV SALGATDRGSPALSSEALVRVLVLDTNDNL\PFVLYPLQNGSAPCTE L\IPGRAAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATEPGLFGVWA HNGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGF SQPYLPLPEAQAQAEADLLTVYLVVALASVSSLFLLSVLLFVAV RLCRRSRAASVGRCSVPEGPPFGHLVD\VSGTGTLSSQSYQYEVCLTG DSGTGEFKFLKPIIPNPLPQSTDLCGGVIDVNDHAPEVTMSAFTSPI PENAPETVVALFSVSDLDSENGKISCSIQEDLPFLKSSVGNFYTL LTETPLDRESRAEYNVTITVTDLGTPLRTHLNMVTVLVS
3942	A	383	703	NRITPTSARINLSILVPSAINNGSMTEINRTVISGTPRQNSIKMTD KIRTIGIWERRPGVVLTCLIMV*HLTSAIANRLNLLRKLGRMVF SHRLKVSSMKSA
3943	A	1887	3072	NFVMC\HGEPLWAGRTVVPVSTLSGPELALQKLKGTPLGRYLFTSST LTRDFIEIGRDAGLWGRSRLRLSGKPLLLTELFRYRHRCTKRKKIC DCISANVWAVLKTVEAAGSDRPVQCLTITAVQRESDTQSLSVITAE EPVSSPHFIREAGQYGTGRSSKEREVPVQVSFNSWIRNNCGDICE LSPTSGDHPPPSGPGLYSARKAIMQHYQARGMRDVTVEDIYIGNGVS ELIVQAMQALLNSGDEMLVPAPDYPLWTAASVLSGKAVHYLCDESS DWFPDLDIRAKITPRTRGIVIINPNPTGAVYSKELLMEIVEIARQ HNLIIFADEIYDKILYDDAEHHSIAPLAPDLLTITFNGLSKTYRVAG FRQGMVHRFFTPRLTVQAI
3944	A	623	2587	SPRKGGGKGGKANRVLLTGAPLDPIDLSQSAVSHSVKEL/ENHTGVR LLDRTTREVVL/TDAGQQLALRLERLLD/ELNSTLRDTGRMGQQLSG K\VRVAASQTISAHLPQCIAESHRRYPDIQFVLHDPQQWVMESIR QGDVDFGIVIDPGPVGDLQCEAILSEPFFLLCHRDALAVEDYVPWQ ALQGAQLVLQDYASGSRPLIDALARNIGIANIVQEIGHPATLFPMV AAGIGISILPALALPLPEGSPLVVKRITPVVERQLMLVRRKNRSLST AAEALWDVCNCAIQPFFTAITRCIGSVTVKLVLPVVGKSEFLAAQHK VVTCPNAGDIAVVASVIGLICITLSKERFEPPTAAGEIVADTVQEH VVEIHAIIRRTVGAIHQVEIKSGVTQAYLQLGINEKLGLSGRPDRPI GCLGTSKIYRILGKTVCYPIIFDLSDFYMSQDVLLIDDIKNALQF IKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAALKKGIIGGVKV HVDRLQGPLENDLVVHVALIAESQRLQVFLNTYGIQTQTPQQVEPIQ IWPQQELVKVTLGAFGHEEEVISNPLSPRVIQNIYYKCNTHDEREA

				VIQQELVIHIGWIIISNNPELFSGMLKIRIGLQNECSLVIQVSTIIPA T
3945	A	102	2392	RKQMNYSLKQLKVFTVAQEKSFSSRAGERIGLSQSAV\SHSVKELEN HTGVRLLDRTRAVVLTDAGQPLALRLERLLDELNSTLRDTGRMGQQ LSGKVRVAASQTISAHLIPOCIAESHRYPNIQFVLHDPQQWVMES IRQGDVDFGIVIDPGPVGDLQCEAILSEPPFLLCHRDALAVEDYVP WQALQGAQLVLQDYASGSRPLIDAALARNGIQANIVQEIGHPATLFP MVAAGIGISILPALALPLEGSPLVVKRITPVVERQLMLRVDLRFQA KFQIGDRKILRSNNVNLPAATCGFPFVCCWRFAYGCCSALLRI PPRLYSVFIIISLLYGFSRAHISSPGACWVFIHERFGQFMYGLYPHD QRWRINLALLIGLVSIAPMFWKILPHRGRYIAAWAVIYPLIVWWLMY GGFFALERVETROWGGLTLTLIIASVGIAGALPFWGILLALGRSHMP IVRILSVIFIEFWRGVPLITVLFMSSVMLPLFMAEGTSIDKLIRALV GVILFQSAYVAEVVRGGLQALPKGQYEA AESLALGYWKTQGLVILPQ ALKLETVRQPOTLAMEEINCHHNYVQKEQHFGEEIYVTRKGAVSARA GQYGIIPGSMGAKSPFIVRGLGNEESFCSCSHGAGRVMSSRTKAKKLFS VEDQIRATAHVECRKDAEVIDEIPMAYKDIDAVMAAQSDLVEVIYTL RQVHSCRAGETGAVAPASDRGKGGDGNLRSNRGRRGAGVAASALPAR HRARGRLPLCYR
3946	A	2	331	LRDRDPFHRIVQISSFIELHAENLKNEDDVTGLLGFWTLLIIISLTAG FSCCSFSWTVTYFDSFEPGMFPPTPLSPARFKKLTGHSFHMGYSMAI LNGIVAALTVAWCLM
3947	A	3	116	CSLLFAILLAFLLAIAYLIVKAFSGLQMAWHLKPNA
3948	A	3	162	CSLLFAILLAFLLAIAYLIVKELHAENLKNEDDVTGLLGIICISRK FSLML
3949	A	181	804	RPLPRIGCCPGAGQVGEARSPRVSLCFAPCRLLRAGGGRALRRRG GTPGPVARPSYSSFTQGD SWGEVDEEBCDQVARD\LRAEFIGMG QWSEPRKLSVLPDRNGSPVLPDK\RNGIFPSGRGQEQPSLRRWPFQ VLSILCSLLFAILLAFLLAIAYLIVKELHAENLKNEDDVTGLLGF TLLIIISLTAGILLQLFLGQ
3950	A	1	149	KQMKLRVMNSQEQCLPSGAEDIMSGGPTLEAAEFDDLIGKCLPDRPI AE
3951	A	1	1896	MPFAPHLLSALEWAAGEETLLFGHHDKGPEARSTGADGLSEPEGISL KRVAVVEDFFDIIYSMHVESAEPGKAPKHAGQKKTIRAIAETYAFL PREAVTRFLMSCTECQKRMHFNNSNGLEPKGGFGLRRPSTFGWYNYN AALRNGRQPVSWPTVPRHKAANVQVAQQRHKVCLYPGWEMLGSGTG GSVARLTHEAKAKVAPADSSASSGTQVQGGQLHSEPVHTVCQPRGL SICYAGFQSV AQPLGGPGDDTSFGAPSVSPYVKGYFRLEKEICVPEI MFLEEDGEQKALPASSPLGSSYLSPLCLPCEPSSSQHPSGAVFLVWQ MELTLPAPVEPSAGWESPRERAQTWGFSFIHLFSKHIWDTYVSGIV LDVGDTAVNRTELCPGLMYIPVGLELPVAQSGPPHCQVAGIPAHLGP GSELSEKQVIWAKSGKGQVSGMEIKKEQLPPGTVIASPOELGIVGDL PHTPPSMPLLDKPSDTRDLKTQGLFLQKSGHLSKLQVFCMEPFK RRAATSPKGPVLAPEENEPSPVLSGIIIDYNMPLTSTYLKQMKLR VMNSQEQSTAGEVYRELTIEKADDSHERSSI FWTL CVCC LQNL TAAH GLIPLSAPFTGEKTEPLTELS
3952	A	3	277	NEPPSPVLSGIIIDYNMPLTSTYLKQMKLRVMNSQEQSTAGEVYRELT IEKADDSHERSSI FWTL CVCC LQNL TAAHGLIPLSAPFTGEKTE
3953	A	2	396	LSPAPAPLTRGSRPPISASLAAQDETSVSSSEDFMSDSTWMSADPHL ASSLSPSQDERMRSPQNLHSQEDDDSSSESGSGNGSSTLNPSTSSST QGDPAFPENMGNGAVAPMDFTTAAEDQPINLCDKLPP
3954	A	1	209	SRPPISASLPAQDETSVSSSEDFMSDSTWMSADPHLASSLSPSQDER MRSPQNLHSQEDGGVCLQGPTA
3955	A	466	3315	EMVPRWAIYQGFQDCLVHHASSRASGLWKLLNPCRGLRCPDTRLPTS RWPNRDTRSASTQLLGKQSLPPAPEADPVFLPQEEENEPSPVLSGII IDYNMPLTSTYLKQMKLRVMNSQEQAGSSPTPIQTERHTAQLLLTADQ

				TLVLPATQHYVVLKKFPRPGAEDIMSGGPTLEAAEFDDLIGKCLPDR PIAGSVRLGDRIWNPRGSPRRRCRLHGQCVPGSGLERRPRDYPIITLQ LWLARRQDPARCGLAENDRRRGGGGHAGGGRWGSRRLGRTVTRRG GASPSPRAAAAAAGAVGLSPPPAPLTRGSRPPISASLPAQDE TSVSSSEDFMSDSTWMSADPHLASSLSPSQDERMRSPQNLHSQEDGW AVGGLLSKSRVEPWLGQVMPTLPWAHPWVTAALSHQEAQNSGLLPP PGPNTHGQTSALEQRAQAQAFQGLAVGHTGSPGSQESVHHQLGRRRH RQCWAVLGPGLPPRESHGGGTASSSHTSGHGRQSARRACWPPVAVYLA YGPRDEPWPTAGATMEIGADDSSSESGSGNGSSTLNPSTSSSTQGDP AFPEMNGNGA/DGPHGLH\QAAEDQPINLCDKLPPATALGTASYPSD GCGADGLRSRVKYGVKTTPEPPYSSGSYDSIKTEVSGCPEDLTVGR APTADDDDDHDDHEDNDKMNDSGMDPERLKAFNVSTGRKQMFVRL FVDENLDRMVPISKQPKKIQAIIESCSRQFPFQERARKRIRTYLK SCRRMKKNGMEMTRTPPHLTSAMAENILAAACESETRKAAKMRLE IYQSSQDEPIALDKQHSRDSAAITHSTYSLPASSYQDPVYANGLN YSYRGYALSSNLQPPASLQTGNHNGPTDL\SMKGAFTTSTTPTP TPSSTSTSRPVPTAQLSPTEISAVRQLIAGYRESAAFLRSADLEN LILQQRNRPRHL
3956	A	11	755	ETHAPPSGVWGLERPSHPADQEIAGGQQTAPAWEKPHSHPTPKSCG DQTKTTLHTERREDKPSFTRAGWGWNELKGPFPVTEGAGSPGSSSHA GLNRDHPLOQSQPGRRAPWPQRAPTHMLFSMTRGQSPGAAPGAQPEI SKLAGYKKQKQKRSCLRKCHP/QEAGHRQVVAHSAGPGLQGEAAGE GRGEGAFWLKARNKYSSSLGINIPPNGAQQSGCLGKVGCRRHDPHRS GLSAPFPRMSQAL
3957	A	175	559	VKRQLRRLRRSPWPDEKPKGVKTENNDHINLKVAGQ\DGSVEQFKI KRHTPLSKLMKAYCE\ROGLSMKQIKIPDFDQGP\INETDTPATVGK WKDERYQLMVFFQARPGGVYLKRELCFLYSQNSVSP
3958	A	140	380	HQKQVRMTTLTHRARRTEISKNSEKKMESEEDSNWEKSPDNEDSGDS KDIRLTLMEVLLLGLKDKQEVMLGLLGLYKDY
3959	A	98	426	LLTPSSSAALKGESVQWHLREAGQSLPRRLTCAGWNKRFLHWIDQLS G*QTCLLLVVFVWIAE*LGESLPL*APIGGTQPW*FLIGAMKKHQ ETGENDHFNSPGPSH
3960	A	234	1050	ARTLKRRWKVRKTVIGRKVQTMKILETLRISALLLWEEVLLLGLKDK EGYTSFWNDCISSGLRGGILIELAMRGRIYLEPRTMRKKRLDDRVL LKSDSPTG\DVYWDETLKHIAKATEPTETVQTIWIELLTGETWNPFLQ YQLRNVRRERIAKNLVEKGILTTEKQNFLLFDMTTHPTVNTTEKQRLV KKLQDSVLERWVNDPQRMKDRTLALLVLAHSSDVLENVSSLTDDKY DVAMNRADLVELDPEVEGTPSATEMIWAVLAAFNKS
3961	A	1	1074	MEPIGARLSLEAPGPAPFREAPPAEELPAPVPCVQGGGDDGGGASET PSPDAQLGDRPLSPKEE/CRPPGAGGAAGMPPPLPRALLFLARRPHL /VRRPSSCSSSSNRWHWAA/SGAEDAQLGPGGCCAKCKKRVQFADT LGLSLASVKHFSEAEPPQVPPAVLSRLRSFPMRAEDLEQLGGLLAAA AVAAPLSAPPSRLRPLFQLPGPSAAAERLQRQVCLERVQCSTASGA EVKGSGRVLSCPGPRAVTVRYTFTEWRSFLDVPALQPEPLEPQQPE APSGASEPGSGDAKKEPGAECFHFSLCLPPGLQPEDEEDADERGVAV HFAVCYRCAQGEYWDNNAGANYTLRYARPADAL
3962	A	42	426	NGFCVQPPYFTGEITVLKMLFLSQDFLCVSSRGDLLYGGGSPEWPR AVCHIHVTVSGHCLLFLPFSAVNKDRHFSCEDCNGNVSGGFDASTSQI VLCQNNIHNQAHMNRVVTHELIAFDHCRAHVD
3963	A	3	899	PPNVFSPASLPFFPAEGGPGRSRWREGGYLSQSRSGRLSQEEAASRS AGGMAGAPDERRRGPAAGEQLQQQHVSCQVFPERLAQGNPQQGFFSS FFTSNQKQCLRLKLTETNPYVKKLLDAMKHSGCAVNKDRHFSCEDC NGNVSGGFDASTSQIVLCQNNIHNQAHMNRVVTHELIAFDHCRA\H VDWFTNIRHLACSEVRAANLSGDCS\LV\NEIFRV\QFGLKHPP\QT \CVRDRATLSILAVRNIKEVAKAVDEVFESCFNDHEPFGRIPI\HN KTYARYAHRDFENRGR\YYSNI

3964	C	165	347	MTGQISNKKCIELENXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXX
3965	A	871	1194	EFVFFFETESFSVT\QLECSGHNGLHCNHLPGSSNAPASASRVA RITGAHHHARLIFVFLVEMGFHQ\TGWAMLVLKLPDIQVICPPWPPQS AGIYRHEPQHPGRK
3966	C	54	197	MVLSSFNFQKAIKLALLKYFKISFQLFPFVHKIGCRHSHFAMNVS* *
3967	A	263	744	SRSHDHLTYTVVPSPNFFRALRISNSKNEMFMSFLFREMKKKKLP SDSGDLEALEGKDKEKESTVHIETHQNTSKNVAAVQPMKR\GQKSKM KKMKEY*DQDEEDRELIMKLLGSAGSNKEEKGGKGGKGT\KDEPVK KQPQKPRGGQVRSDNIKKE
3968	A	189	1393	SHTDFPYDNSTDGGDTSSDEDKEEHETPVEVELMTQVDQEDITLQSG RDELNEELIQEESSEDEGEYEEV/REKDQDSVGEMKDEGEETLNYPD T\TIDLHL\QPQRSIQKLASKEESSNSSDSKSQSRRLHSAKERREM KKKKLPDSGDLEALEGKDKEKESTVHIETHQNTSKNVAAVQPMKRG QKSKMKMKEYKDQDEEDRELIMKLLGSAGSNKEEKGGKGGKGT DEPVKKQPQKPRGGQVRSDNIKKE\TPFLEVITHELQDFC/AVDDP/H LIDQKPEPDLDDQGGNEENLF\DSFDQGP\PEDVL/LGFAIPICAP YTMNTYKYKVLTPGVQKKGKAAKTALNSFMHSKEATAREKDLFRS VKDTDLSRNIPGVKSVCTQSSERKKEIAEMKF
3969	A	192	1510	MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRL QMGEAALARLGDGARESAPYRGMVRTALGIIIEEGFLKLWQGVTPA IYRHVVYSGGRMVTYEHLREVVFVGKSEDEHYPLWKSIVIGMMAGVIG QFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRG LWAGWVPNIQRAALVNMGVTAFIHNRSHPSRNAHRLRLGEPVRQKPL VLLRDGHSABAQDDNALLFAAALHRAAGHAI PARAAPPQASGRRKN LRRPPCIKGWIPWIGVGFEGKAPLEFIEKARIKMRSLKLRSVTKV QQLFDQADLGIQAFITYCAASLWHCVWNLWVLGLTDFKNEATAPRGMK LQTFAVSVTALKATRLDLFVPPGGLVVS LASGVKLQTFSI PPPPPRD LNSSGLNSSDYIMSSR
3970	A	68	382	MSVPDEE\ERLLRLTQRWPRASKFLLSGCAATVAELGTRLPTPGPPG PVARAALGEETAGAASRPGSAQSKRSPSHARLAEVAVEARPRGRR RDLEVSTAFSF
3971	A	3	1451	GAVRTWGRGFQTEKQASLLNFWNPPTTAQVTIEAEPKVS KGDV LLVHNL PQNLGYIWKQGMKDLYHYITSYVVDGQII IYGPAYSGRE TVYSNASLLIQNVTREDAGSYTLHIKRGDGTGRGTGHTFTLYRHS LDSALSLEVTGSSQPL*DTWENCPTLWLHCLMTELTSGLDVLP SAEVPSPRSGFPVSKGFKDNWKFHHPSLGCPWQGLQKHTSGGKVR LKLRRFQHCLMQLVTT\ETPKPSISSNLYPREDMEAVSLTCDPET PDASYLWWMNGQSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIR NPVSASRSDPVTNLNLPKLPKPYITINNLPRENKDVLAFTCEPKSE NYTYIWWLNGQSLPVSPRVKRIENRILILPSVTRNETGPYQCEIQD RYGGIRSYPTLVNLY\TKHSGLYACSVRSATGMESSKSMTVKVS APSGTGHLPLGLNPL
3972	A	1	1008	MATEKRLSAEGGRTAQLTAVLRKFLDPRLISTEENTQAAETMGPLSA PPCTEHIKWKGLLVLTASLLNFWNLPTTAQVTIEAOPPKVSEGKDVLL LVHNL PQNLGYIWKQGI RDLYHYITSYVVDGQII IYGPAYSGRET AYSNASLLIQNVTREDAGSYTLHIKRGDGTGRGTGHTFTLYLETP KPSISSNLPREAME TVILTCDPETPDTSYQWWNGQSLPMTHRFQ LSETNRTLFLFGVTKYTAGPYECEIRNSGSASRSDPVTNLNLLREYLL FLCGPDCHPKYTWEARPLSPSQVQVQRPLPLGIKAGHDFLPQANQN RPRLD PQ
3973	A	3	1374	TAQLTAVLREFLDPRLISTEENTQAAETMGTL SAPPCTQRIKWKGLL LTASLLNFWNLPTTAQVTIEAEPKVS SEGKDVLLLVHNL PQNLGYI WKQGM RDLYHYITSYVVDGEI IYGPAYSGRETAYSNASLLIQNVT REDAGSYTLHIKIGDDGTGRVTGRFTFTLHLETPKPSISSNLPRE

				TMEAVSLTCDPETPDASYLWWMNGQSLPMTSHLSKLNSETNRTLFLGLV TKYTAGPYECEIRNPVSASRSDPVTNLNLLPKLPKYITINNLPNREN KDVLFNFTCEPKSENYTYIWWLNGQSLPVS PRVKRPIENRILILPSVT RNETGPYQCEIRDYGGIRSDPVTNLNVLYGPDLPRIYPSFTYYRSGE VLYLSCSADSNPPAQYSWTINEKFQLPGQKLFIRHITTKHSGLYVCS VRNSATGKESSKSMTEVVSAYSSSINYTSGNRN
3974	A	1	1854	MATEKRLSAEGGRTAQLTAVLRKFLDPRLISTEENTQAAETMGPLSA PPCTEHIKWKGLLVNTASLLNFWNLPTTAQVTIEAQPPKVSEKDVLL LVHNLQNLGTGYIWKQGI RDLYHYITSYVVDGQII IYGPAYSGRE AYSNASLLIQNVTRDAGSYTLHIIKRGDGTGRVGTGYFTFTLYREAM ETVILTCDPETPDTSYQWWMNGQSLPMTSHRFLSETNRTLFLFGVTK YTAGPYECEIRNSGSASRSDPVTNLNLQHSWLDGKFQQAQVFFIP QITKTYRGLYVCFIHNSATAGTNLIIKRTIVPAKKNKRVQHGQYID RKLITKPEWENKDVLAFTCEPKSESYTYIWWLNGQSLPVS PRVKRP IENRILILPSVTRNETGPYECEIRDYGGIHS DPVTNLNVLCIFCSSV QATSLNPNQDQGLSVSLRSKYRQLYFWTSKLAMTPCPGKTWVGTA LTKNIRGVDGLVVGDLGPTSCDGPDLPRIHPSYTYNRSYSGDNLYLSCF ANSNPPAQYSWTINGKFQQSGQNLFI PQITTKHSGLYVCSVRNSATG EESSTSLTVKVS GCREMRREGASGQTPKPGPGSEVSGCMKLWAQYVG HSMEDCD
3975	A	1	1319	VLREFLDPRLISTEENTQAAETMGTL SAPPCTQRIKWKGLLLTASLL NFWNLPTTAQVTIEAQPPKVSEKDVLLLVHNLQNLGTGYIWKQGM RDLYHYITSYVVDGEII IYGPAYSGRETAYSNASLLIQNVTRDAGS YTLHIIKGGDGTGRVGTGRFTFTLHLETPKPSISSNLNPRETMEAVS LTCDPETPDASYLWWMNGQSLPMTSHLSKLNSETNRTLFLGLVTKYTAG PYECEIRNPVSASRSDPVTNLNLLPKLPKYITINNLPNRENKDVLFN TCEPKSENYTYIWWLNGQSLPVS PRVKRPIENRILILPSVTRNETGP YQCEIRDYGGVRS DPVTNLNVLYGPDLPRIYPSFTYYRSGEVLYLSC SADSNPPAQYSWTINEKFQLPGQKLFIRHITTKHSGLYVCSVRNSAT GKESSKSMTEVSEAL
3976	A	1	2247	MAILPKVIYRFNAIPIKLPMTFFTELEERTTLKF IWNQKRACIAKSIL SQKNKAGGITLPDFKLYYKATVTKTAWYQNRDIDQWNRTDPSEIT PHIYNYLIFDKPEKNKQWGDLSLFNKWCWENWLAICRKLKLDPFILTP YTKINSRWIKDLNVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKETTIRVNRQPTKWEKIFTTYSDDKGL ISRIYNELKQIYKKKTNNPIKKLISTEENTQTAETMGLLSAPPCTQR ITWKGLLLTASLLNFWNPPTTAQVTIEAQPTKVSEKDVLLLVHNL QNLGTGYIWKQGI RDLYHYITSYVVDGQII IYGPAYSGRETIYSNAS LLIQNVTDAGSYTLHIIIMGGDENRGVTGHFTFTLYLETPKPSISS SKLNPREAMEAVSLTCDPETPDASYLWWMNGQSLPMSHRLQLSETNR TLFLLGVTKYTAGPYECEIRNPVSASRSDPVTNLNLQHSWLDGKFQ QSAQVFFIPQITKTYRGVYVCFIHNSATAGTNLIIKRIIVPAKLPKP YITINNLPNRENKDVLFNFTCEPKSENYTYIWWLNGQSLPVS PRVKRP IENRILILPSVTRNETGPYQCEIRDQYGGIRSY PVTNLNVLYGPDLP IYPSFTYYRSGEVLYLSCSADSNPPAQYSWTINGKFQLSGQKLFIPQ ITTKHSGLYACSVRNSATGKESSKSMTEVSGGIALADTSFSCS
3977	A	1	1993	MGPLSAPPCTQRI TWKGLLLTALLNFWNLPTTAQVTIEAEPKTVSK GKDVLLLVHNLQNLGAGYIWKQGMKDLYHYITSYVVDGQII IYGPA YSGRETVYSNASLLIQNVTRDAGSYTLHIVKRGDGTGRGETGHFTFT LYLETPKPSISSNLYPREDMEAVSLTCDPETPDASYLWWMNGQSLP MTHSLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPVTNLN LQHSWLDGKFQQAQVFFIPQITKTYRGVYVCFIHNSATAGTNLII KRIIVPDTLRKRGNEKVESDDIENSNOFPFSHPKAFKNIQVQHGQY GIHRKLITKLEKWLDSGLPCVISAETSSPRPGCSVSSGFGHGKSHY YSSLECPWKWLQRNHIYGGKVGWNLEGAHQLHIPAKLPKYITINN LPNRENKDVLAFTCEPKSENYTYIWWLNGQSLPVS PRVKRPIENRIL

				ILPSVTRNETGPYQCEIQDRYGGIRSYPVTLNVLCIFCSSVGQDTS NPNDQGPGLSVLSRKYRHLFWTSEVAMTPCPGKTWVDTALTKNIR RGDALVMGDLGPTACDGPDLPRIFPSVTSYSSGENLDLSCFANSNPP AQYSWTINGKFQLSGQKLFIPQITPKHNGLYACSAARNATGEESSTS LTIRVI
3978	A	1	1006	EENTQAAETMGPLSAPPCTHLITWKGVLLTASLLNFWNPPTTAQVTI EAQPPKVSEKDVLLLVHNLQPONLAGYIWKGMQTYVYHYITSYVVD GQRIIYGPAYSGRERVYSNASLLIQNVTDAGSYTLHIKRRDGTG GVTGHFTFTLHLETPKPSISSNNLNPREAMEAVILTCDPATPAASYQ WWMNGQSLPMTHRLQLSKTNRTLFIFGVTKYIAGPYECEIRNPVSAS RSDPVTNLNLLHGPDLPSIYPSFTYYRSGENLYLSCFAESNPRAQYSW TINGKFQLSGQKLSIPQITTKHSGLYACSVRNSATGKESSKSITVKV SDWILP
3979	A	3	1095	AQLTAVLRKFLDPRLISTEENTQAAETMGPLSAPPCTEHIKWKGLLV TASLLNFWNLPTTAQVTIEAQPPKVSEKDVLLLVHNLQPONLTGYIW YKQIRDLHYHYITSYVVDGQII IYGPAYSGRETAYSNASLLIQNVTR EDAGSYTLHIKRGDGTGRVGTGYFTFTLYLETPKPSISSNNLNPREA METVILTCDPETPDTSYQWWMNGQSLPMTHRFQLSETNRTLFLFGVT KYTAGPYECEIWE\SGSASRSDPVTLESP/RMGPDLPRIFFPSSPLN YFRERNLGFVPGLGDF*TPP\AQYSWTINGKFQLSGQKLFIPQITPK HNGLYACSAARNATGEESSTSLTIRVIAPPGLGTFCFQ
3980	A	3	1442	IRADPAHELENCSCPGKRLSTERGRTAQLTAVLREFLDPRLISTEEN TQAAETMGTLSPAPPCTQRIKWKGLLLTASLLNFWNLPTTAQVTIEAQ PPKVSEKDVLLLVHNLQPONLTGYIWKGMQMDLYHYITSYVVDGEI I IYGPAYSGRETAYSNASLLIQNVTRDAGSYTLHIKIGDDGTGRVT GRFTFTLHLETPKPSISSNNLNPRETMEAVSLTCDPETPDASYLWWM NGQSLPMTHSLKLSETNRTLFLFGVTKYQLDPIECEIRNPVSASRS DPVHPGISCPK\LPKPYITINNLPRENKDVNLFTCEPKSENYTYIW WLNQSLPVS PRVKRPIENRILILPSVTRNETGPYQCEIRDRYGGVR SDPVTNLNVLYGPDLPRIYPSFTYYRSGEVLYLSCSADSNPPAQYSW INEKFQLPGQKLFIRHITTKHSGLYVCSVRNSATGKESSKSMT\VEV SGKVDPKHRWQ
3981	A	79	1565	EASLLEDDDGMYLRPLTSHQYRTAQLRAMLRKFLDPRLSSTEENTQ AAETMGPLSAPPCTQRIWKGLLLTASLLNFWNPPTTAQVTIEAEP KVSQKGDVLLLVHNLQPONLAGYIWKGMQMDLYHYITSYVVDGQIII YGPAYSGRETVYSNASLLIQNVTRDAGSYTLHIKRGDGTGRGETGH FTFTLYLETPKPSISSNNLYPREDMEAVSLTCDPETPDASYLWWMNG QSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPV TLNLLPKLPKPYITINNLPRENKDVLAFTCEPKSEN\YTYIWW\LN GQSLPGSVPRVKRPI\ENRVLI FTPCSRGIETG\PY\QCEI\RDRLW VGLRSLPSSPNVPLMGPDLPRI\YP\YFTYLPFQGGKPSDLSWLSR ES*PHRAGVFFWGQFNGGSFSGIQGQKLFIPQITTKHSGLYACSVRN SATGMESSEKSMITVKVSAPSGTGHLPLNPL
3982	A	1	2045	MLEAAVHAPGNSDVTRTRCATQVLKPLVSYGQAEFGFSVPQLKYPPW DGLLHRDIPPGTLPVEHSPCSLALQFLNATSTHGECSAFARRKLES SFSQHSLOEGHRHGSRLSPSGAPVKDSGSRTPAGSRGGQHQHPSQLLL CGRDDLQFQASSGHGPFLLLPPELPSPRDALQLLREASKFPTDKRQGR SWSVAITNTAATSLEWVPFHAFAPRSTLVSQQLSTERGRTAQLTA VLREFLDPRLISTEENTQAAETMGTLSPAPPCTQRIKWKGLLLTASLL NFWNLPTTAQVTIEAEPKVSEKDVLLLVHNLQPONLTGYIWKGMQ RDLYHYITSYVVDGEI IYGPAYSGRETAYSNASLLIQNVTDAG \SYTL\HIKRRDGTGGVTGHFTFTLHLETPKPSISSNNLNPREAME AVILTCDPATPAAGY\QWWMNGQR/LSPMTHRLQLSKTNRTLFIFGV TKYIAGPYECEIRNP\VSA\SRSDPVTNLNLLPKLPKPYITINNLP ENKDVNLFTCEPKSENYTYIWWLNQSLPVS PRVKRPIENRILILP SVTRNETGPYQCEIRDRYGGIRSDPVTNLNVLYGPDLPRIYPSFTYYR

				SGEVLYLSCF\ADSNPPAQS\W\TINGKVFSL\QGQKLSIPQITTKH SGLYACSVRNSATGKSSKSIITVKVSDWILP
3983	C	302	403	MGSMVVGWVVSFAFLTPFFVFTGCGVAAMMGXVA
3984	A	2	2728	VPGECDGITSMASGPGTRLRNLPMVGDLGLETSMSTTQAQAQPPQ PANAASNTNPPPPETSNPNKPKRQTNQLQYLLRVVLKTLWKHQFAWPF QQPVDVAVKLNLPSPGPFHELQCNLTYHLLMPVGAVAPVDLPVEQP GDYYKIIKTPMDMGTIKKRLNNYYWNAQECIQDFNTMFTNICYIYNK PGDDIVLMAEALEKLFLOKINELPTEETEIMIVQAKGRGRGRKETGT AKPG\VSTVPNTTQASTPPQTQTPQPNPPPVQATPHFPF\AVHPGFL FVQTPVH*QWVPPQPLQTPPPV\PPQPQPPPVSGS*PVQSHPIIAA TPQPVKTKKGVKRKADTTTPTTIDPIHEPPSLPPEPKTKLQQRRES SRPVKPPKDVDPDSQQHPAPEKSSKVSEQLKCCSGILKEMFAKKHAA YAWPFYKPVVDVEALGLHDYCDIIKHPMDMSTIKVSGMCLREGTSLRK SKTSPLALGAQCPRYLAHTVDAPWELGLGLASLFFVEKALLSPLCW RHASKLEAREYRDAQEFGADVRLMFSNCKYNPPDHEVVAMARKLQD VFEMRFAKMPDEPEEPVAVSSPAVPPPTKVAPPSSSDSSSDSSSD SDSSTDDSEEERAQRLAELQEQLKAVHEQLAALSQPQKNPKKKEKD KKEKKKEKHKRKEEVEENKSKAKEPPPKTKKNNSSNSNVSKKEPA PMKSKPPPTYESEEDKCKPMSYEEKRQLSLDINKLP\GEKLRGVVH IIQSREPSLKNSNPDEIEIDFETLKPSTLRELERVYVTSCLRKKRKPKQ AEKVDVIAGSSKMGFSSSESESSSSSSSDSEDSETAFCTSGDFVS PGPSPYHSHVQCGRFRELRLWFLVDVEQTAAGQPHRQSAAGPAITWA PAIAYPSPECARCCVGC
3985	A	190	2406	VPGECDGITSMASGPGTRLRNLPMVGDLGLETSMSTTQA\QAQP QPANAASNTNPPPPETSNPNKPKRQTNQLQYLLRVVLKTLWKHQFAWP FQQPVDVAVKLNLPDYKIIKTPMDMGTIKKRLNNYYWNAQE\CIQ\ DFNT\MFTNICYIYNKPGDDIVL\MAEALEKLFLOKINELPTEET\EI MIVQAK\GRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPP VQATPHFPFAVTPDLIVQTPVMTVVPQPLQTPPPVPPQPPPPAPA PQPVQSHPIIAATPQPVKTKKGVKRKADTTTPTTIDPIHEPPSLPP EPKTKLGQRRESSRPVKPPKDVDPDSQQHPAPEKSSKVSEQLKCCS GILKEMFAKKHAAAY\PFYKPVVDVRPLGLHDYCDIIKHPMDMSTIK SK\LEAREY\RDAQ\EFGADVRLMFSNCKYNPPDHEVVAMARKLQD VFEMRFAK\MPDEPEEPVAVSSPAVPPPTKVAPPSSSDSSSDSSSD SDSSTDDSEEERAQRLAELQEQLKAVHEQLAALSQPQKNPKKKEKD DKKEKKKEKHKRKEEVEENKSKAKEPPPKTKKNNSSNSNVSKKEP APMKSKPPPTYESEEDKCKPMSYEEKRQLSLDINKLPGEKLRGVVH IIQSREPSLKNSNPDEIEIDFETLKPSTLRELERVYVTSCLRKKRKPKQ /ASEKVDVIAGSSKMGFSSSESESSSSSSSDSEDSETGPA
3986	A	212	461	TEEHLYSPHWKGCGRKVKRLFQVRRGRGWIQTRQPGSMVKEPPLSEA GAESHVSC/RQGDCSRPPSFPLSPERVTPWLPDSHTW
3987	A	1	2353	MRPPRAPVVPDGLGGPRLCPVPAAGGARSPSSPYSVETPYGFHLDLD FLKYIEELERGPAARRAPGPPTSRRPRAPRPLAGARSPGAWTSSES LASDDGGAPGILSQGAPSGLLMQPLSPRAPVRNPRVEHTLRETSRRL ELAQThERAPSPGRGLVREQMAAALRRLRELEDQARTLPELQEQVRA LRAEKARLLAGRAQPEPDGEAETRPDKLAQLRRLTERLATSERGGRA RASPRADSPDGLAAGRSEGALQVLDGEVGSLDGTPTQREVAEAVPE TREAGAQAVPETREAGVEAAPETVEADAWTEALLGLPAAARELEL LRASLEHQRGVSELLRGRLRELEEAREAAEEAAAAGARAQLREATTQT PWSCAEKAAQTESPAEAPSLTQESSPGSMDGDRAVAPAGILKSIMKK RDGTPGAQPSSGPKSLQFVGVLNGEYESSSSSEDT\NDSGDSENGGA EPPGSSSGSGDDSGGSDSGTPGPPSGGDIRDPEPEAAEPQQAQVQ RCELSPLRLREACVALQRQLSRPRGVASDGGAVRLVAQEWFRVSSQRR SQAEPVARMLEGVRRLGPELLAHVNVNADGNNTALHYSVSHGNLAI ASLLLDTGACEVNRQNRAGYSALMLAALTSVRQEEEDMAVVQRLFCM GDVNAKASQTGTALMLAISHRQDMV\ATLLACGADVNAQDADGAT

				ALMCASEYGRDVT\VRLLLTQPG\CDP\SILDNEGPSALA\IALE\A ETGMKVAALL\HAHLSSGHPDTQSGVTPLAPQTANTW
3988	A	71	401	RRCKVRPSARGVLRVAVCVVCVCVPCVHVCTCVRMCLCVCVCVCE AQWRFVTGVRDVHAAFASSPKKGGALSRLWLCTVPPSSGGTGLS**S SLWPGSDGISATTPCC
3989	A	205	2190	QIQVSHITETPLPEEAEDELGEIDLRSCDTVTEYAVQRNYGFQIHTK DAVYTLSAMTSGIRRNWIEALRKTVRPTSAPDVTKLSDSNKENALHS YSTQKGPLKAGEQRAGSEVISRGGPRKADGQRQALDYVELSPLTQAS PQRARTPARTPDRDLAKHEELERDLAQRSEERRKWFEATDSRTPEVPA GEGPRRGLGAPLTEDQHNRLSEEIEKKWQELEKPLRENKRVPALTAL LNQSRGERRGPPSDGHEALEKEVQALRAQLEAWRLQGEAPQSALRSQ EDGHIIPPGYISQETCERSLAEMESSHQQVMEELQRHHERELQRLQQE KEWLLAEETAATASAIEMKKAYQEELSRELSKTRSLQQGPDGLRKQ HQSDVEALKRELQVLSEQYSQKCLEIGALMRQAEEREHTLRRCQQEG QELLRHNLQELHGPVVRGDRPAARLHCLAGHGQWLRAQQRAEFLRARG AASRKRKRPVPKEGGAVPPGRAPDDAEGQALHLGKVPGR\LCGAEP \HQDHGSEIREIRAAEGAPASCHGRPSRRRSRCANSLAEVEVPPSCR SKAGGPAALLPSLDGSKKPSFLPTLCWATRALAPTHTHTHTHTHTD TQTHTHTRAHMYTRIHTHTHTHTHCISDARPSHWGLTLHLQLQDFICE EIFI
3990	A	53	364	RSKVEAGLAPEPGPLGARVGS/PGTRARHGRPG\PA\GASIGPGCGP NEQVDEQAGPAQLQGPQGPAPRAIGFPHRLRGSCIKKGDGPGVRR PGSDRLSSSSPT
3991	C	408	620	MKAWKKIKDHPTTSTLTXSNNRDDVTGGRXDPNHSEXSTTLGLRGLYS XXTHEGKQXLXSDSAXXGPFXXL
3992	C	64	300	MDSSHSTTLXPTANPNTGLVEDLDRGTPLSMTTQQSNSQSFSSTSHG LEEDKDHPTTSTLTSSNRNDGHRWKKRPSF*
3993	A	1	530	DTYCFNASAPPEEDCTSVTGPLSMTTQQSNSQSFSSTSHGLEEDKDH PTTPTLTSSNRNDVTGGRDPNHSEGSTTLLEGYTSHYPHTKESRTF IPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHPSGGSHTTHG SESDGHSQEGGANITSGPIRTPQIPEWLIILA
3994	A	1	436	PFAPDTMDKFWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGR YSISRTEAADLCKAFNSTLPTMAQMEKALSIGFETCSLHCSQQSKKV WAEKASDQQWQWSCGGQKAKWTQRRGQQVSGNGAFGEQGVVRNSRP VYDS
3995	A	3	1009	EKVRPTSEAGSLPSGPQPLSGFGRHSRSLRRPLPRAQSSSFFRPR TPFAPDTMDKIWWYAAWGLCLVPLSLAQIGECPPQPGQDGCGLVLSA DPAAAPPAESALGDWSQPQSREKSLDTRATSGTLEGLQYLIQTGSV LCGGYGGEGLRSLVCFYQQHENELMHLVTCQLLDQKGKCAQATFKPA EAVCCLLFYALPPEVESREAVGLVELWSISDCCASSEQGSVGMGLT KPGTGRDLLVCWLGRLGKAQYLGESVPLLQIHLTLGNWAEKCLLTDL ENFNASKAGEHKTMLLFYFSPHGRKIKGNCFESNNSKRSNISGK QANLKE
3996	A	1	2226	MDKFWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRT EAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFIEGHVVIPIHPN SICAANNTGVYILTYNTSQYDTYCFNASAPPEEDCTSVTDLPNAFDG PITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDDVS SSSSERSS TSGGYIFYTFSTVHPIDEDSPWITDSTDRIPATTLMTSATATETA TKRQEAWDWFSWFLPSESKNHLHTTTQAGTSSNTISAGWEPNEEN EDERDRHLSFSGSGIDDED FISSTISTTPRAFDHTKQNDWTQWNP SHSNPEVLLQTTTRMTDVRNGTTAYEGNWNPEAHPLIHHEHHEE ETPHSTSTIQATPSSSTEETATQKEQWFGNRWHEGYROT PREDSHST TGTAASAHTSHPMQGRTPSPEDSSWTDFFNPISHPMGRGHQAGRR MDMDSSHSTTLQPTANPNTGLVENLDRGTPLSMTTQQSNSQSFSSTSH EGLEEDKDHPTTSTLTSSNRNDVTGGRDPNHSEGSTTLLEGYTSHY PHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHP

				SGGSHTTHGSESDGSHSGSQEGGANTTSGPIRTPQIPEWLIILASLL ALALILAVCIAVNSRRRCGQKKLVINSNGGAVEDRKPSGLNGEASK SQEMVHLVNKESSETPDQFMTADETRNLQNVDKIGV
3997	A	2	1599	QPLPGSVRHRPVLRRPLPRAQSSSSFRPRPPFAPDTMDKFWWHAA WGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAF NSTLPTMAQMEKALSIGFETCRYGFIEGHVVIPIRHPNSICAANNNG VYILTSNTSQYDTCFNASAPPEEDCTSVTDLPNAFDGPITITIVNR DGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSER\SSTSGGYIFY TFSTVHPIPEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLV EDLDRTGPLSMTTQQSNSQSFSSTSHGLEEDKDHPPTSTLTSSNRND VTGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGV TAVTVGDSNSNVNRSLSGDQDTFHPSSGSHHTHGSSESDGSHSGSQE GANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKK KLVINSNGGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTA DETRNLQNVDKIGV
3998	A	245	1148	FPGSTPTFPAPDTMDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVF HVEKNGRYSISRTEAADLCKAFNSTLPTMA\QMEKALSIGFETCRYG FIEGHVVIPIRHPNSICAANNNGVYILTYNTSQYDTCFNASAPPEE DCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPS\NP T\DDDVSSGSSSE\REST\SGGYIFYTFST\VHPIPEDSPWITDST DRIPATRDQDTFPPQWGFPLPLHGSEFRWDTHMGSQGRWEQTQPLGP IRDTPNSQLIHLGHPLALGL
3999	A	3	327	AGPGEVAGDGRDGGPAGGRRCLWNWSGSGKSLRKGNPSVSIYCFCL PNHYLFDRN/SCLRSSAGTKSGSYPPQISSMLILVPPCVPQQTHPG LDLKTQKLSLLSALI
4000	A	8	280	SAQMAVTADPRVRPRVRTTVFTSIAHTDTMVHLTPVE\KSAVTALW AK\VNVEVGGEAPGQGCWVVLPLGPPKGPLKPFGGICPNLSNAG
4001	A	405	647	RHVLFLKNGANDVKHHRWFRSVDWKAVPQRKLSRPEAKCLLHGLRT FPVFSVPQIWHCSNLLCMRSQGPVAVAGVSALKK
4002	A	405	608	RHVLFLKNGANDVKHHRWFRSVDWKAVPQRKLPPIVPKIAGDGD TNFETYPENDWDTAAPVPQK
4003	A	1	849	MAEGTGTFRVHLVKEKTAKHFFALKVMSIPDVIRLKQEQHVHNEKS VLKEVSHPFILIRLFWTWDERFLYMLMEYVPGGELFSYLRNRGRFSS TTGLFYSAEIIICAIEYLHSKEIVYRDLKPENILLDRDGHIKLTDGFG AKKLVDRTWTLCGTPEYLAPEVIQSKGHGRAVDWWALGILIFEMLSG LNQSIDCDLCQPIRIQASTSQNSVSVNQLEPNKCQTVRAHRGSGTHQ NSTSVDSSEPKCQTHQNSTSAHQSEPNKCQPIRTQQVSAYQNSMSIS P
4004	A	2	1173	PQOSPECVPLPVSVCSHWSIPTSHRLLRVLVTVECELYVRWPRCNA DLTCTKAVQNGWDLKVPCTCLHLLAVPGVGLFIDEGVKQGFVSVEF RDTRGVLVHGCIMSCLCNNRVRPYLGKKQKSKTTDVGVEVEESGRG CAAGAEVVFQCMQGGSHSAAEGQESSKVESGRHSYNLYLWVISPR PASLQNLQILKCIWFWTWHEERFLYMLMEYVPGGELFSYLRNRGHFS STTGLFYSAEIIICAIEYLHSKEIVYRDLKPENILLDRDGHIKLTDG FAKKL\AYRLMWKSLLEKRWVWRCGGEAKER*Q*QFGWVPASRKV RS*SQDTCPHHRKQGRRLRTWTLCGTPEYLAPEVIQSKGHGRAVDWWA LGILIFEMLSGWVL
4005	A	149	1358	APPSHCLCVSVSRAEPRTRQRRGAWGASVDAAAAAPPSEAAARGVR LPERSGLARRPGPECLPMEAPGPAQAAAAESNSREVTEDAADWAPAL CPSPEARSPEAPAYRLQDCDALVTMGTTGTFGRVHLVKEKTAKHFFAL KVM SIPDVIRRKQEQHVHNEKSVLKEVSHPFILIRLFWTWHEERFLY LMEYVPGGELFSYLRNRGHFSSTTGLFYSAEIIICAIEYLHSKEIVYR DLKPENILLDRDGHIKLTDGFAKKLVDRTWTLCGTPEYLAPEVIQ SKGHGRAVDWWALGILIFEMLSGFPFFDDNPFGIYQKILAGKLYFPR HLDFHVK/DGANDVNHRWFRSVDWKAVPQRKLPPIVPTIAGNGDT SNFETYPEHDWDTAAPVPQKDLIFKNF

4006	A	1	683	MAAEVLTVMAEGTGTFRVHLVKEKTAKHFFALKVMSIPDVIRRQOE QHVHNEKSVLKEVSHPFILRLWPRCNADLTCTKAVQNGWDLKVPCTC LHLLAVPGVGLFIDEGVKQGSVELTAYPLPCPGGALSVCCPCRFW TWHEERFLYMLMEYVPGGELFSYLRNRGHFSSTTGLFYSAEIIICAIE YLHSKEIVYRDLKPENILLDRDGHILKLTDFGFAKKLVDR
4007	A	521	1163	SQDTCPHHRKQGRRLRTWTLCGTPEYLAPEVIQSKGHGRAVDWWALGI LIFEML/SGAFPKHVSSNASPGLQNWGRFPFFDDNPFGIYQKILAG KLYFPRHLDFHVKQCQTPKEKQKTKNKVIIFLHARHQKQKNTNNNNNSN NKMKFIKNGANDVKHHRWFRSVDWKAVPQRKLKPPIVPTIAGNGDTS NFETYPEHDWDTAAPVPQKDLEIFKNF
4008	A	181	1448	APPSHCPRRSVSRAGPRTRRRERAWGASVDAAPSEASREARLP ERSGLARCPGPECVPMAPGLAQAAAESDSRKVAEETPDGAPALCP SPEALSPEPPVYSLQDFDTLATVGTGTFRVHLVKEKTAKHFFALKV MSIPDVIRLQEQHVHNEKSVLKEVSHPFILRLFWTWHDERFLYMLM EYVPGGELFSYLRNRGRFSSTTGLFYSAEIIICAIEYLHSKEIVYRDL KPENILLDRDGHILKLTDFGFAKKLVDRWTWTLCGTPEYLAPEVIQSKG HGRAVDWWALG\ILIFEMLSGFPP\FDDNP\FGIYQKILAG\IDF PRHLDF\HVKD\LIKLLVDRTRRLGNMKNANDVKHHRWFRSVDW EAVPQRKLKPPIVPKIAGDGDTSNFETY\PENDWDTAAPVPQKDLKI FKNF
4009	C	3	167	MPMXAQIEEPQPIQVKTRTNLRLTQLREQDQTQKCLCLYNQQA KFLLLWA*
4010	A	1	2195	MDPGTLQSASQGPTAINPCDYVLKRRNIQTSWQRLTPIIKWHVYILM IGPGEKEAGRNLIIFGKWTPFPKIPAKRLRESNCPVDAQEIVLWPOAF REYLGRRGNFPGRRTCEPWEVESICSVESWELWLRQADSGDSGKCS PDACGIIDTSGLRAGHCYLTRLWHVSGRIPPSFKLHHPGVCKFPKVG GKMTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNLL SVGHQPFHQDTCHFLREEKFWMGTATQREGNSGGKIQTELESVPEA GAHEEWSCQIWEQIAKDLTRSQDSIINNSQFFENGVDVPSQVEAGLP TIHTGQKPSQGGKCKQSFSQSDVPIFDLPQQLYSEEKSYTCDECGKSIC YISALHI\HQRVHMGEKCYKCDVCGKEFSQSSHLQTHQRVHTG\EK FKCG\Q\CGKGSRRSALNVHKLHTGEKPYICEACGKAFIHDSQLK EHKRIHTGEKPFKCDICGKTFYFRSRLKSHSMVHTGEKPFRCDTCDK SFHQRSALNRHCMVHTGEKPYR\CEQCGKGFIRKLYKHQVHTGE KPYNCKEKGKSFWRSSCLLNHQRVHSGEKSFKCEECGKGFYTNSQLS SHQRSHSGEKPYKCEECGKGYVTKFNL\DLHQRVHTGERPYNCKEKG \KNFSRAS\SILNHKRLH/SPEKNPFKCEDCGKRLVHRTYRKDQPRD YSGENPSKCEDCGRRYKRRNLNDILLSLFLNDT
4011	A	1	4559	MDGAKAFFSAVAAGFVILTCQLQWQWQHGGVHAHQLWQLASGYRDA CFCVSTYSSGSPSEFPGLTGLNELAIDLEERKHRRKAKVWKGE LRSPRQSLLAFRAVLASRGTRSCHVSPYLGVSALSSPNPHSTTGA GPIPPVQRWGLPQINQKNREIAIPLTLGMSTHLRRGCKNMSRFS HCCCTPISTNFTDPGSHCKGAHGDICLLIQNLKALPMSINRSYFNA HPLLQISEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNLL SVGNQPIPTQDTF\HFLGKEKFWKMTTS\QREGNSGGKIQIEMETV PEAGPHEEWSCQIWEQIASDLTRSQNSIRNSSQFFKEGDPVPCQIEA RLSISHVQKPYRCNECKQSFSQSDVSVFDLHQQSHSGEKSHTCGECGK SFCYSPALHIHQRVHMGEKCYKCDVCGKEFNQSSHLQTHQRVHTGEK PFKCGQCGKGFHSRSALNVHCKLHTGEKPYNCEECGKAFIHDSQLQE HQRIHTGEKPFKCDICGKSFRVRSRLNRHSMVHTGEKAFRCDTGCKN FRQRSALNSHSMVHIEEKPYKCEQCGKGFICRRDFCKHQMVTGEK YNCKEKGKTFWRSSCLLNHQVHSGQKSFKEECGKGFYTNSRRSSH QRSHNGEKPYNCEECGKDYKRRLDLEFHQRVHTGERPYNCKEKGKSF GWASCLLKHQRLHSGEKPFKEECGKRFTQSSQLHSHQTCHTGEKLY KCEQCEKGYNSKFNLDMHQRVHGGEPYNCKEKGKSGFWASCLLKHQ RLHSGEKPLKSGVWEEIYSEFTASFTSESSGQKLVSIPLGQSFQKKE

				KAAIFAVLQLSLVTTPPGTGKTEATRVSSRPQQTVAALQLLTVSGLTV KNRQKTTRTSTKRPKHNPIQGSATSRLKSKWTPFPKIPAKRLRESNC PVDQEIWLPQAFRELWHVSGRIPPSFKLHHPGVCKFPKVGKMTTF KEAVTFKDVAUVFTEELGLLDPQQRKLYRDVMLENFRNLLSVGHQP FHQDTCHFLREEKFWMGTATQREGNSGGKIQTELESVPEAGAHEEW SCQQIWEQIAKDLTRSQDSIINNSQFFENGDVPSQVEAGLPTIHTGQ KPSQGGKCKQSISDVPIFDLPQQLYSEEKSYTCDECGKSICYISALH VHQRVHVGEKLFMCDVCGKEFSQSSHLQTHQRVHTGEKPFKCEQCGK GFSRRSALNVHRKLHTGEKPYICEACGKAFIHDSQLKEHKRIHTGEK PFKCDICGKTFYFRSRLKSHSMVHTGEKPFRCDCDKSFHQRSALNR HCMVHTGEKPYRCEQCGKGFGRDLDFYKHQVVHTGEKPYNCKEKGKS FRWSSCLLNHQRVHSGEKSFKCECGKGFYTNSQLSSHQRSHSGEKP YKCEECGKGYVTKFNLDLHQRVHTGERPYNCKEKGKNSFRASSILNH KRLHCQKKPFKCEDCGKRLVHRTYRKDQPRDYSGENPSKCEDCGRRY KRRLNLDILLSLFLND
4012	A	125	226	INPSTSHLPHSGAPEPWTMIHPFELFLVLKCVV
4013	A	1546	2204	RICVNILYRALYQINSHMWLLITSSVIPSLATAQWEWSLIWMLPPSM FRPRTVAMVCGLLVSLDWLGLGQYLQSCCFICKNYDPHTPAAAQ GTVIFYTCVDVVFHSSWFITPITLCYNVGTLOASENGISVCDLLLPH FTCSTPDFNLTVAHKTILPERLL\PHTRK\EERCNREAQEAFTWD\R PCLGLNPNFLSQFHLNTAAMLQPMYPIDGLP
4014	A	1	1387	FRAASGRETRAALGASQCLTPHPLPRVGGGGASGGGLRGAGQAWSAM SSPDAGYASDDQSQTQSALPAVMAGLGPCPWAESLSPIGDMKVKGEA PANSAGAPAGAAGRAKGESRIRRPMAFMVWAKDERKRLAQNPDLHN AELSKMLGKSWNA\LTLAEKRPLVEEAERLRVQHMQDHPNYKYRPRR RKQVKRLKRVEGGFMHGMDEPQAAAMGPEGGRVAMDGLGLQFPEQGF PAGPPLLPHPMGHGYRDCQSLGAPPLDGYPLTPDTPSLDGVDPDPA FFAAPMPGDCPAAGTYSYAQVSDYAGPPEPPAGPMHPRLGPEPAGPS IPGLLAPPSALHVYYGAMGSPGAGGGRGFQMOPQHQQHQQHPPG PGQSPPPPEALPCRDTGTPS\QPAELLGEVDRTEF\EQYLHFACKPE MG\LPYQGHDSGVNLPDISHGAISSEVSASSAVYYCNYPDV
4015	A	277	459	DADSMCELPSDLQSCQHAVSDSDTQAWCPRRPGSLCGTGRRAPGS* GGSRVIDRGRPLAI
4016	A	175	370	YYIVCKTFLKYVLLIASFLGRSSVDLEESSTKSLEPKAARIKEVLKE RKVLEKK*P*AKKKKKVD
4017	A	1	2143	MDGTRDYCVISVVLGDNDAPPGTSASQEGDGSVNDGTEGESAVTSTG ITEDGEGPASCTGSEDSSEGFASSESEENGESAMDSTVAKEGTNPV LVAAGPCDDEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGHASTCTGL GEESEGVLICESAEGDSQIGTVVEHVEAEAGAAIMNANENNVDMSG TEKGSKDTDICSSAKGIVESSVTSVAVSGKDEASDDQTTPSYRRKFKP MAKKLKALKKKLDEWITRITNAEKSLKDLMLKTKARELRDECRSL SQCDQLEERVSLMEEEMNEMKQEEEFREKRIKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTLENLQDIIQENFPNLARQANIQIQEIQT MPQRHSSRRATPRHIIVRFTKVEMKEKMLRAAREKGRVTLKGKPIRL TAEGVGDNSIDSWKNAGRVPKDSKDFDANDPILKDQTQEWSSATFT SDGKIRLFYTDYSGKHGKQSLTTAQVNVSKSDDTLKINGVEDHKT FDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQOSAKKRDAELANG ALVLIILLIVTMRRRKKEPLIFDEERDIRENIVRYDDEGGGEEDTEAF HMAALRLNLNVIDRTKTRRDVTPEIQFLSRPAFKSIPDNVIFREFICF RLKAAAVDP
4018	A	4423	9194	SCLEVLTLTDVIVENENITNEGGLVDMAKKENDLNAEPNLKQTIKAT VENGMKDGIAVDHVCLNTEKYAETVKLKHKRSPPGKVKDISIDVERR NENSEVDTSSAGSGSAPSVLHQNRNGQTEDVATGPRRAEKTSVATSTEG KDKDVTLSVPKAGPATTTSSETRQSEVALPCTSI EADEGLIIGTHSR NNPLHVGAEESECTVFAAAEEGGAUVTEGFAESETFLTSTKEGESGE

10289

				CAVAESEDRAADLLAVHAVKIEANVNSVVTTEEKDDAVTSAGSEEKCD GSLSRDSEIVEGTITFISEVESDGAVTSAITEIRAGSISSEVDGSQ GNMMRMGPKKETEGTVTCTGAEGRSDNFVICSVTGAGPREERMVGA GVVLGDNDAPPGTSASQEGDGSVNDGTEGESAVTSTGITEDGEGPAS CTGSEDSSEGFASISESEENGESAMDSTVAKEGTNVPLVAAGPCDDE GIVTSTGAKEEDEEGEDVVTSTGRGNEIGHASTCTGLGEESEGLIC ESAEGDSQIGTVVEHVEAEAGAAIMNANENNVDMSGTEKGSKDTDI CSSAKGIVESSVTSASVSGKDEVTPVPGGCEGPMTSAASDQSDSLEK VEDTTISTGLVGGSYDVLVSGEVPECEVAHTSPSEKEDEDIITSVEN EECDGLMATTASGDI TNQNSLAGGKNQGVLIISTSTTNDYTPQVSA ITDVEGLSDALRTEENMEGTRVTTEEFAPMPASVSGDDSQLTASR SEEKDECAMISTSIGEEFELPISSATTIKCAESLQPVAAAVEERATG PVLISTADFEPMPSAPPEAESPLASTSKEEKDECALISTSIAEECE ASVSGVVVESENERAGTMEEKDGGIIISTSSVEDCEGPVSSAVPQE EGDPSVTPAEEMGDTAMISTSTSEGCEAVMIGAVLQDEDRLTITRVE DLSDAAIISTSTAECMPISASIDRHEENQLTADNPEGNGDLSATEVS KHKVPMPSLIAENNCRCPGPVRGGKEPGPVLA VSTEEGHNGPSVHKP SAGQGHPSAVCAEKEEKHGKECPEIGPFAGRGQKESTLHLINAEKN VLLNSLQKEDKSPETGTAGGSSTASYSAGRGLEGNANS\LAHLRGPE QTSGQTAKDSSVSSIRYLA AVNTGAIKADDMPVQGTVAEHSFLPAE QQGSEDNLKTSTTKCITGQESKIAPSHTMIPPATYSVALLAPKCEQD LTIKNDYSGKWTDAQSAEKTGDDNSTRKSFPEEGDMVTVSSEENAY VPSEEEKNGEILAPPESLGGKPSGIEISSGRKDNAAEISGHSVEAD PKEEENSRLDEELPKTSSETNSTTSRVMEEKDEYSSSETTGKPEQN DDDTIKSQEDDGEEKIVTSVRRRGRKPKRSLTVSDDAESSEPERKQ KSVSDPVEDKKEQESDEEEEEEEDEPSGATTRSTTR\SEAQRQH\ SKPFAR\ATSKLGSPTVSPRNRQKLAKELPTSEKVSNSPPLGRSK TQLSPSIRKREVSPPGA\RTRGQQRVEEAPGARDKRPGEGGGSPCE KSEAIILTTAALGLWRNTVERKETCLGGHRLLFNQEKDMHVL
4019	A	77	407	ESDGGKRKKSRGDPSQLEEKISKGCPQRRKKPRLYRPSNYNRAFRR MRR/ARLPTRTSPETRTPOPH\SPHS\PERTPTPPPGRPPFLGAGQL QRLFMGIPQVGDCPPSS
4020	A	20	464	WWSNLEVTVYAFS IENFKRSKSEVDGLMDLARQKFSRLMEEKEKLQK HGVCIRVLGDLHLPLDLQELIAQAVQATKNYNNDISESLLDKCLYT NRSPHPDILIRTSGEVRLSDFLLWQTSHSCLVFQPVLPWEYTFWNLF EAILQFQ
4021	A	572	1594	SSDWKRTMSWIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYA KKCQVERQEGHFTGFKQ\LAETLRWCLNLGILEVTVYAFS IENFKRS KSEVDGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLPLDLQ LIAQAVQATKNYNKCFNVCFA YTSRHEISNAVREMAWGVEQGLDP SDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSHSCLVF QPVLPWEYTFWNLF EAILQFQMNHSLVQKARDMYAEERKRQQLERDQ ATVTEQLLREGLQASGDAQLRRLRLHKL SARREERVQGF LQALELKR ADWLARLGTASA
4022	A	2	366	EDLLDLDEELRYSLATSRKMGRRQQESAQAENHLNGKNSSLTLTG ETSSAKLPCRQGGWAGDSVKASNGTQTGKQQLDLNACYHKTHRDL GLASLEEADIP IIPDLEEVQEEDFVLQ
4023	A	1	466	RRWRICSTWTRSFATAWLPPAPSANFPRTDRSQGDRGAPAGFALAPI LEFFLWDTSSQKFLQKPHCFMHGRERAKMGRRQQESAQAENHLNGK NSSLTLTGETSSAKLPCR/QGGWAGDSVKASKFRRKASEEIEDFRL RPQSLNGSDYGGDIP
4024	A	254	662	NPQKVENTLSPPASRTVGNFRAFLRFLEPRVTSPEQIDHRRAKMGR RAQQESAQAENHLNGKNSSLTLTGETSSAKLPCRQGGWAGDSVKAS KFRKASEEIEYVSSILIMVSYVDLGQQRLGGHDLHL
4025	A	3	392	MKYSAIQTL DGEIDLKLLTKVLAPEHEVR*VQWWQQFPLSTLAIPI NPAELPGLALCLP*RPWNGREKVS LQLEKALSLSYPAPKPF\EDDV

				GWDWDHLFTEVSSEVLTE\WDPLQTEKEDPAGQARHT
4026	A	63	779	GPIRGPGWPGFGGWWGATPPAPTSLRRLRAAGLAPRRRAKMGRRQQ ESAQAENHLNGKNSLTTLTGETSSAKLPRCROGGWAGDSVKASKFRR KASEEIE\DFR\LRPQSLNGS\DYGGDIPI\IPDLEEVQEEDFVLQV \AAPPSI\QIKRVMTYRDL\DNDLM\KY\SAIQTLGDGED\IDLKLL/ TPKVLAPHEVRERNPSWQDDVGWD\WTHLFTEVSSE/VSFTEWDPL QTEKEDPGGQ\ARHT
4027	A	2	311	AAAKGAAAMSAHLQWVVRNCSSFLIKRKNQTYSTEPNNLKARNFSR YNKNARATLSSIRHMIRKNKYRDLRMAAIRRASAILRSQKPMVKR KRTRPTKSS
4028	A	1	136	VAAAKGAAAMSAHLQWVVRNCSSFLIKRKNQPHQELLSPLPPEQ
4029	A	2	170	HEGQRKPATSYVRTTINKNARATLSSIRHMIRKNKYRDLRMDMLAS TGSGLCSSV
4030	C	64	276	MCKALGTPYSPQQQLGTEASSVHRTCWHLGQGSAAARXXXXXXXXXX XXXXXXXXXXXXXXXXXVSIDPTTQG**
4031	A	3	295	QVAAAKGAAAMSAHLQWVVRNCSSFLIKRKNQTYSTEPNNLKARNFS FRYNGLIHRKTVGVEPAADGKGVVVVIKRRSGEFCLVWARERPLSRV WEL
4032	A	3	279	CTPLTPGRPTRPQVAAAKGAAAMSAHLQWVVRNCSSFLIKRKNQTY STEPNNLKARNFSRYNGLIHRKTVGVEPAADGKGVEVVIKRRSE
4033	A	3	392	RIRHEAAAKGAAAMSAHLQWVVRNCSSFLIKRKNQTYSTEPNNLKA RNSFRYNGLISPARLWGVPEA\ADGKGVV\VVI\KRRSGQR\KPA\T SYLRTTINKNARATLSSIRHMIRK\NKYRDLAHGHAGI
4034	A	2	564	VAAAKGSRQCLRHQW\VVRNCSSFLIKRKNQDPTALSPNNLKA\ RNSFR\YNG\LIHRKDCGTWSRSADGK\GVVV\VIK\RRSG\QRKLA TSYVAGPPSTRNARSHASGRHQ/VHIDPARNKLPPPTCRMGSPFRRA QRPFLAQAGRLVDWLKEGRRDPAPPRSSLKPLGPGQQLKSAGVFSKK KKKSR
4035	A	1	139	DRRAGDPWPRTHEFGSPEASLQASAWRDGKKVSRSELKPLPLRTLS
4036	A	1	299	VGIW*PVTNFGVISGTAKAEMD*G/TPYIHALTNGLLTVEAPHK/ER IALKPGYGKYLINSDELVV/GRSDAIGPREQWEPVFQNDGHPVMRM NSLQLKATI
4037	A	796	911	AMA*YSYVKSSKLVLKGT\SKKKKSTDKKRKREDEETQLD/IVGIW* TVT\NFGEISGT\IAIWNGRKGTYIHALDNGLFTLGAPHK/ERIALK SGYGKYLGINSDGLVGRSDAIGPREQCEPVFQNGKMALLASNSCFI RCNEAGDIEAKSKTAGEEEMIKIRSCAERETKKKDDIPEEDKGNVQ CEINYVKKFQSFQDHKLKISKEDSKILKKARKDGFHETL\LDRRA\ KLEAD\RYCK
4038	A	193	754	EPSRGVWPHEDARINGSKKKKSKKKRKREDEETQFD/IVGIW*TV TNFDEISGTIAIEMDEGTYIHALDNGLFTLGAPHKEG\KMALLASNG CFIRCNEAGDIEAKSKTAGEEEMIKIRSCAERETKKKDDIPEEDIGN VKQCEINYVKKFQSFQEHKLKISKEDSKILKKAQKDGFLHETLLDRG P
4039	A	213	920	YVQSLKQILS/GCI*ESIAIKKKKNKDKKKRKREDEETQLDIVGIW TVTNFGEISGTIAIEMDKGTYIHALDNGLFTLGAPHKEVDEGSPSPE QFTA\VKLSDSRIALKSGYGKYLGINSDGLVGRSDAIGPREQWEPV FK\MGKMALSTSNCFIRI\HEAEDIEAKSKTAGEEEMIQSGP*SSV QPFHLLWTFAFILTQEHRSLLLKIRSCAERETKKKDDIPEEDKGNIK QCEI
4040	A	802	1463	AEATALENPLEESRPHEARINGSKKKKSKDKKKRKREDEETQFD/I VGIWTVINFGGISGTIAIEMDEGTYIHALDNGLFTLGAPHK/ERIA LKPGYGKYLINSDELVV/GRSKAIGPREQWEPVFQNGACAAGFTVI GSEKQSECSLLRESRAKYHGCTHGQISSSLKQHPRWMYSHQEDLKVW SLVEKKVTFEHIYLLKRNNSHHSIAEAMYGRLSNYI
4041	A	879	1051	GGARYHFFFFFFFDGACSVTQAGVQWPILGSLQPPPPRFKQFSCLS LPSSW\DYRRD

4042	A	125	1366	RDSSSSTLSHKSACACGFFPSTHSGTFRFTSVRCLKYKSAKSFLH IGYREAAVWCCQRLVPCTRRTQESSLDFATNLQHSASWRLCRRGASR TSSAARSRSRSPAVEGCNRSFGAPQAPAPRARRRPSRGAPGRAMVKVA \FNSALAQKEAKKDEPKSGEEALIIPDAVAV\DCCKPDDVVPVVGQR RAWCWCMCFGLAF\MLAGVIL\GGAYLYKYFALQPDVDDVYCGIKYIK \DDVILN\ESPSADAPAA\LYQTIEENIKIFEERRSLNFI SVPVPEF \ADSDPAKIVQDFNQETYRPFYDFNL\DKCYVIP\LNTSMCYATPKT LLELLIN\IKAGNLFALSPYLD SMRHMGYLLDRI\ENIDHPGF\FIY RLCHDKETYKL\QRRETIKGIQKREASNCFAIRHF\ENKFAVET\LI CS
4043	A	42	557	QAGKL RPGLDSRSRSSAAGLDRDQGLHRVAF LPKRRTGGTRMDRS ATAATAPPAAPAGEGGPPAPPPNLTSNRRLQQTQAQVDDVVDIMRVN VDKVLERDQKQSELDDRC\ADALQAGASQF\ETSAAKLKRKY\WKN LK\MMIILGVICAILIIIIIVYFQHLNPRGVCPA
4044	A	178	731	SSERCHQQVFIMPALPPGF\SQAGSCVPTGSSSLVL\CLLAASLLLF VPTLALLTGATTWCWLNKRLAV\RRPLAWAGAFGGVSTRLIHGRT \SFYFNSLP\LQTNSSTC\QN\HSWDSGGRGDLWPPLAARRVGLDL CSCQAHTCQQGADWIHALCLMGVTGVPTALPAKHLEQNTSPFVDA E
4045	A	3	155	GAISAH CNLRLPGSSDSPDSASNLIQMSLLRVLLLEMLVTLRTRTKP SEI
4046	A	100	448	WWEVKGMSHGQKNKQEGGAIHFRACVCMESH SVT\RLECSGAISAH CNLRLQSSNSPDSASRVAGTTSTRHEAQLIFVFLAETGFHHVGQAA LELLTSSDPPTSASQSADMLYK
4047	A	151	461	RLTAAATASLCPLRPVTRLPLSRGSKMKEGMSNNSTT\SISKPRKA VEQLKMEACMDRVKVSQAAAD\LLAYCEAHVREDPLIIPVPAENPF REKKFFCTIL
4048	A	1	447	FPVCWNSEAAAAEDPSPDGLRSQNH EPGHQHRS PANRWVGGPCAAS PSSLKEALLVPVLQVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPI QYEFSLTRETKKHVLFGTGVPEHTYRSRTNFTSKYNMKVLYLSAFT SKDEGTYT
4049	A	553	1938	LYQTASCPEYLVLDYENYGRKGSASQVPSQAPPSRVPEIISPTYRPI GRYTLWETGKGQAPGSRSSSPGRDGMQLLACVSLGERSVLPALVS SSEKRAVCSACIAGLGFSTCTLEMITVPVLEDGTWLCAPTALIRQ IHVSVIDDILPRGKVFREDVIIYKAKHRGEVSSPYHYLQLSPIK AASVHSAQNVDVDTLLSELQGTDPRI LPPGSPTGGTYLPLLGGWTSR TGHKHGA AVHKNTLHTKL LLLGDGGMASAIQDCFSYLFSTSFSDMKL NPD PGLRSQNH EPGHQHRS PANSLKEALLVPVLQVSRGQKVTSLTAC LVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTGVPEHTYR SRTNFTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTV LRDKLVKCEGISLLAQNTSWLLLLLLLSLSLLQATDFMSL
4050	A	303	478	DCTSRPSLCPLSARCDVHGLSPGP ELVR*GLIVIEDALPKSHSGGRG EVRQPWDFCGA
4051	A	458	964	DPRTMNLAI SIALLLTVLQVSRGQKVTSLTACLVDQSLRLDCRHENT /SAVSPIQYEFSLTRETKKHVLFGTGVPEHTYRSRTNFTSKYNMKV LYLSAFT\SKDEGTYTCALHSHSGHSPPI\SS\QNVVFRDHGVK\CE GISLLA\QNASWLL\LLLLSLSLLQ\ATDFMSL
4052	A	411	557	YSTDELPNIKISTSGRLQWLMSIIPALWEA/EDQAGRSFEFRNLRLV WTT
4053	A	508	1222	PLPPAATPCPKQLGSQAWACRAARGAEQGVWGRKHPAPSRGRVDK GSTKQKDPSPAHTTSTLNYQMHS CS/HKRRHTHTHTHTHTHTHTH TRQHNIPGGSPDQEEAGQVVEKKAANPSHNPTLQDRRVSSILSCCK RKLEAPSPEQISMVGPRGSNLWFPHWQRRQEPAKCSFGLKEQWGGDF SRMNRMLMGPNPSTSPFWSRKL LHGKDVRCWLHRHAKCLSARCPRI WRVW
4054	A	1609	1808	DRVWLLPRLEYSGMVAHCNTHLLGSSQS\PTSASQAAGTTGAHHYV

				PQLVYIYIYLGLFVETRFR
4055	C	169	297	MILEFHXXXXXXGGGRFKEPLGGPNLPGAGKVLFFSLWGAD*
4056	A	270	614	PFKFILITQVIRDPLFSSEPYLGEKANHPPGFHHVKGQQASHVCKTH PAPSCPP/PDCCLPCPSLGPAPHFRGCCEMEFPGKNFRCLDPFYLDN IFRFFCSLVTPGGKEIARTFF
4057	A	637	890	TKWAGSIVYLSFSFLHMFMSFLLLV/STFLALCMLILVVLFLKLPP KLFSELPLLKLTFLPCELLHLHLFQDLAYFFFNGLRK
4058	A	3	297	ATAARPCPGLGRRAGESRGPBGHIGVRP\GSTLCQIIATCHMSVNDGG C\KYVLCRWEKRLWPAKVLARTATSTKNKRRKEYFLAVQILSLEEK SVVLF
4059	A	2	1942	CPGLGRRAGESRGPBGHIGVRPGSTLCQIIATCHMSVNDGGC\KYVLC RWEKRLWPAKVLARTATSTKNKRRKEYFLAVQILSLEEK\IKVKSTE VEILEKSQIEAIASSLASQNEVPAA/PPEELAYRRSLRVALDVLSE GSIWSQESSAGTGRADRSRGKPMHVSSPCDSNSSLPRGDVLGSS RPHRRRPCVQQSLSSSFTCEKDPECKVDHKKGLRKSENPRGPLVLP GGAQDESGSRIHHKNWTLASKRGRNSAQKASLCNLGSSLSSEDDTER DMGSKGGSWAAPSLPSGVREDDPCANAEGHDPGLPLGSLTAPPAPEP SACSEPGCEPAKKRPRLDGSQRPPAVQLEPMAAGAAPSPGPGPGPRE SVTPRSTARLGPPPSHASADATRCCLPCPDSQKLEKECQSSESMGSN SMRSILEEDEEDEEPRLVLYHEPRSFVGMVLVWHKHKYPFWPAVV RSVRQRDKKASVLYIEGHMNPMMKGFTVSLKSLKHFDCKEKQTLNQG AREDFNQDIGWCVSLITDYRVRLGTWAGGEGWSWAAGVQPLKTPWTG WAGAAWRRGIFPWAWGIPCGWAGVLAWPDYFLNRDAGPAPGTHFLGL LLGLHSALSPPPPAGCGSFAGSFLEYAADISKSTGCI
4060	A	1	2722	MERPLRGSRHPRLPFPVPPGVLGSPQGHIGVRPGSTLCQIIATCHMSV NDGGC\KYVLCRWEKRLWPAKVTAII/RVTSGLRNDFRVTKTSVTGP SILKYLVEFPVTLNQRITFKRQITDDQAAHCSAPIKVKSTEVEILEK SQIEAIASSLASQNEVPAAPEELAYRRSLRVALDVLSEGSISWSQES SAGTGRDN\RSLRGKPMHVSSPCDSNSSLPRGDVLGSSSRPHRRRP CVQQSLSSSFTCEKDPECKVDHKKGLRKSENPRGPLVLPAGGGAQDE SGSRIHHKNWTLASKRGGNSAQKASLCNLGSSLSSEDDTERDMGSKGG SWAAPSLPSGVREDDPCANAEGHDPGLPLGSLTAPPAPEPSACSEPG ECPAKKRPRLDGSQRPPAVQLEPMAAGAAPSPGPGPGPRESVTPRST ARLGPPPSHASADATRCCLPCPDSQKLEKECQSSESMGSNSMRSILE EDEEDEEPRLVLYHEPRSFVGMVLVWHKHKYPFWPAVSWDESTRG WISRLKAARTIALHIPKSNAQNRCHLTSPSLRVPGAHLRSDQPKPS GPRCPPAFRPAQAIGSPVPTCVQISPSHRVPGAHLRSDQPKPSGPRC PPFEQLRAQTCACVSHLPEGPCARRLEPPLSGRNQAREDFNQDIG WCVSLITDYRVRLGCGSFAGSFLEYAADITSRACPGALIPWATSSV SLLWLVAHIRCCEECRPGASFAGYPVRKSIQDVLGTCLPQLSKGS PEEPVVGCPGQRQPCRKMLPDRSRAARDRANQKLVEYIVKAKGAES HLRAILKSRKPSRWLQTLSSSQYVTCVETYLEDEGQLDLVVKYLQ VYQEVGAKVLQRTNGDRIRFILDVLLPEAIICAISAVDEVYKTAEE KYIKGPSLKLPGKRNI
4061	A	57	235	PRVRQKTVGLFILEIPPFVLDCKLSFFLFRPFTTRTENVCSSVTQ KENNFLCIASKR
4062	A	754	1767	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGCLLDRKAVGTPAGGG FPRRHSTLPSKQFHQNLSSSLKGEPAALSSRDRSFRDRSFSEGG ERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYGDQCFAGHI HELRLSTRHPKYKTELCTFHTIGFCPYGPRCHFIIHNAEERRALAGA RDLSDRPRQLHSFSFAGFPSAAATAAATGLLDSPSTITPPILSAD DLLGSPTLPDGTNNPFAFSSQELASLFAPSMGLPGGGSPTTFLFRPM SESPHMFDSPPSPQDSLSQEGYLSSSSSSHSGSDSPTLDNSRRLPI FSRLSISDD
4063	A	568	715	NFISTSPALKISMLGKAKLNILAMVFVTMLVSGMVPCPPPPSPPTPL KI

4064	A	65	347	GLPAPLPPP/PPRSLPFPAPGLRSQRFSTSAAPRHRAPPPVARARAA PPHPQASGRKSQVSAPLVERAPLRAPGLTATAVVTVLGDPAFAFPLE M
4065	A	1648	1974	KVFFCFYRIYVCICVCVCVCVC/TLQTL/CYSIANMLTSSQCLQSCG SQSWCQMHIKSSKAIMTIPCKFISRKPWEGDCSSLEPHGVSAFDIWW PQLCIKKVLNHFSPRKN
4066	A	12	1662	FLRGCCFCYMTQCRPSLRPTALLPERSVPPLPPAAPPRFVRHPPVA APPARRCPAPAPPPPPFPDDWMLDMGDRKEVKMIPKSSFSINSLVP EGLQNDNHHASHGHNSHHPQHSHHHHHHHHHHPPPPAPQPPPPRAAQ QQQPPPPPLAPQAGGAAQSNDEKGPQLLLLPTDHRPPSGAKAGGC CRPGELGPVGPDEKEKGAGAGGEEKKGAGEGGKDGEGGKEGEKKNGK YEKPPPFSYNALIMMAIRQSPEKRLTLNGIYEFIMKNFPYYRENKQG WHNSIRDNLNLNKCFCVKVPRHYDDPGKGNWMLDPSSDDVFIGGTTG KLRRRS\TTSRAKLAFKRGAA\LTSTGLTFMDRAGSLYWPMSPFSL HHPRASSTLSYNGTTSAYPSPHMPYSSVLTQNSLGNHNSFSTANGLE AWDRLV\NGEIP/YTATHLT\AAALAA\SVPCGLSVPCSGTYSLNP CSVNLLAGQTSYFFPHVPHPSMTSQQSSTFMSARAASSTSPQAPSTL PCESLRPSLPSFTTGLSGGLSDYFTHQNGSSSNPLIH
4067	A	3	260	STEQRRSARRAGAHGPPPTASASAGPTPRGRGRPLFPGRLAEVDEF ESCGPLNVAARRAPTYSGPVKVALRLWNFCPALIGE
4068	A	1	1386	MNESKPGDSQNLACVFCRKHDDCPNKYGEKKTKEKWNLTVHYCYLLM SSGIWQRGKEEEGVYGFIEDIRKEVNRASKLVQAINAGVFFRCTI CNNSDIFQKEMLRMGIHIPEKDASWELEENAYQELLQHYERCDVRR RCKEGRDYNAPDSKWEIKRCQCCGSSGTHLACSSLRWEQNWECLEC RGIIYNSALKENLYYEAGKMLAISLVHGGPSPGFFSKTLFNCLVYGP ENTQPILDVSDFDVAQIIIRINTATTVADLKSINECYNYLELIGC LRLITLSDKYMLVKDILGYHVIQRVHTPFESFKQGLKTLGVLEKIQ AYPEAFCSILCHKPESLSAKILSELFTVHTLPDVKALGFWNSYLQAV EDGKSTTTMEDILIFATGCSSIPPAGFKPTPSIECLHVDFPVGNKCN NCLAIPITNTYKEFQENMDFTIRNTLRLEKEESSHYIGH
4069	A	137	611	MKVNLDGDSQNLACVFCRKHDDCPNKYGEKKTKEKWNLTVHYCYLLMS SGIWQRGKEEEGVYGFIEDIRKEVNRASKLCCVCKKNGAFIGCVA PRCKRSY\HFPCGLQRECIPQFTGNFASFCWDHRPVQIITSNNYRES LPWHLLGNLFEPIPSY
4070	A	1	507	MSAYQVFCKEYRVTIVADHPDFGELSKKLAEVWKQLPEKDKLIWKQK AQYLQHKQNKAEATTVKRKASSSEGSMKVKGSDHIPPLLFKACEFC FLAKKLGLKLALEVDLDSQGMVAVSGSLSVLLDSIICALGPLACLT TQLPELNGCPKQVLSNTLDNIAYIMPGL
4071	A	259	1409	FLLWRYFVFGIVTTEEKEKVQPTVYLIQLLDLLKAIT/SPHLEAGSKP SKKT\GEKSSGSSSHSESKKEHHRKKVSGSSGELPLEDGVSHKSKKM KPLYVNT\ETLTLREPDGLKMKLILSPKEKGSSSVDEESFQYP\SQQ ATVKKSSKKSARDEQGALLGHELQSFLKTARKKHKSSSDAHSS\PG PLKGLGLDA\SQFRKSPHSAN\LDLSGLEP\ILVESDSSSGGELEA GELVIDDSS\REIKKKKSKSKKKKKDKEKHKEKRHSKSKSLGLSA VPVGEVTVTSGPPPSIPYAGAAAPPLPLPGLHTDGHSKKKKKEEKD KEREREGKMGPSWKKISSGLPLILHDGPWKNCFPRNRYVPVKRLRT ADLVGLYLGSQKHK
4072	A	436	2063	RRREVEGWYFGGFSHRRTVICIDTPDISSLESSQKKKKKSSPQSTDT AMDLLKAITSPLAAGSKPSKKTG\EKSSGSFKAISGELKREHHRKKV SGSSGELPLEDGGSHKSKMKPLYVNTETLTLREPDGLKMKLILSPK EKGSSSVDEESFQYPSQQATVKKSSKKSARDEQGALLGHELQSFLK TARKKHKSSSDAHSSPGPEGCGSDASQFAESHSANLDLSGLEPILVE SDSSSGGELEAGELVIDDSYREIKKKKSKSKKKKKDKEKHKEKRHS KSKRSLGLSAVPVGEVTVTSGPPPSIPYAGAAAPPLPLPGLHTDGHS EKKKKKEEKDKEREREGKPKKNMSAYQVFCKEYRVTIVADHPGIDF GELSKKLAEVWKQLPEKDKLIWKQAQYLQHKQNKAEATTVKRKASS

10294

				SEGS MKVKASSVGVLS PQKKS PPTM L L P A S P A K A P E T E P I D V A A H L Q L L G E S L S L I G H R L Q E T E G M V A V S G S L S V L L D S I I C A L G P L A C L T T Q L P E L N G C P K Q V L S N T L D N I A Y I M P G L
4073	A	323	539	P F M I C L V H F C A P G N \ P P S A R P R P S P S P R C H P C A P Q E G K M T H P Q F R V M P A P S C Y N W L L E N V P F I I Q N S G V R I S
4074	A	27	425	G G G S G P R A P S A T L L D T G E S V A A V A S G E D K G I A A S A A A A A V F A C S C S P D P Q S S T M N P V Y S P V Q P G A P Y G N P K N M A Y T G Y P T A Y P A A A P A Y N P S L Y P T N S P S Y A P A T L V M \ K Q A W P Q N S S S C G T E G T F H L P V D T G
4075	A	1	434	W T A H E F P G R R F R G G S G P R A P S A T L L D T G E S V A A V A S G E D K G I A A S A A A A A V F A C S C S P D P Q S S T M N P V Y S P V Q P G A P Y G N P K N M A Y T G Y P T A Y P A A A P A Y N P S L Y P T N S P S Y A L F L H G L Q R R G L K T G Q R L H G G G W Q E Q K L Q M K K
4076	C	117	251	M V P G P S L Q N S W Q A S F N I P W P A L P K P D L G P S P S V S P V D I F C G A C C *
4077	A	58	313	S S K Q N K N P K E S K T T K Q N Q I Y T S Y T Q A R P W G F P I F T \ P G L C F E N T Y K F F D Q T T W K T L V K S S S S S S S S S S P I L F L F K M * V P I K F K N
4078	A	1	279	M D A A G G Y P T A Y P A A A P A Y N P S L Y P T N S P S Y A P L G S P Q V A Q Q Q F L K H A G T C L M V Q K S W V G D T H E P S L G Q Q Q R I M A L K G V S Q P N L A A E F Q T N E
4079	A	54	946	G G G S G P R A P S A T L L D T G E S V A A V A S G E D K G I A A S A A A A A V F A C S C S P D P Q S S T M N P V Y S P V Q P G A P Y G N P K N M A Y T G Y P T A Y P A A A P A Y N P S L Y P T N S P S Y A P E F Q F L H S A Y A T L L M K Q A W P Q N S S \ S C G T E G T F H L P V D T G T E N R T Y Q A S S A A F R Y T A G T P Y K V P P T Q S N T A P P P Y S P S P N P Y Q T A M Y P I R S A Y P Q Q N L Y A Q G A Y Y T Q P V Y A A Q P H V I H H T T V V Q P N S I P S A I Y P A P V A A P R T N G V A M G M V A G T T M A M S A G T L L T P Q H T A I G A H P V S M P T Y R A Q G T P A Y S Y V P P H W
4080	A	1	502	R H E G G M W R A G S M A E L G V G C A L R A V N E R V Q Q A \ V A R R P R \ D L P S P S Q P R L V A V \ S A K T K P A D M V I E A Y G H G Q R T F G \ E N Y V Q E L L E K A S N P K I L S L C P E I K W H F I G H L Q K Q N V N K L M G K S E F L I K R E N I M P R T E L N S P F S G V I Y T W E T Y P T S M F I I I W W S F R K I I K N C S P
4081	A	171	1184	I P I L I M K L L C C H K S S G D P P Y L H L F A K S K H S T L P F S L G L G V G P R G M W R A G S M A E L G V G C A L R A V N E R V Q Q A V A R R P \ R G D L P A I Q P R L V \ A V S K T \ K P A D M \ V I E A Y G H G Q R T F G E N Y V Q E L \ L E K A S \ N P K I L S L C P E I K W H F I \ G H L Q K Q N V N K L M A V P N L F M L \ E T V G F C E C L A D K V N S S W \ Q R K \ G S P \ E R L K V M G P G F N T S R E E I Y L F S V S L L E G K H G \ L P P S E T I A I V E H I N A K C \ P N L \ E F V G L \ M T L G \ S F G H D L S Q G P N P D F Q L L L S L P E E \ I C G K K L N I P A E Q V E L I M G M S A D F Q H A V E V G S T N V R I G S T I F G E R D Y \ S K K P T P D K C A A D V K A P L E V A Q E H
4082	A	1	418	Y A T L G T R Q Q I E V A R Q L I D E K V G G T N L G A P G A F G Q S P F S Q P P A P P H Q N T F P P R S S G C F P N M A A K V N G N P H S T P V S G P P A F L T Q G W G S T Y Q A W Q Q P T Q Q V P S H A A S A A P Q A S S P P D Y T M A W A E Y Y R Q Q V A F Y G Q T L G Q A Q A
4083	A	2	2447	K F F M V A L P F V S V A F L A E T E I S E D H R P F D I L Y Q T T Q W T R T H G G A Y V R V P H D Y S C C G A V L N N A S K E G K S S H L F L K E K E G S L S I F T L S L D P E Q E G V G N Q L G A L V H Q R Q A K R L L G Q I V D R C R N G P G F H N D I D S N S T I Q E I L I P A S K V G L V I G R G G E T I K Q L Q E R T G V K M V M I Q D G P L P T G A D K P L R I T G D A F K V Q Q A R E M V L E I I R E K D Q A D F R G V R G D F N S R M G G S I E V S V P R F A V G I V I G R N G E M I K K I Q N D A G V R I Q F K P D D G I S P E R A A Q V M G P P D R C Q H A A H I I S E L I L T A Q E R D G F G G L A A A R G R G R G R G D W S V G A P G G V Q E I T Y T V P A D K C G L V I G K D T V G L C S C K M Q E T V L S F R L N H S E L V W V R V H L P A G V R A G G E N I K S I N Q Q S G A H V E L Q R N P P P N S D P N L R R F T I R G V P Q Q I E V A R Q L I D E K V G \ T F P P R S S G C F P N M A A K V N G N P H S T P V \ Q G W G S T Y Q A W Q Q P T Q Q V P S Q S Q P Q S S Q P N Y S K A W E D Y Y K K Q R C F L L V G R D R V E G Y Q R S G P P G V G I I A R F M A L L G V G G H A A S A A P Q A S S P P D Y T M A W A E Y Y R Q Q V A F Y G Q T L G Q A Q A H S Q A L G K Q V G S H T L D A G V S L H L C L L Y P C Q S T G S L L S S R D T Y V D G I Q V A L P V S N W Y R V L I A A K I D S I P H L N N S T P L V D P S V Y G Y G V Q K R P L D D G E E G L V G P D E T N E I P N A N F R Q Q I R K L I K D G L I L R H R K P V T V H S R A Q C W K S T L A R R K G R H L G I E S K K I D R H M Y H S L Y L K L K G N V F K H K R I L T E H S H K L K A D K A R K K P L A D Q A E A R G S K T K E A R K L R E E H L Q

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				TKKEEIIKTLSQEEKAKK
4084	A	1	271	ALGKQVGSHTLDAGVSLHLCCLLYPCQSTGSLSSRDYVDGIQVALP VSNWYRVLIAAKIDSIPHLNNSTPLVDPSVYGYGVQKRPLDDG
4085	A	1	1814	GPQAEREAGPGSRA/RGVGGVGGGGDGGGGGNGGAGAGAERSCGDEG RG\FVDALHRVRQIAAKIDSIPHLNNSTP\LVDPSVYGYGVQKRPLD DGVGNQLGALDHQRTVITEEFKVPDKMVGFIIGRGGEQISRIQAESG CKIQIASESSGIPERPCVLTGTPEIEQAKRLLGQIVDRCRNGPGFH NDIDSNSTIQEILIPASKVGLVIV\RGGETIKQLQERTGVKMVMIQD GPLPTGADKPLRITGDAFKVQQAREMVLEIIREKDQADFRGVRGDFN SRMGGGSIEVSVPRFAVGIVIGRNGEMIKKIQNDAGVTTHYRPEDAV \SPQRAAQVMGPPDRQCQHAHA\IISELILTAQERDGFGLAAARGR RGRGDWSVGAPGGVQEITYTVPADKCGLVIGKGGENIKSINQSGAH VELQRNPPPNSDPNLRRFTIRGVPOQIEVARQLIDKVGGTNLGAPG AFGQSPFSQPPAPPHQNTFPPRSSGCFPNMAAKVNGNPHSTPVSGPP AFLTQGWGSTYQAWQQPTQQVPSQQSQPSSQPNYSKAWEDYYKKQS HAASAAPQASSPPDYTMV\WF\EYYRQQVAFYQOTLGQAQAHSQEQ
4086	A	1	265	AGNRLRFQLELEFVQCLANPNYLN/WYPQCLHMLELLQYEHFRKELV NAQCAKFIDEQQILHWQHYSRKRMRLOQAL\AKQQQNNNTSGK
4087	A	1	987	MIGPPGSLAGWQLEAFLSWLRALAPWWPLGSSISSGRFFVLAGGRL GRGVGLSAQCRDVSITRDEALTWREVSVRCEEDSTCREDAASMRGS RFPEGEREGPSLRRWEVSTRRDDVSTRQKRGLRYCHSRERHNTMTW KHHGPSKAKTLDSCPSGAPTARAPPPRYFGASAGGAIPLVGDGRSR PAPYPTVPRDRKREPWFPELRPRLWAFALSGWWRFGVFCYGRCCRY GDRGYFKDKAFVNYLYKLLYWKDPEYAKYLYKYPQCLHMLELLQYEHF RKELVNAQCAKFIDEQQILHWQHYSRKRMRLOQALAEQQQNNNTSGK
4088	A	1	491	RGFRNFARVSGLLLCQAGGVLVSSFVMAAAVAMETDDAGNRLRFQLE LEFVQCYANHNTLIFLPQR\GYF\KDKAFVNYLYKLLY\KDPEYAK YLYKYPQCLHMLGAAPNMEHFRKEAGWNAQC\AKFIGWNRQVSTLGKH YS\RKRMRLOQALAEQQQNNNTSGK
4089	A	55	858	EKGRARGRRRRKMLTRCCFVFLVQGSLLYLVICQDDGPPGSEDPE RDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQ PPNRPNHSPPPSAKGGKIFGWGDFYSNIKTVALNLLVTGKIVDHNG TFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNC \RMEWEKVE\RGRTSLFTHDPAKICSRDHAQSS\TWS\CSQ\PFK VVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPSPG
4090	A	1	368	MRARNLMTKLTVISRKEELQEEAAHREVQSLPPGEMEERSSSKTCP QVCDGRILSCMIKVP/VGREKH*RPRGRSH*HEAGCGPFTPPKVDH HEHLPPRRVEAGSRQKSTTEFPQAAGW
4091	A	253	536	YLASLEIPQSKVPESRPSHQVPSSQSLDSETPPSN/RHRQPPVDRKC VCRL\PLPPPPTFRPPKVDHHEHLPPRRVEAGSRQKSTTEFPQAAG GC
4092	A	52	310	SLGSPVLPGSGAAGVSTVAHSSAH*VEANWDSCQGGGLGSARAARRA PAVHWQQLHSGDWVPQIRTRALVHHHFRRPLLRPAHSQQ
4093	A	247	363	DANDGSTVSATVETPAAPDPGRGTGEPRDHAAFEKSSRIS
4094	A	1	608	MEIAITKAKVDFSSVCLPPSVIAVNGLDGGGAGENDDEPVLVLSLA APSPQSEAVANELQELSLQPELTGLHPGRNPNLPPLSERKNDLKL LHGYLRLTFFRLFKLYLSSDSLCHSELLLSFSAYLLNFVTLQHS ALE ERGCFNYDNCNKPCCMGEVKGSGPQDFPELQMPIDSGSSGYPQLLS ELATNQRFQASPQVGSFARTTH*VEANWDSCQGGGLGSARAARRAP AVHWQQLHSGDWVPQIRTRALVHHHFRRPLLRPAHSQQ
4095	A	144	3332	SRSGASRGTRPGAARGVIGGYGWHGIEFHLSVGIVSKIAITKAKVDF SSVCLPPSVIAVNGLDGGGAGENDDEPVLVLSLAAPSPQSEAVANE LQELSLQPELTGLHPGRNPNLPPLSERKNVLQLKLQRRRTREELVS QGIMPPLKSPAAPHEQRRSLERARTEDYLKRKIRSRPERSELVRMHI LEETSAEPSLQAKQLKLRLARLADDLNEKIAQRPMPMELVEKNILPV ESSLKEAIIVGQVNYPKVADSSSFDESSDALSPEQPASHESQGSVP

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				<p>SPLEARVSEPLLSATSASPTQVVSQOLPMGRDSREMLFLAEQPPLPPP PLLPPSLTNGTTIPTAKSTPTLIKQSQPKSASEKSQRSKKAKELKPK VKKLKYHQYIPPDQKQDRGAPPMDSSYAKILQQQQLFLQLILNQQQ QQHNYQAILPAPPKSAGEALGSSGTPPVRSLSTNSSSSSGAPGPC GLARQNSTSLTGKPGALPANLDDMKVAELKQELKRLSPVSGTKTEL IERLRAYQDQISPVPGAPKAPAATSILHKAGEVVVAFPAARLSTGPA LVAAGLAPAEVVVATVASSGVVKFGSTGSTPPVSPTPSERSLLSTGD ENSTPGDTFGEMVTSPLTQLTLQASPLQILVKEEGPRAGSCCLSPGG RAELEGRDQDQMLQEKDKQIEALTRMLRQKQQLVERLKLQLEQEKRA QQPAPAPAPLGTVPVKQENSFSSCQLSQQLGPAHPFNPSLAAPATNH IDPCAVAPGPPSVVVKQEQALQPEPEPVPAQQLLGPQGPSLIKGVAP PTLITDSTGTHLVLTVTNKNADSPGLSSGSPQQMDLEHPLQPLFGTP TSLKKKEPPGYEEAMSQQPKQQENGSSSQMDDLFDILIQSGEISAD FKEPPSLPGKEKPSPKTVCGSPL\AAQSPSAELPQAAPPPPGSPSL PGRLEDFLESSTGLPLLTSGHDGPEPLSLIDDLHSQMLSSTAILDHP PSPMDTSELHFVPEPSSSTHGPGTWANGHL\DSMDWL\ELSSGGPVLS LAPLSTTAPSLFSTDFLDGHDQLH\WDSCL</p>
4096	A	318	543	<p>KSSWSRWAFGTVRSPCGRQHRDIGATDNSGRSGPAEQRPQSS/ASSA MSAAGGSRLTFHPRNLPPRPTQDQAALT</p>
4097	A	42	342	<p>ENEILEVVQLGSRVCVFHFYHLHCCRHHCPENVHAG/CFGDCLG/HG RCSIQNCCTFER*I*VG*NNVAATAVMFGLVFPVLVLSLKYQVYFFKVL ALMNFCS</p>
4098	A	1	1289	<p>MYERVYVSTDIAIKLCKLLNRQFDRLYKKHSTGSASGEGLKALPLI VEGEGERPVCAEITRQEREEGAVHLFGLTWQLQPVGEGLYANGVSKGN RGTESMDTTYSPIGGKVSDKSEKKVFKGRAIDTGEVDIGAQMVTI PPGLFWRFOITIHHPYILKFNISLAKDSSLGIYGRNIPPTHTQDFD VKLMDGKQLVKQDSKGSDDTQHSRNLILTSLETGFIEMDQGPWY LAFYNDGKMEQVFLTTAIEIMDDCSTNCNGGECISGHCHCFPGF LGPDCARDSCPVLCGGNGEYKGHCVCRHGWKGPECDVPEEQCIDPT CFGHGTICIMGVCICVPGYKGEICEEEDCLDPMCSNHGICVKGECHCS TGWGGVNCETPLP/EQCSGHGTFLLDAGVCSCDPKWTGSDCSTEHKG GSSRLFL</p>
4099	A	1	4509	<p>VRLEWPTDLAVNPMDNSLYVLDNNIVLQISENRRVRRIIAGRPIHCQV PGIDHFLVSKVAIHSTLESARAI SVSHSGLLFIAETDERKVNRIQQV TTNGEYII IAGAPTDCDCIDPNCDCFSGDGGYAKDAKMKAPSSLAV SPDGTLYVADLGNVRIRTI SRNQAHLNDMNIYEIASPADQELYQFTV NGTHLHTLNLITRDYVYNFTYNSEGDLGAITSSNGNSVHIRRDAGGM PLWLVPVGGQVYWLTISSNGVLKRVSAQGYNLALMTYPGNTGLLATK SNENGWTTVYEDPEGHLTNATFPTGEVSSFHSDLEKLTKEVELDTSN RENVLMSTNLATSTIYILKQGGDTRHSKSTLTFVSGILWSTATVMV GPGENTQSTYRVNPDGSLRVTTFASGMEIGLSSEPHILAGAVNPTLGK CNISLPGEHNANLIEWRQRKEQNKGNVSAFERRLRAHNRNLLSIDFD HITRTGKIYDDHRKFTLRILYDQTGRPIILWSPVSRVNEVNITYSPSG LVTFIQRGTWNEKMEYDQSGKII SRTWADGKIWSYTYLEKSVMLLLH SQRRYIFEYDQPDCLLSVTMPMSVRHSLQTMLSVGYRNIYTPPDSS TSFIQDYSRDGRLLQTLHLGTGRRVLYKYTKQARLSEVLYDTTQVTL TYEESSGVIKTIHLMHDGFICTIRYRQTGPLIGRQIFRFSEGLVNA RFDYSYNNFRVTSMAVINETPLPIDLYRYVDVSGRTEQFGKFSVIN YDLNQVITTTVMKHTKIFSANGQVIEVQYELKAIAYWMTIQYDNV /RHGNM\CIRVGVDANITRYFYEDADGQLQTVSVNDKTQWRYSYDL NGNINLLSHGKSARLTPLRYDLRDRITRLGEIQYKMEDEGFLRQRGN DIFEYNSNGLLQKAYNKASGWTQVYYDGLGRRVASKSSLGQHLQFF YADLTNPIRVTHLYNHTSSEITSLYYDLQGHLIAMELSSGEEYVAC DNTGTPLAVFSSRGQVIKEILYTPYGDYHDTYPDFQVIIGFHGGLY DFLTCLVHLGQRDYDVVAGRWTTPNHHIWKQLNLLPKPFNLYSFENN YPVGKIQDVAKYTTDIRSWLELFGFQLHNVLPFGFPKPELENLELTYE</p>

				<p>LLRLQTKTQEWDPGKTI LGIQCELOKQLRNFISLDQLPMTPRYNDGR CLEGGKQPRFAAVPSVFGKGIKFAIKDGI VTADIIGVANEDSRRLAA ILNNAHYLENLHFTIEGRDTHYFIKLGSL EEDLVLI GNTGGRRILEN GVNVTVSQMTSVLNGRTRRFADIQLQH GALCFNIRYGTTV EEEKNHV LEIARQRAVAQAWTKEQRRLOEGEGIRAWTEGEKQQLSTGRVQGY DGYFVLSVEQYLELSDSANNIHFMRQSEIGRRYLLQQYSSSQYONLY WSVQAAITRYHRQGG LNNRNLFLTILETGKSKIKVLQIAAIQPSGKQ ELLAGFPADFAMIHSHCVHGLVDSWAGRG GELCKGDAAATAARHKST T</p>
4100	A	338	8522	<p>SEMEQTDCKPYQPLPKVKHEMDLAYTSSSSESEDGRKPRQSYNSRET LHEYNQELRMNYSQSRKRKEVEKSTQEMEFCETSH TLCSGYQ TDMH SVSRHGYQLEMGS DVDTE TEGAASPDHALRMWIRGMKSEHSSCLSSR ANSALSLTD DHERKSDGENGFKFSPVCCDMEAQAGSTQDVQSSPHN QFTFRPLPPPPPPHACTCARKPPPAADSLQRRSMTRSQPSAAPA PPTSTQDSVHLHNSWVLNSNIPL ETRHSLFKHSGSSAIFSAASQNY PLTSNTVYSPPPRPLPRSTFSRPAFTFNKPYRCCNWKCTALSATAIT VTLALLLAYVIAVHLFGLTWQLQPV EGELYANGVSKGNRGTESMDTT YSPIGGKVSDKSEKKVFQKGRAIDTGEVDIGA QVMQTIPPGLFWRFQ ITIHHPIYLKFNISLAKDSSLGIYGRRNIPPTHTQFDFVKLMDGKQL VKQDSKGSDDTQHS PRNLILTSLOETGFIEYMDQGPWYLA FYNDGKK MEQVFVLTTAIEIMDDCSTNCNGNGECISGHCHCFPGFLGPD CARDS CPVLCGNGEYEEKGHCVCVRHGWKGPECDVP EEQCIDPTCFGHGTCIM GVCICVPGYKGEICEEEDCLDPMCSNHGICVKGECHCSTGWGGVNCE TPLPVCQEQCSGHGTFLLDAGVCS CDPKWTGSDCSTELCTMECGSHG VCSRGICQCEEGWVGPTCEERSCHSHCTE HGOCKDGKCECSPGWEGD HCTIAHYLDAVRDGCPLCFGN GRCTLDQNGWHCV CQVGWSGTGCNV VMEMLCGDNLNDGDGLTDCVDPDCCQ QSNCYISPLCQGSPPDLDI QQSQTLFSQHTSRLFYDRIKFLIGK DSTHVIPPEVFSDRACVIRG QVVAIDGTPLVGVNVVSFLHHS DYGFTISRQDGSFDLVAIGGISVILI FDRSPFLPEKRTLWLPWNQFIVVEKV TMQRVVS DPPSCDISNFISPN PIVLPSP LTSFGGSCPERGTIVPELQVVQEEIPIPS SFVRLSYLSSR TPGYKTLRLILLTHSTIPVGM IKVHLTVAVEGR LTQKWFPAAINLVY TFAWNKTDIYGQKVWGLAEALVS VGYEYETCPDFILWEQRTVV LQGF EMDASNLGDWSL NKHHILNPQSGIIHKGN GENMFISQPPVISTIMG NGHQRSVACTNCNGPAHNNKLFAPVALASGPDGSVYVGDFNFVRRIF PSGNSVSILELSTSPAHKYLLAMD PVSESLYLSDTNTRKVYKLSLV ETKDLSKNFEVVAGTGDQCLPFDQSHCGD GGRASEASLNSPRGITVD RHGFIYFVDGTMIRKIDENAVITTVIGS NGLTSTQPLSCDSGMDITQ VRLEWPTDLAVNPMDNSLYVLDNNI VLQISENRRVRIIAGRPIHCQV PGIDHFLVSKVAIHSTLESAR AISVSHSGLLFIAETDERKVNRIQQV TTNGEIIYI IAGAPTDCDCCKIDPN CDCFSGDGGYAKDAKMKAPSSLAV SPDGTLYVADLGNVRIRTISR NQAHLNDMNIYEI ASPADQELYQFTV NGTHLHTLNLITRDYVYNFTYNSEGD LGAITSSNGNSVHIRRDAGGM PLWLVPVPGGQVYWLTISSNGVLKRVSAQ GYNPALMTYPGNTGLLATK SNENGWTTVY EYDPEGHLTNATFPTGEVSSFHSDLEKLTKEVELDTSN RENVLMSTNL TATSTIYILKQENTQSTYRVNPDGSLRVTFASGMEIG LSSEPHILAGAVNPTLGKCNISLPGEH NANLIEWRQRKEQNKGNVSA FERRLRAHNRNLLSIDFDHITRTGKIYDDHRKFTLRILYDQTGRPIL WSPVSRYNEVNITYSPSGLVTFIQRG TWNEKMEYDQSGKII SRTWAD GKIWSYTYLEKSVMLLLHSQRRYI FEYDQSDCLLSVTMP SMVRHSLQ TMLSVGYRNIYTPPDSSTSFIQDYSR DGRLLQTLHLGTGRRVLYKY TKQARLSEVLYDTTQVTLTYEES SGVIKTIHLMHDGFICTIRYRQTG PLIGRQIFRFSEGLVNARFDYSYNNFRV TSMQAVINETPLPIDLYR YVDVSGRTEQFGKFSVINYDLNQVITTTVMKHTKIFSANGQVIEVQY EILKAIAYWMTIQYD NVGRHGM\CIRVGVDANITRYFYEYDADGQL QTVSVNDKTQWRYSYDLNGNINLLSHGKSARLTPLRYDLRDRITRLG EIQYKMEDEGFLRQRGNDIFEYNSN GLLQKAYNKASGWTVQYYYDGL</p>

				GRRVASKSSLGQHLQFFYADLTNP IRVTHLYNHTSSEITSLYYDLQG HLIAMELSSGEEYYVACDNTGTPLAVFSSRGQVIKEILYTPYGDYH DTYPDFQVIIGFHHGGLYDFTLTKLVHLGQRDYDVVAGRWTTPNHIIWK QLNLLPKPFNLVSFENNYPVGKIQDVAKYTTDIRSWLELFGFQLHNV LPGFPKPELENLELTIELRLQTKTQEWDPGKTILGIQCELOKQLRN FISLDQLPMTPRYNDGRCLEGGKQPRFAAVPSVFGKGIKFAIKDGIV TADIIGVANEDSRRLAAILNNAHYLENLHFTIEGRDTHYFIKLSLE EDLVLIGNTGGRRILENGVNVTVSQMTSVLNGRTRRRFADIQLQHGA CFNIRYGTVEEEKNHVLEIARQRAVAQAWTKEQRRLOQEGEGRIRAW TEGEKQQLLSTGRVQGYDGYFVLSVEQYLELSDSANNIHFMRQSEIG RR
4101	A	139	520	LSLPLSPRLECSGTILARCNLHPSPPRSKRFSCLSLPSSWDYRRAPP NLAIFLLLLFLVEMGFHHVGTGLELLASNYLPTSA/FPKCWDYRHE PPCPADKTNFLSLWFIGYNIFLESEVNFFLPWDA
4102	A	7	497	VFTDMSGLRHEPKALRRELPEEAAAAEEERRKIEVPSEIEVPREALEP SVPLMVSLEISLEAAEEEEKSRISLIPPEERWAWPEVEAPEAPALPVV PELPEVPMEMPLVLPPPELELLSLEAVHSPRRMAARVFYLLLVLSAQQ ILHVKQEKPYGRLLIQPGPRFH
4103	B	93	182	PPPKALRRELPEEAAAAEEERRKIEVPSEIE*
4104	A	51	394	WGGPGLKPLMLVDPYRAVALELQANREPDFSLSVSPSPRRMAARV FYLLL/VSVCMCVCGAGTQRPARTGTPTCPLLAS*PVLSAQQI LHVKQEKPYGRLLIQPGPRFH
4105	A	427	499	KTRGTMFYYPNVLQQRHTGCFATIW
4106	A	796	2482	KTRGNMFYYPNVLQQRH\NGCFATIWLAAATRGSRVLKREYLRVNVVKT CEEILNYVLVRVQPPQPGLP RP PRFSLYLSAQLQIGVIRVYSQQCYL VEDIQHIL\YRLHRAQLQMRIDMETELPSLLLPHNLAMMETLEDAPD PFFGMMSVDPRLPSPFIPQIRHLLLEAAIPERVEEIPPEVPTREP ERIPVTVLPPEAITIL\EAELRMLIEIEGERELPEVSRREL\DLL\I AAAAEAILLEIPRLPPPAPAEVEGIGEALGPEELRLTGWEPGALLME VTPPEELRLPAPPSPERRPPVPLLRLLLLRRRLLFWDKETQISPEEF PRNNLQTRAH\CWECMV\QPPERTIRGPAELF\RTPTLSGWLPPPEL LGLWTH\CAQPPPKALRRELPEEAAAAEEERRKIEVPSEIEVPREALE PSVPLMVSLEISLEAAEEEEKSRISLIPPEERWAWPEVEAPEAPALPV VPE\IPEVP\MEMPLVLPP\ELELLLNWKT VHRA\VALELQ\ANREP DFSS\LVSP\LSPRMA\ARVFYLL\LVLSAQQILH\VKQEKPYGR LLI\QPG\PRFH
4107	A	136	424	SPEHPQLPGSLLRPPGAQIPSEWQVAEATALVHTLDGWSVVQTMVVS TKTPDRKLI FGKGNFEHL\KKELEAAWGVFDRFTTVVLHILRCNAR TK
4108	A	1	212	RPPRRVVRGRHQPHGEPVRSAPVRVPGEDDAAQPSAAERVGPRAV PGAGFTVHQHRRGGLHRRRRLRQ*RHQPHGEPVRSAPVRVPGEDD AAQPSAAERVGPRAVPGAGFTVHQHRRGGLHRRRRLRQ
4109	A	1	1746	AGRRTPGAAALPRGPRPLGSAGSRAVLPRARASCRPQEPRESGGAV GRREGPAGGRRTKTERKTTRRSRKMRTTRPRSCCGESLCCRRGPKR VCLVHPDVKGPGKSQMTAEWQVAEATALVHTLDGWSVVHTMVVST KTPDRKLI FGKGNFEHLTEKIRGSPDITCVFLNVERMAAPTKELEA AWGVEGCLTAFTV\VLQHL PACNARTK/ERARLQVALAGDARLHRSN LKRDAVHLYRGVG/SRAYIMGSGESFH/MQLQORLLREKEAKIRKAL DRLRKKRHLL\RRQTRREFPVISVVGTYN\CGKTTLIKALTG\DA I\QPRDQLFATLDVT\AHAGTLPSRMTVLYVDTIGFLSQLPHGLIES F\SATLEDVAHS\DLILHVRDV\SHPEAELQKCSVLSTLRGLRLPAP LLDSMVEVHNKVDLVPGYSPTPNV\VPVSALRGHG\LQELKVELDA AVLKATGRQILTLRVRLAGAQLNWLYKEATVQEVDPEDGAADVVRV IIS\NFPYKG\FRKLFPRMNGRPQKACGVGASPALGELRRYPLCWGQ LGVRCRSRVLLVWFCTRLASQPFAGMYRACR
4110	B	50	382	XGEQLVRQDL DAGVSEHSGDWLDQDSVSDQFSVEFEVESLDSYSL

				SEEGQELSDDEDEVYQVTVYQAGESDTSFEEDPEISLADYWKCTSC NEMNPPLPSHCNRCWAHX*
4111	A	1665	1789	FFVLLVETGFHRVSDGLDLLTS*SAHLGLPKCWDYRHEPP
4112	A	1431	1555	FFVLLVETGFHRVSDGLDLLTS*SAHLGLPKCWDYRHEPP
4113	A	1740	1864	FFVLLVETGFHRVSDGLDLLTS*SAHLGLPKCWDYRHEPP
4114	A	1	752	DL DAGVSEHSGDWLDQDSVSDQFSVEFEVESLDESYPSEGGQELS DEDDEVYQVTVYQAGESDTSFEEDPEISLADYWKCTSCNEMNPPLP SHCNRCWALRENWLPEDTGKDKGEISEKAKLENSTQAEFGDVPDCK KTIVNDSRESCVEENDDKITQASQSQESSEDYSQPSTSSIIYSSQED VKEFEREETQDKESVESLPLNAIEPCVICQ/GST*KWLHCPWQNR TSYGLLYMCKEAKEKE
4115	A	426	815	SSRRFVWRKLLCERAQSGTVYEI*QCAHRHPRHRHPGCCRHRLGYA GTAGPLAGYRPFQHRQSLWRAASAICVDAISMRTSRSTVRPLWPP PSPARFATWSHYRLRDHGDHTRPVDLPTSQFTILL
4116	A	1174	1354	FFVLLVETGFHRVSDGLDLLTS*SAHLGLPKCWDYRHEPLRPAGLF KHSPGLYSQPILT
4117	A	2251	2373	FFVLLVETGFHRVSDGLDLLTS*SAHLGLPKCWDYRHEPP
4118	A	1027	1193	FFFFFFFFFGLVETGFHRVSDGLDLLTS*SSRLGLPKCWDYRHEP PRPAEEGI
4119	A	983	1386	QEVRYRKVETLRCLLFSSCLVPVCAASPVSRPGCRFLRSSLHWPTGR LVFRQGETFLVPEKTVLRGVASAPAKAAGRTVPVGRPRDARLRAD ARS*SC*RAARPRRGASGAVGARCGPRPGFFLRSGGIFV
4120	A	6133	7646	YMLFLFLSTKGWTVIQNRQDGSVDGFRKWDYPKQGFNGVATNTDGKN YCGLPGNEQACKIKSFYKWDFF*LKNIHCWKPVLGS*EEFPDKNVE AKDKGRKAVFSPPKFYFW*EILFCFSFR\EYWLGNDKISQLTRMGPT ELLIEMEDWKGDVKKAHYGGFTVQNEANKYQISVN\KYRG\AGNAL MDGAS\HLMG\ENRDHDPFHNGHGSFQPPYD\RD\NDGWYVWHSLLL L*KSH*YHYSESLTIFLIATTSWALTVSHCPKLFMHHSKAFQL*GRH SYSHFTDEI*RDYVICPM SHNYPEIKLEFEHSYFLNNEHLDKYLYLY ILKCV*KLSFSFPGFSDTKGCKSYSSIK*QTQSLDGLPQRP SYLSF LL*GTGGLWCISVTLCAIPKGKTTVHTSVAVFYG*SAKRNLTTVLF LITPNTFSFRLTSDPRKQCSKEDGGGWYNRCHAANPNGRY YWGGQY TWDMAKHGTDG DVVMNWKGSWYSMRKMSMKIRPFFPQQ
4121	A	333	430	GRGDKPYSPGDSWFWQD*ILVQL*ICPQEPS
4122	A	2	1679	QRGHWEAEVGGRRAGAFVGGAQGRAGGRGVEAGRMRLSKTLVMDMA DYS AALDPAYTTLEFENVQVLTMGNGPSSPHCLTVALLGAWHSDMMI LLPLRLARLRHPLRHHSISGGVDSSPQGDTSPEGTNLNAPNSLGV SALCAICGDRATGKHYGASSCDGCKGFFRRSVRKNHMYSCRFSRQCV VDKDKRNQCRYCRLKKCFRAGMKKEAVQNERDRISTRSSYEDSSLP SINALLQAEVLSRQITSPVSGINGDIRAKKIASIADVCEMKEQLLV LVEWAKYIPAFCELPLDDQVALLRAHAGEHLLLGATKRSMVFKDVL LGNDYIVPRHCPELAEMSRVSIRILDELVLFPQELQIDDNEYAYLKA IIFDPDAKGLSDPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGELL LLLPTLQSITWQMIEQIQFIKLFMAKIDNLLQEMLLGGSPSDAPHA HHPLHPLMQEHMGNTNIVANTMPHTLSNGQMCEWPRPRGQAATPET PQPSPPGSGSGSEPYKLLPGAVATIVKPLSAIPQPTITKQEVI
4123	A	42	1465	GRWPPRGRENALSKTL\VDMDMADYS AALDPAYTTLEFENVQVLT GNDTSPSEGTLNAPNSLGV SALCAICGDRATGKHYGASSCDGCKGF FRRSVRKNHMYSCRFSRQCVVDKDKRNQCRYCRLKKCFRAGMKKEAV QNERDRISTRSSYEDSSLPSINALLQAEVLSRQITSPVSGINGDIR AKKIASIADVCEMKEQLLV LVEWAKYIPAFCELPLDDQVALLRAHA GEHLLLGATKRSMVFKDVL LGNDYIVPRHCPELAEMSRVSIRILDE LVLPFQELQIDDNEYAYLKA IIFDPDAKGLSDPGKIKRLRSQVQVS LEDYINDRQYDSRGRFGELL LLLPTLQSITWQMIEQIQFIKLFMAK IDNLLQEMLLGGSPSDAPHAHHPLHPLMQEHMGNTNIVANTMPHTL SNGQMSTPETPQPSPPGSGSGSEYKLLPGAVATIVKPLSAIPQPTIT

				KQEV I
4124	A	3	1840	TSPSEGTNLNAPNSLGVSALCAICGDRATGKHYGASSCDGCKGFFRR SVRKNHMYSCRFSRQCVDKDKRNQCRYCRLKKCFRAGMKKEAVQNE RDRISTRSSYEDSSLPSINALLQAEVLSRQITSPVSGINGDIRAKK IASIADVCESMKEQLLVLEWAKYIPAFCELPDQVSSFMGSSFM PISQFRQVALLRAHAGEHLLLGATKRSMVFKDVLLGNDYIVPRHCP ELAEMSRVSI RILDELVLFPQELQIDDNEYAYLKAIIFDPPDAKGLS DPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGELLLLLPTLQSIWQ MIEQIQFIKLFMAKIDNLLQEMLLGGSPSDAPHAHPLHPLMQEH MGTNVIVANTMPTHLSNGQMCEWPRPRGQAGKTIPTVTHPIAAGDSQA WALVWEKQSKSAYQINDGGDGCPCCHGVQTEPCEAGSNCGTWGTLTLL LLPPLPPSAVTLTSHPVFSNTTSPAEKEALETIPPVILGTCTWTW VGTWVRIPEGLQPEKTNPGWRLQOELGVERKSIRKQTIHQAFEKGR RGATVSWETNEDTSALDQIMDYVEKQWKQRRPQVAVAVVQKDDGSM D
4125	A	6233	6874	VLIGCIPQVPPSISYSPLFWFSALGNVAEIFFCLCLGNHNSCWRTL VEVPESLCPHC*RLLV*HKSGDIWVLTQMLQLDPAALPCPPSSIVD AKGLSDPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGELLLLLPTLQ SITWQMIEQIQFIKLFMAKIDNLLQEMLLGGPCQAQEGRGWSGDSP GDRPHTVSSPLSSLASPLCRFGQVA
4126	A	1	1481	GFGVGAQGRAGRRVEAGRMRLSKTL\VDMDMADYSAALDPAYTTLE FENVQVLTMGNDTSPSEGTNLNAPNSLGVSALCAICGDRATGKHYGA SSCDGCKGFFRRSVRKNHMYSCRFSRQCVDKDKRNQCRYCRLKKCF RAGMKKEAVQNERDRISTRSSYEDSSLPSINALLQAEVLSRQITSP VSGINGDIRAKKIASIADVCESMKEQLLVLEWAKYIPAFCELPDQ QVALLRAHAGEHLLLGATKRSMVFKDVLLGNDYIVPRHCPELAEMS RVSI RILDELVLFPQELQIDDNEYAYLKAIIFDPPDAKGLSDPGKIK RLRSQVQVSLEDYINDRQYDSRGRFGELLLLLPTLQSIWQMIEQIQ FIKLFMAKIDNLLQEMLLGGSPSDAPHAHPLHPLMQEHMGTNVI VANTMPTHLSNGQMCEWPRPRGQAATPETPQSPPGGSGSESYKLLP GAVATIVKPLSAIPQPTITKQEV I
4127	A	602	800	ENPKQQENLWSQYFTLISTI*KKKSWLCIVAHACDSSTLGD*GGHIA *AQEFETSVGNIVKPPSLY
4128	A	646	1905	EPPFSTTFALHAFTFFSDQONQVSDDDLDPSFTVSTSKASGPHGAFN GNCEAKLSVVPKVSGLERSQEQQPPGPDPLLVFPFPKEPPPPVPRPP VSPPAPLPATPSLPPPPQPQLQLRVSPFGLRTSPYGSSLDLSTGSC GRWGR LHGQEP RPGRAGRPLLVRFGTGRVAAALPGLGAWLYNGAESE NEEESPRQESSGEEIIMGDPAQSPESKDSTEMSLERSSQDPSVPQNP PTPLGHSNPLDHQIPLDPPAPEVVPTPSDWTACEASWQWALTTWN SPPVVPANEPSLREL VQGRPAGAEKPYICNECGKSFSQWSKLLRHQR IHTGERPNTCECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSW SSNLVQHQRTHTGEOPYKCTECEIAFTQSTNLIKHQRSHTEKGP
4129	A	6717	7569	AERSSNRQKSKWELGRKDLDOAKEEVVRLPQEEEEGPGAGDESSCGT GGGTHRRSKKAKAPERPGTRVSRERLGRARAETQGANHTPVISAHQTR STTTTPRCSPARERVPRPAPRPRTPASAPAAIPALVPVPVSAPVPI SAPNPITILPVHILSPPPPSQIPPCSSPACTPPPAHTPPP AQTCLVTPSSPLLLGPPSVPIASVTNLPLGLGGLREELCAQGLGIF QSPWSWLLWPVQKPPHFLLCPLKICQQLLWRSCLCQRRFTLSPLLHP A
4130	A	2	93	DFTMSHHYHSAHGTLVLAPRALGNPLSLYPSNYTFPFQHSPSDPCTQ SYSLPPEYATHGSSCFDTTDGLNASRALAGSCAPVSGSLPCCPTLG IPSPPLPHMHKSLPTYPTPTISMKPP*PCPGSQGPWQSAFTLPI
4131	A	743	955	ESDFTYFTHNSCLFCYNKIYINIIYIKLSLNCNYGNYFLYIVAHTQ TYIYI*NIFCFFCHLLTFCCLGF
4132	A	49	313	PLRIWPC*ALFLKLSLGFSLF*FYSSLFLLSPPLC*SLPRVQYIYMY ILYICICN*YTIQVCICNGYMYSCSWCSNVWYGYTENMRT

4133	A	230	364	SERYLSNPTPPVPP*SAVYLSNPTPHVPP*SDRYLSNPSPPVPP*SN RYLSNPTTPVPR*SDRYMYNNTPPVPP*SERYLSNPTPPVPP*YDRY LSNRTPHVSP*YDRYLSNPTPPVSP
4134	A	508	780	VSFSSFPSPFPHLSLFFSLSFSFPPSLFPSSFFTFFGNHLL*ISCN PNLMYQWGFYKYKYQCIFWLLSDF*LKYNENDMSVAFGLRTSL
4135	A	34	329	DRLKRKNQSLSYLWEYNKKSNIQVTSQSLEREEDDRAEKVVE*IMAS NFPYLSRDVNLKIQDS*RILNWIKLKKSISKYIIDLLETKDII RNLE SSQR
4136	A	582	869	MCQRVQTPKSPSNPYVHSNICTQLFIAPLSIIAKRWKQPKCPSAEE* INEM*YIHSMEYDSAIRKNEVLHVTTWKNFENIRLMKDASHKGLYV A
4137	A	285	346	AVLFYVFHPIPYLLVMTLLLYFLP*LPNQCRFSSLHSKTTAWPSTTVT LF
4138	A	97	298	DNLTLPRLECGGMIMAHCSLNLTFSSDPAASAS*VAGTTGT*HHAW IFVFLCNWLRNRGVTVKKRS
4139	A	147	502	IFHSKMPISEWKLV*TLWQFFKELKIELPFDPAIPLLGI*PKLAVVA PQHS
4140	A	435	660	NLNQHEKLSMLE*ILKSYPKILDNINDHEVSHCSKGNFKNRSKEWW CGTQDSWRLGNLKVGEFFNDLTRNTL
4141	A	293	563	NVWPSSSVRGRNE*GREGRRRTQQAAGLGPAPSDLWWLWLSWCLOK NMSQGENLPAGPGSCCGREAQEGAGTSLEDAPFFEAQLQLH
4142	A	1329	1563	WPRNQPTRRPWLKDKLPGVPGGLTGPNPCGQGPFPPLRPSALWS SHSGPPPNGEPLPPRGE*YLHPSPRRTSYL
4143	A	304	589	RTWWTAASYFRSVGGSASNRPFSPGPIYFQLPGRGHSRKGT\RSRA REPSTLWSTPAAP*RTWWTAASYFRSVGGSASNRPFSPGPIYFQLP RGHSRKGTTEEQSQGAIYTVYACSAVKNLVDSSVYFRSVEGLLKQA ISIRDHMNASAQGHR
4144	A	131	690	VSPAVTSSSLSWARSDLAEGHARCPLCSGWAQHLSNEEADALS TRPIPTTCI*SRTSSLRASTSWPTSHPWCTGCRSMCVRSLELAQH KADNAALGRSRAREPSTLWSTPAAP*RTWWTAASTAAWRVCSNRPS ASGTILNASCPGPQVAPGDRPPPLPFPSLQGPPLSCAGEPLLLAY
4145	C	332	421	MEEKIFSQPGMVAPT CNPSTLGGQGRWIT*
4146	A	685	929	KVGGAKPSLGYLRLGLRPLVFCLHIS*AGDFPRGV*LLPRRSGSVVA HTCNPSTLGGQGRQIT*GQEFKTGPVNMVKPHLY
4147	C	710	892	MCVCAHTCPQTSIYIHVFTHGYDCIQVTAQKCLHMCFHIMSTHACV DTYICIIYHVKLI*
4148	A	98	317	QLTSHLSGGRVNSAWRVLPGRHDSMCVTPVSVSVGSSLSFHFARAWL RIFYGSACEDKPGPPSSHTGNPQRAC
4149	A	656	1037	FVQVQAHKLACKHVQAYFVFKEQQPEGNVFCQGVSTS*EHGASSE PWHGPAGAGVTTSFSSPFSGGDRHKFEVSGRRLPTEGLPSNSSFESF PSSIPWFLFPQVQLSTIWGLKFQFFGDLKILP
4150	A	1365	1503	LKTLQRAGCSAHACNPSTLGGQGRWII*AQEFNTSLGNVAKPCLY
4151	A	397	682	YSKSKCHAYRMKCQLNVGLSCKCCECTEWRDPCELEGQESLWGQVQL AHACNPNTLGGQGRGRIA*GQKFKNLNNIARPHLFFKKRKKISLMRWL K
4152	A	477	686	LYLCSALKKNQ*EPGMVTHAWNPNSTLGGKGRRTA*AQEFQTSLSNVG RACLYKIYIFKISQAWWHAFVI
4153	A	108	419	SHTLGGQHGRIMRSGVRDQPGQHGETPSLLKIQKKKLPGRAGRHL* SOLLRLRLLENRLNLGGGGGSETEIEPLPPQPG*TQ*RLPSQKQKN LETVSKKKS
4154	A	175	190	DKVRVSQVRLTSRHLITLR*IRKGRGKKRGCRERNRENRGK*KYV
4155	A	301	962	IMGDAKNFLYAWCGKRKMTPSYBIRAVGSPNGHRFMPEGDVHGLGKC GMGNSTNKKDALSNAARDFVNYSGRINEIYM*EQGSAIGELSHMYIS FIRPE
4156	A	20	430	RPQTYTMVHLTPEEKCAVTALWGKANVDEVGGEALGRLLVVYPWTHR

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				VFETFGDVSTPDVAVMGIPNGNADGMNVLWASIDGLAHLNLRGTTFAT LTEHD*D*LHVDPEILMLLGNVLICVLAHHCVEGFSPSWQAA
4157	A	31	492	QRILQSRPFEGRVKQGVTWLLQLVGLVSESHIGPELHLPCEEECHL LVSGVNSPEDSSPLLTEWLWTSHPFLLHCLFGASGRGLQTVPPFV STALQNVCFPPQKGIAKAPFLLLSCATGGCSAGLRVYKLSAPSCD*AG RTRGSSGESAPML
4158	A	165	435	GSQADHPCVGVWRQNSVNPQVFLQATG*LISASSGSINTNMAQGT VVCFGPVYPPKAKGRARSQVTPCLTLPSKGRCLKILCYLFLKL
4159	A	132	257	EFLIRKGDVTGENGFTMPTRQAQEQQGERVGCDDVCEAM
4160	A	2	111	QLLKDSARSTLVLYPCWARVSQKSGCCPLKVLSQRPGKKLGLLWVEA WECPGAVARCLCHPGPLCPASGTFTVPGTEPHS*LLLRNELPSPLF* LLGQSEPEKWMPLPPQGAISETR
4161	A	3	116	GWRAPTSQPGGPAQVPCSSF*KILPGQHWSSTPAGPE
4162	A	273	793	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPDIRNTFSMAGGAP TSQPGGPAQVPCSSF*KILPGQHWSSTPAGPE*ARKVDAAPSRCYLR DQPKGPFKVPGETEHS*LLLRNELPSPLF*LLGQSEPEKWMPLPPQGA ISETSLRDLKCLAQNLTHDCCSGTSCPPHCSDSFPYHLAPVLAEIF EIMEKVQPWNRNPTGSAICPLHRPSQKPACTGLRRK
4163	A	391	868	NFQAQTGRRALLRCFQTFYISIVDLCEGNGKRPTTNSSASFTKEQAD AIRRIRNSKDSWMDLVKPGASRDEVNKAYRKLAVLLHPDKCVAPGS EDAFKAVVNARTALLKNIK*KVQKKATCGTQMOTDFP*R*NNQRGGF LPKNLTALFIHVLAFVYQ
4164	A	212	494	FSEAQFLANVAIKAILSEEISEGKGDRRLADHTLILTERGSEGPCC *PQEVPRPTVLSEWGCKCAQANCECSP*PWPBKSRAGHFPPSLGKLL
4165	A	281	587	BIFFNPKREYLSLHWMDEHQCPNFIHVGQGGGLGTIWDVLQEYNQK NFLYNISLKDCKFLGMMW*LTPVIPALWEAEVGSLEPRSSKTSLGNM ARSHPYKK
4166	A	113	564	IDRLDSAKIFGHLSIFDRCEKRRPDLVSGTGTCSGSFRRVTFQPAVP GRTDSPIPRTHGPNFVP*TLVEKKPPAAW*TPACDLTSKPSIGPTIL VPTPKVEPGSLPTPA*DPLEPIQSPEKK*SIVPQTGSFQTASQLTEA VPELVLVAH
4167	A	1173	1432	PIPVDLNTLMFCHYFIYVYHPCLEMFSFTCGLLSL*AQRPSDGYFFE AFIYIILFCTMFFLNQILYSSEKNTVFVDNHSYYTVLR
4168	A	75	270	QYISVVDTYLLMPRLATAIILWITN*VFEKRVAFHGYHWSLMVRDRR ISGVDRYYVSKGLENID
4169	A	271	825	SPPACLVDGQQALPSGGGLYPNSLRQGSVQAGRGCLSWFCMVHFAN PEDQFLGFQASGFLHLVLPKPPQGAATPSGSSQGGPAMFSGPLSEPPT PPATPQNPIHSSSTKLLCEAAAPTRGKPCPTSSIFQPHWRTDGKGRA GFSASGTRGRPHLTPPSPVHQTG*EASQKGPALMPGFPQPPKKG
4170	A	1	211	THPPPAEAPGAEGPQ*G*AKHPSAP*APLL/PRRRARASSRPVTSVT PSSGGSFRPGTPAQGVITAVTVSA
4171	A	1	424	NSRVDDFVRPGSSAAGRQMRGGGQVNPVRPGFRGQPP*RNHGPVP ASPWALAGDAGGMLWNMMRSWPVSGRPTLNPNFNKQSGPRQHEQGPG EVPDVTPEEALPELPPGEPEFRCPERVMDLGLSEDFSRPVGLFPGL
4172	A	1091	1421	RGIITEINKHPDHIHSPHTTCRHTFTNMHAHTHTPTMHHTHTGMFW* K*N*GSLNSRSGFK
4173	A	1407	1609	LSDLNGNFHFSKVMTRVNIKGNLYLKNMRPGAVAHACNCSTLGGQGGQ TA*AQELETSLGNVVRCLCY
4174	A	1	294	FSRPDHLNGHIKQVHTSERPHKCQVWVGSSSGLPPLEPLPSDLPSWD FAQPALWR/CVPFGS*HRLFPFSKKIIPSP*KPGPSTLQQHSDLDPA FISG
4175	A	560	824	FWKVGCLPWELAHAPYLLPPLGITSP*ALGFPRGTGGPWPTFPPLP RVSRPSQRRLGTIPT*SQPHACPLPLPHSGSRSCFHFVWLK
4176	A	3	325	FFHVSRLNLFYFFRYIKCYFIFSLIILVSGSRVNLNLLGLIVYCPL VVFMMNF*TWISHFLSFFFFCRDGVSHCVAQAALFTPGLKCWDSRRE

				PPRPAEMFLFLGT
4177	A	292	543	SPGTYAPKRIGKGAGNWKPGVPPFRSSMWKETQPLSSRVSKVLSVSP SPPIPVVPLLPALPK*GHSPLVSPPLHRSSQGESP
4178	A	3	367	IQMDCVLLFPAQAQISAPPLIMKTTPTISWGLEHICPSYPWNHSPSL YHRYAMGFGMFFQSGPCSSWAWKLSRTLPSLVVALSSAWPLTRG*RL DLGPPAPSSYVGFSSQASPSPPAAQC
4179	A	67	283	MCAYIKIDKGNRMCTNMIYLVGIGVTFSLTLMYKYTKLIIMLSYV KRLTLISCAFYVNLWINLYYAMFI*MCAYIKIDKGNRMCTNMIYLV EGIGVTFSLTLMYKYTKLIIMLSYVKRLTLISCAFYVNLWINLYYAM FIK
4180	A	268	469	GNRRALLRLPALGPPRSSP/DGFTPGTTARPSILKRCMPMPTPLPPDP SAAAPGTSELWTSPDSSSSSR
4181	A	880	1200	GNPTWFLPSYQGNSGPAEIQS*GFTPGTTARPSILKRSPMPTPLPP DPSAAAPGTSELWTSPD*QQQQQDGKEAPQSGRHDSSSALRPAPEA LPVSRPPPPPLAA
4182	A	343	721	SCLLTVISFHQIKKYIYVHTQLTKAGQKEFICRLSLALTNLPPAAP LAMAPCVSPASRQDTVLG\GPQPPSGPAPTAPQPPA*ARWQLGPPSP GPSILPPREGRPSAPSGAGWGDLGAGPSQVHF
4183	A	789	1015	MSLMVPLMPYGP*YLPSPPAYPIWELPLPQRDSADVSRRLGGRGV AVERDSPEKSNISKFGLYQVACAVTHL
4184	A	319	471	IMWYIHIMEYI*PQKGRKILTHATI*MKLEDIMLSEISQSQKNKYCI ISVI
4185	A	68	422	GSPSRCPAFLSSPVAARPLTHFPTGAGLLRASGEPAQLTGVSVSQ* PPRAPSSGLPLKHSHPQCSAQHSGKEGLGGTNTTREN*PSPRPLCM GAQAGRMLLLPAAVRNHVLESGSV
4186	A	135	500	PPWVTPRWERGWGVIKDTGDRVRSQRQQGLPPKLQSGWEVESWLGP PRVF\PGSVPGTPR\SPAAGGSQPRCPDARPAHKGPRAPGARCGPPP APPPGLPPAY*PGRPR/PRPARR*TPLTAA
4187	A	365	1452	IGPEVPEGCHFRSGESRGDATALYRVESEHLGLEGCAGNATLVQGV GRKIPCLGLRGAILGQPQIAVRLGSRIMARPAAPGLSQARSLARRGC PAAGGSQPRCPDARPAHKGPRAPGARCGPPAPPPGLPPAY*PGRPR RGLHGGRRHRSRRPPRRGPAAPGSPPAEVAGASARGRAPGPPCPRPP PPIPAAPRVEAGPSARPSVPAPAPAPSRSPRLPQPPAAPWGGRASGP KDPGTAPPPPTRTQSAARNPSRSPPPAPPSPASAGASADDPGTPWHRT GPPCQSQTRKHTGP*AARDQQRSRKDDSPGLCHCLRPGAPKCLKG LWFAFSVHPWSSTPWLQSGRVNLPLAQDIFLL
4188	A	200	390	GPHAKSAFFPP*LSEQLQGQ*QPGQTPVGRLLALSVAFFQGVGFPA GGGTGEAFGGGLACPLP
4189	A	805	1030	LVLCLPHSQTCKTSHTCLTLQGPL*KLTRLALFRLGAVAHACNPS TLGGPRGPIT*CQEFKTRLANMVKPLLY
4190	A	90	417	LALEILSYFYLLYLPVWHFGFNSVVALSLKILNIIVYLFSSFKSLRN FSALVSIFVFCFSSFSACFSLNSKOFF*NPDIKPKPHVKNSRIYKT QYSKDHQRENQFR
4191	A	2	672	GRVGFTPGSWEAFMVKNIVPKLGMCLGELVINPHQQHMDAFYWVIDW EGMISVSSLVGLLEKHFFPKWLQVLCWSLNSPNYEEITKWYLGWKS MFSDQVLAHPSVKDKLNEALDVMNRAVGSYVG\AYMQPG\ARE\NIA YLTHTERRKDFQYDAMHERRAGPQIGLLRSLGKNLKIACKKEPLEIY LWANLKEYYLAKTGQGPFFFLTRAPEGLITAWALWG
4192	A	1642	2785	RMTSSCPMADRTCLPFSHRLIWEVWMPFVRNIVTQWQPRNCDPMVD FLDSWVHIIPVWILDNILDQLIFPKLQKEVENWNPLTDTVPISWHI PWLPLMQARLEPLYSPIRSKLSSALQKWHPSDSSAKLILQPWKDVFT PGSWEAFMVKNIVPKLGMCLGELVINPHQQHMDAFYWVIDWEGMISV SSLVGLLEKHFFPKWLQVLCWSLNSPNYEEI/TPKWYLGWKS MFSD QVL\AHSIWSRDKFNEALDIMNRAVSSTVGAYKQPGARENIAYLTH ERRKDFQYEAMQERRRPENMAQRGIG\VAASSVPMNFKDLIETKAEE HNIVFMPVIGKRHEGKQLYTFGRIVYIDRGVVVFQGEKTVWPTSLQ

				SLIDMAK
4193	A	264	638	PSRTRIKTKQMATSEILPSFVATMDASNFSFWQVLCSWLSNSPNYEE ITKWYLGWKSMFSDQVLAHPSVKDKFNEALDIMNRAVSSNVGK*GFP FWMSPQVSDFTHVNDTESEFSGSCRQPKP
4194	A	2413	2707	EMHVY/WTERSGSRL*SEHFGPRWVDH*/RQEFETQPGQYGDTPSL LHPLLSTSCPSFLSLFSLVTFFFSSSFLSLFLIYLLSRHDFLACDC FPLFLD
4195	A	835	1050	GSR*HNLQIIGRPRRADHLRSGV*DQPGQHGETPVSTRNTRISQAWW WTPVIPATQEAEGESLEPGRWRLW
4196	A	2	112	SHIPAASRRRIIPQVGHPPPLPLPPFPQSHAGVAAGDE
4197	A	36	172	GQICPENKSHIPAASRRRIIPQVGHPPPLPLPPFPQNHAGVAAGDE
4198	C	1	1482	MVTHACNPTTIGKLEPSYVIRKFLDAQRIHNLATYLTQLHRQSLANA DHTLLNLCYTKLDSSKLEEFIKKKSESEVHFDVETAIKVLQRAGY YSHALYLAENHAHHEWYLIKIQLEDIKNYQEALRYIGKLPFEQAESNM KRYGKILMHHIPEQTTQLKGLCTDYRPSLEGRSDREAPGCRANSEE FIPIFANNPRELKAFLEHMSEVQPDSPQGIYDTLLELRLQNAHEKD PQVKEKLHAEAI SLLKSGRFCDVFDKALVLCQMHDFQDGVLYLYEQG KLFQQIMHYHMQHEQYRQVISVCERHGEQDPSLWEQALS YFARKEED CKEYVA AVLKH IENKNLMPPLL VQT LAHNSTATLSVIRDYLVQKLQ KQSQQIAQDEL RVRRYREETTRIRQEI QELKARVKAMPPPGKVPRKE NLWLQCEWGSCSFVCMTEKFFEHVTQHLQOHLHGS GEEEEEEEEEDD PLENSVNKD IRNKSAILPSRSNC*
4199	A	913	1299	ELGIVGKHAPTGGAGYHFLLGMAAEVLSKFTAVLEGAGTAFPATQHH RVVLADCFVFTETDCVLPHADKTTQDCRRNSVPGATHSAPTNRKWS GISGMTFRLWKSRMQGPRSAWLC*ACSPHCFSLVW
4200	A	1	587	GAEETWEPTDGSGSAAQDGVQWCDLGSLLQPLPPGLKPSSHLNLPSSG TAG*RPCALPGKVPRKENLWLQCEWGSCSFVCMTEKFFEHVTQHLQ QHLHGS GEEEEEEEEEDD PLEEEF SCLWAGMWLLFSGQFCLTSSAMSY FHCYHTKLKQWGLQALQS QADLGPCIPGISRAGTSSLSLTSTSCVWG TTGEILR
4201	A	262	409	RSGGRNISSRKSITAHRSISAPGSISAQGSIPALKSILAHGSIPSQG *DTPLGWDAPMG*DALEGWDAPLG*DASRG*DTPMGRDALSG*YVPS PTPSSWANALPCHFLPQMFPLTNVMPTNPISAE LNCGRGAGWQEWMC PGLLQAPVPNHIHSCSPTASRGLRGQLSSQLPETAKAAW
4202	A	729	922	WFETIEATQLYFNELPDTFHCVLCFLLCHFYNVKAFC CCCCCCSCC* NTCSLIFRPTVYYALML
4203	B	306	392	LTSGETYPKSGKAVEEAQPNSPPAEDVRDR*
4204	A	965	1298	GNLVTAFLQVLVLCIPDESLYRSICFLLHHQKLHISVPQSPRWGWTSLG LAGTPRCSPLPTPPRLLLPQPSRPGATGKI PRPDRTTPVRPLGHKE PRGT*GKSWPAVAQPPG
4205	A	1	324	AGSTTGALAVAVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAR EEGFRGLWKGTS PNVARNAI VSVLVELTFDSVGG LVPARIPSVPSLG KFSQNL RPAPDSPA
4206	A	310	513	VKERKEDVVKTRYMNSALGQYSSAGHCALTMLQKEGPRAF YKGFMP FLRLGSWNVVMFVTYEQLKRA
4207	A	65	191	QEISIMVGFKATDVPPATVVKFLGAGTAACIADLITFPLDTAKVRLQ VRG*SLGVL MVSTLFPQRHRPLKGQCLEHRDDWRWEGHAYPCSYP VLALQIQGESQGPVRATASAYRGVMGTILTMVRTEGPRSLYNGLVA GLQRQMSFASVRIGLYDSVKQFYTKGSEREYGARV*AGNQHHGWVQG HRCAPYCHCEVSWGWHSC LHRSSHLSGGYC
4208	A	12	237	NFKYILPKILHLGEKIYNNVYTCFNNLFHCTTYILYNSTINQPKKIT S*HLNKNLPCKKHSMGHYKVVF KIFFK
4209	A	361	444	QRLKNNCVITCS*QRPRVFSSSPQGLAACHYRGLRSSPQSRGRCLS HFSCQGVHPRSCQRGSAWSPRTTGQRGPTVGTGRTRKRLNTAYLLGA ASADILRPI PSTSR

4210	A	89	198	APP*THKWKIPHTSCDRSLSTCWHTTVDSTSLREK
4211	A	119	699	PTLMLHYIPWGRGRLGGWQCGQSHSARCAGTGTCLPMGTLMHMHEA SRQVWGGCILPLPFPYFLPPQLPS*LGPSNIWVAKDGWLRDLLDPP* YEWTLGVNWPSPGILAYWTVSAPSLGFSGPITDAALPCPYNLGGSSP HPRRGSRFQKTGLSLTEGNLPFPPPIPTPYLPHFLHIRVWPANVEQ MRCRK
4212	A	728	916	FFFPI*SV*KVSAQG*SLWPGVAAHIYHFSILGGQGGRIT*GQEFKT SLGNIVRPHLYKSGG
4213	A	1	319	NTLPPWF*LPSFSAAASVQRPPAPPALASPSTCPAASAPAPAGCARG RRAAAACEARPALLPPPAPPARRRRRPGSPRALCSGSARGRSQGRCA GTGGGLCGMWGP
4214	A	1	416	FFTEEEELFIVGGVWNCRKVSSAVGRDPSQ/PGS*GWAGRHPFRPS PSAHPWGAAITRQIPHQT*GPGEPR*SPPWF*LPYKSGWEL*IKPRW GELAAAKLQEGCGGEPQALLPAKPPGSTSSKREHLGASSSSC
4215	A	582	913	GRAPRLSGPAPAPTTTPVGGSPARAQPAAGGCAAPASGSGRLSRATP APRVPELRWPPQQALQGP*APPRS*S*LRSPGQAPEQALPLRPTP PTGRKVHGPPTLRPAS
4216	A	162	530	LLPYGLDRGPYGGVWCGLPYP/SGTVSTGPPORTASPLPKQSS/GPQ PPEFAACTGDAI*DARDAGDAGEGGSS/GAEPASSPAGAAGGGCGL AARSQVPEIRSGWLKSLPQLASSGALVICP
4217	A	160	835	GGCGRRTVLVKDYQFFAEGRLIQFRWENAAARFSALAPDMQRQNRFP PTPPYPGPGGGWGTGNSFRGTGPGGGPRTALPSRRVRGVRTTRRT GPRS*ARNGSKSLSAKRRQLSRGARFGSPSPGGYPGSYSRSPAGSQ QFGLLPRAAADPPPRVLQGHLLHLDQGVLEKKECLMSWKINFKAFKC LKIPWGWPRTOGICSGYKPNNTAILKHSQAKKEDTFC
4218	A	2	668	TVCQHTQYKESRESGAFERRAWGLSGGDKGKQKPMRSRSPGLSPQASP QKSLWGEQPCIGHRCTKLTVPNPKPPQTSQAACPHPEPSGLPCMESH SQKSLFPESAIVARGHVFPQRLGSGPLCPLPTLSPKSRPPLTSLALH LGVPPSPRYGPR*EGLGMGEAQNAGEMRPGEPWQKPSQGPPTLALG FVSPTFPFSPPLPPTHSGGPHQDSWAQCGSPTCLF
4219	A	198	394	AQPAVRPRFSASCSQPPFTPLSPHLRARARPRRERQKYTPSLDGGF WGETPAGGCGNHIHPWQG
4220	A	318	718	YHHLQGRDIPGNLRVEGVSVPHPAVRPRFSASCSQPPFPPLSPHLRA RARPRWERQKFTPSLDGSFWGETPAGGCGSHIHPWQGPRLFRRRSQ *PRR*AHMEGRVGRRSPLLHPPWEKTPS*LSGLTDRKQA
4221	A	1	563	ETFSSHFERPYLQFKAEPPLTSRGFVEKSTALHRISAEHPESMMSEV HERALQQHPQAQGGLLTETREKMHADNNFTKTQDRHASSDAFSGLRF QSGTSRGYQRMVPREEIKSTSAKSSVSLADTAPNFSRLLSNVTVM EGSPVTLEVEVTGFPEPTLTWVWVAYNDKP*METNSITEKNHSVSTN
4222	A	366	622	LSTMLHQHLLSVLLKLSQSLYVVYSFFLIQSTLQSGTRVTFKCRLO AGAVAQACNASTLEG*GGWIARAQEFETNLGNRRAPCL
4223	A	43	245	NGWVGDDVDDYSLHGGCLVTRGTKWIANNWINVDPSRARQALFQQEMA RLAREGGTDSQPEWALDRAY
4224	A	634	1316	GSGPHSPGKMWVDDSRHSRDVRSRSLTLMVTECLSLQEFNSMDLW DFHKYMRSHKAESSELVRNSHHTCLYQEGGAHHMRAIRQRVLRLTR LSPEIVELIEPLQVVRYGEGGHYHAHVDSGPVYP*TICSHTKLVANE SVPFETSCRYMTVLFYLNNTVGGGETVFPVADNITYDEMSLIQDDVD LRDTRRHCDKGNLRVKPQQGTSSLLVPTTCLMGKVGWVT
4225	A	506	709	FLMRSEFL*KVFPH*HS*GFPCVCSLMSCVG*LLGEGFSTFMTFIR FFPWMCSPDDSGFEIFPLIS
4226	A	1	1662	MIISIDAEKAFDEIQCFMLKTLNKLIGIDGTYLKIIRAIYDKPTANI ILNGQKLEAFPLKISTRQGCPLSPLLFNIVLEVLAIRAIQKEIKCI QLGKEEVKLSLFADDMIVYPENPIVAAQNLKLISNFSKVSQYKINVQ KSQAFLYINNRTESQIMSELPFTIASKRTKYLGIQLTRDVKDLFKE NYKPLLSEIKQDTNKWKNIPCSWVGRINIMKMAILPKGIASFTGYCI PKPEVILKLETGKEPWILEEKFRSQSHLEEPSEYNNNGNSFWLNEDL

				IWHQKIKNWEQPFYEYNECGKAFPENSLFLVHKRAYTGQKTCYKTEHG KTCYMSFFITHQQTHPRENHYECNECGESIFEESILFEHQNVYPFSQ NLNPTLIQRTHSISNIEYNECGTFFS*DRVSLCLPG*STVARSQLS AASISQ\VKRSSH/CLCLLSTSDYRCMPCLANLCIFCRDNCAMLPR LVSNS*AQNKLKISNFSKVSQYKINVQKSQAFLYINNROTESQIMSE LPFTIASKRTKYLGIQLTRDVKDLFKENYKPLLSEIKQDTNKWKNI CSWVGRINIMKMAILPKGIASFTGYCIPKPEVILKLETGKEPWILEE KFRSQSHLEEPSEYNNNGNSFWLNEDLIWHQKIKNWEQPFYEYNECGK AFPENSLFLVHKRAYTGQKTCYKTEHGKTCYMSFFITHQQTHPREN HYECNECGESIFEESILFEHQNVYPFSQNLNPTLIQRTHSISNIEYN ECGTFFSEKLALHLQORTHGPEKPYECHECGKTFQNFTEHLRRHTG EKPFGCNECGKTFHQKLALIVHQRTHIRQKPYGCNECGKSFCVSKSL IAHHRITYTGEKPYECNSGGVRPALWDERSCGYVSAGTKRAEGEVWKG QGEEMGSIVERLVTLSK
4227	C	472	681	MNHKIYVYGHTQQFLYCSYVFKRYEFYSNPTLQGFCLSPHSYFYKYL LLTGRNLAIILNIFAQWYQSL*
4228	A	2	277	RAEIPAGEVWDGAGPMGAELKPWARQRKQVEMDHVGPLLSPPPGRS* SPGPGRGRSRWTMLGPFSPRPQAAVRGPRPGVLGSPREALEPPGARH PRAVTAAPRELQCGSTVRAR
4229	A	1	240	ALLGWFVNLYKEITTTTPSFRRRSYILGFVKLYVSEHFHFFFWVLY FL*MHCEKFYFRRCNAGRRSQIMYIVFLKSLSS
4230	A	1508	1686	IFFQPKCELYKNL*GLGAVAHACNPSTLGG*GGWIS*VQEFETSLGN MAKPRLYKKYKN
4231	A	596	729	YFPNKHGILCRVQWLSL*YQPPLWESEVGVLELKSRTAWATW
4232	A	1212	1344	ATCLSLEKIQLLIQNPGR*ASCDSSLLGCSPLDSSHFTVL
4233	A	2	114	NRPCSQAQWLIPMLSRWFLAWELLSFAAPFPKLCSS
4234	A	1	326	SWTAPEEALFSSRKLDGGSQKWLIGRGQASFGQSAVPSWFREGRAWL SLALSPLCLSIITFPPEEKNYLPCKARFYTDFTNCAKNRCSQETC LEILGWTIEAQKDT
4235	A	37	199	VLQLFKMSSLPLMITDTQQAQVSSGLWIGIQIQSLTQRGRGCAPRMPR KAYISLT
4236	A	3	263	TTHAAHALRIGSRIRDFPGRFRRCYHHRTSLILTDRDKYPFTPVILT SLHSFCFLLPSPFQSPPAVYSNYVGNLYFYLLNKRSDG
4237	A	164	298	SSSKRNRYKFKKRTSYKVNTAELSSLEANWRVCAGSCRDTTRL
4238	A	60	152	RAGWIFSICLVRKSIFLLKKSCLASSAVFST
4239	C	512	805	MSSLPLMITDTQQAQVSSGLWIGIPNYRVFTPTGTWVRXPHATESLHK FNLNRTWEMGLQRRVXTXGTNVKALESAQQPWNQAGRGDNFLWRK GGD*
4240	A	1	361	EPRMLYTRYVSDPEFVISRVDDFVVLQFLRMSSLPLMITDTQQAQVSS GLWIGIQIQSLTQPGSTIS*YCSFFKSVIICHLMIT*YTTSSFFRPC GLASQIPESYPAGTWVRAPHAMEKLT
4241	A	545	865	PNNKHPYKSVTILSLCAVLFSLYIFNSGHFYFTSSIQFRHLNPKFNN LFYQTFVLRTKFL*II*QIKAEPLIVEHK*KIYKKPYLFNTQVLAL KLKR*GFLYIIS
4242	C	47	319	MVFHKARTRMKERTDTAMQAESASETNKRAHPALPPVLPXGRWARR GQEAPRPHLLSPQSGQGQAPPWRERGVTRLKLGEGCRGRLAP*
4243	A	211	472	STLGGSLCAQSGCSFEPLPLRGPHAMPVKCAQPLFS\SPCPPCLPR AAREGEQGEHACWFQMHLLALPYLCVPSSWSWLYGTPCF
4244	B	1	1023	MCWAPSTRGGSPALHPLLLLLPHPLPARCTGFRAPAVPSSPAGIFGH IAVIGSPFPTAGNTSDSFSNGCSQDVGSPLCGCLLGVIWLSVS QGNFATFSPSPSLSAANLVIAIGTIVMTGFLGCLGAIKENKCLLL SFFISPVAELILLILFFVYMDKVNENAKKDLKEGLLYHTENNVGLK NAWNIIQAEMRCCGVTDYTDWLPSAGGEHGRPLHGRTPRAAGATA PRLCGERAAMKRSWGMFSMTLFQHIHRTGGNHVHLGPKIFASFPGA TDISSGLGGDYIICDPKEKKYRKPKREPHLQ*

4245	A	630	841	DTGPCWRERGVTRLKLKGEGCRGRRLAP*HLLPPPKSSSQPCAPLTPTA GWLPEEKAEVCSGCPPCSPSYKP
4246	A	29	360	HSLISQREKESERERARESERE**RASERERERGRDKIPTRKGGEV QFLQTIHFFFLIFLTAFFEYQFKERGSYYRYRGGAKKKGGRGEEKNS RSRNPSSRSFTGRKKRV
4247	A	253	451	NWSAGAALLSAAHAHTPSPHQARPTGSPPSAALWGSPSPSRSPPHF SPTPDL*MRPERHPSSAPF
4248	A	355	500	ARCCGMHLYSQIFGLRLWEHCLR*KVLSQVWWHAPVFADIWEVEVGA LLEARSRL*CAMLLPVNSHGPPWTWAMQ
4249	C	175	387	MLKAQHLQGPWAGPPMPGLFQLRSAHGSHGAAAKAMVQRQMPPQAVT GTXXXQGGHCPQPPRAXYAQDAPG
4250	A	342	608	AGSGTIGMLRPADERGGQSRCRGSAPHPISQAAPCPAFLNRPFTGPS/ CGPSVTSLRNTAGFCPE\GPGCPPSLAEASCPLPSCRAGSHWA
4251	A	56	277	TVSVQRHQAVQSPVVVFTEHIPQDAWCSPSCAPGPN*PPLCPTNKPC ALQQGMKPLALKKSLGGTVCCGSKRD
4252	A	235	721	DLADCSLQLQSRSSWKKCSTMLQKVLVPPEAATSLSHPTPRPLPHPP ALGSPLQPPSNTFGP*CCLSQDAPVFPSPVKLHLVTVPASSLANESR KGPSPRVFSRTPAPSSSITSISDSGIQATVWSGVRLSVSASSFGL LTSPFSASGVSLSVSPLASTL
4253	A	1866	2283	IRILYRSPHLQLPCLTRFLVKKYSVTGNWMVSLKD*SLRLDCWHGP LNLVLKLDEVWQNLGTSTKSL*NNFKNILGKINTFKTLFGGGMKLIP CKVSFSIYLMVNLESHDSTWHLQANQTPHFDVSPVLVLEFPFKF
4254	A	2	767	ELLFDKSTMRPFQKASSLPPIVGSRKSKGSGNDRHSKSTVGSSDN SSPQPLKRKGKEDVNSEKLTCLKQNVKLKNSQETIPNSDEGIFKAG AERSETRGAAEVQEDEDTQVEVPVDQRP AEIVDEEEDGEKANKDAEQ KEDFGSMNGDL*EEGGREATDAPEQVEEILDHSEQQARPARVNGTD EENGEELQQVNNELQLVLDKERKSQAGSGQDEADVDPQRP RPPEVK ITSPEENENNQQNKDYAAVA
4255	A	79	928	TWQRCNLNPLCLHIPVLCSLSSTMWDLPLDRGDLHLSCIDSSNWAL FRCQSKVLYHCVEADSKGLRSVLDELTLNKTNLKLMESQTEKLN LRNNHEEAGTTQNEFKVSVCQYLSRYGGGGYHYKRQSFHKTQSKELM GRHRLLTIANRHEIAELRWTLQTLLELQAQWPLVRMLQ*EP*ER LTC*R*RENQEPVQVVEEQPRANTKETRKSSFSQPMASASTKEESQ DGRRKGK*LKGRAREGKMLHQKSLGFKEYFEGRGAGPTPSGPTVTQL K
4256	A	235	674	SGKQNNPQATAKAEACTETRSQMGATETSSTFDYLGATSLKSPPHRK VVFECFTIETSLHSNSL*ILLPLHSISNIQKQTQTSNLNINLQPATA GPPSQAPPTALSELPGGRSAPEPSHAAPFPARVPPPSSGSPRPNARW AARAA
4257	A	60	473	CLGSLQPPPTRVKQFSYLCLPISFFFFLFFFGLFLRFSLCHRF*AV* L*CSLVLFSSCFLCLGFAMVFGSVGL*FSSSLECFQALFLQTFLLSF PLFFMNSN*PCIRLTEVVPRLSDALFIFKNSFSCCADAADAW
4258	A	392	517	MTLKDVAHAHCNPTSSGGRGGWIT*GQFKISLANMAKPRLY
4259	A	446	767	IWYKSTHSSVIFKCEFFLQFLSQSLASPRHECSGAIMAHCSPLLQ SSDLPASFLNFSWR*CLHYVAQPGLELLGLK*SIPPWASESAGITGL SHHAWPKYELLF
4260	A	119	342	ISICIKININIIYACYVYIIILCIRIYLSKYILLENCI*CTILFYVI FYVYIYLHIYIILLRLCPFFIYSWSPV
4261	A	374	471	GKK*KCPTHLSHLYINPGEKSYLFETSGLNF
4262	A	255	496	LYKFQTSVPLT*FIKALYITFYNSR*RGYYSKFKT*S*RPGMVAH ACNPSTLGGRGGRIT*SQEFETSLANVAKPHVY
4263	A	231	417	CBLPVRTHGAGCVSSDVTLP*PCPFSPVSQSPSVCLSPLFSDPCEE PPYPVLESPLDCSF
4264	A	1204	1398	ASFLAISMVVRVGVFPYHLFFLRQSLILSPRLVGVR*CDRG*LQPL PPGYK*FSCGLPLSSWDF

4265	A	581	705	LLAECGAHACIPSTLGDQGRQIT*GQEFETSLANVVKPCLY
4266	A	3840	4074	AQEYRGQLRQYSETMSLQKKFKNRSAGCGATCL*SQLLRRLGWEDHL SPGGRGCSEP*SHHCSPAUVTEQDLSPCHP
4267	A	173	421	PRPLAHRPRKQYRLLLRSSYQVSLAGWVVRQKQWGRKSHPKSPG GGQAQWLTPVIPALWETKVGGSPVRSRPAWPTW
4268	A	423	595	SCLSINFHLGQAQWLMFPVIPALWEAKVGRSP*VRMVSIS*FRDLPAS ASQSAFNISH
4269	B	1	1224	MPTVGKAQARRRTRDTLLLDITQVLIDQSPRKDTGLAQQTGVIVPSK GIVKYWRAQLKQDMKYASPAFELFYFSVRAQSTDGIVTLLDPTTRED CDISSAPNPEVRTORQAEVAGVGLLAVKVPRDEEVLGGAPGPQKRS RVCGEPTLQRRSGPLPVARPGSRCPPPTSVSSPVPEDYGRVVMIR LDNPGISGRTIENNPPELEKQLPGEPSSENSPYLGPPQVLFLLRDPRE DVMLLLNQTPTTAEKQAVLQAAEIFRNEQQISYNTSKGKKGDRECEE IAETPFQIGSEAVPLDNPWNSSSSAGEWKRRHFLICILEGLERTKA KFLNCSKLSMVDQKPDENPAAFMERLREALIEQTSLSPDSVEKQLIL KDKFVTQSASNIRRKLOKQAIGPISTLKNLLK*
4270	A	1016	1393	IFQLGEYIFLFLFSVFEMESHVTOAGVQWCNLSLQPLPPRFK*FS CLSLPSSWDYRQMPPLANFCIFSRDGVSPCWPGWSQTPDLKRSABL GLPKCWDYRRETTAPSMFLQNLALLVPMQOR
4271	A	825	1246	RAEGFCPNWCCQSNILIPCHDPGSRSAQSDWACHLGWQSGSGQNHG VPAFGDALQLPGNTSRVGAPQGGSGRGRKDGPGNSH*AHGTGWRECY GDRSRKRNRRQFWHLAPPRSEIFLIILACTLRNNGSASCPRSCFDSF LRVPRTRGRFWGSTWGVTPGI
4272	C	442	522	MRCASPSTSKEFSCALLQCLQDLG*
4273	A	322	1025	PLLCVLLAPPEGAVGDICKEDAGNMPSTSEGSYLEMAHFLRNKLA GSSVRKPDGSLFWEALRAWSNMAAPSGGVNCEEFAEFQELLKVMRP IDDRIVHELNTTVPTPSFAGKIDASQTKQLYESLMAHASRDRVOK NCIAQTSAVVKNLREEREKNLDDLTLKPT*EKSRQS*KWVQSELNV VEVVNDRSWKVFNERPNSLQASKE*IKRDSFFFFFFLRTGSSHKS
4274	A	22	54	TSRLFHFSFPR
4275	A	506	623	TRDSAHAYNPSTLGG*GGRIA*VQEFKTTTRAHSYTLIPT
4276	A	296	495	KHVRPYITHSLGGKDFLILEKIWLGIWAHACNPSTFRGQGGRTA*A *EFKTSLGNIVRPLCLYKT
4277	A	270	558	FWIFLRSFYVIRKHLIGHFHPWPRVLKC*KHGGWKVHGGPGQ*RQKG TGKEGRKGLRGRRELTEEGARPLFSSGPVESTQIVPLPQPPYVGAAA S
4278	A	51	113	ISHHPRPHEHKCAVSSAIGR
4279	A	179	387	ILVGFCCLFPPPSNK**THTHTHTHPHTHPVVTNRISLQIGCRKG KQKTSQGPFTATSLSPLSDSAV
4280	A	464	596	EFSPGMGAYTRSPSTLEGHSGQIT*AQELETSANRVRPCSYMW
4281	A	468	564	YAFYRTQVPGGIRLV*CRLRVLWSNILKKQS
4282	A	780	839	SQHFGRRPRVDHEVGRWRP
4283	A	993	1052	SQHFGRRPRADHEARRSRP
4284	A	175	387	HFGAEAGWITRSGDRDHPG*NDETPSLLKIQNISRWWQAPVVSAT PEAEAGEWHEPQEARACSEAEFEP
4285	A	161	409	PPGVIIYLLFVKVRLIWNVMVT*VYMTLLSFYPQICITYIYKYVYI LPI*NIYIYTHICIYIPLFLCLLILAIKEGAANV
4286	A	1910	2120	SVSGFWLEAMLPSELSEGQPCRLQPFIGNKSLTGWAHACNPSTLGG* GKWIT*AEFQTSANMMKPCLY
4287	A	1156	1320	KNSS*FFYFLSYLKNKNRPGAVAHTFNPNTLGGGWIT*YQEFETSLA NIGKPCLY
4288	A	1497	1767	PSASPPQVPIPALPQWTGPRQNPL*CLHIGLCSPQPSDGPWRKACS LFQVPSHCGRIRKKINKVHICVFTASRVWKPKPAAANDQL
4289	C	1434	1655	MKKFSHILKKKFFCTLPVIMLKLMLNLSQCKTKEGKYCTLAENLF HHKIHCPSDDHRSFSLAVVKKL*

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4290	A	275	485	TNWKLSLCEKLYSTHFCTDHKAVLFP*CLSCFVLLCVLFICVLFVGF RFLSFCFVFTTSVISTSFFLAVS
4291	A	889	1199	KKCVCVCVCVCVKC*LLKLMLVGNFRALWGSEWFLHHHLSSTNRKML SLQGHV
4292	A	502	768	SPCDQTPVEEGMLPKFRKSLQGFSLNFDILILPSQK*FCIRGSKTM YIWPQTVSHTCNPSSTLGGQGGWIT*DQEFETSLANKVKPRLY
4293	A	3	309	IFGRDGFHHVGGAGLD*TPDLK*STHLGLPKCWDYRHEPPCLARRYF KNNKKNLNLSSHHTKTVNILPIFSSCTDVFLHNDVECNVFSLDL VNIFQSC
4294	A	204	317	NSLGRSRHCESQADWQGTAKTPFPAPAGKSSALCSP
4295	A	1905	2032	VKHLDTGQK*GCNAFNVGQSGPGPDAAAPRWASRTPGGVNAGI
4296	A	2	225	KWQVTWLSFCSTFMSPPSSWSSCS/PPCSAQPYAPVSCDGPPIRFP PLLD*GRLKTYFPPPCVNWGCWGCQCVISQ
4297	A	299	663	IAHITEIRNLILHSLNNPLWLEPTRIEKFSPRGKVTSLHPRVKMSP SSPKNSHPPEEVGSASSSFLREPSPGGSQHSYPAPSIDAMVPPYRV P*TPFGIKEDLKTPLFWGITFLLPCV
4298	A	1	406	MDWEGSLPLVFNCRDASLIHPRFKGVRPRRDACLGPSPLAASPAF LGKGQITIDAELRVTLTVEDSARLHPGEINSHVAHTKPVWWSLHTDA RETTHLQORTHFQQSWLV/CIRP/MNPAKSTVSSVRTQT*APLP
4299	A	236	768	VPCRESPRALALPRKEMMRA*NQNKTKHDSRHCRISPVGNMEDIAENN YNSFKAELGPNSSSASTPPYNLFIASPPHTCSGLQFHSTITDAELR VTLTVEGNRMSVVRSSFLGLNQLKLAKSMMAAYSIFEEPLASLYSNF HTK
4300	A	302	897	SVAKEGEVEVSHTCGLKWGDIRGGCEGGFGLGEKAAMRCGCSPIGIV READNLVKVSPPSVLIKKGTDLPTVRVTRRSASVMVLTMLPATF LRGNCWAGGGGLVTE*NCKPDQV*GGEMIKGL*GGG/VRGCGRIET* LGLARRSLGRRGEVRLVWRSGLTLLPKYCAFPTVFTTARPGDPLPCLA QWVPCPWSLAHC
4301	A	111	275	SRNETESRTRCEEGR**KDYRVEEQRLRKNWDLARPGKEQLPAFQSG NLSRQLH
4302	A	3	220	SLQPLSREDLGRSQSESLGPEFQGLWEWLPGLNSPICSGVPHRWDV A*EESWAAGSPWPGGQISGTCSKLL
4303	A	2	347	LTMLPATFRLRGNCWAGGGGLVTE*NCKPDQV*GGEMIKGL*GGG/ VRGCGRIET*LGLARRSLGRRGEVRLVWRSGLTLLPKYCAFPTVFTTA RPGDPLPCLAQWVPCPWSLAHC
4304	A	2	265	DFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRK TTLAPNTQTASPRALADSLMQLARQVSRLESQQLLLARPS
4305	A	3	865	LTQQHILTADTNLLCNDYGAGNGIKSIGFVVHACIRATQEDASSHD STIRFLICCFQTTLQAGKQNKHVKTLLKRDTPPGQKTNGEVERNLS FPTSPGNRGSCNGWGWKTQKTGFTSLEYGRSLSVIRSLGQVTATPS STETGANALQSSAAFQVKNIFKAVNGVSGYFEGKPTVEPSVCGGRLE SPWQTAGVSPTVQKLKSLKFDVRGQEEVWEKDEACLHPGEINSHVA HTKPIWWSLHRDAHKKKHRRGHPAGSEAVEVNGGSAKAANSNGGQRAK AQLKP
4306	A	288	597	TDFSVRCKGCRGTGPFRLIFQDRIVGVELIAV/C*RHGPRFSSCRLS CRRPFDKTCRLMCHQRLSGFPQEQTQDRSRCIQLLFRQRFAAASCP HQVLLQTQYF
4307	A	3	188	KPRRSRSESLGPEFQGLWECLPGLNSPISSGVPQRWDVA*EESWAA GIPWPGGQIDFWHL
4308	A	498	803	HLGPEFQGLWEWLPGLNSPISSGVRHRWDVA*EESWAAGIPWPGGQ ISGTCSKLLLEEVLLEGLAAAVQAFGSSCVLEMWLGFSQWRQGIAT FFYYCTP
4309	A	3	338	KPRRSRSESLGPEFQGLWEWLPGLNSPISSGVPQRWDVA*EESW AAGIPWPGGQISGTCSKLLGEEVLEEHLAAAVQAFGSSCVLEMWLG VSQWRQGTATFFYYCTP

4310	C	321	734	MIKHQGAFFVDRRQSFVSTDKTCLLCLSQMKGIEIKRRERLKS GKEKVWLRDRERLEKRTILRASVFKGEKPAAGERGKVWSCDSIHVLQ EKGSRPQISVLCILNHRKYSRFSVWSLKPPSMKLEVRKRCQR*
4311	A	867	1111	RHCYRGTR/ARCRSANAGAMILTMKQLAIVMRVYQHQVRRSMRPGRN GARSGMSAVGAYYSSCIRVMTALQSCCTGDDEAVLL
4312	A	1	560	RQRRHILSVDPKLWRRSWTGKAAFPWCFIIAGTPLIIHPCFRGVRPC RDTWLGPSPLAASPAFLGEGQRIKYLGIQLMRDVKDLFKENYKPLL EIKVDKHKWKNIPCSWIGRINIMKMATVPKRSFSMPSTISPLNNPPA YLCLRTFLIMKTMMAAKMMMEVMMMTVRPLRPSQTQPACTQVK
4313	A	2	268	WMKLETIILSKLLQGQKPNACSHLQSFMSMPSTISPLNNPPAYLCL RTFLIMKTMMAAKMMMEVMMMTVRPLRPSQTQPACTQVK
4314	A	11	783	NLFLRPQKQDTWYHRIRLGQTKHLLKELKVITYLLYATISF*DV*RH C/RSAILAEAKETKETHFIRGPKTLAPVTDWEGSLPLVFNQCRDASL IIHPRFKGFRPRRDACLGPSPLAASPAFLGKGQRLKTDARLPWKPP DHRRRRASGNSHSGRVQPPSRLPSWAHVECLRLFQEHGASCQWIYRS GIWRTVVFMCVRVKRPPNRLCVSNMAVYFTWVQVHYPLYENNKTLR ALRMIHVESLACGVRESSTNDNY
4315	A	177	434	LCLWLQPPF*E* IAGQVGE*SRNETVSRTQCEEGR**KDYRVEEQ LRKNWDLARPGEQLVPSSEKRDPLRVKQGRCPV
4316	A	1332	1602	GPARNRAQHWWAGTAGPSTPSAAAGPGAKSLIARGQQGWPTAPSVG PAKPTPTRNSSWPASAVCSPGSCSRLSLHTSLPLPQKSGTCR
4317	A	797	955	LNTKGRLPSQSVTGARVLGPRIKCVSVFSSVPISDSSSMHDSRCCQR VTAFH
4318	A	1	817	MWESLELPGNIFNGFDQNADNDMDDEIQAQEVISDGDEEFVGNWNKPR DLVPCILATLALTQRQDTAQTMASEGARPKHWQLPGGVGPVGAQKS RIEVWEPLPIFRMYGKACMSRQKFAAGAGFSWYVPVAVVGAKVHDV NLHMLSFPSKWLHTCMKFGAVTQIVTSLGRSSCSLLLEKDPMPVLR PTSPRNISPISNLTKETRFIRGPKTPAPVTDWEGSLPLVFNHCRDAS LDYSPTFQRCQTTQGRLPWSFTLSSKSCFSEGGKARFN
4319	A	3	93	LSPS*AIISVPCTYTPRWPEATEDPQKK
4320	A	874	1114	ESLGAQAEDYCRSGALTESLY*SSSKRKGVGVPKQSLLYSTV*WSC GRGSLSFRPQNDRASSFPQYQEKSTEAKLPKGL
4321	A	264	1259	GDRWEGKKEDLGRVALGTETRGKLMCKRMPGH/AGTSDHLSILGQEL FRSCRMEKLK/RAI/CPAIWNYCRVCIGVKRHCRRK*DA*ILQDLNN SCPDKDKWSEVPDVQAFFYTSVPS
4322	A	607	769	SQVLRPTQPKHELANFKSEDRSVRPLSPS*AIKSPVTCTCTSR*PEA TEDPQKK
4323	A	495	658	GLTGTTHWAHFTHWLVVLSHSTELSGCERLCGPAELGTFTLWLF*RK PFADHWP
4324	C	218	352	MVGSDFLCWDHWLITSXXXXXXXXXXXXXXXXXXXXXXXXXXI
4325	A	444	996	PMTHPFFFFPAEVHEPNQRQAFLVPVSQARWTASSLFSSWVSASTSP QLEELQGSTQTHFSATCSQQPSRCVETVDPSSLLTQQGLAFSAPTG RQAQRCSARMAWNPGLPLPPPSVHPCTPHCP*GPPQPPSPASTPWGS CCSRWGHQAILGCRDRERCRCGTCSSRPWLPLCLLPFPDKWS
4326	C	296	625	MVSEHTSPLAKSSASELHRTSWSTDNGMDFWRECQFRAKEIQGENE ALNKSSKRAQKLVSIDLNMERQVRRKYIVNAGSLHLFILSLLSSIHL KTAFCVLLQGNLTL*
4327	A	221	344	KVLSSDFCSVPFCVCVCVCVCVCVCVLTLL*NSSIYYGH
4328	A	441	656	AHNYIYFQRYIHQTYTDTGRGMRIGMRDQKKRPGTVAHTCNPSTMG G*CRKTSQGQEFKTRLSNTVRPNL
4329	A	409	749	RRGRERKRHTHIHTHTANLFVSFLYFLSFLHLCALCLS*WM*RC SANPILPTGPYASQTFMILPSCCTVISLPCWLLFPQYSQTLYSLFT ELNGQITVTSAKITYTSKI
4330	A	1682	2410	LNKGGQTDIASSQTCLVGHVESDGLHTTMIGPNEPAFLSPENNNCP IWQRERWTIIQKKMNGMHTHRNEAETIAGILTVQELFPRNTSLTV

				IDVHSHSVLFCTTIQVLISQVNHLYLPLPQAFKFPVIFIIITSTGLL PTYVRVVMYNFVISYNGKKNQNI*KVICTELYFSSFLKMICMVRKRR GQPGEGRASRELCTFYTFVLCTALLILHPIMILLEPICKLLRKFC VYVNNNT
4331	A	2	57	NKTQKKLPNACKCVLYSC
4332	A	19	192	WKCSKIRLWLWLNKSVNLPKCVNTLKTAECDLYLVKLFLKYGSTA RDIDIKDAEFE
4333	C	218	364	MTRVSSCFSDLATDRSFTHKGNNIVSSNSKIISLTWMGFELKTQHK I*
4334	A	172	304	PSPVFLAPGGVRAGNSLYPRGPGFH*PRFGPFPPRGTGREPPF
4335	A	258	509	RGHSKQQRDIPRVLDHLMINFSFKIVTVCRSLYSFI*KQAQVKLFLH LHPIPSSHTHTHTKPTLLLTTPSDDSWVFRWC
4336	A	1	2411	MSFLGILCKPLQNESQEESYNAYPLPAVKVSMDWLRLRPRVFQEA VDERQYIWPWLISLLNSFHPHEEDLSSISATPLPEEFELQGFALARP SFRNLDFSQGHQGITGDKEGQRRIRQRLISIGKWIADNQPRLIQC ENEVGKLLFITEIPELILEDPSEAKENLILQETSVIESLAADGSPGL KSVLSTSRNLSNNCDTGEKPVVTFKENIKTREVNDRQGRSFPKKEVR RDYSKGITVTKNDGKKDNNKRKTETKKCTLEKLQETGKQNVAVQVKS QTELKRPVSEARKTPVTQTPTQASNSQFIPIHHPGAFPPPLPSRPGF PPPTYVIPPVAFSMGSGYTFFPAGVSVPGTFLQPTAHSPAGNQVQAG KQSHIPYSQQRPSGPGPMNQGPQSQPPSQPLTSLPAQPTAQSTSQ LQVQALTQQQSPKAVPALGKSPPHSGFQQYQQADASKQLWNPPQ VQGPLGKIMPVKQPYLQTDPIKLFEPQLPPVMMQQPLEKKMKPF PMEPYNHNPSSEVKVPEFYWDSSYSMADNRSVMAQQANIDRRGKRSPG IFRPEQDPVPRMPFEKSLLEKPSSELMSSSSFLSLTGFSLNQERYPN NSMFNEVYGKNTSSSKAELSPSMAPQETSLYSLEFEGTPWSPSLPAS SDHSTPASQSPHSSNPSSLPSSPPTHNNHNSVPFSNFGPIGTPHNRDR RTADRWK\TDKPAMGGFGIDYLSATSFSESSWHQAST\PSGTWGH GPSMEDSSAVLMESLKS IWSSSMHPGPSALEQLLMQQKQKQQRGQG TMNPPH
4337	A	17	300	TFKFYYRNLNLFILKKS YMYATFFIIYLYIYASFLLVLTEIFYFIII SKELLPVFIYQVYFPCFFLG*FIYLSSKNPPYNLFILLPFYNFFNN
4338	A	257	476	KAQMSLLDTLTHPVWLLCLKLCGAV*VKL*EYF*SICNICTAICVCG VCLCIYVTMCVCVRAIERKLKEECLS
4339	A	283	494	GQRCEPPPLPSPFG*DSG*EPFPFPAFQKAGGPASPSGPPGPH*DP TGPASEWKMATMGNRPPPEMVSA
4340	A	766	1083	FKHFGPFHKLHMLVLFKIQNVLFKDGNTFEVRRGGSRLSSQHFRPR RADCLMSSVV*SQPGQCGETLSLKKNTKISQA*WHVPVQATWEAEL GGSLEPRRLRLQ
4341	A	2	163	FVFFVETGFHYVGQTGLELLTS*SARLGLPKCWDYRHEPPRPAYVEY FYSALL
4342	A	192	440	ATVWEEPPCSPPPIPRARFWGPRPECCSSRGQKPKPPAYMSPDPAWR PAWLPSSTPTYD*T
4343	A	1875	2210	PLSQVITGKHQKRKRHLEEGKERPEKEQSKHKRKKSYEDTDLDKDKS IRQRKREEDRVKVSSGKLKHKRKKKSP*VYPPRKKNVSTGKRKRNL KKGQKRKCFGMSLFLGF
4344	C	217	396	MSEETAKEVMRAYLQQLRQETGLRLCEKVFDPQNDKPSKWWTCFVKR QFMNKSLSPGQ*
4345	A	1	546	MPAYHSSLMDPDNKLIGNMAFLSIKSQFKGPAPRETKORDIVDEAIY YFKANVFFKNYEIKNEADRTLIIYIPLYISECLKKLQKCNRSRSGTSP VAGVIVDCEVHGSSSSSHGTYVLISDLHKSLEQKESKIQQLAETIKKL EKEFKQFAQLFGKNGSFLPNIQNKLLQSLYPRLSYSMSYKA
4346	A	216	324	VFFFSL*NEADRTLIIYITLYISECLKKLQKVIKLG
4347	A	71	650	NPGAAKMPAYHS\SLMDPDTKLIGNMALLPIRSQFKGPAPRETKD IVDEAIYYFK\ANVF\FQNYEIKNE\ADRTL\IYITLYISE\CLKET

				AKSGNSKKPKVEERKCFTLGIH*FFPFPQ\EPGFFPL*RQFFAKP\ANKQEDEVMRAYLQQLRQETGLRLCEKVFDQNDKPSKWWTCFVKRQFMNKSLSGPGQ
4348	A	552	874	SGPNCCEEADQLAEESGNASHTSFTV*VRPRRACHACNPSTLGG*G GRIA*SQEFETNLGNTVRPCRNSEVLNRKTVSIRRALRVFSPLHTA RLHPAAAAARA
4349	A	199	375	FSLGGIPPFHRRGNWVSREWPGTVAHTFNPSTLEGRGRWIT*GQEFE TSLTNMVKTCLY
4350	A	368	546	PSMVCSNASCWQLPPVRRFCPDLFVPEVSVCGRHLGFPFPFSAPPGL GGPGGPHSWSLG
4351	A	2	211	YVYIYKIGIESRVSAICTPSMAALVDKRWKKPKCPLMYEWINKM*YT HTMEYYTE*KRKYCSTLSHATI
4352	A	1	676	PK*WGFLPLIYKKGKGGGTWGGDVLPSPSLGQGGGKKGWPKREGGR DLGAERKAGKCREKWKQSKMKGRSRKTGGERVKKPEKHQDTGLFPFQ IGGGGLRLSRVCVPQVQVGRGSVSLAQFLSCTSSD
4353	A	1029	1252	CKFVYSSLLFIYSSFFICLFIFLPPFAPVLIYPLAH*LCKPCSSYMSW VNIQYSIYFRHKCFRNIVQKILYSIKM
4354	A	299	562	FPSWQRDAQASLTSPAPLIYPKATPFRKRPFRRQLWNKGLIQSKLTQ RLYTVAHTCNPSTLGG*GRQMTWGQKFKTSLANMVKPRLY
4355	A	17	195	FMDAQVTFKLYIYIYTYVCTYMYIYTYV*MCEYLFIIYIYARIYMYI *MHYYTYISLTP
4356	A	3	565	NKIPRNPTYKGCGLQGELOTTAQRSKRGHKQMEENSMLMGRKNEE LENGHTAQEENVGNTIQDIGMGKGFNMKTPKAMATKAKTDKWDLIK KSFCTAKETTIRVNKQSTEWEIFAIYPSDNVLTIRISKELKRIYKK ISNNPIKKWAKDMNRHFSKEDIYAAKRHMKNAAHQWSSECKSKPQ
4357	A	1	597	MSELPFTITTKRIKYLGIQLTRDVKDLFKENYKSLLEIRGHKQTEE HSMLMDWKNQYHENGHTAQAIKRLKLDPLTPYTKINSRWIKDLNV RPKTIKLEENLGSTIQDIGMGKDFMTKTPKAMATKAKIDKWDLIK KSFCTAETITRVNRQPKWEKIFAIYPSDKGLISSIYKELKQIYKK KTPPSKSGPRI
4358	A	1	567	MGKDFMSKSPKAMATKAKIEKWDLIKLSFCTAKETTIRVNROPIEW EKIFAIYSSDKGLISKIYNELKQIYKKTNNPICKWAKDMRHSKE DTYAAKHKMKCSSSLAIREMQIKTTLRYHLTPVRMAIKKSGNNRN TTTREYYGHFYAYQPENLEEIDKFLDKYILPRQTSGRIGIPEHTSDE L
4359	A	1596	12368	ENWLAICTKLKLDPLTPYTKINSRWIKDLNVPRKTIKLEENLGNT IQDIGISKFMNKTTPKAMATKAKIDKWDLIKLSFCTGKETTIRVNR HPTWEKIFAIYPSDKGLISRIYKELKQYKKKNPKTPICKWAKDMN RHFSKEDIYVANKHMKMHHPSECKSKPQ
4360	A	48	436	RTGSSSGLSISATCLISQRRYSEDWCNVYSLVRSG*ERGS*LLSTYY VLGSLPDVFTYINSFQKTYLK*MGPGMVVHAWNPSLGG*GRRTA*G RELETSLSNIVRPLNNNNNNNNNSNNEVNGIRKEG
4361	A	2	2552	GQRDVLTTKRDDQAHKPNGLGDARETRWKDPRSLNDLVEPNLSRCSM AVRPAQSPHKRPGKTSIFKNQYHPDLRSSKATGKENFKDKKNKYLDP CTFEEERLLYCRFLDNKLLSRGKTYMCKEPGWFRILFADELPRKL GSPFQVTSYNLETRPDLKELLGSGCHCGPGICEENTLGLDSDRESPAP DIERAPTLWTNPAPPPSPLSGSNAQTSRMAGSDISQPAARNQRRGRC VFCDCGARTLTPALGSELYGEESQSSALPPPLMLRHFSPDAGDGS LTDIAGVOODGGESTARYPHSMRPWNPASGAATAHEEKPSTGRRT SRERRLQVSRQRKDRRQGIIRDGRAEAFKCTEGGLNGFLCKVVD TYLAELEEAVLALGGRPSRVGFSPPGNALRRLTRGPHTTLGEVGFIT AIFNKEKLKTRKARDFADFGTTIKQDFRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLES ECESCLCPTGDLPIRGSDISVFYQSSFQDYNAYQDKYHAKNTLGK KVRGLVLINPQNPLGDIYSPDSLMKYLEFAKRYEFYPLRLEQCCKKA HDQFLADLASILPSNTTPLIVSDAGFKVPWYKSVEKLGWYWSRVRG

				KVQYADLGAENWKPI SNLHDMSSSHSKTLGYKRLTKSNPISCQILLY KSRSKGRKNQRSTRTHCHHPSPKIYSASAKEPWVLATNLPVEIRTPK QLVNIYSKRMQIEETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIAL MLQLTCGLRGSSSRVNWREENGDTYVERVKIPLDHGTLTIMEGATQ ADWQ
4362	A	322	1288	RKNWGLRKIPWSSSLKQEQNLPESEFGSKKAFFGSTWRKKDGEPEFQGS LGCPLLKARPLLSQLPLLRRAISTRKPGQTKWKNKEHHLSDREFVFKPEP QQVVRRAPEPRVIDREGVYEISLSPTGVSRCVCLYPGFVDVKEADWIL EQLCQDVPWKQRTGIREDITYHQPRLTAWYGELPYTYSRITMEPNPH WHPVLGTL*NRIEENTGHTFNSLLCNLYRNEKDSVDWHSDDPEPSLGR CPIIASLSFGATRTFEMRKPPPEENGDTYVERVKIPLDHGTLTIM EGATQADWQHRSQAQNTTLREPRVNLTRFTVYDPDPRGAPW
4363	A	249	906	RIHFPRVSGPSSQSNPKFAVASRGFFSLSLSSAQDPPLPPPLGEALAL SLHPVPRRSTETVAGDSSELQGLRSPQQLAGLAFRLARLFLFPFP *RCKSKPN*NDRRSSVDSQIHLVGRESAHLPLAGLRVCVSLPLARC FGQVLQGVPLWIPSPGGS/AGVSGRRREERHMGVVVMRVREARVS S*ESKI/SRALR*STHLGLPKCWDYRREPPCPAH
4364	A	843	1186	QHSTKNSGGWAQTPYGSSQISVCVYIHTYIHIYIFFFFLVETESH VTQAGVQWHNLSL*PPPGFKRFFCFSLPSSWDYRRTPHPANFCI FSRDGVSPYWPWGSRTPDLR
4365	A	127	601	NLILNVTWPTQLAKQERLHLRLKTSVVWVVRKEKPTRFPRLGAVSHC PQLLILQLVLSPTSTKTL*EPDSESP*PKRKGPWGRTPGAPNLH SPPLSPEGPPWAAWNPLKLPPPQHSSGAVPSSACSPWAGSVPAAPPS VCYLIYWNLSQALHR
4366	A	30	436	RRRCGGCFPALPGSPHKPHEQLPPLCPRVPVA*PSSSAEHPDPRAGK GGGRGL*AGSSPG\AVPHPPSI PGRKNRMGSLEG/RGAPAPRRGGSG AGAAE/ASLTWPGSTGPAPGSHGCSAGVGPSRWAWSLPQRCGR
4367	A	497	924	KRGSRGWFFSTFHHLWGRLLQAHLLGPTPALQPCDPGAGARTARPGQT ASAAPAPLPPRRGAGAPPLRDLARVPAPPCCAQRAPPSSSQPGRNQ* *AASGPWRPPRQAEKEASAGKRRDRPVGARKTAAERDRRGQASGGQT R
4368	C	226	405	MCEKQPQNTTSFQGSYPKYTRGSLPELRQLLKVLFKKNWEHLQPR SMLLVRSGLSQE*
4369	A	3	275	TSMYVGPVAKDLLHPSAEENRKHMTMKRLAQSPNSYFMEAKSP*CYK ITTAFTHAQTVGWVGCSTVLCQPTGGEARLTERCAFTRNQRF
4370	A	266	455	AQWHTSIVLAAWEAAAAAGLLEPRS*SRCLKCTMIIPINSHCTPAWQHM RPCLLKKNFNSNSFISK
4371	C	409	507	MNTRFLTVCVPGWVKNDNYSIVCIDFPLVVIAI*
4372	A	870	1027	HLCMCVRVCVACMCTLLHLFSNGFII*CFCTST*AIHVMG*VAIKM YINDP
4373	A	1	690	FHHLEDSIIEIFDAFLTLLRKKRKKKHNGNMPIFSKLFHVMVNPMS TSLFF*HKYMIVPISPQSHQYSSNGLSVLFLPVYRHSFLFFMILSTLS FRCLANILSHSLFILLGLLINRSLSM*SVLLIY*Y*SYILLQYLLTV LEFFSFHI*VFSLLRILFFFKIFTFSIWMPLSQSYLLRHSVFTDVPY LISYILICVDLFLNTLFCSIGLFILGLTQHCLNSSSFIIIVI*QSIS SHLVQ*DCLCLHLCIFCALSCATKTKNKDVEIFIGLTM
4374	A	393	491	GLYLHRPIFPDHLVQLSCPFHR*THRGTES
4375	A	435	526	GSTRHTHTHTHTHTHTHTQKERERERERER
4376	A	293	1228	NADNSLENFCRKSASCDLEQRRFIIRFIKLRRGSFSEKQQHSVTRK YSFIQNWVLEKDNKALNTRVIYNRFLFMMYKIKQNTDDGDCRLLCSY HVLDRHCKGSTCIDPFLMTNYWCNYHAHFIDEHTEAQRARNGKQG DECEVGIESRRRSGNSGARYVHDSSPPTSGIHSNARPSVRLFLATL SKIAFLLTVSLLYEMTVHIYGEPLPRRQRIITQLLEGVGTLLNGSVASV DPVFRNQQLHLATGSLMASSFCFVSLREIIGQSLIMKTL*ITHTH THTHSHTHTHTERERERERETEREERVKF
4377	A	953	1317	VLTGLVSPLYVSKGFWFFLLFS*TMFSHSPTWAILESWSLARFSG

				MSGEPQMTPIGLQYLA*G*RPRNPTLVTFTEIS*VYFFILPLMSQ*M CLMHLFPLPQTFCQILQLYFFMAHIST
4378	A	9	360	PRKAE LRIFEKVS VTDAMAEDMEKLRPRLKKVHIRELVLAISIMPKT HKPMLTLRV TWREMLR\PRDLK*EVEGGCRRCSSSPR\VDPPGG\RR EPRGGVRVRGRG\SAPPGGPGLSAML
4379	A	223	458	CLRRINPCSPRCRRPAWRRRRPGPRTTRRTDS*IRPKSGAASHPPGG AEGIPRG CQSTRSRTTRRRPEAPASRPCCLRI
4380	A	887	1173	FFPESELAQPEKRF*VPGKGRGLSPRLLPPCRPPAWRRRRPGPRT RRRTDS*IRPKSGAASHPPGGAEGIPRG CQSTRSRTTRRRPEAPASRP C
4381	C	22	255	MPSSSAQ LLLPHEVSPVLSCQLCFLKITRVC SYLWATVILGLDYCNS LIPCLVSYFLLSLSLPCISVVFRTQILLHY*
4382	A	23	361	LTTLVFAGTPGKKRRGNQWR*SPHYSCSGGTGGRPRPAFSLPGAPG QSGQISQSDWRRGPCS*SSGWCNSC/HPGWPGLVRRGGMTS*WSYS*A TGP/GPGYKAIPGAS*RSTSL
4383	A	2	310	PLLPAHPPPWSLPVTS*PRCGSPQRTSSWNRHSHRPA*SLPCLGFAG TPGKKRRGNQWR*SPHYSCSGGTGGRPAFSLPGAPGQSGQISQS DWRRGPCS
4384	A	1021	1565	PHLSPAGTPLLPAHPPPWSLPVTS*PRCGSPQRTSSWNRHSHRPA*S LPCLGFACTPGKKRRGNQWR*SPHYSCSGGTGGRPAFSLPGAPG QSGQISVPPCRVPPLLQSRAGPSPSSFSKWELCYSHHLLPPLLYAH CQESLNTQQRLEASLSSLNASEPTTAKCPHGTAACLLGD
4385	C	361	612	MVARDSRCRSRALVGTGVPVEVLATGKSHDQLVLLNRDAGTGASLAL GATALAQDAASFQALARASPC LWGASAKQRFPLELYC
4386	A	448	683	VNMERKKDLTESSLPAVPTKVPGMRMKLS*TLKTSLATRCQTL SRLC SPPTNQRLSQEGVG VGEKGELRIY LAMWIK
4387	A	1977	2162	VNMERKKDLTESSLPAVPTKVPGMRMKLS*TLKTSLATRCQTL SRLC SPPTNQRLSQEGV
4388	A	145	370	GRVLLVLCFFETESRVA*AGVQWRHRGSLQP*ASVSYELEAAVG GGTTALQPGRQSRALYLKTKTKNFLNLS
4389	A	248	452	GWVFTMLARMVLQ*NHLNPGGGCSEL RSHCTPAWATE*DSVSKKK EKEKKMRNETKTKWTCSPFIT
4390	A	141	354	ARWADWLP LGIANCPRAHLAYLETWELEAHWKRTIVNFCVCVCLCM* VCLVALRLFCSSGMHHSFNRLQ
4391	A	354	592	IRCTQAFALTSVVGPGTVAHASNPSTLGG*GGQIT*PREFKTSLGK MAKPCLYKNLGRHGDLCLQARLLQLAEVEGFT
4392	A	63	353	ATEPVWPPCLWPQPLCAKDCRGVARP*CVRPPKASLVLSPPSSAGNAS SIFMDYKCLSPCPFKQFLSSPPQSTEPSPACELGLINVNLSSRPSLP SR
4393	A	357	561	LILETGSVCVFQAGVK*LCTSVIIAHYSLDLLGSSNPPTS DSRVPGC GDVHLYSQVDAAANLVVVA
4394	A	1048	1599	CRSKWGLASILWLKSFLLGHHLGGDGFKA*FKFHSKFTVLASSKCLL LVGF*SHNYG*VRIHLFIY*IFIHF*KDFKSMFPRLVLSSWPQAILP PWPPKVLGLQVLANC IQPMFHFNLKSSKWLR I
4395	A	24	452	APSPDAMG/HSLWGKV NVEDAGGETLGRLLVVYPWTQRF FDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKL HVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGVASALSS RYH
4396	A	38	553	APSPDAMGHFTEEDKATIT\SLWGKV NVEDAGGETLGRLLVVYPWTQ RFFDSFGNLS SASAIMGNPKVKAHGKKVLTILGEMP*KHL\DDLKG\ TFAQA*SELALVDKL\HVGS*RTFKLPGEMLLVTRFWQSHFRQKNFT PEGARLSWAERWVTWSWPVALVLPRLPLKLNCP
4397	A	74	432	TTGTLES LCSNACFGALLPHPPAPGE*RPWS*HFTRYLGPLNRC AW EGGRG*TGPGLPSLGKALVEGIPSES PGPTVSHPPCCSPRPDPDQSA A SLHQVPPPTVHCSHLTLP MGWPGPQ

4398	A	1	176	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T
4399	A	1	188	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T
4400	A	1	118	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T
4401	A	1	227	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T T H T H T H T H T H T
4402	A	1	157	H T H T H T H T H T H T H T H T H T H T H T H A H T H T H T H T H T T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H A H T H T H T H T H T H T H T H T H T H T H T
4403	A	1	133	T H T
4404	A	1	169	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T
4405	A	1	144	T H T P
4406	A	1	89	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T H T H T H
4407	A	1	166	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T
4408	A	1	190	H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T T H T
4409	C	21	218	M X C V V C X V C V E C V E C X A G V C G X C G X W C V W X X S X W X V C V C V C V C V C V C V C V C V C V C V C V C V C V
4410	A	1	206	T A H T N T A H T T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T H T
4411	A	2	185	T P H P A L H T L H T
4412	C	247	393	M E L F C N G Y N E E V S K N T H T H T H T H T H T H T H T H T H T X T H T H T X T H X W X L
4413	A	1229	1784	R C R R E M G S L S S H S V M V D S G F L W P C W R G P G S R T S N T V E N R N P P P P P R H P L G Q L F I L F Q S L S L H L S L S / C L S L S T S F F Q S L F L N L S V S L C Q S L P S P S L / C F S I P L S N T H T H T H T H T H T H T H T H T H T H T E S G R C * S V L F F P P C P Y L Y H Y R * G * G V G S A A L S L P T P H Y E M T V F K G N L L Y L P A V S I V S R V N L
4414	A	76	297	E I R T L S R S S Q S L W R R D V R W I S G S C L K G H A S D H Q L C Q H * C T H T H T H R T H T H T H T H T H T H T H T H T H T H T H T H T P K M A
4415	A	48	327	E E L E A L R R \ Q R L A E L Q A K H G D P G D A \ A Q Q E A K H R E A E M R N S I L A Q V L D Q S A R A R \ V S E Q G L I E I L K K V S Q Q T E K T T T V K F N R R K V M D S D E D D D Y
4416	A	786	905	V S E Q G L I E I L K K * C Q L T E K T S T V K F N R R K V M D S D E D D D Y
4417	C	58	237	M A A E E L A L R R P E A G R A A G P N T G D P G D A A P T G S Q S T G Q A E M R N S I L A Q V S G S S P A P G P G *
4418	A	115	432	L S K * C N K Y T I H T H T H T H T H T L L N O P L K
4419	A	10	398	E N T V F I G L L K Q Q T R N I I L P L K I F C L R L K I P P L T M P S P P P S P F R K S P D L V P A H T P K E G R L W P W P G P P G P S K A A H A R R P L S T C Q D * P P Q R E I L P G P Q P T S P T H C R M S R E G R S G G T G A R A C Q L P L L R P L A S
4420	A	551	792	I N F F F F * I I D R F S L C H P G W T A V A Q S R L T A T L L P S R F K R F L C L S L P S S

[illegible]

				REIELTNCPPHEPNLATGKMTWLRSSSGFCESNRVT
4434	A	328	333	AFEFKRIDILTFKSSFAGSL*E*LHHTHTHTHTHTNTCFLTVMKEL SNHPGNK
4435	A	1461	1710	SGVLGRAALLKPPSRARSSGGSSLSILRLSSPGLSSPSLPCPTSQ DRGIPFQTFHLNVALT*AAHEMDWREPCVKTRTGS
4436	A	267	499	LLLYCGTNLGIPIINSQEYFLLFGRQVGLQEQTDLHLFLQRQQRVADRV LKQHVQQHHGAICRVGRVGRPGVPAQGPQ
4437	A	5	418	SSWDALWNFFFFLELLLPAASSGPLLTSSSLENFLVFLEPLLWPDSS VSLTVSSSLGEDFFLLGRLVLPVSSRSLLINSSLEKDFFFLGLEKEI DGSSIPFS**ISWGFCFFFLGFSIVSSHLSPPFCPKLTPL
4438	A	1	3297	MGFHHVGHAGLEHLTSGDRLGRRSSSKRALKAEGTPGRRGAQRSQKE RAGGSPSPGSPRRKQTGRRRHREELGEQERGEAERTCEGRRKRDERA SFQERTAAPKREKEIPREEKSKRQKKPRSSSLASSASGGESLSEEE LAQILEQVEEKKKLIATMRSPWPMAKKLTREAEQEFVEKYEGALG KGKGKQLYAYKMLMAKKWVKFRDFDNFKTCIPWEMKIKDIESHFG SSVASYFIFLRWYGVNLVLFGLIFGLVIIPEDVYVPIEEPSVMLQE LAGKAPLDDKFMYPSSNTGSYGLGFDQGYNYLEAELKKIRFQASHG YWQISEDITISSLLTWLLAGLRKSASNLTYVAVPKVQGYIKYSALFYG YNNQRTIGWLRYLPMAYFMVGVSVFGYSLIIVIRSMASNTQGSTG EGESDNFTFSFKMFTSWDYLGNSSETADNKYASITTSFKESIVDEQE SNKEENIHLTRFLRVLANFLIICCLCGSYLIYFVVKRSQOFSKMQN VSWYERNEVEIVMSLLGMFCPPLFETIAALENYHPRTGLKWQLGRIF ALFLGNLYTFLALMDDVHLKLANEETIKNITHWTLFNYNSSGWNE SVPRPPLHPADVPRGSCWETAVGIEFMRLTVSDMLVTYITILLGDFL RACFVRFMNYCWCWDLEAGFPSYAEFDISGNVLGLIFNQGMIMWGSF YAPGLVGINVLRLLTSMYFQCWAVMSSNVPHERVFKASRSNNFYMGL LLLVLFLSLLPVAYTIMSLPPSFDGPFSGKNRMYDVLQETIENDFP TFLGKIFAFLANPGLIIPAILLMFLAIYYLNSVSKSLSRANAQLRKK IQVLRVEKSHKSVKGKATARDSEDTPKSSSKNATQLQLTKEETTPP SASQSQAMDKKAQGPPTSNSASRTTLPASGHLPISRPPGIGPDSGHA PSQTHPWRQSLGLGLGLGLGLRLRLPWERPADAVALTLAPRLP FQVLLHVLFEHAVGYALLALKEVEEISLLQPAACTARSHVAGRPEE SVLNLGQIPQHRSSGGLLSLCLIPGCLGKMPTPCLKGVVHEDLRLLL EDPPAVQKEEKYSWELGD
4439	A	3	451	QTQREPTMVLSPADKTNVKAANGKVGGAHAGEYGAEALERMFLSFPTT KTYFPFHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALS HAHKL RVD PVNF KLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4440	A	26	529	NSTDSETHPWLLSPADK\TNVKA\AWG\KVGGAHAGEYGAEALERM LSFPTTK\TYFPFHFD\LSHGF\AQVKG\HGK\KVA\DALTKAVAHV\ DDMPKRRCPP*SDLHAHKL\RVGPGSTFKLL\SHLPCLGEPWAAHLP RPSFNPWRLQRLPWGQSFLGFLKHRCLNLPNTR
4441	A	294	600	ISCFLCSETLSNFALFLKESNGPVKVWGSIK/AMTENLHGPHVHEFG DNTAGRVLCFFLECIWEL*FII*LFLLLLINR\CTSAGPHFNPLSRK HGGPKDEER
4442	A	517	758	CFPIIRHVGLGNVTADKDGADVSIEDSVISLSGDHCCIIGRTL VVH EKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ
4443	A	80	725	SPAASGGFPLQSLPRTLGRGLSDFGDRSPVCVLKGRRPKCRGIINF \EQKRESNGP\VKVWGS\IKGLT*KALHGF\HVH\EFG\DNTARL YQVQGP\NPLSQKTTVGPK\DEESH*DLGQCDCLTKNGVADVSI \EDFVNLTQGD\HCI\IG\RTLVPWKKPDDLGPKVGNE\ESSKT\ GNAGKSVWPCGV\IGIARINIPLGCSLRPPKLCIVSC
4444	A	415	635	QQTLVYSAACVICFPFHLLSPNPILFFFFFFAFLFFFFFFSYLLYLVC LFLVASQVRKLFTERFPLCICTKMN
4445	A	2	478	MAGKQAVSASGKWLMIKRWYNAEFNKLGLMRDDTIYEDEDVKEA IRRLPENLYNDRMFRIKRALDLNLKHQILPKEQWTKYE/EGLCCSSS

				ALCFLLR*KDQPIECPSRSQEELL*SKLSPL*TAFET*AKENFYLEP YLK\EVIRERKEREWAKK
4446	A	323	400	ENFYLEPYLKEVIRERKEREWAKK
4447	A	2	396	RPPTTTTKFAAARQMAGKQAV*STQAKGLNG/IFKKWYY\NAARIQNK LGLM\RDDTIY\EDEDVKRSP*EDFPENLYNDRMFRH*EGHWTNLNK \HQILPKEQWTNF\EEKNFY\LEPYLKE/VLFRERKERE\EWAKK
4448	A	3	316	ATVLLDYHLNLYLKEVDQLRLRLQIDEQLRQIGASSRPPPNRTDKEK SYVTDDGQGMGRGSRPYRNRGHGRRGPGYTSES DHRDELS DWSLAPT EERESFLRR
4449	A	5	340	GSGETSAKAFRSIWGPLPPVHRHGS PRSSVQR/DGPGLGTGEPRVYIR NKVANTGVPGAPGPSIGGV TAPATDYCHRIAPILAARRRRRRRRRRR RRRRRGGGGVAGGGGGGG
4450	A	1	117	LSRMERLRSFNNNNFFFLFFFCFLKCGGLVLFESFFPK
4451	A	1	1973	DGGARARGRAAARRRRRPRRRRRRRRRRRRRRRRRRRRRRRRLGLER PQPTSRGRAPGASRAEEKMEELVVEVRGSNGAFYKAFVKDVHEDSIT VAFENNWQPDRIIPFHDVRFPPPVGYNKDINESDEVEVYSRANEKEP CCWWLAKVRMIKGEFYVIEYAACDATYNEIVTIERLSVNPKNPATK DTFHKIKLDVPEDLRQMCAKEAAHKDFKAVGAFSVTYDPENYQLVI LSINEVTSKRAHMLIDMHFRSLRTKLSLIMRNEEASKQLESSROLAS RFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDCTCTFHI YGEDQDAVKKARSFLEFAEDVIQVPRNLVVGKNGKLIQEI VDKSGV VRVRIEAEENEKNVPQEEEIMPPNSLPSNNSRVGPNAP EKKHLDIKE NSTHFSQPNSTKVQRGMVPFVFGTKDSIANATVLLDYHLNLYLKEVD QLRLRLQIDEQLRQIGASSRPPPNRTDKEKSYVTDDGQGMGRGSRP YRNRGHGRRGPGYTSGTNSEASNASETESDHRDELS DWSLAPTEER ESFLRRGDGRRRGGGGK\QGGRRGGGFKGNDHSRTDNRPRNP AKGRTTDSLQNTSSEGSRLRTGKDRNQKKEKPDSDVGQQLVNGVP
4452	A	1	2115	TASAGGGDGGAAARGRAAARRRRRRRRRRRRRRRRRRRRRRRRRRR RRRLGLERPQPTSRGRAPGASRAEEKMEELVVEVRGSNGAFYKAFVK DVHEDSITVAFENNWQPDRIIPFHDVRFPPPVGYNKDINESDEVEVY SRANEKEPCCWWLAKVRMIKGEFYVIEYAACDATYNEIVTIERLSV NPKNPATKDTFHKIKLDVPEDLRQMCAKEAAHKDFKAVGAFSVTYD PENYQLVILSINEVTSKRAHMLIDMHFRSLRTKLSLIMRNEEASKQL ESSROLASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLD EDTCTFHIYGEDQDAVKKARSFLEFAEDVIQVPRNLVVGKNGKLI QEI VDKSGVVRVRIEAEENEKNVPQEEEIMPPNSLPSNNSRVGPNAP EEKHLDIKENSTHFSQPNSTKVQRLVASSV VAGESQKPELKAQQG MVPFVFGTKDSIANATVLLDYHLNLYLKEVDQLRLRLQIDEQLRQI GASSRPPPNRTDKEKSYVTDDGQGMGRGSRPYRNRGHGRRGPGYTSG TNSEASNASETESDHRDELS DWSLAPTEERESFLRRGDGRRRGGGG RGQGGRRGGGFKGNDHSRTDNRPRNPREAKGRTTDSLQIRVDCN NERSVHTKTQLNTSSEGSRLRTGKDRNQKKEKPDSDVGQQLVNGVP
4453	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAAWGKVGAGHAGEYGAEALERHFD LSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVD PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
4454	A	1	456	RPRRPQREPTMVLSPADKTNVKAAWGKVGAGHAGEYGAEALERCFLS HHQDLLS\HFDLSHGSSQVKGHGKKVADALTNVAHVDDMPNALSAL SDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHAFLDKFLA SVSTVLTSKYR
4455	A	25	640	EFHRLRENPPWCLSPA\DKTKAQRPPRLKLGHAH\GEYGGEPLERMF LSFPTTKDLLPALRP*ATVSAQG*RAHGK\KVA\DALT\NAVA\HVD \DMPQTALSAPERTCNGAQAFGWDPVQLSSS*SHLPCLGEPWAAHLP RPSSTPGGCKASLGTKFPGLFVEAPLLEPSKLPKLGLSLRVGHCFFA PLGLPPSPSSPSCRTPTPVFE
4456	A	906	1046	PDHHNWSQ*TTTGAQRQT*KRTVKEV*SAHNEAMCFGTCASDCLYR
4457	A	1	383	MVLMPPVSAIPEAEAKSSLIENDVCLSAKENHKS KRAITRTAERFPT

				E/SPHD/YPRKTARTGLRHAQQASL\PNWSTPLAARIAPVPPAANPQ GVLLKSAGPHLLLLARTTTCNR*VPIASPTTHRME
4458	A	1	1509	MGSKLSQPLSPGVAWQLHVILRRDDWMDGRAVVTLMIRMCFSVYTM YRRAANVWLSSGMAASRQAELDGMPAINAKRVGTGSCARMRCCLSEN LLSAIETGTYRQSGRERKHQRWCSDGFECDDNGEDCVSRSRWTAVI VRHCMGGHYRRLQQRVNGSKELAEAFEHYNEWHPHSARVIARHGNIC GSGLVMGEVPENAMHDANIRVAIAGAGGLWAARLIQAALALEGVHWA LRWSVKDLLYWAATRRYRAKQLDAVKDDFDVFIDFTRPKRWVNVMLK LLEKAAKVMGATPISKLLKHIIDIKLIAVRHRTGNNGRDRPRPDKDL KDCAVYSREGHTVNVCLAPLVLPVCVQVVSMTTAGFTTDTLPAGRS FCRYCFYVQPYRRLRRVNGRWPEODPILLLFKQGNLTNRQYPANHAM FQDNGFQQLCRVGRYGGNCMIISTSGSTAFQQAATIPVEIQLLNM PHSKYLTGCFNSTVSIRPRYADCVDRAKLHPQ
4459	A	579	919	PGSM/IPLSVSHSTGDDGRSLPKRRSTAPSMSTSVYCFNCERCLVSCS LLLLSSLGPPCLAVLLAPFFAPFF*VFLLCVVVAGLPALLLLLVSSL LFLVLLSFCAASACFGFLSV
4460	A	1477	1691	YCNVSFGANLERA*TSFSALFIDLQPPGYRTTTSKHKVSSSLIKGHV LLDHSFHDLTNTQLWISTNAFRGN
4461	A	1076	1354	QQKCAVNLHSLFIPITKLCRLFASCRAARCCSHLTSQPVTA*LAGKVN PLPLGNLWECDTKAGSQAMRTHLSITWRAVMQLPVINTTYQRGKR
4462	A	880	1242	RTDAVLFDQVVSQRVEVRLFRHSLVERGVKYSNVFVQLWERFQSFF DTDQVSRVVQRCKRSCIFDTLNNRLIDHYGAGILFAAVYDVTVDSSQ LRRQFWFLCQNSINDKVERFAVSGACT
4463	A	832	1386	TIIRQPLHWRRRKIVAEAAFHRSQHDVLYCFTVEAAGSDRPVQCLTI TAVQREERDTQSLSVITAELEPVRAPSLIAFFHGHSACMCPITARYS RFSLKQQRILAHDPVNTFGIDRRHTIKFCLSAKQRPYPTITIRWQLS DNMVTYKHIRIISVTTAAAIHPVIGSENDVQLRTHPETTAD
4464	A	46	492	HPVTLGDNTRYRTHIKQLIKGEVFLHFTPDADVDFRTT/MTLPL*RL QLSSQRADDQRTLRCSSVRGRDAVHAADVQFVCIRLD\EVTEAVIFQF PFQLSDSETVSQRCVDVGTLCRQYTFIFRRIFYFAQMSNTLRLFDD YAEIIDHRQ
4465	A	7259	7441	IASPGWS*QECSSRSCAQCCCQSTTTTCRHAKQRSLLALAHKPLAKLA NGITPRLRQICR
4466	A	538	1056	TIIRQPLHWRRRKIVAEAAFHRSQHDVLYCFTVEAAGSDRPVQCLTI TAVQREERDTQSLSVITAELEPVRAPSLIAFFHGHSACMCPFRWRYSR FSLKQQRILAHDPVNTFGIDRRHTIKFCLSAKQRPYPTITIRWQLSD NMVYTEKHIRIISVTTAAAIHPVIGSFPIPGQ
4467	A	1	1134	MIDVLGPEKRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAAASQLF LWRKQYQEGSLTAVAAGEQVVPASELAAAMKQIKELQRLLGKKT MEN ELLKEAVEYGRAKKWIAHAPLLPGDGRHTDDTDVLLRIHHVIGELP TYGYRRVWALLPRQAELDGMPAINAKRVYRIMRQNALLERKPAVPP SKRAHTGRVAVKESNQRWCSDGFECDDNGERLVRTFALDCCDREAL HWA VTTGGFNSETVQDVMLGAVERRFGNDLPSSPVEWLTONGSCYRA NETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKRDYISIMPKPD GLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRACNGLSDNRCL EI
4468	A	745	1263	TIIRQPLHWRRRKIVAEAAFHRSQHDVLYCFTVEAAGSDRPVQCLTI TAVQREERDTQSLSVITAELEPVRAPSLIAFFHGHSACMCPFRWRYSR FSLKQQRILAHDPVNTFGIDRRHTIKFCLSAKQRPYPTITIRWQLSD NMVYTEKHIRIISVTTAAAIHPVIGSFPIPGQ
4469	A	3506	3826	EVWRPARRSRDVSCSRSHAYYVVPGTADWLWPS*RPSTTGVC*PVT WRWLEGQWTPHLGRVLQEDSDSPTFPSALGIQETRPEPLKSPREVPT SGRTGVFHYPA
4470	A	1	751	MRDFAGCPRSSVSETGNRRPNAGHNQEWNGGKDETHDTNQSRTRHYG VRNFSTIPNYFEGNPKWGPEKRRRRRTTQEKIAIVQQSFEPGMTVSLV ARQHGVAAASQLFLWRKQYQEGSLTAVAAGEQVVPASELAAAMKQIKE

				LQRLLGKKTMEHELLKEAVEYGRAKKWIAHAPLLPGDGERTDDWMDG RRSRHTDDTDVLLRIHHVIGELPTYGYRRVWALLRRQAELDGMPAIN AKRVYRIMRQNAPVA
4471	A	482	1200	VFSGPFGSGVFFPFGSLCPCELSATVLEVAPPLLPGNRMSSRITMLS ESCQRMVIVGYGRCFADRQNLMLVCLRSMNPVFTGSCARMRCCLSEN /PVPPSKRAHTGRVAVKESNQRWCSDGFEFCCDNGERLRVTFALDCC DREALHWAVTTGGFNSETVQDVMLGAVERRFNGDLSSPVEWREGVF VRNIDEEFGNESAQTGMLHHQLDPSVEGELHQNTGSTACCRADSTHI SHWRFM
4472	A	1271	1681	TVITTGIGRPFMSMESVFALNALQNSMMFTPC*PRAGPTGGLGCTSF DEPILDGWPPQSSQLMIRMCFSVYTMLSESCQGMVIVGYGRCFADRQ NLMVCLRSMNPVFTGSCARMRCCLSENLLYRHRNGHIQAEWP
4473	A	739	1257	TIIRQPLHWRRRKIVAEAAFHRSQHDVLYCFTVEAAGSDRPVQCLTI TAVQRETDQSLSVITAELEPVRAPSLIAFFHGHSAACMPFRWRYSR FSLKQQRILAHDPVNTFGIDRRHTIKFCLSAKQRPYPTITIRWQLSD NMVYTEKHIRIISVTTAAAIHPVIGSFPIPGQ
4474	A	1	2661	EGRTKEHERKKERKTTTTKDNERNRTEQKRKKAQNRKKERKQREHQ TEDRKKERTTERTKEGRKDGKEGTEGTEGRKERKNTTGNLQNTINQK VQTPLAFVTAGEDQDNYLEPVWRKR'TTNHRHGGGDSAFEIKPVLLRA FR'TTKVIFMTQTFIPGKDALEDSIARFQQLSDLGFIIEASWLN VPNVWSVHIRDEKALCFTNGKGATKKAALASALGEYFERLSTNYFF ADFWLGETIANGPFVHYPNKWFPLTENDDVPEGLDDRRAFYDPE NELTGSMLIDLQSGNEDRGICGLPFTRQSDNQTIVYIPMNIIGNLYVS NGMSAGNTRNEARVQGLSEVFERYVKNRIIAESISLPEIPADVLARY PAVVEAIAETLEAEGFPIFAYDGSGLGGYQPLHWRRRKIVAEAAFHRS QHDVLYCFTVEAAGSDRPVQCLTITAVQRETDQSLSVITAELEPVR APSLIAFFHGHSAACMPFRWRYSRFSLKQQRILAHDPVNTFGIDRRH TIKFCLSAKQRPYPTIPYVGSSPIHGVYGEAHPYHQDDCGGIHPVI GSSENDVQLRTRHRRQLTKLTPHPRAIRARKTLGGDSCTMTNCGSE EAVATNALQPMPKSQTHLGELQSLRLTYNFDVIDGVNYQIDVTQPAR YDGEQMINANAEIRIKNLTFNGKPIDPNAMFLVATNNYRAYGKFGAG TGDSHIAFASPDENRSVLAAWIADESKRAGEIHPAADNNWRLAPIAG DKKLDIRFETSPSDKAAAFIKEKGQYPENKMVNTTVSLVLLKYPMPV CEFAVAPGAFENQVGKQSRQAQLKTVANIESSFRSAPVSETREARFR QTIWKGESSYCLCGKTGQKYLSPVPVDVAWGNNTLHPIDR
4475	A	1	2370	MSKSANRIKPKKNTQINNTQSKATRTYNTNTQYKPGKCRTOGWIPVC RAYRQYDRGRDQRSSEYSRRRLRPSAPTSKSHRRRHRWSVYQQSGH SDAGFSSRERFLNLASPWCHIVEENGHREGNLPFGDSVVANTVDK ETNFFIAQRMTITFTTNFLCEKQAAGALTVAVTQRFQACQAGSA KAVVTRICPVSTEQFICNGEIFLRIFRSTHAARRFETNGFFYAHITD HFHHDARAFRRRVHSHFTGRGFDEVTRTFDGFRRFTDQRFVVFQFAG FDDHFQQYIRCRASLFTGFHQVKTNLLVTRHQRVREHNVNFISTVG DCRTGFCQRDQDVVVTVWEVGYRSDTDFGVPCSPRVCEHSDNAMIDT DRVCRAEFGMLTQAITSRRCSSKQVVPASELAAAMKQIKELQRLG KKTMEHELLKEAVEYGRAKKWIAHAPLLPGDGERTDDWMDGRRSRHT DDTDVLLRIHHVIGELPTYGYRRVWALLRRQAELDGMPAINAKRVYR IMRQNALLERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFCCDNG ERLRVTFALDCCDREALHWAVTTGGFNSETVQDVMLGAVERRFNGDL PSSPVEWLTDNGSCYRANETROFARMLGLEPKNTAVRSPESNGIAES FVKTIKRDYISIMPKPDGLTAAKNLAFAFEHYNEWHPHIRYRNQDDH ELQITHGTRFYVELCGESLPAEGTGLTPLRTHARFQVDHNAIVSRRV VRSCCTCLYQVPKLRSPDTIAQTALSLAISYHTASGH
4476	A	421	972	TIIRQPLHWRRRKIVAEAAFHRSQHDVLYCFTVEAAGSDRPVQCLTI TAVQRETDQSLSVITAELEPVRAPSLIAFFHGHSAACMPFRWRYSR FSLKQQRILAHDPVNTFGIDRRHTIKFCLSAKQRPYPTITIRWQLSD NMVYTEKHIRIISVTTAAAIHPVIGSSSENDVQLRTRHPETTGD

4477	A	766	1073	HRQLVIVFQQPLVSGFHEAELSLDDAKWVLHPGPDAGFHVFDVGRF VLA*CCFKVLTLPGRSAISQST\PPRPAPRAVAPLGSRHRLRQIAP LHAADYPAD
4478	A	1662	2045	PTALAAFRRIVRITFLPVGDPGFHQSGSLRLS/NPDALQIQPACRI FSSALITSVFACSVHEGE*LPVDPGIIRALLHR*R*KAESACAVPCI *AWTDREYGCNNRRKSGVILRRTDDWMDGRRSRHT
4479	A	1	1803	MTRDNPVPIPRFIHRREVVFQENGIGIQNARFIAALFFQHGVLNCQR VGGLLKIGIVEVFRYTSVVERVVVDYIIRPAGFSIDTNDRGSVTDDF APDQGLAKAIPGFKPREPQRQMAVAVTQAIEKGQPLVVEAGTGTGKT YAYLAPALRAKKKVIISTGSKALQDQLYSRDLPTVSKALKYTGNAVAL LKGRSNYLCLERLEQQALAGGDLVPQILSDVILLRSWSNQTVDGDIS TCVSVAEADSQAWPLVTSTNDNCLGSDCPMYKDCFVVKARKKAMDADV VVVNHHLFLADMVVKESGFGELIPEADVMIFDEAHQLPDIASQYFGQ SLSSRQLDLAKDITIAYRTELKDTQQLQKCADRLAQAQDFRLQLG EPGYRGNLRELLANPQIQRAFLLDDTLELCYDVAKLSLGRSALLDA AFERATLYRTRLKRLKEINQPGYSYWECTSRHFTLALTPLSVADKF KELMAQKPGSWIFTSATLSVNDDLHHTSRLGIEQADSCSIGNSYVF RLVIGEOMIDVLGPEKRRRTTQEKIAIVQSFEPGMTVSLVARQHG VAASQLFLWRKQYQEGSFICCRPPENRFLPLNLLPP
4480	A	230	368	LGPLPQGTFSPEGWRQP*PCGWPPCRAFMESSLQKRMRSVLDPLE
4481	A	3	334	QGYEYDNLVYHFFVELPTAHWSSPAFQQLSGVTQTCTTKSLAMDKVA HFSYPFTFEAFFLHEDESSDALPEWPVLYCEVLSLDFWQRYRVEGYG AVVLPATPATMTWPH
4482	A	47	296	QKTKKQTNKKTQ*KIPPS*QKGLSTAFSLHLLRNNSYLNLSKPQAVE *GFPGKRLRLTGWGFKTLSPSTFLPSLVLEDERLHF
4483	A	2	1317	YTDSDRYTNLEEHCQRMTTAASEVPSFLVERMANVRRRRQDRRGMEG GILKSRIVTWEPSEEFVRNNHVINTPLQTMHIMADLGPYKKLGYYKY EHVLC TLKVD SNGVITVKP DFTGLKGPYRIETEGEKQELWKYTIDNV SPHAQPEEEERERRVFKDLYGRHKEYLSSLVGTDFEMTVPGALRLFV NGEVVSAQGYEYDNLVYHFFVELPTARELTI FGLWLSDWSSPAFQQL SGVTQTCTTKSLAMDKVAHFSYPFTFEAFFLHEDESSDALPEWPVLY CEVLSLDFWQRYRVEGYGAVVLPATPGSHTLTVSTWRPVELGTVAEL RRFFIGGSLELEDLSYVRIPGSFKGERLSRFGRLTETTTGTVTFRLHC LQQSRAFMESSLQKRMRSVLDRLLEGFSQQSSIHNVLAEFRARRRM QEARESLPQELMGPF
4484	A	875	1075	TSLTFFSDFPADASKGDDLLPAGTEDYIHIRIQQRNGRKTTLTTVQGI ADDYDKKKLVKAFKKVGLQ
4485	A	2097	2179	DQEI KDCVCVCVCVCVFKCLNLVYLSL
4486	A	4274	5255	HTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL RLVRPEVDVMCTAFHDNGETFLK*VIRCL*FKIKKHGVT*ANTL* KLP*QKYFQH*DLEVLL**FFKEVVDFTTKFYTAKNMIKDILKFIET GYNLSQKF KIDKFNVFRYVYVVIIDFVLVSNIILPKFNHLC THT HTHHTLTLFSTYLNDRDKTIMCKLSLIG*L\ESLEFGSGGENVDYN YFCNIVCYRK/ADCFSLKFRYLYEIARRHPYFYAPELLFFAKRYKA AFTECCQAADKAACLLPKVLCTRIEKKSLLSNLILSLWLDLGTLSV
4487	C	102	230	MFLSCRSVXXXXXXXXXXXXXSPLFLSPLLFLFHTYMRA*
4488	A	2	567	VKVRMLREYKVVLGSGGVGKSALTVOFVTGTFIEKYDPTIEDFYRK EIEVDSSPSVLEILDTAGTEQFASMRDLYIKNGQGFI LVS LNVQS FQDIKPMRDQIVRVKRYEKVPLILVGNKVDLEPEREVMSSEGRALAQ EWGCPFMETSAKSKSMVDELFAEIVRQMNYSLSPEKQDQCCTTCVVQ
4489	A	125	522	NTPQQGRRSYTTTWMNPKNLTLKTLHNLVLTFISSIVTSFPLITPWS ILILEDCLSLIRSIKVLTYFFFYVKSDDL SFLN ILYFLIPKFPPI SFLLPRMPLLSYAYPKPHLSRTSSKPTLTHQNALGLS
4490	A	195	473	TSEAQSTKVFGSGCWGWSNQLNSNFPILIFSLIPLSAVARPLCAEP CVSIGSCPFHFSVQSGTISHLLCIFPKKCWTS LGYILFFLILCNS
4491	A	1	966	MSVGNLEEIIDNHAIVSTSVGSEHYDSIISFVEKDLEPGCSILLR

				HKVHAVIGVLMDDTGPLVTMMKVEKAPQETYVNTGGLDNQIQEIKES MELPLPHPEYYEEMGTKPPKGVILCGPPGTATFLRVVGSSELIQKYL DGPKLVRQVFQVAEEHAPSIMFTDEIEAIGTKRYDSNSGGEREIQQT MLELELLNQLGGFDSREDVKVIMATKQVETLDPVLIRPGRIDKKIEF HLPDEKTKKHIFQIHTSRMTLANDVTLDDDLIMAKDDFSGADIKACT EAGLMALREHRMKATNEDFKKSIESVLYKKHEGIEPEGLYL
4492	A	1	960	MWESLELPRDLEGSEDFLNGFNQADVDNEVQAKVSDGDEELVRNW SKGKSGETLYLRRLKAGNKFLPGGILHNIVIKHGLSLAEADGNKSN RGEELSESEKLFYTSIHEANQLNKTVKSQAISESDNFPSVSSESH PTDSGSILCECTVQRPVQGPASRATLLQLPLVENPPLPPSSGCC HSLWLHRPNLCFHFHMAFSSVPSNQVLAMTTGLSCSDSSKEVLEET SKSGERAVPHSADFLKKRIFQIHTSRMTLADDVTLDDDLIMAKDDL SGADIKACTEAGLMALRERRMKVTNEDYIDFSKIEIREG
4493	A	1743	1935	LPNLFVPAGRIDRKIEFPLPDEKTKKRIFQIHTSRMTLADDVTLDDL IMAKDDLSGADIKVRA
4494	A	1	1540	NSGGSGGGTSGSGSSGQKMGQSQSGHGPGGGKKDDDEDKKKKYEP PVPTRVGKKKKKTGPDAASKLPLVTPHTQCRLKLLKLERIKDYLLM EEEFIRNQEOMKPLEEKQEEERSKVDDLRGTSPSVGTLEEIIDDNHA IVSTSVGSEHYVSILSFVDKDLLEPGCSVLLNHKVHAVIGVLMDDTD PLVTVMKVEKAPQETYADIGGLDNQIQEIKESVELPLTHPEYYEEMG IKPPKGV\ILLVPPG\TGKTFLPKAVANQT\SATFLRVVGSSELIQY LGDGPKT\LSRELFR\VSEELAPSLRFIDRILPPLGHKRYD\SNS\G VRRELQRTMLELELLNPVGMGFDS*GRL*KLSWATNRI\ETL\DPAL IRPRPAFDSKIE\FPLH\DEKTKKRIFQIHTSRMTLADDVP\LDD\L IHGLKIDLS\GA*HSRAICTEAGL\MGL*GERRMKVTNEDFKKS KENVLYKKQEGTPEGVVSLMNHGLSSGKWLGDFSIPERDEVGGSCPEESL FPLIFY
4495	A	125	320	KDATGLFLIFETGSRSVTPAGAQWCNYSSLQPELSRFQSSYLSLPS GLGTIGVRHPPHVAVTGLV
4496	A	1376	1509	ERKMGGFFSDHGPLESIPWPLPSIQYKPEIRTYVLTVCCEVCV
4497	A	2120	2313	NSLRFFFFLQFSIFLSSSTMVSVSFYMWPCKILPMRSREAKIL DTPCLGEHCFFVYLVS
4498	A	2	266	KGSTEFISGTAGWGTGLLPSSAGLPGGWGPAGGWAGTDRRGPRARP IPQKSPWPWWSGDAAGQSGFLPVAAWAGQGRLPGGGIIVH
4499	A	918	1475	PEPTTVFEWHGVGPAPWESVPRWGRAGLPERDWVGGCPRITRDGGG GVSGSWLRSRLRGPLWRCPLATELPPQLRKPRARSQSGRQMEPDNRG RQRDRSGWQGGPWTAKAKPGVEKLFPRPKTQALCPNPTQTVPKTRLC LDPDRVRRQPTAYSQVRPSSQSRARAVGRPRRRGRSEGLTKPSNR
4500	A	1	822	FFFFKKGSTEFISGTAGWGTGLLPSSAGLPGGWGPAGGWAGTDRRG PRAQHPTEKPSLAMVGRCSQRTVRLPPGGGVGLGKBGFPEEASLST EKHRGAWPLPVCLLGAGHGWAQTLLQPWEDSRVRGVAGWGAWWGRE GAGGTTGGTCRGLGHWWLGEDSVLQRLCDMSSYTTTHAAEFLSRHE HSFFICVLASTHATPRPSPRRKEITARAAGRAEAAGGSGRAEAVCGS GRAEPVGGAGRAEALGGASEHLCHPWDCSSVTRTRVPEP
4501	A	158	668	MEVYHPLWAAFPSNPTSGKTRAPARRGPLPASHRPRAGPRSEGLGPP TSGAGERVFPYATCPAHRRGAGIRALGSSLFTRRLRESWLVSFPPL TNMLKFSGSPRLLPNSARTVMPLDVRCCTRATLTGSACAYPTPAGA GNPLNPIRDGDRGLQLFPHERGIPSKCGS
4502	B	151	336	ANSDSMVGVLGPPFFLITLVGVVAVGGPAAHLLPMYSYDPAEELH EAEQELLSMDGDPKV*
4503	A	748	949	HQQPEGWVWSMGSWREGRAPPLGSLPPLQPRQERPRLAGPGRKSQA RDQRTRGNGPGLSTRTOPIR
4504	A	1139	1241	WYEFKMKMSSLGKEYSRKMEHVQRLSVQTVWKA
4505	A	334	466	SSGRGGGPLGSLSSGWRCFWRLGAGHSVAPLTRLPYREGNLFPAK
4506	A	1235	1446	NYLQPPLSRDNISVGILFCQARWLTPLIPVLWEAEAGGSLEPRNSRL HHCTPAWETEQDPNPPPAKKKKK

4507	A	41	489	RLQLNSNYVKPPSLSGGFPRGIQDPPAGCQAAGISAGEEGSPIPTA MRCPGDWRSSGRLGSQSPAYSSSRECRALQDQAASADTESLQGEVR SLFLSYFSLRLPSQQAIEHSAIARQSPSGLQNALRQAHRENQSRL APVGKMAL
4508	C	187	342	MICKNKNKVILLXXXXXXXXXXXXGGAXXXXXTTPRRRGKKQFFL PPKQ*
4509	A	1304	1434	KKLPEMEGPDETLLKHTNTHTHTHTHTHTHTHTRLHESKLLHEV
4510	A	1	1383	MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRPCQAPQ WEGRQVMYQQSSGRNSRALLSYDGLNQRVRVLDERKALIPCKREIFR EEGLLGIAWSGTGRGAAPTEGGLLAGDSVTPSEAVAECIPKMTQNG AMWSKSGSENTILEIVVVVQVTDQASVALDATQGHAGPFPAQLCWQL LPGSLHGALESSILTEMIELSSIKSCKPKMKESLLEQRKLIVTLLFE YILLYKDGVMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIG GPQEQUITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVIL STRFFDIQLGIKDPVFTPPSTCQMAQLEKMSDCSWTLIHYLGCEL LGYGYLQKEVKKEQEGEEDTKKKRKKKKKKRKKRKKRKKRRRRRKR RRRKRKRKREKEKEKRKRGRREEEREGRGMEEEKRRM
4511	A	1	674	MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRPCQAPQ WEGRQVMYQQSSGRNSRALLSYDGLNQRVRVLDERKALIPCKRLFEY ILLYKDGVMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGG PQEQUITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILS TRFFDIQLGIKDPVFTPPSTCQMAQLEKMSDCSW
4512	A	19	249	KFLWLLTTQVCTHVAARQSRPTRLPVSTQTCGQIVASGCLRHFPLC IGFSCISNYSNCRHPPHCAHWFLCPQELI
4513	A	1000	1174	GNRKMGRWPMGNQVRARQTPNPMQQHSCPRSLPGPSSSHSHNLSSGT RPSSPDTPPER
4514	B	60	378	NAVLEADFAKRGYKLPKVRKTGTTIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAADTDMTTQLISSLAAMAVFEDKF RPDMEEBEAKNLX*
4515	A	1	437	DPRATEGMVVADKTCQKSTGRLPPELVTAIRMLKQMLFRYQGYIGAAL VLGGVDVTGP/HLYSIYPHGSTDIAAGIFNDLGSGSNIDLVCVSKNK LDFLRPYTVPNKKGTRLGRYRCEKGTAVLTEKITPLEIEVLEETVQ TMDTS
4516	A	1	1059	MRKKFLGSTILDHYSGRALGYSCGDHYVADVDFVPFTSAAHLSC SGKWNCTLESRD TLCDAEEEAKNLVSEAIAAGIFNDLGSGSNIDLVCV ISKKNLDFLRPYTVPNKKGTSPEEVSTTFCLASISHCTHNSTSGVI HKEGMERSEPAIHCGLHSTLRKLSGLLMGWGSTGPNAGTGVGECW WLAWWLPANQSVLEMELNQMTSNEPTKSLGPLAGRQATFQAQSCVGE PGFAELQPSSTRSCSPLARKAEALNACRKNRALSPOCPCVQGRGWVF REHKAMAQPAAFWQFLKDSKFDRTITPAGARAEQLGRYRCEKGTTA VLTEKITPLEIEVLEETVQTMDS
4517	A	1115	1307	FGRGHYCRRSVSQEEEAKNLVSEAIAAGIFNDLGSGSNIDLVCVSKN KLDFLRPYTVPNKKGTR
4518	A	3	866	FLGKMAAVSVYAPPVGGFSFDNCRNAVLEADFAKRGYKL\PRPRKT GTTIAGVVYKDGIVLGADTRATEGMVVADKNCSKIHFI SPNIYCCGA G\TAADTAMT\TQLISS\NLKLHSL\STGR\LPRV\VTANRMLKQM LFRYQGYIGAALVLGGVDVTGPHLY\SIYP\HGSTEKVP\YVTHGFL APLA\AMALFER*V*APDMEEEEE\KNLVSEDSPPQFPSPSWRIFN\ DLGSRKPNIDPLPSSARNKLGFSPPHTQLPNKKGTRLGWV\RYRCEK G\TTAVLTEKIPLLWST
4519	A	4	181	SCVHHWEWREINDWMVAANISFKIEHSKTKGCLKPVPCPSDLHKHSS PGKVEPPSLSPE
4520	B	55	372	MERFLMDGFQPPQLSTYALTLYKHTATVDGKTILVADINVTQKSNF AKKFSPLPLYFVSAADGTNVKLFNDAILAVSYKQNSQDFMDEIFQE LENFSLEQEEEN*
4521	A	1	270	VFDVQRKVTYRNLSTWYTELREFRPEIPCIVVANKIDDRPMSYLLST

				ADINVTQKSFNFAKKFSLPLYFVSAADGTNVVKVWLTAEVASK
4522	A	3	347	FWDTAGQERFQSMHASYYHKAHACIMDAVLTAAPPDGPVVKQSLQEK NAAEERAEEKGRSSVYLCPVEVPTREFPGWVFDVQRKVTYRNLSTWY TELREFRPEIPCIIVANKID
4523	A	531	686	TQACCFLSSSRPTQWSAET***HSGQACFSWGCSSEDIWAASGVAV SWAA
4524	A	2	274	LDQGGYDADDNVKIIICLGDSAVGKSKYVGRGLGNKYQPQRGSRSPFKKS SRGRGAWLLGAGEGAVLAGAQMFMGERGESHDPLCVSGGGGRS
4525	A	26	410	RERQAKSSFMAPCLKTFFLLFRDRVSLCRPGWSAVARSRLTAASNS WTQAILPPRHPWTIGVSHRLRAKTCLSVSSPSKWVCYLSINVSGHQ CPGIARLPVPPPTTASRSHLSVLPPTTRTPFRPPR
4526	A	791	1407	PECSQPQQLSTYALTLYKHTATVDGKTIILVDFWDTAGQERFQSMHAS YYHKAHACIM/LDINVTQKSFNFAKKFSLPLYFVSAADGTNVVKLFN DAIRLAVFYKQNSQDFMDEIFQELEVGQVHISGGMEETAPLQG*GLQ PSRVTLA*VCPTKCIRAAVEQMQGQASPATLFT\NFSLEQEEEDVPD QEQSSSIETPSEEVASPHS
4527	A	203	928	EPMAEDKTKPSELDDQGYDADDNVKIIICLGDSAVGKSKLMEFLMDG FQPQQLSTYALTLYKHTATVDGRTILVDFWDTAGQERFQSMHASYYH KAHACIMVFDVQRKVTYRNLSTWYTELREFR*IPCIIVANKIDADI NVTQKSFNFAKKFSLPLYFVSAA\DGTVNVVKVWLTAEVASKLFNDAI RLAVSYKQNSQDFMDEIFQELENFSLQEEEDVPDQEQSSSIETPSE EAASPHS
4528	A	674	1910	SLSTTPTARSPSPALGRMRTPCGPPARRRWAASDRRGPSRSAGQPPS GSLRGCVAAARTRGEPEVESLRRELGRRAWFESAQSPDWRQGPKGPT. RSVPGLSSPHSEPHEPMAEDKTKPSELDDQGYDADDNVKIIICLGDSA VGKSKLMEFLMDGLYPSRFEVLLVPVGLPTLMYQCPTAHPFVPAQ EQEGGLDFDGDTLSSPPTPHPSMELVPVCSQPQQLSTYALTLYKHT ATVDGKTIILVDFWDTAGQERFQSMHASYYHKAHACIMVFDIQRKVTY RNLSTWYTELREFRPEIPCIIVANKIDADINVTQKSFNFAKKFSLPL YFVSAADGTNVVKVWLTAEVASKLFNDAIRLAVSYKQNSQDFMDEIF QELENFSLQEEEDVPDQEQSSSIETPSEEVASPHS
4529	C	58	447	MLRYVETLLTHMGVNPLEAEELIRDESDPDEFIVYDSWKITGRTAB NTFNKTHTFHFLLSIYGECVPKPRVDRPRKVPVIEERAMPAHLI PPMSFFDFVGDPHSFPRPTVENIFHVSFIIRDGXAE*
4530	A	2	329	PKPRVDRPRKVPVIEERAMPAQLRRMEESHQEATEKEVERILGLLQ TYFREDPDTPMSFFDFVVDPHSFPRPTVENIFHVSFIIRDFARIRLD QDRLPVIDTENMASV
4531	A	207	318	WSVPSKRSSPGCPLSCFGFRFGQRESKAAALRPELL
4532	A	1	178	IFSRRSDTQWSSFFDFVVDPHSFPRPTVENIFHVSFIIRDFARIRLDQ DRLPVIDCEDL
4533	A	1	440	SGRGPEGRGRGRDPRDRTRSRSRSRSPSPRSRRGSARERREAPER PSLEDTEPSDSGDEMMDPASLEAEADQGLCRQIRHQYRALINSVORK AAPPGAGPDGPLSPPCAGRGGRAPEAGARRPGAALVETRRVPAPR RTLNC
4534	A	23	370	TMNSKSGLSSSRMSSSASSGFTPICVSRVSTYLNMSKELRSERSCFA FSLPKSEAKTRKWAARTASLARDTSLNRLVASSRTSVNLSPAFSMSS RFSIFKNTNFGKFVQHSLISS
4535	A	600	997	QGRTAENTFNKTHTFHFLLSIYGECVPKPRVDRPRKVPVIEERA MPAQLRKNGKNLIKSTEKEVERILGLLQTYFREDPDTPMSFFDFV DPHSFPRPTVENIFHVSFIIRDFARIRLDQDRLPVIDK
4536	A	195	489	NLVYISKVRIKKLPCFFRWFMKYQHVDPEEAVRIHTDVQTKKSMAIH WGTFALANEHYLEPPVKLNEALERYGLNAEDFFVLKHGESRYLNNND ENF
4537	A	535	1631	EDVKIQHGIPEQVILLGFLGKASNWDYRLEEGVTKSKKGKDRFVNP WPTWKNPSIPNVLRWLIMEKDHSSVPSSKEELDKELPVLPYFITNP EEAGVREAGLRVTWLGHATVMVEMDELIFLTDPIFSSRASPSQYMG

				KRFRSPCTISELPPIDAVLISHNHYDHLDYNSVIALNERFGNELRW FVPLGLDWMQKWCENVIELDWEENCVPBGHDKVTFVFTPSQHWCK RTLMDDNKVLWGSWSVLGPWNRFFAGDTGYCPAFEBIGKRFPGFDL AAPIGAYEPRWFMKYQHVDPEEAVRIHTDVQPKKSMIAHWGTFALA NEHYLEPPVKLNEALERYGLNAEDFFVLKHGESRIP
4538	A	1511	1687	GESVPLEDRVLRFCFSKQSDNSTALLPSLAPFLSHLLGLFASCKLC GWTLRDPEFRI
4539	A	425	619	EKKTENTCQVFLFSAVLCAPAPGAVQMGSLLSWGNRCLVPGCTPP TSSAGSVPIPTRSCCP
4540	A	122	621	TFARWMPERSWLNSQMEGEKPHLHCPSPTGQTPLPPSTPPSSRKSCP HTGFHRAPLSSGHLEAGWELTHVCRLKKDSAGSAQPCRGFCLCPDVC FPVAFSLGEENRETLVKCFCLPCCVPPPPGAVQMGSLLSWGNRCL LVPGCTPPTSSAGSVPIPTRSCCP
4541	A	2315	2790	AATTPALRPLRRSSFLMATTITKASTGTWSSSPSLPTPPPTSTLRKA PTTLIQKWRPGAQQPSCPKPRS*PSSSTPRTGPIPGTSTSEPMITTQW P*STPSMR*LPPALTHPRSCVPSRTAAWVLGWYATHIERWLSAYSRO PDSGLGWQTCFAQNLPK
4542	A	645	766	PSYIAYMCICMVCVYVYINICVCIYTHVHTPYNPVISKN
4543	A	294	504	FFYFPQVVFIPPQGLELVLVKKNKKKSTLDREESRQENHLNSGGGG CGEPRLLCHCPPSWATRTKLCLK
4544	A	969	1160	GSISLTESWATVSCGPHPQTLEDSSHHPWKGGCHCCRAQGCDSGVPH CRGAGAGSASTCKMGI
4545	A	147	402	GRGIQLFHEIQLQLSKTLCEPAVPVQRLRGRTAARWPGSRESPLRPV FDVEYCGVLIFIIILFI*WRHFHSLCWSGDDIIILACLL
4546	A	240	433	SWSAPSRPGHVCGSFSFLLFFFFFKKKKGSAEISVASSQRISIREK LCVCVCVCAHVACARV
4547	A	3	310	GGQPPHPPAARPGRWGCQPPARQPLRPGGSVSTGTGFPGRWQPET SWVSCRHCGPHLSAVWGLPR/LSPLPAGPNRQPOLSEFPRPKFLT PRTQKTKPN
4548	A	3	195	WPPGQLQPRGTEHRPPTPDTPRAARSTRSHSPSEPRTRTWPQQR*L PRPSKPSHGPDVIEAA
4549	A	1	1439	MATEIGSPPRFFHMPRFQHQAAPRQLFYKRPDFAQQQAMQQLTFDGKR MRKAVNRKTIIDYNPSVIKYLENRIWQRDQDRDMRAIQPDAGYNDWTP EGRRLVTGASSGEFTLWNGLTFFETILQAHDSPVRAMTWSHNDMMW LTADHGGYVKYQSNMNNVVMFQAHKEAIREASFPTDNKFATCSDD GTVRIWDFLRCHHEERILRGHGADVCKVDWHPTKGLVSVGSKDSQQPI KFWDPKTGQSLATLHAHKNTVMEVKLNLNGNWLLTASRDHLCKLFDI RNLKEELQVFRGHKKEATAVAWHPVHEGLFASGGSDGSLFWHVGF WTRNRPGDKMRDRYNLNLPGMSEEDGVEYDDLEPNLAVIPGMGIPE QLKLAMEQEQMGKDESNEIEMTIPGLDWGMEEVMQKDKKVPQKKVP YAKPIPAQFQQAWMQNKVIPAPNEVLNDRKEDIKLEKKKTQAEIV YRNGYITIY
4550	A	292	573	VFFCFDFFKYIYICGVYIHICIYIYIYTYTYIYTHTYIYIYIYIY IYIYIYTHTHTHTHTHIYIYIYIYIYIYIYIAASWAANAISWRQVSC
4551	A	376	456	GEEPTSVF*RNQWNLPHKHFGNASPW
4552	A	1663	1984	PQSYKSHLRFTKPSCEPLSSPAAPNYIFKQTSRILALMLVLDIGH SCYQNRDTGWRVSTSPQHRIKLISGAEMIAKDLSHVNPKATPSPLWN QMGNRPNTNCFILI
4553	A	1735	1868	LDHGGFTIVAKWWEVAYLKMVVCVCCIFSHFVNKAHLLKILNFL
4554	A	138	279	EKPQISLQIDFVCRSQFRMHTHTHTHRDVFIFPNWILVSEIESWYK
4555	A	72	192	ILFADLSSECTHTHTHTHTHTHTHTMYLSFQIGFWFQR
4556	A	571	690	CQQGFSFLQAYGPAQHAIS\MRKFKAKYPDYEVTWANDGY
4557	A	130	943	TGEAEHLGLARADTWLGEEGPRDGAFFPGGSLEGKAWCEQPRGPPNCP VPRVPPDPAGEELLRWLISSPPIADSTFPLSGAGGAARRQGTGLRLV STCLGPRYNWLLRRWALGSI PRRDWSSLSQSPPPAVQAAPGWGEGGD

				SGRRNMAVADLVLI PDV DSDCVFKYVL IRVHSAPRSGAPAAESKE IVRGYKWA EYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIH VYGYSMVSRSPVPPCRRPQYQLRGPPEPAALTRGPS
4558	A	45	405	GIPGRRNMAVADLDLIPDV\ DSDSGVFKYVLIPSPLGIPAPGIRPA ESKEIVRGYKWA\GHHADIYDKSVGATCRKQGLRTVSILGGGRIS/H TKSPGQERFTVY\GYSMGLWSCPRTPIST
4559	A	613	866	NSVLTLLALLFSLHVLPPPPSGVTD TAGALPTGGPPSPSTSVTGRGPA HSHASQLPPAPGEFAPLNE SCRGWAGEAFLEKVSLLI
4560	A	69	432	GGGQRAIERSLSSIPEDCAMGLSDGEWQVLNVWGKVEADIPGHGQE VLIRLFKGH PETLEILSMLFLT VVIGSLCPLFMTDRVIVLLFISFLY HHYCYDSYHLFLT YNILYRSCLSMLP
4561	A	144	294	ELLIWTS LWELCAYTCLCVCKCAGSFVCMCTCGNLCLSYFSSFHKG FF
4562	A	13	759	PGDPRVRGRVAWRSNNSRKSSADTEFSDECTTAERVL MKSPSPALHP PQKYKDRGILHPKRGTEDRSYQPSL KSTDSRSYPSRGARPSPRGSGK GSKSPSPRPNMPDRYFIMKSSNLRLNLEISQQKIWT TTTTSNERKLN AFWESSIVYLVS SVQSGHLQGF SRMSSEIGREKSQDWGSAGLGGVF KVEWIRKESLPFQFAHLLNPNW DNNKKVQISR DGQELEPLVGEQLLQ LWERLPLGEKNTTD
4563	A	177	328	INAH LKFKVYFLSQAPL KCTWKTS AARENHV*LTFLMFYGT LGTGVC FCL
4564	A	218	343	LHVYIKTLTH THTHTHTH TQFCMSVNNIAKLLCNFYLG IKQ
4565	A	708	916	CSRYSVPRGMFPRHTLLSTALGSSRTTSQIITQIFKIVETCPNIGLC HREKGLLLRLTGTCCKSHLRSPQ
4566	A	829	1002	YTQMEEQNHFHLQENSKQSDPFSSKICGLASELLENKLISSTLEEF CWL GAGSIARK
4567	A	51	209	LPGARPGDCGSAGEGTLDDLSSLAHKAPPIKRGSLCHTHTHTHTH THTHTQ
4568	A	8	218	LPGARPGDCGSAGEGTLDDLSSLAHKAPPIKRGSLCHTHTHTHTH THTHTMIGGLYDPALASWCAKHA
4569	A	3	359	LLKYPINHFVGWVSSIYRMILQQDFTSIRFPAL EHCYTGGEVVLPKDQ EEWKRRTG LLLLYENYQ QSETGLICATYWG MKIKPGFMGKATPPYDVQ VIDDKGSILPPNTEGNIGIRIKPV
4570	A	2	217	ECGDVCDTGDRASVDEEGYI WFLGRSHHTINAS/GVVKALIVLTPQF LSHDKDQLIKELQQHVKSVTAPCIGC
4571	A	1	846	MYANVHSSFTLNSQNLKTTIQMAFNRLYVNAELIAGDPEKTAKVECG DFYNTGDRGKMDEEGYICFLGRSDDI INASGYRIGPAEVESALVEHP AVAESA VVGSPDPIRGESKGWRONGISAMWLPNIHALKTGILLRDSR NYRGSPDASVLVSRSSLSRGNLGSDSIGQLAASIQRQSPVAVAVRIW VDQTQHKAVEATKSGGVKGI RDKDLRVHKVGP GDQHWYGGCEDPKLW EPTLFIGDQTKKQVTLLKYPINHFVGWVSSIYRMILQQDFTYGRSGL
4572	A	361	916	FTGLLLQVIDDKGSILPPNTEGNIGIRIKPVRPVKLFMCYEGDPEKT AKVECGDFYNTGDRGKMDEEGYICFLGRSDDI INASGYRIGPAEVES ALVEHPA VAESA VVGSPDPIRG EVVKAFIVLTPQFLSHDKDQLTKEL QQHVKSVTAPYKYPRKVEFVSELPKTITGKIERKELRKKETGQM
4573	A	128	416	RQVLLFWGRGKYHNFPSPCLYPFSAFLGEGQVPLNPFSTLSGKSRF SRGQEP/LNPLFPHPDLLSVCNPLFPHPDFFAFLEGKNPRTPRTR GST
4574	A	127	135	NKIVLKCWGGENFWGVVWRENGRCFSGLLQAGLGA AWEPRVG/IVRR NICCIE*LVMAWIRFCMN* KTK
4575	A	35	386	QLKTDTAQSPRSPLDHGHGRASGN SHSGSIHPDGLK*LKNH KRSEKP CPTLTDDIPPQKKCKWPVLALSADITL*KSFSWLILAQKAPPLSTL* PPLLPAREQMSFDCNFPLPTQIL
4576	A	148	336	IRTPLKIGLFNSPGSHSQSPWN SGPRLS D/WTPSQIFSA*QLKTDAA GSPRKPPRPSRTPSFR

4577	A	4418	5132	DTISYQLEWRSLKSQETTDQAPMSSL*NFLRSNPWLS*RLGA*/WNA DEQGVPLIQEMLESWASICKVPKYPNAEAVRPEEQTPHLHPGEINSH VAHTKLWVWSLHTDTHEIWCRSDRGTSLSGRSIPCPALCSVRKIHL RPQVLRPTSPRNISPISNPHTRT/SQTPEPQRPVGPPEPPSPGACYK CQKSDHQAKECLQPRIPPKPCPICAGPHWKLDCAHLAATLRAPGTL AQGSL
4578	A	522	923	PSAAGLLEFAGGPLQTLFAWVSAEAAEQRVLLNSQ/WLLPDRSSGS FVS\GSIWPCVSVCPSSRCWRPRRKPLEAHLVQPQPPTLLAPVLVL LAVCYGWSRPLAHTLFAASRLAHHGVDQRNNLVDKAQILN
4579	A	1	569	MGKKQNRKTGNSKKQSTSPPPKERSSSPATEKSWMENDFDELREEGF RRSNYSELREDIQTGKEVENFERNLEECITRITNTEKCLKELMELK TKARELCEECSRLRS/LMRSTGRLLIKKTPFSSG*SRI*FNN*ASNS LY*NINSNKSLP*PLKGPILSKPSASNIPCSLQWVQAFQKSESLPA PR
4580	A	23	660	FIDSMPSPSRYQ*LSSQNWKLL*SSYGTKEEPASPSQS*AKRTKLE ASHYLTSNYTRLQ*LFQKHTMLSPRENLTQPACTQVK*TAMLLTQ/ RPVWWSLHTDAHEIWCCSDRGTSLSGRSIPRPPALCSVRKIHLRPQV LRPTSPMNISPILNQLSSLRLTLPLDLRSLPDHHRASARLHPGEI NSHVAHTKPVWCSLHTDTHENDKNKQ
4581	A	1	764	MIQEHADKQVQRLQGVLLGSIPTAASRARLHPGEINNVAHTEPVWV SLHMDAYEIWCRGSDRRTSLGRSIPLPALCSLRIHLRPQVLRSTS PRNISPISNPGHLSDYTPTFQGCQTMQGRLPWSFTLSGKSRSFSGEGA TORQYPIPIQQALKGLMPAITRL/STAWPFKAYKLSLPFPHTCPKTR QALQVSSGSAPYQPNCFAYPPHGAKPIYSSILNTCLYNPLFCRSRQT SFLYYSFAPFIPASLRIHLD
4582	A	1	400	MWNAVTLWQQRESCIEESEEIGTLETKEHFIIRGPKTLAPVTDWEG/ SPSLGV*SMQGRSLDYTPTFQGFQTTQGRLPWSFTLSSKSCFS/AGR GKLLLARPS*VPILQPPLLHPTILLSPPLLTPGQAYSFIP
4583	B	1	933	MEEKBEERKRRRKRKRREEGRDGERKRMKQKENQDPKDPPTTSGPQ TDQPKKHLTNFKSETKETRFIRGPKTPAPVTDWEGSLPLVFNHSRDT SLIHPGFRGVRPRRDACLGPSPLAASPTFLGKGPAAPRQTELGPNS SSASAPPPYNPFIASPPHTWSGLQFPSMTSPPPPAQQFTLKKVAGAK GIVKDLINLTFKVYNRKKLQFLASTVTRQTPATSPAHNKFNQTPELQQ PGVPPEPPRGACYKFQKSGHRAKECLQPRIPPKPHPICVGPWHKSD CPHTLAATPRAPGTLAQGSLLTPSQIFLA*
4584	A	1	582	MATAVHLPASQPGTHQKI IDAMKALDAGQQPALWALASTDFTSLKK LRPQSVTSRNSRAVTSSSERKGGTPDYSPTFQRCQTTSLYTCRKSG HQAKECPQPGFLLSRVPSVRDPTENRLFNPSGSHSQQSPWNSGQGSLLT DSFPDLLGLSAETDTARSPKRPRRPSRTRASVSQFIQNHIAITIIIL YDKCFE
4585	A	1	622	MAKFSFGSGKSVCKSPKGNNTWETRMIGDGGQLEGSLLTMKFEDGKY LFGFNIIEGDFCEDSNFQTGESVSDVYFENVSAHQRESTGSGIAQER NDEGLESGRAVLCIEECLSASLASTSQSSIEQPLPTSS\PTKTKQNM TPDIAEYPQWAIWTSKTTTIVLRPS*VLILQPPLLHPIIFLSPPL LTPAPAYSFIPPSQTPSFG
4586	B	102	1151	MEEHFMLMGSKNQYRENGHTAQEKLLYAFHNISLKQSSSLSLSQNFP NNENNDGSKDDDDGGDDDDDCQASEAKPNSACLHPGEINSHVAHTKP VWWSLHTDTHENDNGDVGDDNVDDDVDDGGDDGKDDGDDDDGDTVM VMMIMMMVLMVVMIVVVVVVVVVASRKAFLFLINGESEELESHLT GFANIPNHHLTVQHIYTPTLPSGETKETRFICGPKTPALVTDWEGSL PLVFNPCRDASLI IQPRFKAASPAILGEGQVPLNPFSTLSGKSRSFS GEGARAYYKCRKSDHQAKECPQPRIPPKLCPICAGPHWKSDCSTHLA AAPRTPGTLAQGSLLTDSFLA*
4587	A	258	479	TAAARRSSRTSSHRSLHVPETIWPLGQGMPAARDSS*AASHLCRTPP KIGLFNLPGSHSQQSPWKSGPRLSD*LLPRSSRLSS*RALGQISRGSG SGCQVS

4588	C	259	531	MSPAHNQFOTPEPQRP GIPPEPPPPGACYKCQKSGHQAKECLQPRIP PKPRPICAGPHWKLD CPTHLASTPRAPGT LAQGS LTASQIFLA*
4589	A	1	446	MNLNRNALVLT LFS DSARLHPGEINSHVAHTKPVWWSLHMDTHEIWC RDS DRGTS LGRSIPCTPV L/VLSRFKKIKACYHSPATSWPFKTYKLS LQLPHFTCPKTRQALQVSSGAVPYQPNCFAYPPCGAQPVPSFVLNTF LHNSLCRA
4590	C	228	260	MFLGLVGLRT*
4591	A	268	390	KQHSSFKNIQSRPFSAMSKLRPWRFRWKENCKASNYLLKKD
4592	A	1	499	MAPTNCKGSRKCGRPHEQMHPYLP LLT LFS DSARLHPGEINSRVPH TKPVWWSLHTDAYEIIWYHDSWDGDLPE\TIPCPPALCSMRKIHLRP QVLRPTSPRNISPINPEK*NGLKVF*KHTSPSSATNLKRPQGQYFYH FPFSEFRPVLGMLQVTSAFQKFTLL
4593	A	1	355	MEVYTQKAYWRVPLGSTVG DQGGHGRFIHPFAIKIEQGSTNRCPSGS PATKYVLLCLHGEKVDLLPADQQSIFSPGRSTQGH LISITGVLMNRH STYMDKEKVKMTALWTDEELSKLTWTRMKFDAMTQLGDLPEINPL SSCSLLREKDPPTSGPQT DQPKHLTNFKSTTNHAPLTIP LKPNHS YPAECQYPVPQHALKGLKSIITRLLQHGLLKPINCPYNPILPVLKP DKAYRLLQDLRLINQIVLSIHPVLPKPNLTLLSSIPSTTHYSVLDLK HAFFTIP LHLSSQPLFAFTWTDPDTHQAQQITWAVLPQGFTDSPHYF NQAQISSSSV TYLGIILMKTHVLSLLIVSG*ESIWFQHGVDQRNNL VDKAQILK
4594	A	260	487	AQACMYTSRWPEATEEPQKK*KWLVPALTDDITL*HSFSGTVSLRSS PLSTL*PPPLPAREQPPLTVIFHHLPKS
4595	A	1	508	MNMNIKKIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSH ITRHDMLQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSPK DADDTSIYMFYQKTA/PSPGQA/TV PILPQPPLLHP IILLSPPLLTPSPAYSFVP
4596	A	1	1246	MKGRRSLWLLPADGSSGNGNELQGTSPHDYFSIAIKSTHIGLEYP TSRQSNRVSPQSKRIRQPLGLPSGSITERGPPNNRQKGYTRQQFCHE STPNKGD RVIYNLTCLLYCCVRFPLAGTGPHILYLSRLASNLELFR DKGRGEQRKEEVTCFHKL LAEKENNPFFSFIYPNPIKRPHPYLP SLT LFS DSAHLHPGEINSFMAHTKPVWWSLHTDAHEIWC RDS DRGTS LG SILRPPALCSMRKIHLRPQVLR LISPRNISPISNPHALKGLKPVITR LLQHGLLKPINSYNSPILPVLKPKPKYKLVQDLCLINQIVLP IHPM MPNPYTLLSSIP/CHNPLFCSGSQTCLFYSFVPVIPASLRHFLD* P*HSS/WFSKLPGLYCRKASQTAPITSVKPKFHPHLLPISA
4597	A	182	750	KWPYCPSSAGQQTQLCSSSTNSNNCLPYRGTS LGRSIPCPPALCSMR K/MPPTTSGPQT DQPKKHLTISNPVAEAKGIVKVNAPFSLSD\PPKI S*RLGSFSSNHPYLGQRQYPIPQALKGLKPVITCLLQHVL LKPVNS PYNPILPVQKLDMPYRLVQDLCLINQIVLP IHAMVPNPETFIPLTV LNP
4598	A	3	504	KRPHPYLP LLT LFS DSAHLHPGEINNHVAHTRPVWWSLHTDVHEIWC RDS DQGTFPWEINPPSSCSLLREKDPPTSGPQT DQTKKHLTNFKSG KRPLFT\PSPTSLTIPQLSPFN LGATLQSLPSLNFNSFHLVFTKE TCFIEHPKTPAPVTDWEGSLPLVFNHC
4599	A	1	1032	MWIPPQFMTCTFQCGRSSCTLAHLSHDWGSQEMLHWNMGSRKLKQPW DVLALRACDGKGGTDSAPLHPGEIKSFIAHTKPVWWSLHTDAHEIWC RDS DRGDLPEINPLSSCSLLHEKDPPTSGPQT NQPKELLTNFKSV PTPSVAESFQSSFSTDPSPSSPPQAAPRQAKPGPNSSSASAPRYN PFITSPHTWSGLQFHSATSPPPPAQQFPLKKVAQVKGI VKHALKRL KPVITRLLQHGLLKPINSYNSPILPVLKPGKPKYKLVQDLRLINQIV LP IHPVVPNPYTLLSIPASTTHYSVLDLKHAFFTIPLHPSSQPFFA FTWTDPDTHQAQQIT
4600	A	72	724	FQIAGKWHFQFFHPTRSK*FLS*N*QMV*GA*CPGILLHISPFLVSV PSATRPKSSFFPSHLSPQYQPVSLSLSNLPFLQTHVTS AFLPRLLL ARPS*VPS/RSSASA/LSTLQSLYHLPSHLVRLTVSFRDYPSTCP

				AIYS*KGGWSQRHSQG*CSF/SLYPKSDSV*ALFHQI*KSSPVHGSF GSNPKTLYSPSP*KVKRPSYSQYTFYYPICSRH
4601	A	2009	3197	NLVVSI RHMEETNSSSKDMYQSPGEAEGWRWKKGSDRGQNLFRKHSK CLILLIRERFESPHSYICSPVTFQFFYAQSVKHVNVITIDCLPEGAAT RGTARTSKPTTKSQKTL PSTSPGHWTQSTPWASALRSSPWTETAAPS ETEETLNTGRPPPEL PARATATWFSASHTLPALATRRVARTQWLTADR QTWASISSVPWAQTISEKKPGGSLWETRSSPPTTAGTEAMNTTSL APAAEIMATPGSPSQASPTSGAFTHGTQTPSPTKATAPRYPQTGDLS AEWPFTAGEEPVLVPRPHQVSRCPQPLFKVGAMAAAPLTALQRLNP CLMELCQFFQOCLCMSQRSPTEDMRYCLEYYSWFLKNATYICQVRK RVSHSHTLKQKCLENICKSV
4602	A	3948	5007	VLQTFAVSVTAHGGTTPRVVCSQWVRGLADFRNEAADPHDQGMEN PTDFLERLRGALVKHMSLSPDLVEGQLILKDKFITQAAPDIERKLQK QNGPSLRDIFFSPQNGYNWRMASFYLPVANKWKILKSLYQILHLGPD WEGPYTVFLSTPMAVEVTGIDSWIHYTQVKAWKADGATS VNPPEHPK YQGEINSHVAHRKPVWWSLHTDVNEIWCRRSDRGTS LGKS/ HPRSSC VLC SVRKIHLRPQVLRPTSPRNISPILNQELATRA/VKSGH*AKECL QPGIPIKPHLICVGPB*KSDCS/TSPGSHSQSPWNSGPRLS D/WTPS QIFSA*RLKTD TARSPQKPPRPSRMPSFR
4603	A	567	678	RNKTCWAWQYTPVVPAAWEAKAGGSLQPRSLSPAMG
4604	A	1	305	SDIETLDIPEPPPNNGYECQLRLRLSTGKDLKLVVRSTD TVFHMKRR LHAAEGVEPGSQRWFFSGRPLTDKMKFEBLKIPKDYVQVIVSQPVQ NPTPVEN
4605	A	3474	3657	QICVCVCIIYICICLYIYICICLRKWFFKMYVYSTHMDTLQSSDFPCA TSCVSLLMRICNG
4606	A	796	937	HRSLLRLPASVSPHTAARAPLCCSSGPHSPAFGSWTFGILPSTLVLSE
4607	A	1	2722	MAWRRLSRRRVAGNDRTPAPQRHWRYTTLFEMKRSKELPVRWCDFS AFTPMMRTHEGNRPGDNWQFDGDAETIAHFARMTTFTTLKPYLKEA VALNAKSGLPQLVDIREEMPEQTAKRMLSLLGILKYKPSGNATDMGK EHRTL PANFAFNEFVARHLRHRTVNQLQPGENHLGGGVAVASSFGT SIIATPIAVTPPINLPTIIGKIMAFMLAAAKPKWSPRAKAAETAKAQ LMTLPRNSVILFASRLSSHAPAGLQGHINF TISTKILDSNEPCGGQK GFVPQKGRSDTLIKPVLVKDPMVSQGLRCLKNSATSTTNLYTQALLA YIFSLAGEMDIRNILLKQLDQQAII SGFILVTVIKSSNADDTSIYMF YQKVGDNSIDSWKNAGRVFKDSKFDANDPILKDQTQEWSGCDPQLG CDFVVSEARAFASDHRQA EWSSKDDFMRLGKPI LFFGVTAGNMDSMI NRYTADRRRLRHDDAYTPDNVAGKRPDRATLVYTQRCKEAWKDVVIL GG/VGMMCS/LSEQGKQLA/IQVSN I/LGMDVCC/IDLLMKD/DG/S FCV/CEANANVG\YPALGSTMGCSNSGMVTTPIKWLMSISVQCLANG TFLSPSLTKCPKGIRASVPLSGGPRSLKARTFSAFSGQPSSQPSQP TNYPSTICGHNSGIQPKFQLNG
4608	A	17	1507	VCGSVSVLEWEGEGEADGTRGCEKLGECARTPGQPAGAAVGGGERRRL PVSRRPPPPPLLPPLPAARRPALSRTPQPGSVGRERGRSPPTQVSGRR YIQEBIIQARKHKLIKMCSSVAAKLWFLTDRIREDYPQKBILRALK AKCCEEELDFRAVVMDEVVLTIEQGNLGLRINGELITAYPQVVVVRV PTPWVQSDSDITVLRHLEKMGCRMLNRPQAILNCVNKFWTFQELAGH GVPLPDTFSYGGHENFAKMIDEAEVLEFFMVVKNTRGHRGKAVFLAR DKHHLADLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRRVVGTM LR CSTDGRMQSNCSLGGVGMCSLSEQGKQLAIQVSNILGMDVCGIDLL MKDDGSFCVCEANANVGFI AFDKACNLDVAGIADYAASLLPSGRLT RRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSDPESTER ELLTKLPGGFLNMNQLLANEIKLLVD
4609	A	664	1059	EGTLGSGIPCLSRQCFVSFPLFFLLTGIITIEKEVPLSMYVSASRMS SEREMTQCLTQAPGSLATSFYFVFMTEKGKPCSDNRHFRQPCWLST PAWPPPPSTLPLCPPRPPTSTKQGGVGDICGIPTFNLW
4610	A	775	944	IFTWINELFAQILLKLYLVPIKLMDTVYMSIYLSLELCFVISPFLLT

				GIYLNLYIY
4611	A	279	416	ALSKTIDVARNLERRHTHAHTHTHTHTHTHTHSFFLPCDEKGL
4612	A	36	4704	TGAQSLTLCQVFILSCFFFFLNEVKMPIRPDLOQLEKCIDDALRKND FKPLKTLQIDICEDVKIKCSKQFFHKVDNLICRELNKEDIHNVSAI LVSVGRCGKNISVLGQAGLLTMIKQGLIQKMWAVFEKSKDIIQSQGN SKDEAVLNMIEDLVDLLLVIHVDVSEDEGKKQVVFVPRICSLVIDSR VNICIQQEIIKKMNAMLDKMPQDARKILSNQEMILMSSMGERILDA GDYDLQVAIVEALCRMTEKQRQELAHQWFSMDFAIAKAFKRIKDSEF ETDCRIFLNLVNGMLGDKRRVFTFPCLSAFLDKYELQIPSEKLEEF WIDFNLGSQLSFYIAGDNDHQQWEAVTVPEEKVQIYSIEVRESKKL LTIILKNTVKISKREGKELLLYFDASLEITNVTQKIFGATKHRESIR KQGISVAKTSLHILPDASGSQILVPESQISPVGEELVSLKEKSKSPK EFAKPSKYIKNSDKGNRNNSQLEKTPSKRKMSEASMIVSGADRYTM RSPVLFSNTSIPPRRRRIKPLQMTSSAEKPSVSQTSERNVDNAASL KRSRSEGRHRDNDIDKHIKTAKCVENTENKNVEFPNQNFSELQDVIP DSQAAEKRDHTILPGVDNICGNKIHSKWACWTPVTNIELCNNQRAS TSSGDTLNQDIVINKLTKQKSSSSISDHNSEGTGKVYKKEQTDHI KIDKAEVEVCRKHNOQQNHPKYSGQKNTENAKSDWPVSETTFKSV LLNKTIEESLIYRKKYILSKDVNTATCDKNPSASKNVQSHRKAKEKEL TSELNSWDSKQKMKREKSKGKEFTNVAESLISQINKRYKTKDDIKST RKLKESLINSFGSNKPVVQLSKEKVQKSYRKLKTTFVNVTSECPVN DVYNFNLNGADDP I I KLG IQEFQATAKEACADRSIRLVGPRNHDELK SSVKTDKKIIITNHQKNLFSDETETEYRCDDSKTDISWLREP KSKPQ LIDYSRNKNVKNHKSGRSSLEKGPSSKMTPSKNITKMDKTIPE GRIRLPRKATKTKKNYKDLNSSECEQEFSSHFKENIPVKEENIHS RMKTVKLPKKQKQVFCATEKELSKQWKNSLLKDAIRDNCLDLSPR SLSGSPSSIEVTRCIEKITEKDFTDYDCITKSI SPYKTSLES LN SNSGVGGTIKSPKNNEKNFLCASESCSPTPRPLFLARHTPTKSN TIV NRKKISSLVLTQETQNSNSYSVDSRYSSEERFMEIESPHINENYIQS KREESHLASSLSKSSEGREKTWFDMPCDATHVSGPTQHL SRKRIYIE DNLSNSNEVEMEEKGERRANLLPKKLCKIEDADHHIHKMSSES VSSL TNDFSIPWETWQNEFAGIEMTYETYERLNSEFKRRNNIRHKMLS YFT TQSWKTAQQHLRTMNHQSQDSRIKKLDKFQFIIIEELENFEKDSQSL KDLEKEFVDFWEKIFQKFSAYQKSEQQRLHLLKTS LAKSVFCNTDSE ETVFTSEMCLMKEDMKVLQDRLLKDMLEELLNVRRELM SVFM SHER NANV
4613	A	124	672	WSCSNKKYPLPPGNLMQSLPPEEAEPCHREISSFYVSEPOQGDQDRV SSEKQHEQLWQQRHTSAAAPPSAAAPHVLCNPKSVLKRVPVTSEELL TPGAPYARKTFTTIVGDAVGWGFVVRGSKPCHIQA VDPSPGPA AAGMK VCQFVVS VGNLNLVHDYRTVNNLILTGPR TIVMEVMEELEC
4614	A	688	940	NSLGEIGIKPFLKVPFCFLPPPKLLLLFVAFSSRLWALPSCFGLT PHFPGFPSHFLTRISSICLPLFLPSFLSCLFFFEYN
4615	A	561	663	WESHISPPFNGIYIHTHTHTHTHFLKVVYLQIC
4616	A	217	378	RETDKTLASLKKRVKTQINKIINEIRGVTTDTTEVQRIIRDTLNNPV GRSTGRE
4617	A	552	973	NWAGAQRLTMTHGSCLPQLSDKVAPAKHWRPKPRSITPIVTPPISSA SAVKGKREKGSEALVPPHLVGRYASSRSHPSQGGEGRPQAGCGHSWL TLSSATDRLSHSWAGLNPRCPPAATWPPCSTFSPFASSGCRQPSSF
4618	A	198	347	AADVLIQSQSHIQHPCWPPFSKPSCAPKVGQPALPLPDPLAVRALHV LT
4619	A	201	426	FSPWSWCCYGHWTSSAQVGSRLPLPSASVSPVSTWPLCCLLQGGLL AYTIFHTQRLCGPFPILLPIPSLHSST
4620	A	3	299	HASVLPPRSCRWFVHSGTTMSKVSFKITLTADPRLPYKVLSVAEST PFTAVLNACMQNTVQSLGRCNHYQPGNTDLALRILESLPLSFWPTE NEVI
4621	A	305	440	LKINERGRAQWLRPILPAPWEAESGSGFGRSSRTAWGISGEASS

4622	A	936	1380	VLNTINSSLSHVQGTSVLSPFLHIGSVITLAAMIYKKS AVQLFEKHP CLYILTFGFVSAKITNKL VVAHMTKSEMHLHDTAFIGPALLFLDQYF NSFIDEYIVLWIALDFSFFDLIRYCVSVCNQIASHLHIHVFRIVKST AHSNHH
4623	A	9	1230	DWEGDPPEGPATSPLTNSGHPGSGGSSSSDAAATAQSREAAPAGRP ERAAPGPLPGHPAFMQRLVAWDPACLPLPPPPPAFKSMEVANFYEA DCLAAAYGGKAAPAAPPAARPGPRPPAGELGSGDHERAIDFSPYLE PLGAPQAPAPATATDTFEAAPAPAPAPASSQGHDFLSDLFSDDYG GKNCKKPAEYGYVSLGRLGAAGALHPGCFALHPPPPPPPPAELK AEPGFEPADCKRKEEAGAPGGGAGMAAGFPYALRAYLGYQAVPSGSS GSLSTSSSSSPPGTPSPADAKAPPTACYAGAAPAPSQVKS KAKKTV KHSDEYKIRRERNNAVRKSRDKAKMRNLETQHKVLELTAENERLQK KVEQLSRELSTLRNLFFKQLPEPLFASSGHC
4624	A	1	932	RTRGRET KPHTKERGMMAKKPKPGPRRIFQERLKITALPLYFEGFL LIKRSYREYEHYWTCLRGTTLFFYTDKKSIIYVDKLDIVDLTCLTE QNSTEKNCAKFTLVLPKEEVQLKTENTESGEEWRGFI LTVTELSVPQ NVSLLPQGVILHEVLEREKKRRIETEQTSTVEKEPTEDYVDVLN PMPACFYTVSRKEATEMLQKNPSLGNMILRPGSDSRNYSITIRQEID IPRIKHYKMSVQNYTIELEKPVTLPNLFSVIDYFVKETRGNLRPF ICSTDENTGQEPSMEGRSEKLLKNPHIA
4625	A	942	1293	MGNFFFFEPGTCYVAQAGLELLNSSDPLTSASQIAETTGTHTWTLK TIFLKNKSTALHLYLLVSLQFKHTINDYNILFKAGRSGSWLQLEQFI TSGYLRARKIQKKKLGV CNTV
4626	A	40	154	RCWLCPHALFLWLASHLCHFYTFCVQAEC*VMPHPPL
4627	A	4	436	EGGGASLNIQPVHTQRCRSDKDDSTNRTSHDWPARGRHEDTASSY WVMTQTCRDPVGSRHWMGLRAEAGALAGMALEATCLALQGSILLEA SMKRSFPWATHCLAPQRRTTQPALPRI FLVLALNVHSLRNPSVSGKW DVW
4628	A	465	748	VLFVPIYIHKLVYIPYLQKHASNHQKEQKVMGNFLFYNKALLSFW TYFTSLERLSAHTSTIIFLLCQLFSAHVHLHQWHLDDRSSKSHICL
4629	A	92	394	WPRSGPLRLRTVCCCVLPLLSHSHKLHKISVSAPGP**QIPPPFQNR SFSCDTERG*GGETPLVPGKFSSPHQTL*GTSSGRTGSAGQLPLLY LSYKTR
4630	A	1	1614	MSLHGKRKEIYKYEAPWTVYAMNWSKGKVKEAAQRYQYALKKFPREG FGEDLKTRELKVSLLLNL SRCRRKMNNNSSSCVHILSSRQFAAALE DLNEAIKLCNNREIQRLLLRVEEECRMQQPQQPPPPPPQPPQQLPE EAEPEPQHEDIYSVQDIFEEDPPVGGQGKEYSPPPPSPLRRGPQYR ASPPAESMSVYRSQSGSPVRYQQETSRPYQMPQLPVAVPQQGLRLQP AKAQIVRSNQSPPAVHSSTVIPTGAYGQVAHSMASKYQSSQGDIGVS QSRLVYQSGIGGIVDGRPVQHVQASLSAGAI CQHGGLTKE DLQRP SSAYRGGVRYSTPQIGRSQSASYPVCHSKLDLERSSSQLGSPDVS HLIRRPISVNPNEIKPHPTPRPLLHSQSVGLRFPSSNSISSTSNL TPTFRPSSSIQOMEIPLKPAYESNIAFYNKTNNAQNGHLEDDYISP HGMLANGSRGDLLE RVSQASSYPDVKVARTLPVAQAYQDNLYRQLSR DSRQGQTSP IKPKRPFVESNV
4631	A	1	410	KGKVKEAAQRYQYALKKFPREGFGEDLKTRELKVSLLLNL SRCRRK MNNNSSSCVHILSSRQFAAALEDLNEAIKLCNNREIQRLLLRVEEE CRMQQPQQPPPPPPQPPQQLPEEAEPEP*RT*TRPSSCVPTTVSRD FC*EWKKSVD/TMQPQQPPPPPPQPPQQLPEEAEPEPQHEDIYSVQD IFEE
4632	A	1	972	RPYQMPQLPVAVPQQGLRLQPAKAQIVRSNQSPPAVHSSTVIPTGAY GQVAHSMASKYQSSQGDIGVSQSRLVYQSGIGGIVDGRPVQHVQAS LSAGAI CQHGGLTKE DLQRPSSAYRGGVRYSTPQIGRSQSASYP VCHSKLDLERSSSQLGSPDVSHLIRRPISVNPNEIKPHPTPRPLLH SQSVGLRFPSSNSISSTSNLTPTFRPSSSIQOMEIPLKPAYESNIA FYNKTNNAQNGHLEDDYISPHGMLANGSRGDLLE RVSQASSYPDVK

				VARTLPVAQAYQDNLRYQLSRDSRQGQTSPKPKRPFVESNV
4633	A	196	390	HGALERTRTTYPQSLFSALSPNSCSRKWQTGGVPFALGTRGSGSPAK PPRSSATIQHSAPGPLCR
4634	A	2	4417	DEDFIILIDGLNEAEFLKPDYGDITIVLFLSKMMGKFPSSLKIIVTVR TSLQEITKLLPFHRIFLDRLEENEAIDQDLQAYILHRIHSSSEIQNN ISLNGKMDNTTFGKLSSHLKTLSSQSSYLYLKLTFDLIEKGYLVLKSS SYKVVPSLSSEVYLLQCNMKFPTQSSFDRVMPLLNVAVASLHPLTDE HIFQAINAGSIEGTLEWEDFQQRMENLSMFLIKRRDMTRMFVHPSFR EWLIWREEGEKTKFLCDPRSGHTLLAFWFSRQEGKLNROQTIELGHH ILKAHIFKGLSKKGVSSSILQGLWISYSTEGLSMALASLRNLYTPN IKVSRLLILGGANINYRTEVLNNAPLICVQSHLGYTEMVALLLEFGA NVDASSESGLTPLGYAAAAGYLSIVVLLCKKRAKVDHLDKNGQCALV HAALRGHLEVVKFLIQCDWTMAGQQQGVFKKSHAIQQALIAAASMGY TEIVSYLLDLPEKDEEVERAQINSFDSLWGETALTAAGRGKLEVC RLLEQGAAVAQPNRRGAVPLFSTVRQGHQIVDLLLTHGADVNMAD KQGRTPLMMAASEGHLGTVDFLLAQGASIALMDKEGLTALSACLKG HLSVVRSLVDNGAATDHADKNGRTPLDLAAFYGDAAEVVQFLVDHGAM IEHVDYSGMRPLDRAVGCRNTSVVVTLKKGAKIGPATWAMATSKPD IMIILLSKLMEEGDMFYKKGKVKEAAQRYQYALKKFPREGFGEDLKT FRELKVSLLNLNLSRCRRKMNGESQNSPWTFFIVSLDFGMAEEFATKAL ELKPKSYEAYYARAKRSSRQFAAALEDLNEAIKLCNNREIQRL LRVEEECRQMQQPQQPPPPPPQPPQQLPEEAEPQHEDIYSVDQIFE EEYLEQDVENVSIGLQTEARPSQGLPVIQSPSPSPHRSAYISSSP LGSHQVDFRSSSSVSGSPTRQTYQSTSPALSPHNSHYRPSPPHTS PAHQGGSYRFSPPVGGQKBYPSPPPSPLRRGPQYRASPPAESMSV YRSQSGSPVRYQQETSVSQPLGRPKSPLSKMAQRPYQMPQLPVAVPQ QGLRLQPAKAQIVRSNQSPPAVHSSVTIPTGAYGQVAHSMASKYQSS QGDIGVSQSRVLVYQSGSIGGIVGDGRPVQHVQASLSAGAICQHGLTK EDLPQRPSSAYRGGVRYSTPQIGRSQASYYPVCHSKDLERSSSQ LGSPDVSHLIRRPIVNPNEIKPHPTPRPLHLSQVGLRFSPPSNS ISSTSNLTPTFRPSSSIQMEIPLKPAYERSCELSPVSPQTGGYPS EPTRSRTTFFMGIIDKTARTQQYPHLHQNRRTWAVSSVDTVLSPTSP GNLPQPEFSFPPSSISNIAFYNKTNNAQNGHLLLEDDYYSPhGMLANG SRGDLLERVSQASSYPDVKVARTLPVAQAYQDNLRYQLSRDSRQGQT SPIKPKRPFVESNV
4635	A	158	358	LEAAEAPSRRERTAQQCPPSPPPHPSHPLVFSPPPEGPPRVNGFPCPRC GGQRKGEADPGAGRGWPGS
4636	A	4	152	FQGGEGEQADPKRHEPVCVIVITHQQGPDGKAQEDEMEKLIIFLYIQ SS
4637	A	382	458	SSSFKTSGSPCPGPEEEEEDEEDED
4638	A	46	314	SSSFKTSGSPCPGPEFPFWGYAPRLRRCFPVALGCWSSSLLSEEB EDEDEDEDEEEEEDEEDLFLSYCSWEKSPAFPSCLWKSVP
4639	A	46	271	PRRVPPPPRSISRVEAHPKQAPHAPGPBEEDEDEDEDEDEDEDEE EEDLFLSYCSWEKSPAFPSCLWKSVP
4640	A	1	1815	MTLVAYERYFNAEDDYTRESALQEHASVRNHIRLLGRKDYQQESAA YLDVSAHIRDPYPWELRLMISAPGSGNDTVILKLTAFTVSVGTA LTWNWNAQCANFQLSGYIPRHGPCNNHFPGEPEWDWIFTSPOKGTG REKRGIKIMRGISKVAQRCVPFKSDAARTRQRLSARKGRTLPPGRGK FPHSTTESFRNTFWLKKIMEHCFNMVDQQTTTAQTANFLQIRFTTM SKKIAVIGECCMIELSEKGADVKGFGGDTLNTSVYIARQVDPAAALTV HYVTALGTDSFSQQMLDAWHGENVDTSLTORMENRLPGLYYIETDST GERTFYWRNEAAAKFWLEMSITLRRDTRSGGSSSEGIIQFFFEETQ DENGFNIIYILDESNRVEVYHHCEGSKEELVRDVSRFYSSSHDRFTYG SSPINFNLPPQFYQIVKVDGREQQIPEGFAAAITNPLIAFQVKMVAAL FGCQPYLVQRLLAVDNDFAAAILKNGQYAAVDFAVDIAVAPVQAF FNGQPELISQAMKFPVVHCCILFLSDCGSLAAWPGSKLCLWGGFAG

				ISGRIARFQERIKWVYELFPR LHERRIQRAGTMSGGEQQRN
4641	A	1	1284	MDKKQVTDLRSELDSRFGAKSISTIAESKRFLHEMRDDVAFQIIN DELYLDGNARQNLATFCQTWDDENVHKLMDLSINKNWIDKEEYPQSA AIDLRVCNMVADLWHAPAPKNGQAVGTNTIGSSEACMLGGMAMKWRW RKRMEAAGKPTDKPNLVCGPVQICWHKFARYWDVELREIPMRPVRLQ QSVPHVLVVEFQTMQENHFLQRYGFFLSAVIRKTQYTLGHQLQQHHL GMSQLSCNPLSSPRGITRWCLGERLSRSSTRVEGILRGRISPDGFQE RIKWVYELFPR LHERRIQRAGTMSGGEQQMLAIGRALMSNPRLLLLD EPSLGLAPIIIQQIFDTIEQLREQGMTIFLVEQANQALKLADRGYV LENGHVVLSDTGDALLANEAAWVWSGNMLNLHDLVGLIRRLRRIRHE TMSNL
4642	A	1	1650	MFILWYSASSTFGKSDIVMGVRAQQKEKTRRSLEAAFSQLSAERS FASLSLREVAREAGIAPTSFYRHFRDVELDPNFGEKGNMAPLDCFG RTRAVASRVKLLGIEEVELNPPLFDLFLKHDAMHDPMVNESYCET GWVSKENLARMKELTYKANDVLKKLFDDAGLILVDFKLEFGLYKGEV VLGDEFSPDGSRSLWDKETLEKMDKDRFRQSLGGLIEAYEAVARRLV RHKMEKVMLSFDKVS AHYKIQALHEVSLHINQGEIVTLIGANGAGK TTLLGTLCGDPRTSGRIVFDDKDITDWQTAKIMREAVAIVPEGRRV FSRMTVEENLAMGGFFAERDQFQERIKWVYELFPR LHERRIQRAGTM SGGEQQMLAIGRALMSNPRLLLLDEPSLGLAPIIIQQIFDTIEQLRE QGMTIFLVEQANQALKLADRGYVLENGHVVLSDTGDALLANEASER KLWLEMLSPPKDDSKDPQAKLFITAATEGRGMDALREHLLQLPEREH ASQHSFRLAIDRAFTVKGAGLVVTGTALSGEVK
4643	A	1	1605	PMYFLCPLALVQCALKDPRSKYSLGGRTTLIITLQSGSKKNNIPH PSSLSERVMTAKDGFVSRCHLLMQPKQKQWSLMPMEGEVLENGCWP TLQDSSLCTALVDKLLVFLGRCFCTAVEVVMLVTCRTAAAVSAFLIV GRVSSPVCRAVSVQPWTLTADHTPGRYCLKLVCRQLCLCPSSTPLTE VFCSKEAFFIILDCSNLPHALLPVDS PKGLSKCSNPREKARRKLQGH YHVASEVSFVPVRRFPKGEIGANQPGTHRKFYHLTHYRQNLKQPDVP HGRIVFDDKDITDWQTAKIMREAVAIVPEGRRVFSRMTVEENLAMGG FFAERDQFQERIKWVYELFPR LHERRIQRAGTMSGGEQQMLAIGRAL MSNPRLLLLDEPSLGLAPIIIQQIFDTIEQLREQGMTIFLVEQANQ ALKLADRGYVLENGHVVLSDTGDALLANEAVRRGDELTEDRSRSLDG ELIRSLPCGASYGGLSLRPWSRGHIPQSHQSSSVRVMFINTSKGAS IISSSATMPGGLPKHLGP
4644	A	303	410	FNVGGKGNGLRCIPLLCLLFRLKRRKRRKMRQSK
4645	A	92	395	HHHSLTVTLSPFPCKKPLPPMKAKLVEERKRNRARG*SAKRRKMRQ RSQVNPSPFVAPVEATQEHETWNAQTLGMLGTSCGTACYCLELVSMG SRTSSAL
4646	A	362	498	DVNVLITYTVILKEALWLMVISALCDAEAGELLEAKSLRPAWVTK
4647	A	609	701	LRGVWGGRGWAGGVPALGPCRGCPQGRRG
4648	A	1	104	TYV*PSVFKVN*HPT*SSS*HRKDQTDILNAINQ
4649	A	1	1398	MTKKRRNNGRAKKGRGHVQPIRCTNCARCVPKDNAIKKFVIRNIVEA AAVRDISEASVFDAYVLPKLYVKLHYCVSCAIHSKVVRNRSREARKD RTPPPRFRPAGAAPRPPPKPMSGAGRGRSHLDEGREGAGDEVGELS QQEIDKDP LGGALGAGSRGTKTGMQAGIGGGEQVLVFDSSLPVAV DSCFHPVSPDTSALSWCLLSFSRTPQQPSPGNFRPEHLPLFLST VLPQSVAQQTASGKYLPSRWSQDRCGESREAPLPSKTLEGETPEGVG AELRCVRLPGPEWNSVLKPGFSLQLDSSSARMALVFVYGT LKRGQPN HRVLRDGAHGSAAFRARGRTLEPYPLVIAGEHNIPWLLHLP GSGRLV EGEVYAVDERMLRFLDDFESCPALYQRTVLRVQLLED RAPGAEEPPA PTAVQCFVYSRATFPPEWAQLPHHDSYDSEPHGLRYNPRENR
4650	A	1	1149	MTKKRRNNGRAKKGRGHVQPIRCTNCARCVPKANAIKKFVIRNIVEA AAVRDISEASVFDAYVLPKLYVKLHYCVSCAIHSKVVRNRSREARKD RTPPLDLANEKKVDQPP EAKKPKIKVNVNVELPIEANLVWQLGKDLN MYIETEGKMIMQDKLEKERNDAKNAVEEYVYEFDRDKLCPYEKFICE

				QDHQNFLRLLTETEDWLYEEGEDQAKQAYVDKLEELMKIGTPVKVRF QEABERPKMFEELGQRLQHYAKIAADFRNKDEKYNHIDSEMKKVEK SVNEVMEWMNNVMNAQAKKSLDQDPVVRQAEIKTKIKELNNTCEPVV TQPKPKIESPKLERTPNGPNIDKKEEDLEDKNNFGAEPPTSGMVNVT PNEENFC
4651	A	3	242	RASKMTKIRRNNGRAKKGRGHVQPIRCTNCARCVPKDKAIKKFVIRN IVEAAAVRDISEASVFDGKWVTGANCVRIPVS
4652	A	213	658	EGPARHRLSPVRASKMTKKRRNNGRA\KKGRAPRQGTAPLKIFPSG PLPPNCARCVP/RRDKAIKKFRHSET*WEAAAV\RDSEASVFDAYL \LPKL\YVKLH\YCVSCAIHKQK*SGNRSS*SPAKTRTPPPRF\RPA GCWPHGPPTKSP
4653	A	161	295	DLLGEIYVYIFIQLMYTYIYVYTQTHHTTNNHHTTHAYNRH
4654	A	2	394	QLMGADLCRIKMKHLLTTFVLVILWLYFYRGNGRYQPELSPQPLIILE GKNCSLRICIYASPFSLWRYNHDTRGPVSLTIMTFSENTKPNGRY TATLDADTKQSSHLITAYQLIDSASYICVVSALCST
4655	A	355	476	MPHTHTHTHTHTHKHMLIKLIGWGEANCFQGRWHILEKT
4656	A	662	979	EVLYLKNLSPRVTERDLVSLFARFQEKGPPIQFRMMTGMRGQAFI TFPNKEIAWQALHLVNGYKLHGKILVIEFGKNKKQRSNLQATSLISC ATGSTTEISGS
4657	A	960	1387	NTDKQVSWRARIASRTQKLRSKRHFVGHLLAQKPQKQSPGRTHAN LNSFSLQQAQEAQPAEPCLTLTAAQPAQKAQKQSPRQNHANLTAQP AEKHRSKAQAEPMPLNSLSLCPFKKRERQTDTWGLRLLTQAGLKL TG
4658	A	696	998	SLPTTSQPVRLQATDTPIPAKSKRAQLSPEGAGTGQAEVAQREPTG RGGGAFRPPTRAGDPRRRDSRSGGRNVPRAPGSRKSGDCPSLLPPQ SAPSPH
4659	A	240	463	GLVFSRLSPEYYDLARAHRLDEEKSCPCLAQEGPQGDLLTKTQELGR DYRTCLTIVQKLKMKVDKPTORSVSNA
4660	A	2939	3295	PVCTVSGPMAPGASSHPVLPLLGLLEPAGLAELGRTHPITMSTVVL LLQRSVSNAATRVCRTRGRSRWRDVCNFMRRYQSRVIQGLVAGETAQ QICEDLRLCIPSTGECRGDSRDT
4661	A	44	319	LPRSQGFPERTCAAAGTGVLSFRRSEGLSSCRGSRPPFSAPSLIAEP TEQGTGMAKAGEIGIDLGTYSVGVESHGPNKEIIRFYQINLSF
4662	A	2	896	FVLARRRPLRSRKMSRSGAAAEKADSRQRPQMKVNEYKENQNIAYV SLRPAQTTLIKTAKVYLAFFSLSNYQLDQLMCPKSLSEKNSNNEVA CKKTKIKKTCRRIIPKMKNTSSKAESTLQNSSSAVHTGKNKLQPKR TADAMNLSVDVESSQDGSDEDTTPSLNPSSTPPSPNPGEISMEKV KVKRYVSGKRPDYAPMESSDEEDEFQFIKKAQEAEPEEQEEDSS SDPRLRLRLQNRISEDVEESRNGVHHVGGNQRELARQKMKKQSDSVK GKRRDDGLSAAARKQR
4663	A	68	439	GARPSRPSCFPQLPDPLSSVFLWVFTSSRCLLAGHS SPDPQLCA VPQRTQGSQAQPDLAGRRLISPSLLLPHSPLPQGPLPQGPLPQSPCCF KPWEFMAKHRPHLPRADVAQTRGGEKEEA
4664	C	208	345	MSPDRNIECKATGFTETTIYDLLFCKSVDSFYQLLISSSGSKSIT*
4665	A	1	320	RPVPAKLNPRSWPRTAGALPLRPPLTMVAFHDEVEIEDFQYDEDSE TYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDKDQFVCG RNSPSPFQPTKN
4666	A	54	230	RWVLLFFLSFVNAVMLCAQVGSHHPALPWASPECCRDHICPHVGP PGPP\ P*PFQPG
4667	A	1	2303	MARGSLGVSPRAPLAAPRFSQCGMWRVCAFTQTRSRLECCVCLRSEPV GYTGSDDRGRHPRHSPAVALMVQSRVWQWRVPLVTKNVRLGTGVRGR PCTRFGEIKSPAAINTLQFEYALCLGRVQRPBGHDFCVPAERGVTED VRGCFRPEGQDMLALLLVGRLSQPGLSAPVTVSPRDCPTIPWWRG TGLLDLFTAVPPALSVPVPGWAEQEERLRLEQEREQEKANSRLA HTLPVEEPRMEAPPLPLSPAPPAPPPAPPPPLATPAPLTVIPIPVVNTS

				PQPLPPPPPLPAAQPLPLAPRQPALVGAPGLSIKEPAPLPSRPQVP TPAPLLPDSKATIPPNGSPKPLQPLPTPVLTIAHPGVQPQLAPQQP PPPTLGTLLKLAPAEVKSSEQKKRPGGIGTREVNHNKLEKNRRHLKE CFETLKRNI PNVDKTSNLSVLRTALRYIQSLKRKEKEYEHMERL AREKIATQQRLLAELKHELQWMDVLEIDRVLRQTGQPEDDQASTSTA SEGEDNIDEDMEEDRAGLGPPKLSHRPQPELLKSTLPPPSTTPAPLP PHPHPHPSVALPPAHLPVQQQPPQKTPLPAPPPPPAAPAQTLVPA PAHLVATAGGGSTVIAHTATTHASVIQTVNHVLQGGPGGKHIAIAPS APSPAVQLAPATPPIGHITVHPATLNHVAHLGSQLPLYPQPVAVSHI AHTLSHQVNGTAGLGPPATVMAKPAVGAQVVHHPQLVGQTVLNPVT MVTMPSPFPVSTLKL
4668	B	1	651	MQKEDCVIVLVKLAVEGMAPTQQIHLFVAITFSGWPRQCTGSSFKAI DLFLDPDSVMQQIYSPHFGIMCNFDNHAQNLMAVIDNIKQDRDMDE AGSHHSQQNTGTGNQTPHVLTHKWELSNENTWTQGEHHTPGPWVL GLADFKNEVVDPHGVKQPQFTVSVTALKDDVSGIHSFLLVGSWSANF RNEAAEPSALFTIAKIWINLSIHQMNG*
4669	A	1	112	ETHQYTSKDSIDQDLGFIWMNLFFPLRQDKKERKYWE
4670	A	474	616	HTKGLATSVFSQHRIPILPECFIVKLDVCVCVCVCVFIYINIQMYVF
4671	A	197	334	LNQVFLFCLLVFVFLIRCSPHISLEVNTPCVPLRIFSFYKGLHLI
4672	B	82	402	MGLEKLHPFDAGKWGVINFLKEEKLLSDSMLVEAREASEEDLLVVH TRRYLNELKRVLRPLRTQTGGTIMAGKLAVERGWAINVEAIXRKVE LEWGTEDDEYLDK*
4673	A	1	1524	MGEKLAPGNMFEGLDQAVLEVHPCTLGSGTSESEAPDETSLGWRGHW KVKATWGDIPSAATVERVGLGLSIHPSAFTPTLLGAPTTRPIFQIEK LRIGDKSLMMQAPGAQAQAMLNSHEKATYYTIAFMNRNVQNRHIYRSK MWINGFQWMPGGRKWMTAKRLHTTQLYQHVPETRWPIVYSPRYNIT FMGLEKLHPFDAGKWGVINFLKEEKLLSDSMLVEAREASEEDLLVV HTRRYLNELKWSFAVATITEIPPVIFLPNFLVQRKVLRLRTQTGGT IMAGKLAVERGWAINVGGGFHHCSSDRGGGFCAADITLAIKFLPER VEGISRATIIDLDAHQNGHERDFMDDKRVYIMDVYNRHIYPGDRFA KQAIRRKVELEWGTEDDEYLDKVERNIIKSLQEHLPDVVYNAGTDI LEGDRLGGLSISPAGIVKRDELVFRMVRGRRVPILMVTSGGYQKRTA RIIADSILNLFGLGLIGPESPSVSAQNSDTPLLPAPV
4674	A	39	786	GQGGQEAQPSLGEAKGCLLSESACSLCPRVMTTPNKGKALKVKRE PGENGTSLTDEELVTMSVRELNQHLRGLFKEEFVQLKQRRRTLKNRG YAASYRVKRVTKQGELEKQKAELOQVEVEKLASKNASIKLELDALRSK YEAMQTFARTVARSSVAPARGPLAAGLGPLVPGKVAATSVITIVKSK TPRPVIGTRVCPGRILCGATRHMANLAALSLCFLFLFSFLPLFPPTLLS SLQSTTCTPGAPG
4675	A	434	1333	GASLCQWLNAHCLARHPAPGWRSPSSLWTGSLASTTYCRLCPSSSTG FFSNVAPSAEGHQLFLCNVERSVSHFADKLLSKYVPVANRYEGTEDD YGDDPSTNSFEKEKQDYVYCLESSLQTYNPDYVLMVEDDAVPEEQIF PVLEHLLRARFSEPHLRDALYLLYHPERLQHYINPEPMRILEWGV GMLLGPLLTWIMRFASRPGVSWPGMLFFSLYSMGLAELVGRHYFLE LGRVSPSLYSVVPAPQCCTPAMLPAPAAARLTLYLSQVYCHKGFGK DMALYSLVEGPRERGPM
4676	A	772	1107	GLSGRERGNQAALTSEEWALAQDFNRPEAHRDQSTSKFSCPGPRVEP TGVPGCGSTHMPHCQPRQEPSWPGSGSACSPARSPSPDASWHCTLT LHKHLYADGLRDPASLVC
4677	A	282	377	TGEPLLQCGCKRWGRLHTESPLAHCLVEL
4678	A	233	459	THKAPESSPNSFPPPRGTLEERWGRPPQEWVDRETNDGTDVGGEGR EKSGPGTWGRGIGEGKGWGLPHCPHQR
4679	A	761	962	EILRNTWFPSSLGWVFNSEMHIDEHTSHRAHTHTHTQTRSHTLPS VNIFLPKNGSSFLRTFLID
4680	A	3	190	FFFFCHLSPRLDCSGAIMSYCSLKLGGSSGPPASASQVAGTTGMCHH PQPKHPYFLEWFTL

4681	A	150	338	AAGLDGKHWIGGSCACAGSCKCKCKCTSCCKSCCSCPLGCAKCAQ GCICKGASEKSCCA
4682	A	168	375	ATSPRLAMDPNCSCEAGGSCACAGSCKCKCKCTSCCKSCCSCPLG CAKCAQGCICKGASEKSCCA
4683	C	55	444	MLAKRVQGCYKKKKKKNPRFNIGCLYLHLKSTAVPGIQAQQLHLSDV PLQMXAPGQSYCTAHRAAGAAARLCQDGAICDSIAICQEPAPAGAN RRAGAVGSPFRGQGEARSSRSKRKTRSGTDEKRPEL
4684	A	64	322	DLGWGFFVKGSTKKMGPLKKTGYQKKFWSFPGIKGPKPKAFEAKNL GPRGPAHYSHPFGLNQRIGLTRGVPGPPGPHNEALFFF
4685	A	2	38	LALPRPQHFKV
4686	A	185	451	SQHFRPRQVDHLRLGVGDQLDQHGETPSLLKIQNWPGVVAHACNPS YSGG*GRR/RLTLGGGGCGLRSCHCTPALATRAKRLK
4687	A	344	468	MGYNFETGCLMDGSGFLSVGNKRFGHEGIPSRMGVPTDSK
4688	A	204	286	LLKLRRSLFGFVKVLRKYMIYIYTKTI
4689	A	206	395	TFCLVFFQFSYNFQLVPVFNTALVC*RH*LIAFLNLRII*F*YKIS YIFVKL*QNQISKPF
4690	A	2112	2221	KPYQWFTSYCNVFISFFFLSLNLAKEYCKEIFGCHK
4691	A	116	382	GHVSQELYLWELICTILPFFFFFFETELCSVTRLECSGAISAHYNLC LPGSSDSPASASQTSGITGVTTAPSHFISLKSGPSIKPIL
4692	A	11	666	SSAVEFGVALGRNQPLKKEPKWKSDYPMTDGQLRSKRDEFWDTPA FEGRKEIWDALKAAAHAFESNDHELAQAIIDGANITLPHGALTECYD ELGNRYQLPVYCLAPPINMIEEKSDIETLDIPEPPNSGYECQLRLR LSTGKDLKLVRSTDTVFHMKRRLHAAEGVEPGSQRWFFSGRPLTDK MKFEELKIPKDYVVQVIVSQPVQNPTPVEN
4693	A	47	241	RPDSHCLFSPQLTHASPSLPTEDRGPPQPETFPEDMGNTAEATAHP PRSCPPHCREPAPRAAR
4694	A	246	485	CQRSKNSGEAASWDQRRASSRQPGDRTLTHASPSLPTEDRGPPQPET FPEDMGNTAEATAHPPRSCPPHCREPAPRAAR
4695	A	2428	2657	HPVKHIIRPPKHTSGKKPNKRVTNRNSIFMDEV*PRKIEVEFQEEVV IRGMFPWSTSCSLVLLCCSLSWSTQIVNF
4696	A	1137	1491	AVFKRRLTLPVASGWNMTMDHTGAIDTEDEVGLAHLAPSPQSEAVAH EFQELSLQSSQNLPLNERKNVLQRLQQRRTREQLVDQGIMPRKIY TITAI PNVTEDGRVQEEPASCS
4697	A	3	728	YNSARPRPPAPPAPQONSAQRSRAPGSRPAAQSGGETDRSADRDSG RDSGETRVCERAGPSGPRSGSAAQRAPSANMSVDPLSSKALKIKREL SENTPHLSDEALMGLSVRELNRHLRGLSAEEVTRLKQRRRTLKNRGY AASCRVKRVCQKEELQKQKSELEREVDKLARENAAMRLELDALRGKC EALQGFARSVAAARGPATLVAPASVITIVKSTPGSGSGPAHGPDPAH GPASCS
4698	A	825	941	KVHWCRAWWHVPVFPASGKAEAGRFLEPRSLRQAWTTQ
4699	A	236	449	GRMAQDLSEKDLLKMEVEQLKKEVKNTRIPIISKAGKEIKEYVEAQAG NDPFLKGIPEDKNPFKEKGGCLIS
4700	A	1	299	MALRKNEVFEGWDGRKGVSHGEGCFSGKSNIGAYLGKSQEQFEGNIR GNRQIIVNNESKLKISEEDLTPMRQRSNTLPKSFSGLEKEDEKKQ ELVDKAIKPSVEATLESIQRLQEKRAESSRPEDIKDMTKDQIANEK VALQKALLYESIHRPVTKNERQVMKPLYDRYRLVKQILSRANTIP IIVSRIPSRGWYNTFP*CPQGGCFPLASPGASSE
4701	A	1	238	AVSHKPFGLKWPNNHQSLNEPVSDPPLVPPSPCRLLPPPLTPPTSP QILFSSSAAATVAVSAPVFLQSFPPQYLQI
4702	A	1082	1436	VPPAGGRGVPPCVRGQHSVQPDPHLQGPWGLLLQHPGREYHQDTSV PQDPGVALQNPAGCLCFPMCYTYHCDVGLHHVHDPAECHSAKGHGGE PGATLWGQVLLPDVLWAFLAGDSI
4703	A	126	417	PCAQRQAKYSYRSKYRWPDNSTALDPVFFPIDGPVQVLRLLPLPHPT PPHVRIIQGLWPSPGPIPPQLGRSRLSWGEKGTMLGRWSGPCREWS GP

4704	A	867	963	RIVICWAQWLTAVIPPLWEAKAGGLPELRSS
4705	A	3	242	GSQGSRRRCSGRPGMHLWLSVPTDVTASASLPQSPPAAKPGPHLGVIS CLTSSRHLGFFGLISGSLALTALTLQIPASP
4706	A	3	3082	ASQAFLRVPALPMDVLP LLVVEDPPTGAARGPGPDPTTHQPPEVAIF AASRVEGGLRPEQENRRDAGRPQIRTPKQGRAEQTRHPARVSSGGGG SQEPTQVNTFMSFIFPMVVISVLNTIIANKLTMVMRQAAEQGVCTV GGEHSTFSMAIEPGRVQALRHGVRVLRVAVIAFVVCWLPYHVRLMF CYISDEQWTFPLYDFYHYFYMTNALFYVSSSTINPILYNLVSANFRH IFLATLACLCPAKAQGLCQDTTWEGAQASASRSSAVASRARQKGRRI RGLVSSSTCPSGRGQDGDGPGSTEHMTSQAPGLRRSPKPKRRQSQECLA GTSQELGATGSKSRDTCPRTTDTPTTDLVSLACGQVMMWPKLALR AMSASVMESGAPEPAPGDGTALTAQTPTPTPTICRVSLLAQSGTRA LDCCPPRAPCLNLSTPRFVPRVGHSMFKGSLGSPRRKELEQGNK ADGRAHVRTTREPVPDQFPRPQLSPRRSEGHRRSLHPNRRNTDIDDN IIGMEIQPNSSSVMEREIWGHWPGLPQAPLNSSPLKPEPGPTNQV TSRATGDTSPQAQTPANYPGPGARPCQLNPHHLTWFKAHGHREPVC WAKGQTGPGEVDVSCITYTSSRQEDARRTDGETGWERECDLPVIEVW LPELELKPPEFTKSSSQDLSPWPMNPVRCLSCLYRGIRALPASHYWT LVKELGDRVAAEGTEPAVSRVQRRTRQSAKGSVRRSMGRACHFQ QGAHREGPPVKHPSPKSPAGIGCSSLCVETSHSGVFTTQGLHLGVH WGGLSLSRVLHPHTLSLGSHEQEHRGQQAEGSARAKGTFFALASCSP GTRSRTSADPKGVHSGYGPSGVPLKAGRGQDFILFLPPLRAVTNCSP DEVNSMSDGVVPSLPDGVVPSLSDGMVPGLSGDDGVVPSLSDGVVPSL DGVVPSLSDGMVPGLSGDDGVVPSLSDGVVPSLSDGLVPGFLDGVVPSL SEGVVPSLSDGVVPGLSGDLVPGFLDGVVPSLSEDEGERS
4707	A	3	347	GGLRPEQENRRDAGRPQIRTPKQGRAEQTRHPARVSSGGGGSQEPTQ VNTFMSFIFPMVVISVLNTIIANKLTMVMRQAAEQGVCTVGGEHST FSMAIEPGRVQALRHGVRVL
4708	A	280	417	YEIRCRGCVCGAWTRVPTFASCGSQLLAGPGQLLLGLSSRLRRPS
4709	A	1	1626	SSSPRAARAGLGA VLGG LGNRAVWRSEAPGTRGKR RAGRPQEEPRVL ELGAGSWESGGERSPEPGARGGASGSGASRLDGAPAGLRHAPSPGLA FIGPRLRRAHSCPDFQPRRRRTEPRTPAPTMR LNSSAPGTPGTPAAD PFQRAQAGLEEALLAPGFGNAGNASERVLAAPSSSELDVNTDIYSKV LVTAVYLALFVVGTVGNTVTAFTLARKKSLQSLQSTVHYHLGSLALS DLLTLLLAMPVELYNFIWVHHPWAFGDAGCRGYFLRDACTYATALN VASLSVERYLAICHPPKAKTLMRSRRTKKFISAIWLASALLTVPMLF TMGEQNR SADGQHAGGLVCTPTIHTATVKVVIQVNTFMSFIFPMVVI SVLNTIIANKLTMVMRQAAEQGVCTVGGEHSTFSMAIEPGRVQALR HGVRVLRVAVIAFVVCWLPYHVRLMFCYISDEQWTFPLYDFYHYFY MTNALFYVSSSTINPILYNLVSANFRHIFLATLACLCPVWRRRRKR AFSRKADSVSSNHTLSSNATRETTY
4710	A	244	318	RKLLHIYIYIYIYIYDLYWQFYL
4711	A	1	1605	MGIVEPGCGDMLTGTEPMPGSDEGRAPGADPQHRYFYYPEPGAQDADE RRGGGSLGSPYPGALVPAPPSRFLGAYAYPPRQAAGFPGAGESFP PPADAEGYQPGEGYAAPDPRAGLYPGPREDYALPAGLEVSGKLRVAL NNHLLWSKFNQHQTEMIITKQGRMF PFLSFTVAGLEPTSHYRMFVD VVLVDQHHWRYQSGKWVQCCKAEGSMPCGNRLYVHPDSPNTGAHWMRQ EVSFGKLKLTNNKGASNNVTQMIVLQSLHXYQPR LHIVEVNDGEPEA ACNASNTHIFTFQETQFIAVTAYQNAEITQLKIDNNPFAKGFRENFE SMYTSVDTSIPSPPGPNCQFLGGDHYSPLLPNQYPVPSRFYFDLPQG AKDVVPQAYWLGAPRDHSYEA EFRAVSMKPAFLPSAPGPTMSYYRGQ EVLAPGAGWPVAPQYPPKMGPASWFRPMRTLPMEPGPGGSEGRGPED QGPPLVWTEIAPIRPESDSDGLGEGDSKRRRVSPYPSSGSDSSSPAGA PSPFDKEAEGQFYNYFPN
4712	A	1	816	VYIAAFVSAYSSTYHRAGCKPFNPVLGETYECERPDRGFRFISEQA VTAMNWVSWKVKICVLEALQAASGSPSFTSTICSRGCMYTSVDTSIP

				SPPGPNCQFLGGDHYSPLLPNQYPVPSRFYDLPQAKDVVPQAYWL GAPRDHSYEAFFRAVSMKPAFLPSAPGPTMSYRQGEVLAPGAGWPV APQYPPKMGPASWFRPMRTLPMEPGPGGSEGRGPEDQGPPLVWTEIA PIRPESSDSGLGEGDSKRRRVSPYPSRGDSSSPAGAD
4713	A	395	1374	KVTLMRWLYKG*NSGPMSV/TEEMDLAIEASEMIVLQSLHKYQPRLH IVEVNDGEPEAACNASNTHIFTFQETQFIAGTAYLNAEITQLKIDNN PFAKGFRENFESMYTSVDTSIPSPPGPNCQFLGGDHYSPLLPNQYPV PSRFYDLPQAKDVGGSSRVNREVSKDFADFGTTIKQDFRLLGQTS VDRLLQLSQQAQVKGQQLLPVSLVKRKTTLAPNTQTASPRALADSLM QLARQVSRLESGQDFADFGTTIKQDFRLLGQTSVDRLLQLSQQAQV GNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLESGQ
4714	A	1	2109	MQEIHGALDSPGDTSDMDKMRQTQTRYRDKASSEAHSPRDPLARGG AGPRRLREGASPPRMGIVEPGCGDMLTGTEPMGPSDEGRAPGADPQH RYFYPEPGAQDADERGGGSLGSPYPGGALVPAPPSRFLGAYAYPPR PQAAGFPGAGESFPPPADAEQYQPGEGYAAPDPRAGLYPGPREYAL PAGLEVSGKLRVALNNHLLWSKFNQHQTEMIITKQGRSALVVVVVV AVVVVKRKAQPLELVMELVLVEVVVVVTVLLVVVVTVKVVAVDGGARA GAGGDRGYRDGGGGSCSDGGCGDGGDGRMFPLSFTVAGLEPTSHYR MFVDVVLVDQHHWRYQSGKWVQCGKAEGSMGKALHPPGFLSPGLEC KRGELSTGTRLYVHPDSPNTGAHWMRQEVSGKLKLTNNKGASNNVT QMIVLQSLHKYQPRLHIVEVNDGEPEAACNASNTHIFTFQETQFIAG TAYQNAEITQLKIDNNPFAKGFRENFESMYTSVDTSIPSPPGPNCQF LGGDHYSPLLPNQYPVPSRFYDLPQAKDVVPQAYWLGAAPRDHSYB AEFRAVSMKPAFLPSAPGPTMSYRQGEVLAPGAGWPVAPQYPPKMG PASWFRPMRTLPMEPGPGGSEGRGPEDQGPPLVWTEIAPIRPESSDS GLGEGDSKRRRVSPYPSGSDSSSPAGAPSPFDKEAEGQFYNYFPN
4715	A	251	623	RKSAGPPGRTEGSRQVPGRRCPAALQAPVPLVPALAMPYLPSEPEP IFSYPHMQGAPSPRNTHRQTHTHGHSPQLPGPFMCSGKGPAPKEQP PLNLDAHLSSFQLPSEDQGAQIRRKGEGLR
4716	A	36	69	PFFMHQSHFP
4717	A	328	441	LKFWDETFLYFKTTSPCKHHTHMACMYAHATHHTHTPQ
4718	A	2	786	GRVGEAQHYLSKTPESSAQPSETILWDVQTDSPNPQEKDSSSNEKQT ISLPVSTSKSRKESTEPKTCIESMEKKTDSLQVNGNERSDDTVSNIS LIDQKMPDIEPNSENNCSSSDIVNGHSEIEQTPLVSSDPALKIDTNR IRTENGSIPLSVVPQEHNTLPVSQAPSKPNLTSEHTSYGLILTKPYV RPLPPSYLDERYLSMPKRRKFLTRVDACSDQDNVYKKSVKRLRCGK CLTTYCNAEALEAHLAQKKCQTLFGI
4719	A	560	688	ARYNPPKKKMLQKCLFPRVLVNSWPQAILLPWPSKVLGLQA
4720	A	245	382	CCWCCWCCWCCWCCCCCHRRRCLIHLEFVVAGLAKPAQENKKN
4721	A	235	425	PVLCRGNSSGSLSRKFPPKQKPADKDHPRTCVYLENRS PGKSES KKI PAYAETNPSPQLSPWS
4722	A	253	363	CQQFLLLCQGSQAEPTEHGFSRVFPPEPPPPYWNPSV
4723	A	235	320	QKNQEPAGHQPGPIPPCVLGLGNEILRS
4724	A	1	1326	MVGERSQPDATANRAPTGLTQIALQSPSAHRPDTAHHAPPTDLTQPM ALHPQPDAMALCPQAPKRRTHPVLNECTVNDRVNDPPNIQVPRPPG LLSAPPPPIHLTLQASPDMLRYGLVFLFLSGGTRQRCSPPELLVR AAGMCAPSTCTRVLFTQRDRGQSPGPLQGCPHYLAPHMTSCRLFWF FAGRQTTAGVPVLKQVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLL VAMPLPPRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHS VPWWVIRIPILISIIVNFVLFISIIIRILLQKLTSPDVGGNDQSQYKR LAKSTLLLIPLFGVHYMVFVFPISISSKYQILFELCLGFSQGLVVA VLYCFLNSEVQCELRKWRSRCPTPSASRDYRVCSSFSRNGSEGAL QFHRGSRAQSFLQTETSVI
4725	A	2	1502	CIERAPAAGTEGAAPALGALGYSCGARGLRALAPGPCWRRNRNRLG RRRRALGGPRHAELGMRTLLPPALLTCWLLAPVNSIHPECRFHLEIQ EEETKCAELLRSQTEKHACSGVWDNITCWRPANVGETVTVPCPKVF

				SNFYSKAGNISKNCTSDGWSETFPDFVDACGYSDPEDESKITFYILV KAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLRA ISVLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWL LVEGLYLHTLLVAMLPPRRCLAYLLIGWGLPTVCIGAWTAARLYLE DTGCWDTNDHSPVWVIRIPILISIIVNFVLFISIIIRILLQKLTSPD VGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFEL CLGSFQGLVAVLYCFLNSEVQCELKRKWSRCPTPSASRDYRVCGS SFSRNGSEALQFHRGSRAQSFLQTETSVI
4726	B	144	2704	XHGSVVVWDLREDSRLHYSVTLSDGFWTFRTATFSTDGILTSVNHR PLQAVEPISTSVHKKQSFVLSPFSTQEEMSGLSFHIALDESGLNV WVVVELPKADIAGSISDLGLMPGGRVKLWDSSTD SHAVTGLQWSPTR PAVFLVQDDTSNIYIWDLLQSDLG PVAQQVSPNRLVMAA VGEPEK AGGSFLALVLARASGSIDIQHLKRRWAAPEVHSCVERKWSGHTASRV HTHSPSLLLFCNPLDDWSRSFETEAPKHWWFFEPYRNVKFVKKETS KANDLPLSLTPREELARCLWAPPSPSVEGPMTAEAVPWNESSHSSKG RREGPEPHRRRSSAEQEVQAARLQGKERKARGEHGRS IKGRENGAKQ DKPROAPPTVSVFRQSPPSRESAHSSTRFQLGCSHTELTGCHLAS LCDYLLQTPRPGVPEHRASPGSKCTRHSHTLGRGEGVVCTCPSAT DTPQVVERESNPLDEVRRGHAGEHRLLSQSLSTVGAESISKSSTGWA PLNAPVRTFLGESLGSASFSSASIALRTSVKRRHKWARPHNTGARQPP GGKGTTPGGKEHPYIEIKAPPCVSRWLSPPPGTPTCTTVRRSWLPS ALKHCCVLRREMAVCHRLSKCPANAIVKHPCEGKSPPYRALWHRSGV WTVAGTQRSPNIRAHRDQTLRNNYTILIPNGNWRHGAYAGVSSFSRX *
4727	A	8	3281	SKINEYDMYIRNFGKKNTKQAYVQCNEEDNVERDIQTEDIETREVTQ HPGESTVVSQSGSEQRDTS DAVVMPKIDTPRLCSFLRAACQVMVLL EDRLAAEPSWNLRAQDRALYFSDSSSQLNTSLPFLQNRKVSSSLHTSR VQRQMVSVDLPEKSFVPLLD SKYVLCVWDI WQPSGPQKV LICESQ VTCCCLSPKAFLLFAGTAHGSVVVWDLREDSRLHYSVTLSDGFWTF RTATFSTEMSGLSFHIALDESGLNVWEEDGLPRAACFLRKRTASR ALPASSGRGRPPARCRLPQEEDGLPRAAGFLRKRTASRALPASSGRG RPPARCRLPQEEDGLPRAAGFLRKRTASRALPAFSGRGRPPARCRLP QEEDGLPRAACFLRKRTASRLLPVSSGRGRPPARCRLPQEEDGLPRA ACFLRKRTASRALPVSSGRGRPPARCRLPQEEDGLPRAAGFHRKRTA SRALPASSGRGRPPARCRLPQEEDGLPRAAGFLRKRTASRAL LALSG LLRFSFECHHTHTCDSFPPQRETSEWTSSLSVRAKCTQFCSVTTSTT GQCEVFELVLTENCQLPKDLGALLPTPGASIRVRSVVTLSAHFSYY MRDSSRTCSESRFTMSDTLYSLRQETFSLDTISAQHYYSPAPDEVCO RPRGGYTAQIVDRVAMQPAYLSHKGNEFWGTTQTLNVKFLPSDPNHF IIGTDMWDSSTD SHAVTGLQWSPTRPAVFLVQDDTSNIYIWDLLQSD LGPVAKQVSPNRQTEKQNKKRMFGRKEFRYKQGFNTFRVTLSLT MTYPLHVVEKQVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAML PPRRCLAYLLIGWGLPTVCIGAWTAARLYLED TGAPLSVWVRVTTA PKTVLDARNAGHLLFVVISRDTPGHLKFSFYIQVERPGHLYDPAPRV HTVRGHAASALKHCSSATRDVCHRLSKCPANAIVKHPCEVKSPPYR ALWHRSGVWTVAGTQRSPNISAHRDQVCGQSQARSGAAAAGPPRSGR WVPFQGDLTGAHCSSCFSPRELSVPLGTQHS LCTVLHMDLCGHLLA FIPSSSSLPC
4728	A	162	347	SQHFGRRPWADDLRSGVLPASASQSVGITGMSHCTQPLFLMLITYFY LLMHQLGQSVQHEQ
4729	A	201	522	AETEPKQEHLCPRSSWLEGARARPHRPLGTRRLAAAVFTWAGVHPVT PTWIMGAGNIERVSTPKGR LKMPRLGLETS LPTKRRWLSFPRAINS QQQGFTPQSLYA
4730	A	205	424	GYTRLGRLAHPGSSAPVPCPSYRSSPPPPHPEIARDTRPPASPG AGRGTPGVEEGPIYMLFSLPTRAGLA
4731	A	343	500	GSLVVAMLSFFLFLSFSFSLFFAFFSFFLFFFFFANNLQAYVKYS

				KNTGS
4732	A	103	361	FWLRGLMACGRFAQRPANHQARPRRLGSAPKPSPSAWPAMPCTLAES GVAQPGVGFPGPARWSALPRSPGGWGRFGGEWPVAKTKGIW
4733	A	1097	1298	FIVESQLFLVFFVFETLSWSIRAGVFTFLWSRWISYVCLFAYFVYEF CNLNWQVSYIYVFTINSIKR
4734	A	874	1184	PWLGLLIFSLPLPFLSLSSRSHLPGLKYFVGIAIYYIILADEPQDNVY THHTYTHTKSQLLKSGLGIRLLCPVKNSCTGSHCDLSSYRLIPVEL DSNFLFDSN
4735	A	451	641	YLRRERKERGRERERKERKKERKKERKKERKKKKRRKKERKRQEEEE RDRKNKKTAILMRIN
4736	A	1	1215	MTLKEHAAFKHLFNKAHLAPPLIHLTLSGHSTCFREHWVGDIVHRDL KLENIMVKSSLIDDNNEINLNIKVTDGLAVKKQSRSEAMLQATCGT PIYMDRGWNSLEGSEQDRKMWDSLELPRDLLNVFEQNADNDMDDEIQ AEVLSGDDEELGNWSKGDSCYVLLKQLAAFCPLRDLWNFKLERDD LGYLVEEISKQOSIQEATWVLLKAFSFIREAHEKNLENLQPDNAIEK KIPFSEEKFKLAAEICISNQEANVNPQDNEKNVSRACQRSSQQLPLPL PRVLGGKSGFVGWAQDSHAEIYTFGRILGKSGFGIVIEATDKETETK WAIKKVNKEKSTAYEKQFPATSKDNFDMCSSSTSSKLLPAEIKGEM EKTPVTPSQGTATKYPKSGALSRTKKKL
4737	A	1	417	PRSPTMPADLSGTWTLSSDNFEGYMLALGIDPATRKIAKLLKPQKV IEQNGDSFTIHTNSSLRNYFVKFKVGEKFDENDNRGLDNRKCKSLGIW DNDRLTCIQKGEKKNRGWTWHIEGDKLHLEMFCEGQVCKQTFQRA
4738	A	19	345	AATLGHCPSSTIQCWSAGSCPRASSSGPQASPMWV*STDLR*MSWA TSLQGWCPWPPTPSCSQSSWAA\LHHRCGWVCHCHLTGEDLRPEAR LPGGQQPGAGGPGPQ
4739	A	40	209	DGRCSNQSRRLLQGRWVHTEGPGPASARLPQHPGPGCPLLCHGCV PQEPEEYFP*LPQHPGPGCPLLCHGCV
4740	A	2	4097	PCPPHADCRDLWQTFSTCQPGYYPGCVDACLLNPCQNQSGSCRHLP GAPHGYTCDVGGYFGHHCEHRMDQQCPRGWWSPTCGPCNCDVHKG FDPNCNKTNGQCHCKEFHYRPRGSDSCLPCDCYPVGSTSRSCAPHSG QCPCRPALGRQCNSCDSPPFAEVTASGCRVLYDACPKSLRSGVWWPQ TKFGVLATVPCPRGALGLRGAGAAVRLCDEAQGWLEPDLFNCTSPAF RELSLLLDGLELNKTALDTMEAKKLAQRLREVTGHTDHYFSQDVRVT ARLLAHLAFESHQQGFGLTATQDAHFNENLLWAGSALLAPETGDLW AALGQRAPGSGSPGSAGLVRHLEEYAATLARNMELTYLNPMLVTPNI MLSIDRMEHPSSPRGARRYPRYHSNLFRGQDAWDPTHVLLPSQSPR PSPSEVLPTSSSIENSTTSSVPPPAPPEPEPGISIIILLVYRTLGG LLPAQFOAERRGARLPQNPVMNSPVVSVAVFHGRNFLRGILESPI EFRLQLTANRSKAIQVQWDPPLAEQHGVTARDCELVHRNGSHARC RCSRTGTFGVLMDDASPRERLEGDLELLAVFTHVVVAVSVAALVLTAA ILLSRLSLKSNVRGIHANVAAALGVAELLFLLGIHRTNQLVCTAVA ILLHYFFLSTFAWLQVGLHLYRMQVEPRNVDRGAMRFYHALGWGPV AVLLGLAVGLDPEGYGNPDFCWISVHEPLIWSFAGPVVLVIVMNGTM FLLAARTSCSTGQREAKKTSALTLRSSFLLLLVSASWLFGLLAVNH SILAFHYLHAGLCGLQGLAVLLLFCVLNADARAAMPACLRKAAPE EAPAPGLGPGAYNNTALFEESGLIRITLGASTVSSVSSARSRTQD QDSQRGRSYLRDNLVLRHGSAAADHTDHSLOAHAGPTDLVDAMFHRDA GADSDSDSLSLEERSLSIPSESEDNGRTRGRFQRPCLCRAAQSER LLTHPKDQVDGNDLLSYWPALGECEAAPCALQTWGSERRGLDTSKDA ANNNPDPALTSGDETSLGRAQRQRKILKNRLQYPLVPQTRGAPEL SWCRAATLGHRAVPAASYGRIYAGGGTGSLSQPASRYSSREQLDLLL RRQLSRERLEEAPAPVLRPLSRPGSQECMDAAPGRLEPKDRGSTLPR RQPPRDYPGAMAGRFGSRDALDLGA\PREWLSTLPPRRTRDLDPQP PPLPLSPQRQLSRDPLPSRPLDSLRSNSREQLDQVPSRHSRE LGPLPQLLRAREDSVSGPSHGPEQLDILSSILASFNSALSSVQS SSTPLGPHTTATPSATASVLGPSTPRSATSHSISELSPDSEVRSEG

				HS
4741	A	2	10321	<p> ISHSTPSQSYENAHGHQNFPRPKSGTRFRTSGQEGGTRDLEGQKKAGR RSWDSALEGGSQEELGGGGHQWDPGLAATTGPRAHIGGGALALCPE SSGVREDGGPGLGVREPIFVGLRGRRQSARNSRGPPPEQPNEELGIEH GVQPLGSRERETGQGPVSVLYWRPEVSSCGRTGPLQRGSLSPGALSS GVPGSGNSSPLPSDFLIRHHGPKPVSSQRNAGTGSRKRVGTARCCGE LWATGSKGQGERATTSGAERTAPRRNCLPGASGSGPELDSAPRTART APASGSAPRESRTAPEPAPKMRMRSGLFRCRFLPQRPGRPPGLPAR PEARKVTSANRARFRRAANRHPQFPQYNYQTLVPENEAAGTAVLRV AQDPDAGEAGRLVYSLAALMNSRSLELFSIDPQSGLIRTAALDRES MERHYLRVTAQDHGSPRLSATTMVAVTVADRNDHSPVFEQAQYRETL RENVEEGYPILQLRATDGDAPPNANLRYRFVGPAAARAAAAAAFEID PRSGLISTSGRVDREHMESYELVVEASDQGGQEPGPRSATVRVHITVL DENDNAPQFSEKRYVAQVREDVRPHTVVLRVTTATDRDKDANGLVHYN IISGNSRGHFAIDSLTGEIQVVAPLDFEAEREYALRIRAQDAGRPP SNNTGLASIQVVDINDHIPFVSTPFQVSVLENAPLGHSVIHQAVD ADHGENARLEYSLTGVAPDTFFVINSATGWVSVSGPLDRESVEHYFF GVEARDHGSPLSASASVTVTVDVNDNRPEFTMKEYHLRLNEDAAV GTSVSVTAVDRDANSASISYQITGGNTRNRFAISTQGGVGLVTLALP LDYKQERYFKLVLTASDRALHDHCYVHINITDANTHRPVFQSAHYSV SVNEDRPMGSTIVVISASDDDVGENARITYLLEDNLPQFRIDADSGA ITLQAPLDYEDQVYTLAITARDNGIPQKADTTYVEVMVNDVNDNAP QFVASHYTGLVSEDAPPFTSVLQISATDRDAHANGRVQYTFQNGEDG DGDFTIEPTSGIVRTVRRILDREAVSVYELTAYAVDRGVPPLRTPVSI QVMVQDVNDNAPVFPAAEFVVRVKENSIVGSVVAQITAVDPDEGPNA HIMYQIVEGNIPELFQMDIFSGELTALIDLDEARQEYVIVVQATSA PLVSRATVHVRLVDQNDNSPVLNNFQILFNMYVSNRSDTFPSGIIGR IPAYDPDVSDFLHYSFERGNEQLQLLVNQTSGELRLSRKLDNNRPLV ASMLVTVDGLHSVTAQCVLRVVITEELLANS�TVRLENMWQERFL SPLLGRFLEGVAAVLATPAEDVFI FNIQNDTDVGGTVLNVFSFALAP RGAGAGAAGPWFSSEELQEQLYVRRRAALAARSLLDVLFPDDNMAFLRE PCENYMKCVSVLRFDSSAPFLASASTLFRPIQPIAGLRCRCPPGFTG DFCETELDLCSNPCRNGGACARREGGYTCVCRPRFTGEDCELDTEA GRCVPGVCRNGGTCTDAPNGGFRCQCPAGGAFEGPRCEVAARSFPPS SFVMFRGLRQRFHLLTSLSFATVQQSGLLFYNGRLNEKHDFLALELV AGQVRLTYSTGESNTVVSPTVPGGLSDGQWHTVHLRYNKPRTDALG GAQGPSKDKVAVLSVDDCDVAVALQFGAEIGNYSCAAAGVQTSSKKS LDLTGPLLLGGVPNLPENFPVSHKDFIGCMRDLHDIGRRVDMAFLVA NNGTMAGCQAKLHFCDSGPKNSGFCSERWGSFSCDCPVGFGGKDCQ LTMAHPHHFRNGTLSWNFGSDMAVSVPWYLGLAFRTRATQGVLMQV QAGPHSTLLCQLDRGLLSVTVTRGSGRASHLLLDQVTVSDGRWHDLR LELQEEPQGRRGHHVLMVSLDFSLFQDTMAVGSELQGLKVKQLHVGG LPPGSAEEAPQGLVGCIQGVWLGSTPSGSPALLPPSHRVNAEPGCVV TNACASGPCPPHADCRDLWQTFSTCQPGYYGPGCVDACLLNPCQNG GSCRHLPGAPHGYTCDVGGYFGHHCEHRMDQCPRGWAGSPTCGPC NCDVHKGFDPNCNKTNGQCHCKEFHYRPRGSDSCLPCDCYPVGSTSR SCAPHSGQCPCPRGALGRQCNSCDSPPAEVTASGCRVLYDACPKSLR SGVWWPQTKFGVLATVPCPRGALGAAVRLCDEAQGWLEPDLFNCTSP AFRELSLLLDGLELNKTALDTMEAKKLAQRLREVTGHTDHYFSQDVR VTARLLAHLAFESHQGGFGLTATQDAHFNENLLWAGSALLAPETGD LWAAALQRAPGGSPGSAGLVRHLEEYAATLARNMELTYLNPMLVTP NIMLSIDRMEHPSSPRGARRYPRYHSNLFRCQDAWDPTHVLLPSQS PRPSPSEVLPTSSSIENSTSSVPPPPAPPEPEPGISIIILLVYRTL GGLLPAQFQAERRGARLPQNPVMNSPVVSVAVFHGRNFLRGILESPI SLEFRLLQTANRSKAI CVQWDPPGLAEQHGVTARDCELVHRNGSHA RCRCSTGTGFGVLMASPRERLEGDLELLAVFTHVVAVSVAALVLT AAILLSLSLSKSNVRGIHANVAAALGVAELLFLLGIHRTHNQVQDQG </p>

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				QGTCVLMTLLAQEAWQNSGSELVCTAVAILLHYFFLSTFAWLFBVQG LHLYRMQVEPRNVDRGAMRFYHALGWGVPVLLGLAVGLDPEGYGNP DFCWI SVHEPLIWSFAGPVVLVIVMNGTMFLLAARTSCSTGQREAKK TSALRTLRSFLLLLLVASWLFGLLAVNHSILAFHYLHAGLCGLQG LAVLLLCVNLADARAAMPACLRKAAPEEARPAPGLGPGAYNNTA LFEEGLIRITLGASTVSSVSARSGRTOQDSQGRSYLRDNVLR HGSAADHTDHS LQA HAGPTDL DVAMFHRDAGADSDSDLSLEERS LSIPSSSEEDNGRTRGRFQRP LCRAAQSERLLTHPKDVGNDLLSYW PALGECEAAPCALQTWGSERRLGLDTSKDAANNNPDPALTSGDETS LGRAQRQRKGILKNRLQYPLVPQTRGAPELSWCRAATLGHRAVPAAS YGRIYAGGGTGSLSQPASRYSSREQDLLLRQLSRERLEEAPAPVL RPLSRPGSQECMDAAPGRLEPKDRGSTLPRRQPPRDYPGAMAGRFGS RDALDLGAPREWSTLPPPRTRDLDPPQPPPLPLSPQRQLSRDPLLP SRPLDSLRSNSREQLDQVPSRHPREALGPLQLLRAREDVSVP SHGPSTEQLDILSSILASFNSSALSSVQSSSTPLGPHTTATPSATAS VLGPSTPRSATSHSISELSPDSEPRDTQALLSATQAMDLRRRDYHME RPLL NQEHLEELGRWGSAPRTHQWRTWLQCSRARAYALLQHLPVLV WLPGYPPWA
4742	A	157	273	NFHSFLLFPKHPILLGRDLLTKFGATISLNQDRIEVF
4743	A	469	676	LECPRFSGTRSWGCLAEAPHLPPRVLSSPEVPKPLQIKLSPNPPAE PLGNTLPTKRYPVWNP GPYFRD
4744	A	237	497	GGLSQRKAGRSSVS RSPLEPEAPPAQASKVQEASHLETSADLTTHP RASKGPTPEPTSDPTVPRDRSQPCPSLLDPRVP CGHYC
4745	B	40	285	MPKKAGATTKGKSQSKEPERPLPPLGPVAVDPKGCVTIAI HAKPGSK QNAVTDLTAEAVNVAIAAPPSEGEANAELCRYLSK*
4746	A	3	292	SSSQAGMLRLRSGRLRHLRATPNTRGSARLLRAEMPKKAGATTKGKSQ SKEPERPLPPLGPVAVDPKGCVTIAI HAKPGSKQNAV TGIPGHWGGI QV
4747	A	3	163	GDMIFNLQSRKTAFNK*SKDLGSS/SPACMVQS*VSLSTSGYRKS KA PQONERC
4748	A	3	307	SARGCAPQRAEALRATPNTRASARLLCAEMPKKAGATTKGKSQSKEP ERPLPPLGPVAVDPKGCVTIAI HAKPGSKQNAV TALLFHSSTIGGDS GGRFRYS
4749	A	2	478	PSQAGMLRLRSGRLRHLRATPNTRGSARLLCAEMPKKAGATTNGKSQS KEPERPLPPLGPVAVDPKGCVTIAI HAKPGSKQNAV TDLTAEAVNVA IAAPPSKGEANAELCRYLSKVLELRKSDVVLDDKMRDLLKIVPCKLA TRTQILGLLAECSFSRL
4750	A	303	1978	RIYKVQQTTPQSQLFQDHPESLVKIFGSKAMQTKAKAVIDNFVKLEE NYNSECGIDTAFQPSVGKDGSTDNNV VAGDRPLIDWDQIREEGLKWQ KTKWADLPPIKKNFYKESTATSAMSKEADSWRKENFNITWDDLKDG EKRPINPTCTFDDAFQCYPEVMENIKKAGFOKPTPIQSQAWPIVLQ GIDLIGVAQTGTGKTLCYLMPGFIHLVLQPSLKGQRNRP GMLVLTPT RELALQVEGECCYSYKGLRSVCVYGGNRDEQIEELKKGV DII IAT PGR LNDLQMSNFVNLKNITYLV LDEADKMLDMGFEPQIMKILLDVRP DRQVTMTSATWPHSVHRLAQSYLKEPMIVYVGTLDLVAVSSVKQNI I VTTEEEKWSHMQTFLQSMSSTDKVIVFVSRKAVADHLSSDLILGNIS VESLHGDREQRDREKALENFKTGKVRILIATDLASRGLDVHDVTHVY NFD FRNIEEYVHRIGRTGRAGRTGVSITTLTRNDWRVASELINILE RANQSIPEELVSMAERFEAHQRKREMERKMERPPQGRPKKFH
4751	A	142	408	LKFDKSKPGLPSPAPRPLFFPLGQRDSKTRHYPSTSRPLGLSSTYPG HWGAPLISVPGPEAPPTPGIGPAPVSQDPASSCGGGKAASYS
4752	A	500	665	TKEQMSGPLFPVCSQP LPFMLS PCHMHHHPGHVALSQT VSPASLLT QGLGLPQH
4753	A	49	163	QIIFKFISLFKYKAKPQTGIIKTLCLTFTLPSDPLPIC
4754	A	665	733	AQEP/LTWCLLPTLVPGKCEWRQV
4755	A	334	520	GAKGFHLNCEGRNRLTASSRPFHRTDSHTLVPSVQGAGA QEPMTWC

				LLPTLVPGKCEWRQA
4756	A	3	222	PRDKVSLCHRLECNGRITAHCSLKLNNSSDLPASASQVAGTTGVCHH AWPLLFFLMKEEMYRIDIKTKCRKN
4757	A	133	205	DLPQAQSNLQWPRKTS*LKIPHERL
4758	A	250	532	AYEVGYNTVATSEGGNRARRVGELPEVTELVSGPDWNPNTSQPMPGS PAPAPRRLPGCQRHPHPFKCCPVPAQSLPFNTRPHLPPTPQQQASR
4759	A	524	678	ARCEWLMPVIPALWEAEACGSLEPRSSRPAAWATWLMNTKHSFDFVFI KDFL
4760	A	110	1520	HLSQACPPFAGHQGSWGRSSPHLQPRMIGDGLSEENDTKQNAQSSDE SFEPYPERKVSGKKSESKEAKKSEEPRIKKPGPKPGWKKKLRCE ELPTIYKCPYQGCTAVYRGADGMKKHIKEHHEVRERPCPHPGCNKV FMIDRYLQQRHVLIHTEVRNYICDECGQTFKQKHLVHQMHRSGAK PLQCEVCGFQCRQRASLKYHMTKHKAE TELDFACGQCGRRF EKAHNL NVHMSMVHPLTQTQDKALPLEAEP PPPGPPSPSVTTEGPGRCEVCGFQ CRQRASLKYHMTKHKAE TELDFACDQCGRRF EKAHNLNVHMSMVHPL TQTQDKALPLEAEP PPPGPPSPSVTTEGQAPPRPPDRAAPEAAVLRV QRPVSRREQSSRASPRLLPPDPQPRKPTAAALAEPLHAVPARAQRS PAAPGQSPHAPTPTPRGRVSLTPGGHRIWIARQQLVRGPGAVPGDV
4761	A	1	635	YALLGTRAASSRSCGAATRATTTTPWIPAPAARPCSWTVRWQSSGHGT KKRASRLPPRRVKPWGFPLSPSKLEGQGPQGGLRPKTLPSRNVAKL LSDSNALGPRSGFPFPQPSLPLCRAPGQLGEKQLPFSTSDDRVKDEFS DLSEGDVLSDEENDKKQNAQSSDESFEYPERKVSGKKSESKEAKKS EEPRIKKPGPKPGWKKKLRCE
4762	A	2	4398	AAAGAVGAKAMSDSWVPNSASGQDPGGRRRRAWAELLAGRVRKREKYNP ERAQKLKESAVRLLRSHQDLNALLLEVEGPLCKLSLSKVIDCDSSB AYANHSSSFIGSALQDQASRLGVPVGILSAGMVASSVGQICTAPAE SHPVLLTVEQRKLSLLEFAQYLLAHSMFSRSLFCQELWKIQSSLL LEAVVHLHVQGIVSLQELLESHPDMAVGSWLFRLCCLCEQMEASC QHADVARAMLSDFVQMFVLRGFGQKNSDLRRTVEPEKMPQVTVDLQR MLIFALDALAAGVQEESSTHKIVRCWFGVFSGHTLGSVISTDPLKRF FSHTLTQILTHSPVLKASDAVQMCREWSFARTHPLLTSLYRRLFVML SAEELVGHLEQVLETQEVHWQRVLSFVSALVCFPEAQQLLEDWVAR LMAQAFESCQLDSMVTAFLVVRQAALLEGPSAFLSYADWFKASFGSTR GYHGCSKKALVFLFTFLSELVPFESPRYLQVHILHPPPLVPSKYRSL TDYISLAKTRLADLKVS IENMGLYEDLSSAGDITEPHSQALQDVEKA IMVFEHTGNIPVTMEASIFRRPYVSHFLPALLTPRVLPKVPDSRV AFIESLKRADKIPPSLYSTYQACSAAEKPEDAALGVRAEPNSAE PLGQLTAALGELRASMTDPSQRDVISAQVAVISERLRAVLGHNEEDS SVEISKIQLSINTPRLEPREHIAVDLLLTSCQNLMAASSVAPPERQ GPWAALFVRTMCGRVLPVAVLTRLQLLRHQGPSLSAPHVLGLAALAV HLGESRSALPEVDVGPPAPGAGLPVPALFDSLLTCRTRDSLFFCLKF CTAAISYSLCKFPSSQSRDTLCSCLSPGLIKKFQFLMFRLFSEARQPL SEEDVASLSWRPLHLPSADWQRAALS LWTHTRTFREVLKEEDVHLTYQ DWLHLELEIQPEADALSDTERQDFHQWAIHEHFLPESSASGGCDGDL QAACTILVNALMDFHQSSRSYDHSNSDLVFGGRTGNEDIISRLQEM VADLELQQDLIVPLGHTPSQEHFLFEIFRRRLQALTSQGSVAASLQR QRELLMYKRILLRLPSSVLCGSSFOAEQPITARCEQFFHLVNSEMRN FCSHGGALTQDITAHFFRGLLNACLRSDPSLMVDFILAKCQTKCPL ILTSALVWWPSLEPVLLCRWRRHCQSPLPRELQKLQEGROFASDFLS PEAASPAPNPDWLSAAALHFAIQQVREENIRKQLKKLDCEREELLVF LFFFSLMGLLSHLSNSTTDLPKAFHVCAAILECLEKRKISWLALF QLTESDLRLGRLLLRVAPDQHTRLLPFAFYSLLSYFHEDAAITREEAF LHVAVDMYKLVLQVLFVAGDTSTVSPAGRSLELKGQGNPVELITKAR LFLQLIPRCPKKSFSHVAELLADRGDCDPEVSAALQSRQQAAPDAD LSQEPHLF
4763	A	2016	2227	EKSTLNNPMFCIWEIVFKNKKERKYIKLLFIPAFPYISIALSVYPFW

				YILPLHIYICICNSELYIYINCK
4764	A	1388	1520	SITFWLKGCMCIGVCVCVCVFLVWRMKGFLGICKYSMAS
4765	A	2	110	GGVGGGGGHGLG*DSKGR*GWGPWLAGGDCIKENT
4766	A	120	233	LPAATNRLKRGKGSSTGSSSGNHGSGGGNGHKTREL
4767	A	3	796	GLQGFPPACGGQQLRFKSLRSSEYPRPHLAFSMLGITSCSDQQA EGEGLEGSSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESQIQ FRGQGVSSNMREISKEGNRLGGSGDNYRGQSSWGS GGDAVGGVN TVNSETSPGMFNFDTFWKNFKSKLGFINWDAINNNQVPPSTRALLY FIRLWEDFLTEHSFSSTWKQLFEGRVITAETCRQSRFRITITTS RIPLPMVGKYSVKTPCKRGGSLTFFLGLP
4768	A	1	1263	MTRQCQASNQQLGPQPLATTPPDLFLGFQQLFGTFASWGREPHCGGP DFPQPIQTVEDALRKPSGLQLINYIHTYLPLPAKVLDFPPKPPQFGM DVQGFVLYLMSPPASQGHVPKYQIHRTPAPPQGVAGVLVGHFPD TVKVRLQVQSVEKPQYRGTLHCFKSIKQESVLGLYKGLGSPMLGLT FINALVFGVQGNLRLALGHDSPLNQFLAGAAAGAIQCVICCPMELAK TRLQLQDAGPARTYKGS LDCLAQIYGHEGLRGVNRGMVSTLLRETPS FGVYFLTYDALTRALGCEPGDRLLVPKLLLAGGTS GIVSWLSTYPVD VVKSRQLQADGLRGAPRYRGILDCVHQSYRAEGWRVFTRGASTLLRA FPVNAATFATVTVVLT YARGE EAGPEGEAVPAAPAGPALAQPSL
4769	A	1	1285	MTRQCQASNQQLGPQPLATTPPDLFLGFQQLFGTFASWGREPHCGGP DFPQPIQTVEDALRKPSGLQLINYIHTYLPLPAKYQIHRTPAPPQ GVAGVLVGHFPD TVKVRLQVQSVEKPQYRGTLHCFKSIKQESVLGL YKGLGSPMLGLTFINALVFGVQGNLRLALGHDSPLNQFLAGAAAGAI QCVICCPMELAKTRLQLQDAGPARTYKGS LDCLAQIYGHEGLRGVNR GMVSTLLRETPSFGVYFLTYDALTRALGCEPGDRLLVPKLLLAGGTS GIVSWLSTYPVDVVKSRQLQADGLRGAPRYRGILDCVHQSYRAEGWRV FTRGASTLLRAFPVNAATFATVTVVLT YARGE EAGPEGEAVPDRLR GLPWRSPACDAHPALLPQGSFSETWDINWPLSRLPCFLLGCCELWS LSDVG
4770	A	620	904	GMVLNGSAGPHAS PWSNHGSQRDGS LTASLGHLP RCCGHMPLTEGQK CSWGQQREQPPQSSEECRHRSHRAAPHHP CALHPSTIELGKVLIVLV
4771	C	230	487	MLNLASPLDKLT LQNTTQNGDSSTHISSNSIHKHTSSSSSVLFPDGT LEALFVSSPKVEASPLEAXVPCSASHSCNTSSKLNRRRL*
4772	A	1	350	QASNGDASTLGEETKSASNVPSGKSTDEEEEAQTPOAPRTLGPSPPA PSSTPTPTAPIATLNQPPPLLRPTLPAAPALHRQPPPLQQQARFIQ RPTLNQPPPLIRPANSMATPS
4773	A	76	1941	RRRFSAGGRSVRRVGESVRCNSQHTFLSDQAPSLKSSAIALAMLQ DWCRRMGVNAERSLLILDIPDDCEEHEFQEA VRAALSPLGRYRVLIK VFRKELGARAALVEFAEGLNQSLIPRQIAGKGGPWKVISLPQALDAE FQDIPSFPAQPQQQAVARGAGEAGAAGEAGSVGEAGGVNEERSAGED EAGGIGEAGGVGEAGAAGEAGAAGEAGAAGEAGGAGEAGGAGEAGGA GEEGGTGEEGGAGEAGGAGEEGGEDEAGAAGEAVGAGVVEAWTQSWR QTLRPLVKTMAYREL RPFSGREQPGCVESFESWLEDADMLQLWCH ASERERRRRLLDSLDGLALDIVSGLLEEDPDFSAQDCLTALGQVFRS RDTWMTSRMKFLTCTQGPQEG LFAFVVRLEGLLQKAVEKGAVHPAMA NHLRLRQVLSRARPSEALQDTLRRMQLERRPPDFLRLLRLIRDMEAW AASLARSQQGVAAWAAAPVESEDPAQAQSPAQGDASEADPGAEDADE AASTTKEAARVAPATGEDENAPAGLEGLCQGRSPDAPGGLPARMGSA VDMAPGGPSWEPEGLVQVGQEA EPPQEG LKPILEESENEDEDGAG EAGKPKSPPGK
4774	A	619	2097	VVLAGSRNRI LRTRTFWVGRFSEYCPSCLENDQRWLCNENYKVVEQV PTKKNFSILARNLNTIQVEEMSACNISIQGPSIYNKEPKNIINPHEK VQMKSI CANSPIKAQQDQLQVKNNIKASLHNKSSLPFNTKSSTSV GQLQSP TLNSPIYMQKGKNEHLAFNTKSKASTVGSSELVLVSTTVPT VHVSDLEMSSTLDCLPVLADWEDVLLPASQPEENV DCTVPISDSD LEISFN SGERLMVLKELEMSSHENFGDIEETPQKSETSKSIVYKSPH

10345

				TTIYNVKEAKDPGSDISAFKLPEHKSSTFNRVNANMSHPLVLGKHPL LSGGTKRNPSPQAFPPAKKQPFTIHEEKPTSSDCSPVRSSSWRRLP SILTSTVNLQEPWKSGMTPLCKCGRRSKRLVVSNNGNHGVFYC CPIGKYQENRKCCGYFKWEQTLQKERANSMPVSHSTGGLTFSSPETS HICDRNLSISTKNSLRRLRPSMRN
4775	A	97	185	FMFFNQICKCICCCIVIVLQNKIACHLTA
4776	A	845	942	MEECTDCGDPSPHTHTHTHTPYNTASRGII
4777	A	510	636	AHAYLYGKVRKSTMTKPCGRTRKRRRRTSSSSQDGLALPP
4778	A	22	333	ERGLLSPDRLSLVPWHWERRGAGPRTPVGRGLYLLAPKAYKEVSGP VHGQMGPGKTLRVGIQWTRRSQMCCFYGCPLPPPVLCPGNKEPLR TQESPHPPSC
4779	A	310	422	GVGTATTGQWYFGQLAVCGVCGFLGLHSIKTSGWLSA
4780	A	1	140	KIRCEGLSRLDKGE/RR/RGKGHDG/LYQGLSTATKDTYDAFHMQUAL PPR
4781	A	17	283	PLESGGIPKLVQPRLLPVGPGLFLGLWRLGGWSQGCAAETPVGLWV GSCPHRLLTHSLFSDLLSRQGLSTATKDTYDALHMQALPPR
4782	A	2	673	GECEFLGLSAGAFSKAPQSSTSWGGSCRIKPAETPFLLTVPATAASA SASQPLSEGKDKMKWKALFTAAILQAQLPITEAQSFGLLDPKLCYLL DGILFIYGVILTALFLRVKFSRSADAPAYQOGQNLYNELNLGRREE YDVLDKRRGRDPGEMGGKPHRTKNPHEGLYNELQDKMAEAYSEIGMK GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
4783	A	105	1378	ELIPALTSPLFLEESEKSRAEGAPDTGRGRARGAWRVFPGLSGWSAP PASWPRTPLQMSRRAGVTKMSDPFLKLVFIKDTTFRPKRKLEPGTQR LELHKKAAQASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNL YGTISDGCTEQSCPVMSSGGPKYEWQDEHKFRKPTALSAPRYMDLL MDWIEAQINNEDLFPTNVGTFPKNFLQTVRKILSRLFRVVFVHYIH HFDRIAQMGEAHVNTCYKHFFYFVKEFGLIDTKELEPLVRGLGAEG VRLRWRPRLELPGDPADGTSGEVAGRDPAFSHGTNAGDRSENADSL ASWGSLLPLVSRNDRPDVPLRRPAGLPVPEPPLGPRRLGGGRSGTI IPLLSGLSISGRPGAEP LSRWSSGAPTRGLQMPSSVSSLSLPSGKT T
4784	A	131	524	DCMTHCLQPFSSWCMFPFNATLLFQHCKTMSANQAPPYRHVVFKHKTTK KEKEKRERRSLPQNPFSSMCLDSKCTGMQLLPSVNSFKPLEMVALCAQ YPGHQGIHRAGPAPGCWLSKQDKCPSLFVKAVSVL
4785	A	197	582	ALISNNYHDMCYLCAYCCTAFFGFLTRATAEQKHFSLVWHLNMLINV CYGKSIPLYNFMGEAMCKSEFKKKEKKKPCAELLPTQYI IYMPEMAK AAICQGLQKHEEAGMEINTLVVCNVFKVGVFNDT
4786	A	235	416	GQGNRKKGFGLGLERGHAGAGGREPFSPAGKLQGGKRAFAPGI IWGVP NPQLNIGVGMPPW
4787	A	280	569	KSPSHQPENRRRRCPHSCHAPTTCVSRKSGFSFKAKTLGTVLEQGR SGGIYSHGHCVAGSLTQTAGETGPWEGQHVGLQTSLSSSLPLQFLRM GH
4788	A	208	487	VQRHCLAGLIHHPFQKWNPKDQILDPIWRQGRRSTSPRAPGRRGPGA RGPAPSPAPRG\RRRWAGFRQRTPHTPGPPAPTAKTLLAGREPPR
4789	A	190	594	SFVVDNEKKEVQHVRDDADDAELLQHKVQNVGQVQGP HARHDGGRHE DQSRHSACCHAWRQGRRSTSPRAPGRRGPGARGPAPSPAPRGRWR AGFRQRTLHTGPPAPTAAPTLLAGREPPSSRGRVGGRVGRP
4790	A	523	722	SQHFGSRWVDCLSRVRDQPGQCHETPSLQKITKISWAWWRMPIVP ATWEVEVGGLLEPRRQRLQ
4791	A	171	320	QDLFSSSRQLEAFSNTCKRTQRTCRNRMYS*RYSCGGTE*GSYPTN LE
4792	A	243	445	LRRQLQTVTCGLGHLFVMCFTFPCFPVNWLPWFCRVVSRSCGCSRAG DACPSGSNPPPCPQCLTPGF
4793	B	320	434	XQCPLNRMAGHISSPYRSEAVVSSPGAPVRTGPSWEPPK*
4794	A	146	609	ALSSWPARELALLSERHPSLLLLQRCPLNRMAGHISSPYRSEAVVS

				SPGSTSEDRPQLGARARWESSVLTTLGARVSEPRLEKVRNPCVLLP TPARLARPHSSPSLAQSPGPGGRGRGWLRSRAGPSHSATHIAPSPLS SQLWSLRWCHDRL
4795	A	874	1126	YHIGINIKYQTHKVIKMENLQFYLFISSAPQCVSTKGCSGYL RPVGL VQVTICPLPLQIKVQIEKYLGFRTHQRYFCCIFHLKN
4796	A	1	957	METSSPRPPRPSSNPGLSLDARLGVDTHLWAKVLFTALYALI WALGA AGNALSVHVVLKARAGRAGRLRHHVLSLALAGLLLLLVGVPVELYSF VWFHYPWVFRDLGCRGYFVHELCAATVLSVAGLSAERCLAVCQPL RARSLLTPRRTRWLVALSWAASLGLALPMAVIMGQKHELETADGEPE PASRVCTVLVSRTALQVFIQEAIVVMYVICWLPYHARRLMYCYVDD AWTDPLYNFYHYFYMVTNTLFYVSSAVTPLLNAVSSSFRKLFLEAV SSLCGEHHPMKRLPPKQSPPTLMDTASGFGDPPETRT
4797	C	209	406	MTRCGSLGPSPLQGVYMATVRRGDSVWVGTECGRDSPAVRVSFLLC SCWGWWSRGLTPWRPCGP*
4798	C	133	237	MFMDXXXXXXGGRFGKSLGGPKFTRACKVKFFSL*
4799	A	250	422	ASAMVTSTSTPGSILMEVICLTISEGLCKSMSRL* ILIWKRS HVLEP SPQGVFLVVI
4800	C	33	158	MRMQQPSVKPGFKDLQCKTmplLLMKYIVLENIGLKIFLR*
4801	A	3	344	AQDRLHWGQTQNRQGGHALVPAEV*WDHPSWQINSRFYPKEQ*KVF STSSSSSSGGAVLKNPWGGQSLRGLARKNLFPYRGPKNLPGNFGKE TLLWGGDKLGQPPSRNLRL
4802	A	7	1268	EGGSAGRGSGMETSSPRPPRPSSNPGLSLDARLGVDTRLWAKVLFTA LYALI WALGAAGNALSVHVVLKARAGRAGRLRHHVLSLALAGLLLLL VGVPVELYSFVWFHYPWVFGDLGCRGYFVHELCAATVLSVAGLSA ERCLAVCQPLRARSLLTPRRTRWLVALSWAASLGLALPMAVIMGQKH ELETADGEPEPASRVCTVLVSRTALQVFIQVNVLSFVLPLALTAFL NGVTVSHLLALCSQVPSTSTPGSSTPSRLELLSEGLLSFIVWKKTF IQGGQVSLVRHKDVRRI RSLQRSVQVLRAIVVMYVICWLPYHARRLM YCYVDDAWTDPLYNFYHYFYMVTNTLFYVSSAVTPLLNAVSSSFR KLFLEAVSSSLCGEHHPMKRLPPKQSPPTLMDTASGFGDPPETRT
4803	A	65	376	IKPREPNFPAARLCRLVYPFYPLKFFIFPKAFNFCREVGPICSPPKG RVLSONSQVADFPVPAFLKHGPGGLGFNSAPHKEKNFTLQARVKFGPP QGSFKTGPP
4804	A	2	903	CCPCSPRSWPPPARCRPSAAGPRTRPASSGCPPMLQSTRPPTSPSP RGCWPRRPPGPPSARARRRRRRRRRLCNISVQRQMLSSLLVRWGRPR GFQCDLLLFSTNAHGRAFFAAAFHRVGPPLLIEHLGLAAGGAQQDLR LCVCGWVRGRRTGRRLRPAAPSAATAAGAPTALPAYPAAEPPGGL WLQGEPLHFCCDFSLEELQGEPPGWRNLNRKPIESTLVACFMTLVIVV WSVAALIWPVPIIAGFLPNGMEQRRRTASTTAATPPQVPAGTTAAAA AAAAAAAAAAVTSGVATK
4805	A	64	1355	PPRRVPADMAESWLRLSGAGPAEEAGPEGGLEEDALDDSLTSLQW LQEFSILNAKAPALPPGATDPHGYHQVPGSAAPGSPLAADPACLGQP HTPGKPTSSCTSRSAAPPGLQAPPDDVDYATNPHVKPPYSYATLICM AMQASKATKITLSAIYKWITDNFCYFRHADPTWQNSIRHNLSLNKCF IKVPREKDEPGKGFWRIDPQYAERLLSGAFKKRRLPPVHIHPAFAR QAAQEPSAVPRAGPLTVNTEAQQLLREFEEATGEAGWGAGEGRLGHK RKQPLPKRVAKVPRPPSTLLPTPEEQGELEPLKGNFDWEAIFDAGTL GGELGALEALELSPPLSPASHVDVDLTIHGRHIDCPATWGSPSVEQAA DSLDFDETFLATSFLQHPWDESGSGCLPPEPLFEAGDATLASDLQDW ASVGAFLL
4806	A	2	451	AQKESRSVQRSWKLKPLIVLSPLQTGLTVQSTWSTCPVSRLVTLTSLQ LLGVHSRSLSSRCRDEGFSDDTPEATEPQGNPNP\ PSC*GAGTAWGR MEPPAPQHPGDFPTPL*MSWC*DCVNPKTTHGPVLWPPFEAKTKQPD TLCSGAGLY
4807	A	239	580	ASTREVSLSGRTWPMIMVVPPTSAAWGMSLLSCTPLCFLPCRLSDR* PCSKASFSSDPRSSRRQVEWHLVKALPSPSPSEDAPPPPARNSPAEAS

				PVMPQNFLISAKPNPLASL
4808	A	1	180	FPGLGPHPCSNGCHLP*APSPLLPG*PPLSSQPLSEERGSEGRSEG VDAHTARLAPNG
4809	A	1018	1284	ESTSRSLSSRCRDEGFSDDPEAKRTTRKPKPPAAEGAGTAWGRME PPAPKHPGDFPPSPVKCHGAKTVSTPRRHMGVLPWPPFLGKN
4810	A	704	978	NRLQSHHSHPLHRPQKRRNHLYFLPHTDYSHPPPFETPREKEDHC STPHFHEAPLYKTPYFPHPRFSWIFNFVELLPDPELNPLLSFAT
4811	A	72	813	NNCLWVSCSAVGSERRNVLPCHTHALPCERARERERGRARECASPRR SGTSAAARQOQLRRRPTQOREARGGCLEEAASRMKCKPNQTRTYDP EGFKKRAACLCFRSEREDEVLVSSSRYPDRWIVPGGGMEPEEEPGG AAVREVEEAGVKGLGRLLGVFEQNQDRKHRTYVYVLTVTTELLEDW EDSVSIGRKREWFKVEGMQSKVLKCNKPVKADYLNKLNLGGFPTNWK FMGPFLADSDS
4812	A	63	131	PDKTNHILILLEHIAVVKNNGL
4813	A	204	448	TCFFIFLSFFQVFFIFLLFNVIIFTVFSSHFFNLFFLLFCLFFIHHF FFDQPLHHAGLDLDLSHARIGHGPSRRRRRRRGGE
4814	A	397	553	GFYLINAGSFRRLLFTYFMRIYTVKQNHQLFLPFLVKKEQNVGNLWN YNIFR
4815	A	361	766	RSKYAASKPALAIWDHHPGNLVRISAVH*RHTWFKLLFNVIIFTVFS SHFFNLFFLLFCLFFIHHFFDQPGHCHLCVTPATCVRHGLIMRKSC
4816	A	137	262	GRALLKYVSPSSSLWNSVPPDPNSPQPCPLKKKNPGVLGTP
4817	A	265	394	IPELLVSSDPPDSASRVAGTTGTCTCYCTSLQDRFFYFIQVNTSC
4818	A	1817	2233	RITFQERLQARSRREVGSARPKTARQVCRLPAAAKSPILARSACF RCLQKVTEERECGRITGSP*TSSFTKTLRTITPFTSHKRRVGIIQSN QPPEPDSNDRTLREPECEGCWSESWAPPHFASSNRGLPGSESM
4819	A	569	950	PLESRRLARSSGGWAGITGTPMNIIFTGPDGPSPERSAQPRVWDSTCC LKSNCFWKVKATTPMSSMMRQIPRMYNNAWRRYRLSRDASTPMK ETMNMTTTPRRMRMMAGARKALSRVLYFCRSTSA
4820	A	1868	1912	TFVKN*DRSKHITY
4821	A	1003	1094	RERLREREREREREREREMFRPQLLLPFFF
4822	A	810	970	PCPDSTQLKFFFKHNFQWQVQWLTSVIPALWEAEAGLLECQEFKTS TVKDLA
4823	A	133	261	DYCNHSEKRRWQLGPGVSSRVVTRKFVTPVTPILLRENTER
4824	A	76	475	DIRPTPKSPFAMSLCVLLTNTPGRAGHGRRGLCGKPGSGRRRTGAPA RTWQGGHEGDKMGREGAESQAQVQLLTASPPACPAASFSSSPSSASA VGSPASPGSTPQAKATSTDNCSVLSDTSAMAGSSWSGAC
4825	A	1	1647	FRSRKARSDLRYLPGRFIFPGTLPFPRRRRGKMTKFQEAFTKDVAV AFTEBELGLLDSAQRKLYRDVMLENFRNLVSVGHQSFKPDMISQLER BEKLWMKELQTORGKHSNDRNQENMATLHKAGLRCFSLGELSCWQIK RHIASKLARSQDSTINIEGKSSQFPKHDSPCQVGAGESIQASVDDN CLVNHIGDHSSIIENQEFPTGKVPNSWSKIYLNQNYQRSCKQTOM KNKLCIFAPYVDIFSCISHHDDNIVHKRDKVHSNSDCGKDTLKVSP LTQRSIHTGQKTYQGNECEAFNDSSSLELHKQVHLGKSPACSTHE KDTSYSSGIPVQQSVRTGKKRYWCHCEGKGFSSQSNLQTHQRVHTGE KPYTCHCEGKSFNQSSHYAHLPIHTGEKPYRCDSCGKGFSTRSTDNLN IHCVRHTGEKPYKCEVCGKGFQTRSHLQAHERIHTGEKPYKCGDCGK RFSCSSNLHHTQRVHTEKPYKCECGKCFSLFNLHSHQRVHTGEK PYKCECGKGFSSASSFQSHQSARGQIFKSIR
4826	A	1	1459	MHSSVYSSPAAAGLRFPGIRVSIITEGVFKTMSSEPLNNGSRDSED EETSLHGTRQVPLQLLLEVIGAEFFPGGSPAGAAAQRGQNPSSDPCHA ALRPYRSHFPHGQGIQFMNRKALLQORDVKHAQLDNGHEQQKISVAAA EAAASEAAGETSEQRRRRRPSRLPGPRLQRRASRPPSPSPSFL TFPLSLNRLLLPPGGLTATLLLRASPHRPLFLSSASLSAPPSLRVTL PPGSARLQTFEQNTSLGKRVLPQLLLLLPLVPAASAQTPTPDGDASRV VTPAQELEALCPPSYLAALLAAGGVEGMTMCSGARLALLVYGIIMH

				SSVYSSPAAAGLRFPGIRPEEEAYGEDGNPLPDFGGSEPPGAGSPAS APRAAAAWYRPAGRRDVAHGILNEAYRKVLDQLSAGKHLQSLVARGV GGSLLGGAGDDAEPLSKRHSDDGIFTDSYSRYRKQMAVKKYLA AVL GK RYKQRVKNKGRRIAYL
4827	A	456	705	CFLPFLQPRVAPITPNKTRTRAQDVPKCPGFWLSCAWTCPEGSRAR PYAGLPCPGRRCDSPSGRPWGQPVLTWLPFCFAYV
4828	A	417	793	ENAAWCRWDSTVLCSRGGKQEKRPWTAQELGAGRAEGEFAAYGRAGQ RRGVQPWARRMSWSRLWRPAAYRGELVERIRECTAAREACQEQECGC ERRESSFLPKRGEVFDAGHGGESMVVVRHGR
4829	A	553	734	NTH SFSLSNSRCSVRL
4830	A	246	346	AFEENLLRVCKKLYSVF\TQMPKMNANFANVFIGAN
4831	A	3	241	SCERARFWAAAVAGVAATRVRRRLAITGLTMRKVLALHARKKRTKA KKDKAQRK*/RLVPQHPILWIFLRHLLCSGFTS
4832	A	195	266	GVWRPLSGCNASSA*SQEPCTT
4833	A	1	1278	MGRFSQFEKKKKKKRPGESSLPQGFCSDDRSLRVGLCPSPASPGSSPS LSAQRTOGPEPQGRITGEGPSAPGRQGDPOGSGSPSGACCRAATLR EGKAQGASQNRAPAPPPTSRSGPECCTRWAYLRHEAWHQIGPRSRI AKPREKEPWTGLPNTKGIPLRLEYEGDPGHNGSGTAAGIRVRSAA SQARAVWDPSARTPAPAKEPGMAQLERSAISGFSSKSRNSFAYDVK REVYNEETFQOEHRKAKASSGNMNIITFRHHVQCRCSSWHRFLRCV LTIFPFLEWMMCMYRLKDWLLGDLLAGISVGLVQVPQGLTSLARQL IPPLNIAYAAFCSVVIYVIFGSCHQMSIGSFLLVSALLINVLKVSPF NNGQLVMGSFVKNEFSAPSYLEMGYNKSLSVVATTTFLTGTI IQKSST DLG
4834	A	2854	3176	PVISSSVCRASPKSRIFSSQSSFTARLLGFRSL*IMSAECIYFRPRR IW*IRN*TWSSVSF*HFHNVVQICPHEMGHQIHIIEFLQRPCRCKNV QQTNHIFMFHMFK
4835	A	1	2991	VIGLLDVFTPARSLEEFNDVHCSRYFRYREQKITLSSTNIVQADNN KQQLVTHLMGADLNNIVKCQKLTDDHVQFLIYQILRGLKGLNKQVN NFSNGKFKHIKSQDLKPSNLAVNEDCELKILDGFLARHTDDEMTGYV ATRWYRAPEIMLNWMHYNQTMQAQLERSAISGFSSKSRNSFAYDVK REVYNEETFQOEHRKAKASSGNMNIITFRHHVQCRCSSWHRFLRCM LTIFPFLEWMMCMYRLKDWLLGDLLAGISVGLVQVPQGLTSLARQL IPPLNIAYAAFCSVVIYVIFGSCHQMSIGSFLLVSALLINVLKVSPF NNGQLVMGSFVKNEFSAPSYLEMGYNKSLSVVATTTFLTGTI IQLIMGV LGLGFATYLPESAMSAYLAVALHIMLSQLTTFIFGIMISFHAGPIS FFYDIINYCVALPKANSTSI LVFLT VVVALRINKCIRISFNQYPIEF PMELFCLRSRPERKGP RPRTKPKGTTWPRGSSGSRPATMWKRAA VAERQAWLAAPGLLERAVGGPEPARFLLPVTPDFSLLPKIILOAF SLSLVSSFLLI FLGKKIASLHNSVNSNQDLIAIGLCNNVSSFFRSC VFTGAIARTIIQDKSGGRQQIKLQQANLRGVPSQLCRVTKCQRAIGI ETGVARGMSQHS DARETVAEVKDLLQKHSKRKIDMLLTQKASVA DRDQYVPDGFSP TGSVSSVCISGRRRCDAA PDGEDGTLFLHTAKCRI TAGAHSSLEHKTGGQKGETARNKRWRIECDERRTQERQRMKGDNFW SQIPEELRGDGAKILLGQIPNTNIYRSINDYREVMVKVPLKEEIE FSLNSSDTNLQGGKICRCFCNCDDLEPLPRILYTERFENKLDPEAS SINLIHCSHFESMNTSQTASEDQVPYTVSSVSQKNQGGQYEEVEEVW LPNNSSRNSFTRDCLDVGGKQGGGRSLIPYSDASLLAQCPHHHPGFL HGTLRGFHGG
4836	A	472	575	APKRCKQPKCLSTNEQVNKTWPVHTTEYYSSKKN
4837	A	1	248	SISKRGLMEEKGSLYEEMGPSSAHSLSVLLAPGSGFCGRLTSLQKRGV QOSSPPRSKSKQKQARARREDKSLFFLFFTYANHL
4838	A	676	788	LCTKHTYTH TH
4839	A	212	677	SRTPALCLSPVSSLSWQHOLTAPSSPLGAEDLLSDSSEPPGLNQ VSSEVTSQLYASLRLSRQAEATARAQLYLPSTSPPHGLDGFQAEQS

				RSLSVGLEKNLKKKDGSKHIFEMESVRGQLQTMLQTSRDTAYREGSS HSWRWLRETGRGLL
4840	A	455	2705	PKI I KRKACLLMILTSPKKREGRAQIVVPVTFRDVTVIFTEAEWKRL SPEQRNLYKEVMLENYRNLLSLENFHSSAEPKPEIYTCCSSCLLAFSC QQFLSQHVLIQIFLGLCAENHFHFGNSSPGHWKQQGQQYSHVSCWFEN AEGQERGGGSKPWSARTEERETSRAFPSPPLQRQSASPRKGNMVVETE PSSAQRPNPVQLDKGLKELETLRFGAINCREYEPDHNLESNFITNPR TLLGKKPYICSDCGRSFKDRSTLIRHHRHISMEKPYVCSECGRGFSQ KSNLSRHQORTHSEKPYLCRECGQSFRSKSILNRHQWTHSEKPYVC SECGRGFSEKSSFIRHQTHSGEKPYVCLECGRSFCDKSTLRKHQRI HSGEKPYVCRECGRGFSQNSDLIKHQRTLDEKPYVCRECGRGFCDK STLIIHERTHSGEKPYVCGEGRGFSRKSLLLHVHQTHSGEKHYVCR ECRRGFSQKSNLIRHQTHSNEKPYICRECGRGFCDKSTLIVHERTH SGEKPYVCRCMGKAFVITHHRENLHVGTWSSAQMTFSGVTPQLLER TVLLLAEMHSRDALRSGTHSQPQGAACCTTGAMHLCRGTFWPQPLTQR GQLQKVIPDPEIPIELKDHVADTLQVPPINLI IMAIEFQHEFWRRH SHHSINYAVAPQSGLMREKDVHVWECGPPPFARTAPITPTSDQNRWP LREKKGHYQDLSTPSQKETELKRTRVSLRRKRDNASPLQDYGFGA
4841	A	92	316	YKQGYQTLIKPSDLVKLTHYLKNSMGETALMIQLPPPGPALGTWGL WDLQFKMFTASVYMCLPVFTCLPSTKH
4842	A	1	578	MGETALMIQLPPPGPALGTWGLWDLQFKTNTTSTDTDP RSHLQETGD NILTLFTMHPPLESEWTICNFRQIWLSSWSTLETRAQPLHSYFRKL KGRGTAIAGIVFGIVFIMGVIAGIAICICMCMKNHRATRVGILRTH INTVSSYPGPPPYGHDHEMEYCADLPPPYSPPTQGPAPQSPPPYPG NARK
4843	A	99	413	TAGFIWLFKHHRFLKKTQKLTVCPIINGEDHLRLNLFQHNFITRIQ NISNLQKLISLDLYDNQIEEISGLSTLRCLRVLLVGKNRIQKNLHLE NLKKPKRPWI
4844	A	2	639	LEGRSNREPGLSPIMIPGKYRSVSGRAANNVNCGLHLVIQTSSLPEK NKVEFKLNKDTSSFPGRLLQHDLEARNYSCRQGDHINLVSSSLPSFPI LQRSSEKILYSDRLSLERQKLTVCPIINGEDHLRLNLFQHNFITRI QNISNLQKLISLDLYDNQIEEISGLSTLRCLRVLLVGKNRIKKNISNL GESKKLRMSWDLHGKSGLPKIGKY
4845	A	788	1174	PSCTRLRRRQNRSLKTNISPRKRATVCLKPSQMLGLVPGVDGRSP RGGRGGLGWRSCFLSDGEWILRTGSGVSGLVGSRGSAGGPRLEMDPN CSCTTGGSCCTCAGSCKCKECKCTSCCKKSCCSCP
4846	A	35	406	SGTPASPCLEMDPNCS CSPVGSACAGSCKCKECKCTSCCKKSECRF PANLQDGPS* SREPRALQAGAGQ* PASPNPSFNT* FRIRPQIALKMG CCSCCPVGL/ CAKCAQGCICKGTSDKCSCCA
4847	A	299	981	ALVPAGAAPPTRVAAMEVLRRSSVFAAEIMDAFDRSPTDKELVAQAK ALGREYVHARLLRAGLSWSAPERAAPVPGRLAEVCAVLLRLGDELEM IRPSVYRNVARQLHISLQSEPVVTD AFLAVAGHIFSAGITWGKVSL YAVAAGLAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGWTD VLKCVVSTDPGLRSHWLVAALCSFGRFLKAFFVLLPER
4848	A	152	797	DPPNLYLDFDGDVTKLETFGVTTTKASKPRSPASTSTVTNVTDAPTA PKAGTTPVAPSAPDISANSRSLSQLIEQSQKEKQLVTGMDGGPKEC KNKDDQGFESCCKKVSNTDKSSRQSDSKTSDALQLENSQEIETANK YDMTIDMVHVDAERP NVLENLDNSKEKTVTSEAAKTEDTVLCSSD TD KECLIIDTECKNNSDGKTAVMGSNLNS
4849	A	1	124	GTSLLLPYHIHHGRIPCTFPKSLDTTTQQKVRSLKLVH
4850	A	2	719	PNAEKLVSRYHPQIALTSQSLFTLLNNHGPTYKEQWEIPVCIQVIPV AGSKPVKVIYINSPLPQKMTMRERNQIFHEVPLKFMMSKNTSVPV AVFMDKPEEFISEMDMSCEVNECKRIESLENLYLDFDDDVTELETPG VTTTKVSKSPSPASTSTVPMNTDAPTAPKAGTTTVDAPSAPDISANSR SLSQILMEQLQKEKQLVTGMDGGPEECKNKDDQGFESCEKVSNSEQA FDTR

4851	A	98	263	LVNTPSTCALLSLHYRLRSPALPRLEMDPNCSCCTGGSCCTCAGSSCO VTLFHLQE
4852	A	741	965	AHLPEFLLSPCPSLGGPRPRSHCRW*HCPRLRAAPPPA*SALCLGGC CECVAAPGRWYCWVPGDRACSPHTCAR
4853	A	105	284	LVNTPSTCALLSLHYRLRSPALPRLEMDPNCSCCTGGSCCTCAGSTHS RADGSQQAMLRH
4854	A	407	1815	TRATRWRKRTKRYTLRKTERWSRPRVIMDSASR/HAPGNGLYVNYGLKA LNIHGGQKLTAEHGGAYGATADMSAKIGGEGDLAINTVRQVLSNG QNDYQGATYVQMGLTRTDADGALGNTRELNISNAAIVDLNGSTQTVE TFTGQMGSSTVLKKEGALTVNKGGISQGEITGGGNLNVTTGTLAIEGL NARYNALTSISPNAEVSNDNTQGEFSSKRRQTRKEIFLSRMEQILPW QNMVEVIEPFYPKAGNGRRPYPLETMLRIHCMQHWYNLSDGAMEDAL YEIASMRLFARLSLSDALPDRTTIMNFRHLLLEQHQLARQLFKTINRW LAEAGVMMTQGTLDATIIEAPSSTKNKEQQRDPEMHQTKKGHWPL WHEGPHCLVTTAANEHDLNQLGNLLHGEEQFVSADAGYQGAPQREEL AEVDVDWDLIAERPGKVPARHRLSAHGCVLTYTALSRRIVALPLPVSAP P
4855	A	1020	1352	RAEARAPGDWGKEQDDEQVQMSYPPVRLTCWLRLVSPQHQPFGFPLH GLMCGNHWTSSRLPCSVPPTRYAPPLPPSVQNGAVPPDGHPPSW HRENHSAYRVENLHTR
4856	A	491	628	KTITNWRCSRWPTCFGRK*YDWHRQMTTPRQRAVLWTKSPKTV
4857	A	1	1872	MVIVPIGYAAQELFDVSQVRGCTPYGATTIAGGDSRQPSQEELSIA RYQGEYVAGVRYRSTFYPGIS/ALSVLSHILVLYCTAGLHIGA\AIV PTRYAYCNSEFSSKRRQIRKEIFLSRMEQILPWQNMVEVIEPFYPKA NGRRPYPLETMLRIHCMQHWYNLSDGAMEDALYEIASMRLFARLSL DSALPDRTTIMNFRHLLLEQHQLARQLFKTINRWLAEGVMMTQGTLM HQTCKGNQWHFGMKAHIGVDAKSLTHSLVTTAANEHDLNQLGNLLH GEEQFVSADAGYQGAPQREELAEDVDWDLIAERPGKRSASCIQKLT TMIYVTHDQTEAMTMATRIVIMKDGIVQQAERNDWHFTIGAMYEIE NVEGYGEDLDGLADPSVYFNAANGPCRIALGYHEGPENITRAPEEM RSFLLDAGAEYNGYAADLTRTWSAKMTNDYAQLVKDVNDEQLALIA MKAGVSYVDYHIQFHQRIAKLLRKHQIITDMSEAMVENDLTGPFMP HGIGHPLGLQVHDVAGFMQDDSGTHLAAPAKYPYLRCTRILQPGMVL TIEPGIYFIESLLAPWREGQFSKHFNWQKIEALKPFGGIRIEDNVVI HENNVENMTRDLKLA
4858	A	1231	1407	QVTGHRFRGAYQHTACSFTEDGFHRLRFSFIASRRRSTVRVNVANLT RFNACITQSICH
4859	A	491	553	KTITNWRCSRWPTCFGRK
4860	A	3	278	KLSCPDQSEKLGKREGQIRETGEEGGAKEAAVPPQSSSDSAPG ATQLRRQRQCCSSSEGGQAGRQTEVLGLEGLSPQPLGAWPNGL
4861	A	2455	2871	RWLIVTLFIGEDLNTQITVYIREQQQFKVINRTGCQGMGLRLNIRNI QLVIKYLDIEYRTKQRFITCRSPAVTDNLFQIVTLMTHFFQLCCQS GCQFRQRFLRRNVNTQRQNVHSGSRQRRRAQSTHKDKSGGVVH
4862	A	656	949	LLHRFCRWPALAPGAILRQIPKKQQRVGLHYSFMSYVSWRYRVCHWT ITVFCLSKTLATSYPASISVKNTKWRCFPLPKVKTNH*NIRICLP PPR
4863	A	448	582	GPSTAISPSRVLLVAHLVPRCLHFLGGGSALVADPAANFSFWCS
4864	A	495	920	WRRRDRCASHHFAVSVTTIGSSRDPDAGSLPVHSWRRKERRSALYLH RSSRSHRRTPRRDRRAFWFVQPRCWLAAILSGH*TGGCT*NIRSH QLGTSQTLRCVQNHRCRCRSSDRPRLRVLSWHARKYQTPGRCSE
4865	A	1	2799	MTQIFTGTLEADPFHAVTLVANHDTQPLQALEAPVEPWFKPLAYAL ILLRENGVPSVFYPDLYGAHYEDVGGAGQTYPIDMPIEQDELILA RQRFAGHVQTLFFDHPNCIAFSRSGTDEFPGCVVMSNGDDGEKTIH LGENYGNKTRWDFLGNRQERVVTDENGATFFCNGGSVSVVWIEEAA NNRQYDYGAGHKIPVINYTDVHLRIERSCRFRADPRQHELQLSSKL AVHDVLTNIYNRRYFFNSVESLLSRPVVKDFCVMLVDINQFKRINAQ

				WGHVRGDKVLVSIVDIIQQSIRPDDILARLEGEVFGLLFTELNSAQAKIIAERMKNVELLTGFSNRYDVPEQMTISIGTVFSTGDRNISLVMTEADKALREAKSEGGNKHWNLSGAMEDALYEIASMRLFARLSLDSALPDRTTIMNFRHLLQHQQLARQLFKTINRWLAEGVMMTQGTLVDA TII EAP SSTKNKEQQORDPEMHQTKKGNQWHFGMKAHIGVDAKSGLTHSLVTTAANEHDNLQNLGNLLHGEEQFVSADAGYQGAPQREELAEVDVDWLIAERPGKVRTLKQHPKXKNTAINI EYMKASIRARVEHPFRI IKRQFGFVKARYKGLLKNNDNLAMLFTLANLFRADQMIHSQYSALRRHQDGSVSFKPETHTCDAHRPALKPANDYVRTFFRGVDISQVFSAKDIARRTPNGLIRKTPGFGPRSALKLLQDEDEYGYVIERGNKFVGAVSIDSLKTAAVPPVQLLTGWCVTAKAPPDISAISALTAVKHGNCSSLTPLLNP GSDVIVCAEMDEQWGYVGAKSRQWLFYAYDSLRTTVVAHVFGERTMATLGRMLSLSPFDVVIWMTDGWPLYESRLKGLHVISKRYTQRIERHNLNLRQHRLARLGRKSLSFSSKVELHDKVIGHYLNKHYQ
4866	A	3675	4064	VSSDQNRRCNRCYGRQLPGGCFSLWCQFSASKSYLSPSDL**W*/QLSPSASRLPLASLTISSSSLSCAGSASFHS\RHIPGRCTCRYLRVFGVAFWAVW**HVDFLKSQQGKS AKKRQIAEKGRNYTQNP
4867	B	1	2325	MNLMEQPAKQYLLSTQGLPVLVNSLARYPQEALPITNYFAASELAPAVARAFNKLKTLRENARSWLLKYPEHALTGLLPAALGKAGEAQDNARAALRMLTENGHQPLLQEIARRYNQPEVTDVAVNALLALDPLDNHPTKIP TLPAFYQPSLWTRPVLKANAQSLPDSALLHLGEMLRFPQEEALYPGLLQVKDVCSADSLAGFAWDLFTAWQTAGAPSKESWAFTAEFSSKRRQTRKEIFLSRMEQILPWQNMVEVIEPFYPKAGNGRRPYPLETMLRIHCMQHWNLSGAMEDALYEIASMRLFARLSLDSALPDRTTIMNFRHLLQHQQLARQLFKTINRWLAEGVMMTQGTLVDA TII EAP SSTKNKEQQORDPEMHQTKKGNQWHFGMKAHIGVDAKSGLTHSLVTTAANEHDNLQNLGNLLHGEEKQFVSAMPATKEPQREELAEVDVDLLIAERPGKVTLKQNP RKNKNTAINI EYMKASIRARVEHPFRI IKRQFGFVKARYKGLLKNNDQLAMLFTLANLFRVDQMIQLPTYELSSGIGAVRRQAELDGTAPAINSKRVYRIMRQNALLERKPAVPPSKRAHTGRVAVKESNQWCSGDFEFCCDNGERLRVTFALDCCDREALHWAVTTGGFNSETVQDVMLGAVERRFGNDLPSSPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKRDYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSA LGYRSPREYLRQRACNGLSDNRCLEI*
4868	A	82	199	GLLLGTGP ERKPEQKMCLLVHLLTSGGLPGLPSGTPRC
4869	A	882	1091	VCHAAPPI LRTTATSVPAVPGAASDSGYAAQFAAYIAC*LRAAFPSGGIHTAASHPSSISPRQRTAGS
4870	A	3	274	LSCPDPQSEKLGKREGQIRETGEEGGAKEAAVPPQSSSDSAPGATQLRRQRQCCSSSEGGQAGRQTEVLGLEGLSPQPLGWAWPNGL
4871	A	2888	3076	KTITNWRCYSRWPTCFGRK*YHWHQLLSMVRQLMVLWSKKISSWFMGPPIIRKSILAENSI
4872	A	1	2043	MVARAAALTATPQVDKVLSRLIDITDAAIDSGVLLERLIAQNPVSYNFHVPLADGGVLLGASPELLLRKDGERFSSIPLAGSARRQPDEVLDREAGNRLLASEKDRHEHELVQAMKEVLRERSSELHVPSSPQLITPTLWHLATPFEGKANSQENALTACLHPTPALSGFPHQAATQVIAEL EPPDRELFGGIVGWCDSENGEWVVTIRCAKLRENQVRLFAGAGIVP ASSPLGARMSIPFTRWPEEFARRYREKGYQDLPLTDILTRHAASDSIAVIDGERQLSYRELNQAADNLACSLRRQGIKPGETALVOLGNVAELYITFFALLKLGVA PVLALF SHQRSELNAYASQIEPALLIADRQHALFSGDDFLNTFVTEHSSIRVVQLLNDSGEHNLDQAINHPAEDFTATPSPADEVAYFQLSGGTTGTPKLI PRTHNDYYSVRRSVEICQFTQOTRYLCAIPAAHNYAMSSPGSLGVFLAGGTVVLAADPSATLCFPLIEKHQVNV TALVPPAVSLWLQALIEGESRAQLASLKLQVGGARLSATLAARIPAEIGCQLQQVFGMAEGLVNYTHESSTYLRRHEFSSKRRQTRKEIFLSRMEQILPWQNMVEVIEPFYPKAGNGRRPYPLETMLRIHCMQHWNLS DGAMEDALYEIACHASVCPVIPG

4873	A	222	513	PEGAPRTPGPLPRAPGRTSEGAGRRGGPLGPVVTMCLPRRQLSYPDV G*AEGGLPALDPWPGHARGSEGPRRQGGAVLAVRLGGRVYVHLHTPG GQ
4874	A	20	161	RALPIDEREHQPEGPMVVHCSDCILHPPLASGRCVTSRASLRPKLV
4875	A	1	2251	MAGVGAGPLRAMGRQALLLALSHRRQGLYFHIGETEKRCFIEEIPD ETMVIGNYRTQMWDKQKEVFLPSTPGLGMHVEVKDPDGKVLSRQYG SEGRFTFTSHTPGDHQICLHSNSTRMALFAGGKLYREERFRLTSEST NQRVLWWSIAQTVILITGIWQMRHLKSFFEAKKLRVRAALLSSAME DSEALGFEHMGDLPRLLQAVTDLGWSRPTLIQEKAIPLALEGKDLLA RARTGSGKTAAYAI PMLQLLLHRKATGPVVEQAVRGLVLPVKELAR QAQSMIQQLATYCARDVRVANVSAEADSVSQRAVLMEKPDVVVGTPS RILSHLQQDSLKLDRSLELLLVDEADLLFSFGFEEELKSLLCHLPRI YQAFLEMSATFNEDVQALKELILHNPVTLKLQESQLPGPDQLQQFQV CETEEDKFLLLYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIP TCVLNGELPLRSRCHII SQFNQGFYDCVIATDAEVLGAPVKGKR\GA EGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGR** CDGPGICM\TARANNPGIVLTFVLPTEQFHLGKIEELLSENGRGPIL LPYQFRMEEIEGFRYRCRDAMRSVTKQAI REARLKEIKEELLHSEKL KTYFEDNPRDLQLLRHDLP LHPAVVKPHLGHVPDYLESKVPEPTAQL QAQRKEIQTHSQALLRLLGLSGAEHIVEHRLTPFVDRRGSGAYCTA
4876	A	2	2318	FVSGGLGCRWGGRRLLLLLALCATGAQGLYFHIGETEKRCFIEEIPD ETMVIGNYRTQMWDKQKEVFLPSTPGLGMHVEVKDPDGKMLQVLSR QYGSEGRFTFTSHTPGDHQICLHSNSTRMALFAGGKLRVHLDIQVGE HANNYPEIAAKDKLTQLRARQLLDQYREERFRLTSESTNQRVLWW SIAQTVILITGIWQMRHLKSFFEAKKLRVRAALLSSAMEDSEALGF EHMGDLPRLLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSG KTAAYAI PMLQLLLHRKATGPVVEQAVRGLVLPVKELARQAQSMI QLATYCARDVRVANVSAEADSVSQRAVLMEKPDVVVGTPSRILSHLQ QDSLKLDRSLELLLVDEADLLFSFGFEEELKSLLCHLPRIYQAFLEMS ATFNEDVQALKELILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDK FLLLYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGE LPLRSRCHII SQFNQGFYDCVIATDAEVLGAPVKGKRGRGPKGTSV ARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIVLTFVLP EQFHLGKIEELLSENGRGPILLPYQFRMEEIEGFRYRCRDAMRSVTK QAI REARLKEIKEELLHSEKLKTYFEDNPRDLQLLRHDLP LHPAVVK PHLGHVPDYLESKVPEPTAQLQAQRKEIQTHSQALLRLLGLSGAEHI VEHRLTPFVDRRGSGAYCTA
4877	A	866	1150	QPPQEGTAEAGKPSLCVFISTFPGIWGGLLFLRFQVQHCIRTEAVTE DSVPRKGASCVSLGFGALLKKPTTPTPYCSPSTPHSSMKMCEPPV
4878	A	417	872	SFKLSKVEQFQEGGPKRMPWVIHVFPWVHFQLCIPALQLCSQPRAN TLHPNLRWGKGQSPWIWDPSIEGQPGLLPAGCLCYTCRMCMTFSLDN TPSFLPHQPQTSRPFPPFLPVAEPPTIAHTVLVQLLTVPGLRSVMLA FPQQRKPAG
4879	A	3	284	AASRGDGGALAGARVAEAAAVGRGECPPFGRRQSGPEPAAQGGELRA EMAADAAPHGGPRLPTGGPRAADEAGRASTGCGISKPLPSVFSHL
4880	A	2	437	AAASGGEWRGSGWGSVAEAAAVGRGECRFPGRQSGPEPAAEGGEL RAEMAADAAPHGGPRLPTGGPRAADEAGRARVRAGAPPGAQRGPHS RSHPPISQESLCLWRWPKEEEEPTLWKNALPVLVVCPLAPADTAKC PIPK
4881	A	336	442	EIGWVQWLMPIPAVWEAEVGGLEPRSLRAARAI
4882	A	523	630	VKQKPRIVAHVLAYSVYTHQTQTHKHTHTQCHTGSDP
4883	A	1	1004	MAPWPHENSSLAPWPDLP LPTAPNTANTSGLPVWPWEAALAGALLALA VLATVGGNLLVIVAIWTPRLQTMNTNFVTSLAAADLVMGLLVPPA ATLALTGHWPLGATGCELWTSVDVLCVTAS IETLCALAVDRYLAVTN PLRYGALVTKRCARTAVVLVWVVSAAVSFAPIMSQWWRVGADAEQR CHSNPRCCAFASNMPYVLLSSSVSYFLPLLVMFLVYARVFVATROL

				RLLRGELGRFPPEESPPAPSRSLAP/APGYANSAFNPLIYCRSPDFR SAFRRLRCRCGRRLPPEPCAAARPALFPSGVPAARSSPAQPRLCQRL DGERHL
4884	A	144	1423	FGRPPPSFFPYRPTRDPGMAPWPHENSSLAPWPDLPPLANTANTSG LPGVPWEAALAGALLALAVLATVGGNLLVIVAIWTPRLQTMNTNVFV TSLAAADLVMGLLVPPAATLALTGHWPLGATGCELWTSVDVLCVTA SIETLCALAVDRYLAVTNPLRYGALVTKRCARTAVVLVWVVSAAVSF APIMSQWVRVGADAEARQCHSNPRCCAFASNMPYVLLSSSVSYFLPL LVMLFVYARFVAVTRQLRLLRGELGRFPPEESPPAPSRSLAPAPVG TCAPPEGVPACGRPARLLPLREHRALCTGLIMGTFTLCWLPFFLA NVLRALGGPSLVPGPAFIALNWLGYANSAFNPLIYCRSPDFRSAFRR LLCRCGRRLPPEPCAAARPALFPSGVPAARSSPAQPRLCQRLDGASW GVS
4885	A	1309	1702	IGQVRWLTIVILALWEVEVGGSPKVTSSRPQLITHLGLPKCWDYSLE PLCPTCLFFEIQSCSITQVECSGTITAHCSLQLLGSSDSPASASQVA GTTGALHAWLIFKFIVEKGSFHAAQACQTFSYKKLHA
4886	A	1	648	MVMEMVMVMVMEMVMVMEMVMVMEMVMVMEMVMVMEMVMVM VMEMVMVMEMVMVMEMVMVMEMVMEMVMEMVMEMVMEMVMME MVMVMVMWRCDGYGDGDDPLMALPPCHALCQFYVNSELSQLYQ RSGDMGLGVPFNIASYALLTYMIAHITGLKLQREPRPFPKLRLRKV EKIDDFKAEDFQIEGYNPHPTIKMEMAV
4887	A	1	1049	GGGGTTWPASVPPRHLACLRLPAAPLRLPPSPARRAMPVAGSELPRRP LPPAAQERDAEPRPPHGLQYLQIQHILRCGVKDDRTGTGTLVSF GMQARYSLRDEFPLLTTRVFWKGVLEELLWFIKGSTNAKELSSKGV KIWDANGSRDFLDSLGFSTREEDLGPVYGQWRHFGAEYRDMESDY SGQVDQLQVRVIDTIKTNPDDRIIMCAWNPRDLPLMALPPCHALCQ FYVNSELSQLYQSRGDMGLGVPFNIASYALLTYMIAHITGLKPGD FIHTLGDHAIYLNHIEPLKIQLQREPRPFPK\LRILRKS*RKIDFK AEDFQIEGYNPHPTIKMEMAV
4888	A	437	851	NGHLQETLHRWIVSLSSVPSLQRLWLSLQPSGSLSWSPPYEMASVS LLFYFAFSCGLSNHPSLSSSGSSDLPMALPPCHALCQFYVNSE LSCQLYHRSMDLGVPFNIASYALLTYMIAHIHGPEGGLSRER
4889	A	1	1063	MCPAAALTPTSVAQSEAPWSFMLIRECNTMTVPSLRGEMQTTTLHA ATPSSNSDRHVSMPLLLYLEQVTFLQEHAGTGRRWWSIVWRRRTFPA AGAMEMPLPDDQELRNVIDKLAQFVARNGPEFEKMTMEKQKDNPKF SFLFGGEFYSYKCKLALQQRHSRGSPLPGLGLRARGNGGGAAA TRAHWDDGRATYVYQWPWTLLLLAVSGFCNFAQNVIAFSILNLVSPL SYSVANATKRIMVITVSLIMLRNPVTSTNVLGMMTAILGVFLYNKTK YDANQQARKHLLPVTTADLSSKERHRSPLEKPHNGLLFPARGLSVR PQQLNRPLPIQPAELPKLVQFEPL
4890	A	496	701	FTKGPPPSKKRFISSINIFDKGFQFGFHRGVPGHDFGNLGPLPPGIK RFLSLSLSNSWECKPASLERP
4891	A	875	1156	LHTVCVVCVCVCMCMCVCLKGYSVFTLKIQRSHSFSQNYKGEVKK NSKAPSVYLVLKEIRVCICSHRAYINAHTHTHTHTHPKYISAH
4892	A	76	382	FSHWIFFPAVRGDLGPVEGHCLNLSGVCRRDVCKVVEDQIGAFWKFL KSPQVSRGDCSCTESHCLDNWPGVVAGVGLNPGVKILELGVFLYLFW DSAPLANI
4893	A	71	228	FSHWIFFPAVRGDLGPVEGHCLNLSGVCRRDVCKVVEDQIGACRLFF LFSEC
4894	A	69	242	FSHWIFFPAVRGDLGPVEGHCLNLSGVCRRDVCKVVEDQIGAWGSCR SRPKSRCEDP
4895	A	146	431	LPHKLIHNSVGKWSRVPGQSAISTGTETPPVQGSRRDLGLHLQLPQ ASYPGSDFLYSYSHLWTPAETLKISRRSGIFGDLGYGVACKGESIS F
4896	A	3	262	SKRWFGSCGRSLSQFVWCLQNRCLQHSRRSNWCLCRQCSHEKGLQKF LTFWKFLKSPQVSRGDCSCTESHCLDNWPAGCFSYFSEC

4897	B	185	338	MSTTFMGRSQATGGCVQTDTPGPPTLLQDTQQLSVVHPDIOLEVGFPGGGGX*
4898	A	69	303	FSHWIFFPAVRGDLGPVEGHCLNLSGVCRRDVCKVVEDQIGACRRRMKCCRTWILMPIPTPLIMSDYQEPLKHKLK
4899	A	260	881	MTVTHITIYNKAQVSILKCRGRVKGCESAERRSHPNQHVAARTPSDASKTTTAQRNGGGKPRSSTTCVSVNSVDSSSDVCRSMSVESQSIVAYFLHSQVQAAGYLNPLHLAVKLCQAPGTSNNSDCLRPRRRRCHRQHTPSDHFTCWPSNVQQRIRKHPARTLESAPWPAKSPAIFADGPTGGAACILQALFRAGSTAKAAMVASR
4900	A	373	491	ASDHFEVLVRWLTPGIPALWEAQEGGLFGPGSSRPTWATF
4901	A	1	232	GMGVSTVTAARILKGQKKDKLGPETPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTPRPADLCFSP
4902	A	3	703	LGVPTVTATRILKGQKNGKLGPEPLAMDRFPYVALSKTYNVDRQVPDSAATATAYLCGVKANFQITIGLSAAARFNQCNTTRGNEVISVMNRAKQAGKSVGVVTTTRVQHASPAGTYAHTVNRNWYSADAMPASARQEGCQDIATQLISNMDIDVRPPGQGLGLGRGEGGTGSDPGNQKPDGLQQVLEVILGGGRKYMFPMPGTPDPEYPADASQNGIRLDGKNLVQEWLAKHQ
4903	A	3	1622	CPPDMLGPCMLLLLLLLGLRLQLSLGIILVEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLDGCVGVSTVTAARILKGQKKDKLGPETPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQITIGLSAAARFNQCNTTRGNEVISVMNRAKKAGKSVGVVTTTRVQHASPAGTYAHTVNRNWYSADVPASARQEGCQDIATQLISNMDIDVILGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKHQGARYVWNRTLMRASLDPSVAHLMGLFEPGDMKYEIHRDSTLDPSLMEATEAALRLSRNPRGFFLFVEGGRIDHGHESRAYRALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHVFSFGGCPRLRGSIFGLAPGKARDRKAYTVLLYGNPGYVLKDGARPDVTESESGSPEYRQSAVPLDEETHAGEDVAVFARGPQAHVLHVGVQEQTFAHVMAFAACLEPYTACDLAPPAGTTDAHPGRSVVALLPLLAGTLLLLLETATAP
4904	A	26	168	TCLTHTHTHTHTHTHTHTGLLSLVQVCQVCRQNMSSEGFVTTDHKPT
4905	A	258	486	GHTGPLGSPWSSVWVCLAGRQVPGPQHPHRPPGCSWGCRRPPAGTGPRLPSASAPRCCPPMRLEPRASRRSGTSG
4906	A	1121	1518	LLPGSTNKAILQKDGQASHTIMQGTGALTGPAPPARGPWPLLRWPPQPTAARASEIWHRSQPQHVALIRRESCGSQGAPRGRPPPPPAVPADHGSARPPGCCLASPRIROGSPGAHQASASASERGGSSMA
4907	A	19	541	YARTLCLTCHIFFFFLETDPCSIQARVWVWCEHGSGLQPRPSGSSDPH ASDPQSAGITGESHHAGLNQGLRLKCHLLNHPCKSVGGHPVSAA DLAWTLGCEREGWAGLEEPEALVMSQAHLAGHPLRCTCPRWPPQQR ATGGWRASTGRSSGGEGRAPRRLRPEPGVR
4908	A	288	561	ISLHYKEENPPNETDMNIVYGLHTHTHTHTHTHTQIYFNPVTTRN LETTYQQRGTERLPFSKMSKKRRVGVWEVLVYLDEQGSEMARHE
4909	A	1	1857	MLESKEEDVEVEKWSPLSLHLHTLKGYGQVQEARYSPKVIIEIWKMGV DWSGTGLVLKAEQHSFAFGVMETGIRIRKKKTSNESKSGGPPSPQMG GSGNLIGRGRKGGVKNCKEENLRTDPAKKVRQVQKCSWCVCLEGES VEIVSEVRVEVGELNIIKDWGRESVEKGGAVISMEAERVKGQAMIA TGGVITGLAALKRQDSARSQQHVNLSPSPATQEKPIRRRPRADV VV RGKIRLYSPSGFFLILGVLISIIGIAMAVLGYWPQKEHFIDAETTL TNETQVIRNEGGVVVRFFEQLHSDKMKMLGPFMTGIGIFIFICANA ILHENRDKETKIIHMRDIYSTVIDIHTLRIKEQRQMNGMYTGLMGET EVKQNGSSCASRLAANTIASFSGFRSSFRMDSSVEEDELMLNEGKSS GHLMPPLLSDSSSVVEGLYPPPSKTTDDKTSGSKKCKETKSIVSSSIS AFTLPVIKLNNCVIDEPSIDNITEDADNLKSRSRNLSMDSLVPPLPN TSESFPQVSTVLPRNNSIGESLSSQYKSSMALGPGAGQLLSSGAARR QFGSNTSLHLLSSHSKSLDLDRGPSTLTVSGRTTETSKLGLGLDREQ QAKGIYGN
4910	A	81	416	PSLHPKASPVSPIKGKEAVSRDEQNNHQGSHFLLPKIPSWRDPPE

				LEEQNAPRERPEGPAAAKKPPRHCELVVTLGCPEIHGDLRPWDRKR QPRSLRGSHLGGQRLHG
4911	A	1	507	ASPKPVLCHQSKERKPSAEMNRITTKATSSCPPKSPLGETRQKLWR SLKMLPERGQVRQQLKKPPRHCELVVTLGCPEIHGDLRPWDRKRQP RSLRGSHLGGQRLHGS LCGHISQKPLTAPGTRQKQKPHQEGREESKP EHQGLAEPENDQLPEEYQQPPFFAPGYC
4912	A	519	858	GLSEILAIGFCPHQVQRGPGKVLQS\LAQPLGPFTRLVHRRQSLH AVPKCIHAVPCSFTLPHLPQEGLRPEFLAPWGLHLKATPVWPFANP RCCSILGAGGYFVQTLGMS
4913	A	67	467	QRPSCPYRYPHGWTGLCTPRWASWPKTGSPSGSMVQSQERMLRTCW SHSHWDPFSSGSVTAMWATHSPTS KAWAGIQGRGRWALGFPWRGQGV LHVIASQKAAVTEAVDLRTGAASQAMSEAFSRSGMFYLR
4914	A	2	307	PPETLEEQNAPRERPEGPAAAKKPPRHCELVVTLGCPEIHGDLRPW DRKRQPRSLRGSHLGGQRLHGS LCGHISQKPLTAPGTRQKQKPHQEG REVGQLH
4915	A	1	2112	MEPVEANGKDPKEGIQNPQAESGGLQQTGHTHGA LRHSQS QLDEVA ACPOYGAAASVRKRPHWGWLTC LRKQELPRGSQPRPIDVQTLNRNPG SCRHWHSYSEGLGHPRV SQVCDPRASALEETERSRAVLLWDWDLGMQ GSASRDHQGASTGQKPRLGDPGQATERGLPKASPVSP IKGKEAVSR DEQNNHQGSHFLPPKIPSWRDP PETLEEQNAPRERPEGPAAAKKA TSPPVNIVVTLGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGS LCGHISQKPLTAPGTRQKQKPHQEGREEMTEAGKLPLPLPRLDWFVH TQMGLAQDGVPEWFHGAISREDAENLLESQPLGSFLIRVSHSHVGY TLSYKAQSSCCHF MVKLLDDGTFMIPGEKVAHTSLDALVTFHQQKPI EPRRELLTQPCRQAEAGDHHKDPANVDYEDLFLYSNAVAEEAACPV APEELFPPHIRLFYRYQDLAPQLVPLDYTTCPDVKVPYELIGSMPEL KDNPFQRRIAQVSEDDGDMTLDNFDLMFSVMSEMAPRDLKAYYAF KIYGLQMETPGCKEFRSLQTF LWKMEQCETAWNSMDAFGNCVEALSP LPQLPDGGPQEQSSNCTSSFSHLPYLYISRGDNMDKPGKWPGQLGS QRFVKPFQVLFEPDEDKSQWPIISESPQKCTDIPFFVHGDRRLST
4916	A	796	1018	RSEGPVAVFSWMRQTPEGKELAPWPAVCRAQDPAPAPFQASSSFG PMLSAPAGREATCNYA AFRLLPPQPPGH
4917	A	3	113	SCSGDMAGVKALVALSFSGAIGLTFLMLGCALEDYG
4918	A	2	134	SGLGRLPGPWQAEAGSSRGPSGDMAGVKALVALSFSGAIGLTF/LHM LGCALEDYGLGPTDSVYWPLFVLIFHGISP IPHFIAKRVTYDS DATS SACRELAYFFTGTGIVVSLWISPVILARVALIK\WGACGLCV/VAGN AVIFLTIQG\FPFI FGRGDDFSWE\QWGYWTD FS
4919	A	512	625	CPTLCVWGRSGSQPPSPTIAPMFAYPPPPSPFTYACC
4920	A	206	366	IGGVTKFVIYCMEDNFVLCCLNHTN ILKSCTSQMIVILQMLCKMGQ GVEIYI
4921	A	504	690	GKIYTYTVCVCLCVCVCYIYFHALPRLTKQCGSRSSGKCMTLGY WYDLGNSTVQNYLP
4922	A	3	336	TKFRSRSLTSGLFAGGVGAEPDWSGQRHAGAVPRAQPRRGRGRGWRA ARPSSPKHAGRVAPSLVGS LITTWPVNHHPKEAGNESGAFSAPGLSP SFLGFQGHSL EARWRV
4923	A	22	129	ASFQGTYSDDHREKLTSVIFFLTYTHTHTHTHS
4924	A	852	1366	RDTVSLAPYLEKCLFGVRGRGGA WPKVKAEGRNAWPLHPVPSIIPGS HPMPAELKHKTREVPARKARSGDAEH PGVSADHPLLLGPGPGPTLHH TFPGRGSPWLCPNWVPFLYMCEPRGCLLLCSPLNPKNVGSHHFN LNI FKKHFFFWRQSLAVSPTLLTPGSLSSPRAT
4925	A	1	897	MCLSLDPCKLLSPVKIVAYIDRCVCAGRSSSQSPVIARKGKCLVSPK GFSVVKVAALSRRLLPVLPTARKSEKGETAPNRLPGCHAALAGRKT GCGILSPGPVSALPLPSHPFFSSSPVPHEAASESFINMSDPV IQGSL SPGVTVQGQLGTWPHKQEYTLVYIIDGVDFVTSN SSRVVIETYF KELARGIVPGNLKSAEKAAAEIQTALRALLLRVGGRVP CNLLEG NFTDRKTAGEEKRVS PFELMSTHTSI IHRSAHGPHLDPYNRHTYLYN

				RPYATNYP SNITPQDHS
4926	B	449	2578	MLLECEEEAVCVIMCASVKYNIRGPALIPRMKTKHRIYYITLFSIVL LGLIATGMFQFWPHSIESSNDWNVEKRSIRDVPVVRPADSPIPERG DLSCRMHTCFDVRGCFNPKNKIKVYIYALKKYVDDFGVSVSNTISR EYNELLMAISDSDYTTDDINRACLFVPSIDVLNQNTLRKETAQAMA QLSRWDRGTNHLLENMPLPGGPPDYNTALDVPDRALLAGGGFSTWTY RQGYDVSI PVYSPLSAEVDLPEKGPGRQYFLLSSQVGLHPEYREDL EALQVKHGESVLVLDKCTNLSEGVLSVRKRCHKHQVFDYPQVLQEAT FCVVLRGARLGQAVLSDVLQAGCVPVVIADSYILPFSEVLDWKRASV VVPEEKMSDVYSILQSIQORQIEEMQORARWFWEAYFQSIKAIALAT LQIINDRIYPYAAISYEEWNDPPAVKWGSVSNPLFLPLIPPQSQGFT AIVLTYDRVESLFRVITEVSKVPSLSKLLVVWNNQNKNPEDSLWPK IRVPLKVVRTAENKLSNRFFPYDEIETEAVLAIDDDIIMLTSDLOF GYEVWREFPDRLVGYPGRHLWDHEMNKWKYSEWNTNEVSMVLTGAA FYHKYFNLYTYKMPGDIKNWVDAHMNCEDIAMNFLVANVTGKAVIK VTPRKKFKCPECTAIDGLSLDQTHMVERSECKNFASVFGTMPLKVV EHRA*
4927	A	533	804	HWREEAGLTAQRPDTHCFLYIQENEIYTGNTGCTFGGGVSYKANVAH HQPARGRKVTEPPPRWERDARRPTEPSGLPWPEHTQRACGWS
4928	A	965	1109	PVWATRD CNLQEISTVCQDLCPLPPPNPHCSAQGGGEGDPLFRLTT L
4929	A	1	1337	MASSKLRPVDDEVFDLDAVPETARLDSSSLHKAQQLLAKGRRHRPS RSRLRDSASSAEDGEGSDGPGGKVTDCGSPHLRLRSPHSGPGSPA GGSFCLDPPGLRRSLDEDEPPPSPLTRYRPLHNAASHEGLAAASCSP PRSAPSSDSSPSFVRHPRAEPHSEDDSRDASPPPEASPTIGLDKKT RRKFLDLGVTLLRRASTGKSREKGSNRLSMGSRESVEGSGRSGGSPF LPFSWFTDSGKGSASSGTTSPTCSPKHEGFSPKKSASQAQLLAHAQ EALSNSWCLVQDFGSTQIGMESTLSDDSTPPSSSPKIPSGPWQEAAC SYPYHTLSQSSDEFLEPLPPVHHWTSQQVGQWLQSLNLEQYAAEFA ARQVDGPQLQLDGSKLKSLGLSNSHDRALVKRKLKEMAAAAEKERK AQEKAARQREKLRRREQEAKKS
4930	A	507	981	CWRSTATCYQWVIKSANRCTLQVGTTRRTMDNGDERHSRICPGM*EA ARSLFIPT/CQTRH*RPVPQRLRSNTAPIRT/RPRPSVHRPTGRES MPRTRPPEPEPLQTPLAATKRRSTSENASYS DALLRGLGLSGKDRE ARRGPRSRPGSRVQTAGAAL
4931	A	1121	1272	YDDTNEYFAIKTYFYFKIYIYIYLYICIFLQNYKLCCLMMVSYKKQGG KGP
4932	A	54	245	KSESGSFADASRCDPAHSQVWVLRGETTSA*EEQREE*RGLRLELRY QLSHSGKEHQASSLGP
4933	A	1025	1176	KLFHEKSQCMPMINLCICFLKGEDGEKNRKLADIRGHKMSSSFVQMT FSC
4934	C	178	360	MGQELRHFGTVTWPMHRKMERRXFPREQGPGXQLLPQWRGNEKTLGS AGRQGEDHRLRAE*
4935	A	409	516	YPPPGPLQIMNTHSIPPPPTPYVGFQGGQLKNRWDKN
4936	A	288	573	GLLSSSATHEAHGCHIDLYQQMLRRSHSDFAMGRGRRRAWGEGGREGT RWSPPWMGSLGGLAGLGKNPGNNGTWRSSSVRMPCQGRKASGKIPVVT
4937	B	1	1152	MGSEAGCLVRAERFQLIVERDVRSSFPWKELSMGFIQKQARVYV QFFLADALILPVPRPCLHSATPSTPQTDPTGPEGPHLGQSRLFLLCH KEALMKRNFVPPGASPEVPKPAISFYVLGSWLGGTQRKEGTGWGLP EPQGNDDNDQKVHLIFFGSSVRWFEFLHPGQVYRLIAPGPATPMLFE KDGSSCISRRPLELAGCASCLTVQDNWTLLESSQDIQDVL DANKSL PESSLTDLLSDKSHNVYCCFRSSTYVQVLSFPPETTISIPLPHIYLA ELLQGGQSPFQATASCHIVSVFSLQLFWVCAYCTSI CRQSSARVDEP MTMFLWTLCTSPSVLRPIVLSFELERKPSKIVPLGTSPSRSSSFQPPFA ARAKGGK*
4938	A	409	701	KEKVKNWLLNPLPKAQEFGYPSPLPATLHLKLSRCPCKLQDH/CC

				CHMVIHTGHHGFGSPILHQEPMGSRKYSRL
4939	A	301	573	KKKDSVRPGPPLTLRPFCSRRPPTCPAANSIAAWLGPGSVCCPLPS AQPRFYLGFWWLHLIKVVCNFGTKVVPCACCWPSTLNPSVTHG
4940	A	754	999	MTLGITSFISFYFCFIYIFQYLIIGKKNLTFSVLKFFIIKYISLII ISKEBKNTFKISHWIWKIIMELWFLMSTHISFRY
4941	A	339	494	CVHSQETRGAASTSPGSRRTTSQPSTHSTATTTPPPNRAPPPSRPPP RPSV
4942	A	408	548	CLEVCAGYHHHHHRHHHHQTSLERSKPKCTLGHMALWHSEKYSSC
4943	A	1421	1581	VRAGPLTLKKEHSQFLKLSFQKEMENFEAPFHCLAKRFHQLYREKVE VFRALA
4944	A	1	1113	MHQEDLRAWYLDLGLPSHQNAQPTAWKCQRAPSPYTHQDMALIPSPT ARWLSPEKEPKQGEVGEKSLLPDPTLPLTDPRLTGSTEQAHAEGLAA LMSALRVSHLQGRGGVTVLVDSQLGVIASVSTQFNKGPSYRLLADVQ NRLLPKYDSQKEAELRSWIKGFTGLSIRPDFQKGLKDGIILCTLVNK LQPGSVPKIN\ASV*NWH*LENLSNFLKAMVSYGM/NPVDLFEANNL FESGNNMQVRVSLLAGAKATKGLRSGVDIRDKYSEKQNFDDTTMK ASQCVIRLQITNKCASQSGMTAYGTRRHLYDPKNRILPPMDNSTISL QMGITNKCASQVGMTAPGTQRHIYDTKLIDKCENSSMSLKMGYT
4945	A	272	902	LQHRLLSPALTAETLQPLQLRRLGRNDSSKPAADPSPACTPPA VVHCRWSSALSSSSHPHGLLTAQLSASLPSLLYRWSSQOPTYSWGS AI PVSPVQSLPLSPPKAALSAAPPPGERSAGESNREKRTGRGWLTNTN LQLDRSNEHTYDTKLIDKCDNSSTSLKMGYTQGAHQSGQAFGMGLQ IYDPRYYWGGPVAHGAPSGSGP
4946	A	281	471	TGWSWQCTPSC*TTMCVYTFMTYTAWGCPPNHVQPHA*PVSPTVLL NVGFRAKAVFSGHGYL
4947	A	1192	2248	APSKKLRSATLRRPGSSKDTARGPVSVGWCPSEQEPLGARCATSCPW L CRLPSSVFSRALAIRLGGGSGSLSAGCAARLQGSVPCWPLARLSA SATPLSELRQQPAPPPRCDPGSRLSVPVAPCPAPRAPQPRRLPSGP RFCRCPSLSVCRSLG/PVSPPPQFLPPLCLPRWLARSALGRGETAS QANPRNLCKLAMKFKFFDFGAIFEWSQSFPSPRPVRFPLEPEGS PVPASLPERPSRHPASSSGLQDPGLILCSLCHYLFIRTDYAVVTR AGNGGECVWLQKFPVKLASLMSFGLYIGHFLGVPPANPQAPRTRS FFTPKSVMEPSAVPGTAERVLHPG
4948	A	654	730	VCDPSVMCCPPKVPMSGPRPCSMEE
4949	A	1574	1881	KHLRWPLRTGDSEPPVPRGSSEAEGLPSPTTAGGHGQGSRRPGKV SIRPPGIHHSYFLKCNBPQGLSGMRALCTPLALAWGVPSVRLPGRR GHSPAMQV
4950	A	207	315	SCCRGTACGPESGTTKVPRAHVSREAVAQSGPKPL
4951	B	199	420	MSLPIGIYRRAVSDDTLEDPA PMTPPPSDMGSVPWKPVIPERKYQH LAKVEEGEASLPSAMTLSSAIDSVDK*
4952	A	336	594	HLSVRLVITSFHCALEASAPLGKMSLPIGIYRRAVSDDTLEDPA PM TPPPSDMGSVPWEPVISEKRYQHLAKVEEREASLPSPA
4953	A	401	1301	VAPSKARMSPAHRDYTAGAVSYDDTLEDPA PMTPPPSDMGSVPWKPV IPERKYQH LAKCGGRRGQSTLPCHDPVIKPFDSVDKAPKWVKAKATH VIMNSLITKQTQESIQHFERQAGLRDAGYTPHKGLTTRGDQVPFELA EALHKLKLSQGEVNNRRRGS LHQSPPPQAPLRTPLPKQRPGRWFTSG SSTGLPGPNPSIMDSGSGWIKDKKLCSDKWSLFGPRSLQKYDSGSFA TQAYRGAQKPSPLELIRAQANMAEDPAALKPKPKMDIPVMEGKKQPP RAHNLKPRDLNVLTPTF
4954	A	388	681	PFESICSPIGANESSCCTG IKCVCSRRRCGCTYKANS LIQGE GEM EELTDLVGLCCLKLGFCTHMPCMCVYNCNLEPSGSKNLFSGSFLSKK VIRV
4955	A	272	452	LHWPGSLAAAEFLKGRSPPVRAGLLTMWGLYYVGGLGFSFTEMLS HQLCPTCPNSSPL
4956	A	256	381	EREFCFATQVGGQGGDFGSLNPLTPRLKFFSCLTPPISWITG

4957	A	58	301	VMRLKPSSTGASCNSLVCNMPSWSVTRFWLAAGSRPPPRSHRNAGS LPPGPRSCSAPLSHPHCLRRSGNHRKSSPQTGAE
4958	A	562	1221	RDVAVRCFEVTGLHDVDQGWMAVRKHAKGLHIVPRLLFEDWTYDDF RNVLDSEDEIEELSKTVVQGGKEPAFRWLRGGGLEPAAKPRSALGLI HMLTHFGRGSAPGPAAGPPGSSRLPSPPGTWSWACSRTRSFEQLAPV LGWFSAFIDLTDYFYSAFSLALIAPLSWVRACVPGPGPESPKWRSKN PSWGFNFWLYGTTRPPRMPVSLVVGPPQVHPRH
4959	A	152	358	CGLFKISNTPLVSSIDTTSFKWIPRCNCSYCLCLSCSSHCLNTYHC LNGNYFAIVKKHYQLGLIVGS
4960	A	184	361	GGPFKKTLGGPKFNGGWKGKIFSLKGGVLKTTWGFLEKNLFFGGGKY GPNPPPKFKGFR
4961	A	2017	2406	GSQAVGVSQHHTIPKVPGLDLWLIGGSSGVGCCPAVEEEQQSDMSP FGDQASALWWGPGTRHTGGHSPMDNTNCPQQRARNPLGASSVSSPK IPILKNTISGMLLHQRRFFEIAHLPELSKYRSFHFL
4962	A	198	629	IQSVFVRSSFGLLAVTPACCLLRLISSWVHLSRSLAGLSTLPDQKLS WHAQRNSTHMSRWLRPSRSRIRRI SLAHPAKFGF\RLMVR*SSPCQT STLRRSGLLLSPTCRSELQHPVSPQKGRFLAGQRIRQNSLTNNLFF FLL
4963	A	132	326	YVHCKDLWMDCAHVSSPRKNS*PFHRRHPLQGDKKPLSPRNSSMPA VYPYWL PQRSIRIFQHI
4964	A	3	396	GLGPGRQPRPPWRGPPSAALQVRSSGR*LGGAVLQVRPSKCGPRGG NFAGQERNVADLDDGYARLSNMLLEAYSGADLTQRQFKVLLAILRKT YGWNKPMDRITDSQLSEITKLPVKRCNEAKLELVRMNI IKQGGMFG PNKNISEWG
4965	A	1	2463	MKLCRELSDLVVYTNVAAQDIVDDGTTGNVLSFSETRAHQVVQKS EQFMIYNQQLTRIYPSAYRIDSSNFNPLPYWNAGCQLVALNYQSEG RMMQLNRAKFKANGNCGYVLKPQCMCKGTNPFSGDPLPANPKKQLI LKVISGQQLPKPPDSMFGDRGEIDPFVEVEIIGLPVDCCKDQTRVV DDNGFNPVWEETLTFTVHMPEIALVRFLVWDHDPIGRDFVGQRTVTF SSLPVGYRHVYLEGLTEASIFVHITINEIYGKNRQLQGLKGLFNKNP RHSSSENNSHYVRKRSIGDRILRRASAPAKGRKSKMGFQEMVEIK DSVSEATRDQDGLRRTTRSLQARPVSMVPDRNLLGALSPLVSETAK DIEGKENS LAEDKDGRRK GKASIKDPHFLNFNKKLSSSSSALLHKDT SQGDTIVSTAHSVTEQQLGMSSPRGGRTTSNATSNCQENPCPSKSL SPKQHLAPDPVNPQTQDLHG VKI KEKGNPEDFVEGKSILSGSVLSHS NLEIKNLEGNRGKGRAATSFSLSDVSM L CSDIPDLHSTAILQESVIS HLIDNVTLTNE NEPGSSISALIGQFDETNNQALTVVSHLHNTSVMSG HCPLPSLGLKMPIKHGFCCKGSKSSFLCSPPELIALSSSETTKHATN TVYETTCTPI SKTKPDDDLSSKAKTAALSNLPGSPNTSRGWL PKSP TKGEDWETLKSCSPASSPDLTLEDVIADPTLCFNSGESSLVEIDGES ENLSLTTCYRREGTSQLASPLKLKYNQGMGLPDSWTVVIVIACLGL ATQWGYQAPAWYSGISAKSPVK
4966	A	1	607	MTNTAKILNFGRGNFAGQERNVADLDDGYARLSNMLLEAYSGADLT RQFKVLLAILRKYTGWNKPMDRITDSQLSEITKLPVKRCNEAKLELV RMNI IKQGGMFGPNKNISEWCIPQNEGKSPKTRDKTSLKLGDCYPS KQGDTKDTITKEKRKDYSSSENSGESSDQPENDLSVVKPDAAIQSGSK WGTAEDLTAARVDV
4967	A	1	3105	MTKLVALWREEAENDLSVVKPDAAIQSGSKWGTAEDLTAAEWMFDMV KTIAPSARKPNFAGWANDIRLMRERDGRNHRDIDL RGGSMKNIAAQ MVNFDREQMRRIANNMPEQYDEKPQVQQAQI INASYWQLSRRALAN RDQNEVNEIRRGVLA FRENGINQDGTGNARKPDRRNDHFLPSTRAD LVHGGREENNPLPDRNGQNRGGRDLALFAASLFSGTAPASRGFARLF RSPSPTLTNSPTYELRYPTTRATYPAGVLSIPNKKHTQPSPHMNNV TTDYCLDIKKFEVSEENKVNVLGIEGFTNFMRSACDI FNPLHHE VYQDMQPLCNYYIASSHNTYLTGDQLLSQSKVDMYARVLQEGCRCV EVD CWDGPDGEPVVHGHYTLTSKILFRDVVETINKHAFVKNEFPVIL

				SIENHCSIQQORKIAQYLKGFCDKLDLSSVDTGECKQLPSPQSLKG KILVKGKKLPYHLGDDAEAGEVSDEDSADEIEDECKFKLHYSNGTTE HQVESFIRKKLESLLKESQIRKEDPDSFTVRALLKATHEGLNAHLK QSPDVKESGKKSHGRSLMTNFGKHKTTKSRSKSYSTDDEEDTQOST GKEGGQLYRLGRRRKTMKLCRELSDLVVYTNVAAQDIDDGTTGNV LSFSETRAHQVVQQKSEQFMIYNQKQLTRIYPSAYRIDSSNFNPLPY WNAGCQLVALNYQSEGRMMQLNRAKFKANGNCGYVLKPQCMCKGTFN PFGSDPLPANPKKQLILKVISGQQLPKPPDSMFGDRGEIDPFVEVE IIGLPVDCCKDQTRVDDNGFNPVWEETLTFTVHMPEIALVRFLVWD HDPIGRDFVQRTVTTFSSLVPGYRHVYLEGLTEASIFVHITINEIYG KWSPLILNPSYTIHLFLGATKNRQLQGLKGLFNKNPRHSSSENNSHY VRKRSIGDRILRTASAPAKGRKSKMGFQEMVEIKDSVSEATRQDQ GVLRRTRSLQARPVSMPVDRNLLGALSPLVSETAKDIEGKENSILVQ I
4968	A	1	396	NKKKKRDGDDRWFRVLVSFDEEKRREKAAIEEIKQRLKEEQRLREE RHQEYLKMLAEREEALEEDELDRLVTAKTESVQYDHPNHTVTVTTI SDLDLSGARLLGLTPPEGGAGDRSEEEASSTEKPTKAL
4969	A	67	180	VVNDLVTGEGRRNWSQTSQQKQQRQHAVGTPGEEQQALW
4970	A	2	415	LQGEAGGLTAMGRNKKKKRDGDDRRPRLVLSFDEEKRREYLTGFHK RKVERKKAIEEIKQRLKEEQRLKEERHQEYLKMLAEREEALEEAD ELDRLVTAKTESVQYDHPNHTVTVTTIISDLDSGARAARADPT
4971	A	1090	1203	SVFCQNCSEKAPVSNVSGVFMGKNKTKQKRWLIRPRCC
4972	A	3	356	VQNRTHLHFSLLYEPKRKSKPESYLYCYKIFQDEPLAP*AFL*IPASL SQIQ*FTSRKGKASQNLIIYIVIKYSKMSLWPPEPSCYLPCLKSNS SQLSWLLWCVLVWGVGWKYCQGWGGPPLHLVSLWGGYSASRWEDIGK QHTSLRGVPKGVIFIIYI
4973	B	148	305	MDNSASVEQLQETLLRALRALVLKNRPLDTSRFTKLLKLPLDCGPF SSLGHN*
4974	A	484	927	GREGGLTGWEVTSAPAEPTLPFRHLLLLGQRPGRRYGTPSPSPSAFW GASGRGCIACQVLADLRFLLRGARGVRLTAVVFPTDRSGMENSASVE QLQETLLRALRALVLKNRPLETSRFTKLLKLPLDLRTLNNMHSEKLL SFRVDAQ
4975	A	2053	2615	RGCPFGGRKAPFGLLFNVKDQTMFLSRTTYSLQELGAMGMGDLISA MF\DFSEKLNLSALTEELGLF\TA\VLLVSADR\SGME\NSASVEQ LQE\TLLRA\LRALVLKNRPLETSRFTLLLLKLPLDLRTLNNMHSEKL LVLSGWTAPVTPPRAGLSAGCPLCTESELCTSLSPFYETEKEKQTRIL FILL
4976	A	173	520	VLMVRFASLFNVKDQTMFLSRTTYSLQELGAMGMGDLISAMFDFSE KYNLSALTEELGLFTAVVLVSAGRSGSRLTRGRRQTQFNSTHLLWS TYSMPGPAPGTGVYRHSDTV
4977	A	44	213	RVFCPRLKNFPLPPGKKRFLEKGGKGDWPREGKGPFPPLISPPQSL NPVLFWGFF
4978	A	840	980	KLQVLLPLHWSVLCSPWPTCWNFLTKLILGFSLKQGNPLQNVSQEI
4979	A	72	464	PCPIALPTFKFNIVFKQGFSPFPLTKSNPREGATEMGKTGTGTGILK LQRTGTVPPNETLKKWNPSSRPTLCPQNSCPHPMKHRVNTLAGLRIS GLPGPMGQROGSPRTATWFPSSPATLASLGPPPLLSL
4980	A	1	132	LPRDASREGCRLWDILNQCCSRDLSIDVECSLCCQTGOPLATCG
4981	A	99	212	CARTMGGTPSGWHCCTPAEPSCSPRLCGTHYHHACHH
4982	A	84	196	CARTRGGTPSGWHCCTPAEPSCSPRLCGTHYHHACHH
4983	A	2	186	ECLTSLSSSLQRWHAPPALPAQVNKPHAACFKWQLKASQCWAVLTPL WSSWRGTGSLWGKG
4984	A	87	347	SLNFHIGQ*AOPHAGFLRGS*GPCPPCCQANAC*APEPNDSMEDQA PGVRHPPLSNVKIQGSE
4985	A	176	1554	VFLASLPTISCLGNVAVVESYVLGNCRPSDPYSMNSVYSYHSYYAQP SLTSVNGFHYSKYALPSFSYYGFPSSNPVFPSSQFLGPGAWGHSGSSGS

				FEKKPDLHALHNSLSPAYGGAELPSQAVPTDAHHTPHHQQPAY PGPKEYLLPKAPLLHSVSRDPSFPAQSSNCYNRSIKQEPVDPLTQAE PVPRDAGKMGKTPLSEVSQNGGPSHLWGQYSGGSPMSPKRTNGVGG WGVFSSGESPAIVPDKLSSFGASCLAPSHFTDQGWGLFPGEQQQAAS HSGGRLRGKWPSPCKFGNSTSALAGPSLTEKPWALGAGDFNSALKGS PGFQDKLWNP MKGEEGRIPAAGASQLV FYQHKNLNQPNHGLALWEAK MKQLAERARARQEEAARLGLGQQEAKLYGKRWGGTVVAEPQQKEK KGVVPTRQALAVPTDSAVTVSSYAYTKVTGPYSRWI
4986	A	1	1863	GGGRAPPGVFAEPEGASGASVPAAGGPERLEERSGNWEELARLEG GPLRPGAGSQAPLGAKPRVFSQSQFHTRLCVPGIPWRGAHLRGGM SEKSLTLAAPGEVRGPEGEQQDAGDFPEAGGGGGCCSSERLVINISG LRFETQLRTLSTLFPDPTLLGDPGRRVRFFDPLRNEYFFDRNRPSFDAI LYYYQSGGRLRRPVNVPLDIFLEEIRFYQLGDEALAAFREDEGCLPE GGEDEKPLPSQPFQQRQVWLLFEYPESGPARGIAIVSVLVILISIVI FCLETLPQFRVDGRGNGGVSRSVSPVSRGSQEEEEDEDDSYTFHHG ITPGEMGTGGSSSLSTLGGSFPTDPPFLVETLCIVWFTFELLVRFSA CPSKPAFFRNIMNIIDLVAIFPYFITLGTTELQQQEQQPASGGGGQN GQQAMSLAILRVIRLVRFRIFKLSRHSKGLQILGKTLQASMRELGL LIFFLFIGVILFSSAVYFAEADDDDSLFPSPIDAFWVAVTMTTVGY GDMYPMTVGGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHRETEQE EQGQYTHVTCGQPAPDLRATDNLGKPDFPEANRERRPSYLP TP HRA YAEKRMLTEV
4987	A	1171	2784	WRGAHLRGGMSEKSLTLAAPGEVRGPEGEQQDAGDFPEAGGGGGCC SSERLVINISGLRFETQLRTLSTLFPDPTLLGDPGRRVRFFDPLRNEYF FDRNRPSFDAILYYYQSGGRLRRPVNVPLDIFLEEIRFYQLGDEALA AFREDEGCLPEGGEDEKPLPSQPFQQRQVWLLFEYPESGPARGIAIV SVLVILISIVIFCLETLPQFRVDGRGNGGVSRSVSPVSRGSQEEEE DEDDSYTFHHGITPGEMGTGGSSSLSTLGGSFPTDPPFLVETLCIVW FTFELLVRFSA CPSKPAFFRNIMNIIDLVAIFPYFITLGTTELQQQEQ QPASGGGGQNGQQAMSLAILRVIRLVRFRIFKLSRHSKGLQILGK TLQASMRELGLLIFFLFIGVILFSSAVYFAEADDDDSLFPSPIDAFW WAVVTMTTVGYGDMYPMTVGGKIVGSLCAIAGVLTIALPVPVIVSNF NYFYHRETEQE EQGQYTHVTCGQPAPDLRATDNLGKPDFPEANRER RPSYLP TP HRAYAEKRMLTEV
4988	A	176	464	NALRIPRGLLAFYSVLSIKISIPFFTNKRGFFNPKEGLQAGKRGR QWWVKSPVPSRTCHQHHLPRKTPSPACGPLPLPPGYPPFIAFDKI NI
4989	A	1	2190	MPEPPAPGSCAARASKTSAAPGSTAPSP IHR SRAEERGT TARNWQA APTAAPVRDPLGEASWAPESANLVGIWRTFVSSSGIVNAPISTLSKR TNQLSVKQTNRLSVKWTNQQDVARGSATYREGEHGCWLLAPGGFRAL QLDNCRDGV CVR DPLRQVLGEAPPLQLACRFPPTAASPERGPGE KRVCGKDVSEVTHCTHDLHATLEDSDVSSQLDRQQENWKRLHLS ASTQKKIITPQENFEQNKFGENSRLNTNLVTQLNIPARIRPSECETL GSNLGHNADLLNENNILAKKKPYKCDKCRKAFIHRSSLTKEKTHKG EGAFPNGTDQGIYPGKHHECTDCGKTFLWKTQLTEHQRIHTGEKPF ECNVCGKA FRHSSSLGQHENAHTGEKPYQCSLCGKAFQRSSSLVQHQ RIHTGEKPYRCNLGSRFRHGTSLTQHEVTHSSEKPFQCKEKGKAFS RCSSSLVQHERHTHTGEKPFECICGRAFGQSPSLYKHMRIHKGKPYQ SSNYSIDFKHSTSLTQDESTLTVEVKS YHCNDCGEDFSHITDFTDHQR IHTAENPYDCEQAFSQQAISHPGEKPYQCNVCGKAFKRSTSFIEHHR IHTGEKPYECNECGEAFSRSSLTQHERHTHTGEKPYECIDCGKAFSQ SSSLIQHERHTHTGEKPYECNECGRAFRKKTNLHDHQRIHTGEKPYSC KECGKNFSRSSALTKHQRIHTRNKL
4990	A	7	396	HHELQYPIRFCPIKSCCKGRNSLQNKIYDLSLQNFPPATLRQNLALS PRLECSGTISAPCNLHLPSSSDSPASASRV\AGNAGMHCHKQ\LIFV FLVETGFHHVAQAGLRTP*PCGSGPPRGPKSAGDLQ

4991	A	1	2201	MTNLMAMVERDSEAGTAASRFPGNHAAKGKAQAHYKVRPAEVRCLKL GPEWVTLLRYTIKHPYKLCGKRQHVFVFTSRSDVGFMLTTLKPFSGV SVESKMNNKAGSFFWNLRQFSTLVSTSRMRLCCLGLCKPKIVHSNW NILNNFHNRMQSTDIIRYLFQDAFIFKSDVGFQTKGISTLTALRIER LLYAKRLFFDSKQSLVPVDKSDDELKKVNLNHEVSNEDVLTKETKPN RISSRKLSEECNSLSDVLDAFSKAPTFPSSNYFTAMWTIAKRLSDDQ KRFEKRLMFSHPAFNQLCEHMMREAKIMQYKYLPSLHAIVKLGIPQ NTILVQTLRLRVQERINECDEICLSVLSTVLEAMEPCKNVHLRTGF RILVDQQVWKIEDVFTLQVVMKCIGKDAPIALKRLKLEMALRELDRE SVLNSQHMFEVLAAMNHRSLILLDECSKVVDNIGHCPLRIMINILQ SCKDLQYHNLDLFKGLADYVAATFDIWKFRKVLFILILFENLGFRPV GLMDLFMKRIVEDPESLNMKNILSILHTYSSLNHVYKCQNKEQFVEV MASALTGYLHTISS\ENLLDAVYSFCLMNYFPLAPFNQLLQKDIISE LLTSDDMKNAYKLHTLDTCLKLDLTVYLRDIALSLPQLPRELPSSHT NAKVAEVLSSLLGGEGHFSKDVHLPHNYHI\DFEIRM\DTNR\NQVL PL/SLDVGTTSAT\DIQRLTYISFAGLSELKS
4992	A	3	485	LHTLDTCLKLDLTVYLRDIALSLPQLPRELPSSHTNAKGGQRS*AAL LGEGTTPPSKDV\HLAPHNY\HIDFEIQNGTPNRNPSAYPLS\DVDT TSCLQIFKE*LCYVFPRSAICLSSHPRGFLAMKMRHLNAMGFHVIL VNNWEDGQTRDGRCSPLKT
4993	A	40	131	ATKAFEENEVYKTTLVVYCFKCVILKASL*FRILLTEWFYMRWLKK YHIVCF/PLGDAKIFCFMYITVLFKLTLEDSC*TLVVYCFKCVILKA SL
4994	A	2437	2762	GIILFWAQLFPASFFFFF*DGVSLLCCPGWSAVVRSQLTASSASRV QAILCLSLPSSWDYRHLPPCLANFFVFL/CRDGGFTMLARLVLS*A S*VHPPWPPQSGDY
4995	A	1	299	FSLIKISMMLLMKMEK*NLQFIW/KPRRLQIAKARLNASSSSSSSS SSSSSSSSSVVWYWHKKRHIDHWNRLSNSINRHICSQILTKVPGA NTKDH
4996	A	3	358	STSHLSPLAGSRALSSSSPRVARSDMAVAQVLGTDGNRRGCTSSWE ALEDQVGEDRHQGESGRPTRVRQEWVWSGQRHPPAKIKGKPSHTPR HVHEAPSPFPFPFRTLSLSLSEF
4997	A	76	388	VLPPPSSPALHSPAPPSTCPYLPGA/PPPLPPCAGRSPAAAAPH PAPCAPRH*GSR*LESPAPQGPQSRARMPAWPLPPAPPTDPTAPPA PRSHWPAAPT
4998	A	66	381	VLPPPSSPALHSPAPPSTCPYLPALPPL/PPSRPPRTFIGNPG GQGPGEVSPIVLRSPSQPH*PGNQGPCSSQPPGSPRSEHGC*HRCW ALYGQKEKPAPS
4999	C	36	236	MGPTIPDXSXFWRKPIITWMPTEGTSNVGPQPLSSSKSLHSXRGHP APIPTGQAGPRDSGPGASP*
5000	C	231	521	MRAPVCQSQSVYFTQTISLKPTITVPGRCDAFQVTNNKLAQATQSEG VAGASNPDLESHEPAHGMQREFSGVTAVSQADTMVNYPVSNWENRG SG*
5001	A	46	1438	LSTPTALVWPGHRPP*PIP*WPLCPQEGGPGGLPRGWSSGTVAP*S* AGGCEGKIQSYPPQSASWSEPAPSPS/PAPFAPFLMLNCSGLALSL SGPKWAREQL*CVPPRALATGLPLEVWL*LRPFPWP*CLPPPG/PWV QLLHSLSSCWGPPMPRTIRGIPPGSICRLCFCPAAGL/PPWWLSSG QLPHPPGTPLCSVS*GGPDQPPLLCLSPWAPGLSSTALCHSRVLPA TPIPVVTWPSCGLSTT/PPAPGATPTAACFQOVPSAPDKPLLVS PAKHPPVPPVGLGLRAMDR/PPGPIPETPRD/LPCHPTPPKSKLQA RGPWPWVD*TTSGWKLRKEALMGPTIPDPKSSSWAGPLVSLPLVLG GNPSPWNALRGKRDPRKCGNPQPPSPKLRKSPPTA\PGKTPAPYSPR EKAGPQKTLGPRGPPP*SRDPPL*L\RTPADPGVTRGAGPPAPRR NP
5002	A	1	874	LDDALESCDEHYRTASSCLRKGVMVKSSSNRELVSRYTDITI/S GSTSEFPDWAAGQGRSSHPRRWAARQRRSSLHLFYSEPDTDAKHQDD

				ALTEEET*G/SRSASCAHWL*SNCCTATGSSTLLPLTSRL*LPRMAV KSSRASAALPSSRFSSWHRACASAPAAATTAAPSAGLSSNIPSGPA GCAPRPPTSFSPLPGALPTTTRRRHSS\DRSRRSPSRGLTSARESGSK SPPQG/TARDSRQALRSAMVTKTSWRMELDREGRSSCTSTFCVSAA SRGFLLQTSFRWE
5003	A	1	2487	MLRSLRLQEWLEWEDRRRAAAQCCRSRRCPSSPRARLTRPHRSCR PAVHQALFSGNLQQVQALFQDEEAANMIVETVSNQLAWSAEQGFVWL TPKTKQTAPLAIATARGYTDCAHLIRQGAELDARVGGRAALHEACA RAQFDCVRLLLTFGAKANVLTTEGTTPLHLCTIPESLQCAKLLLEAG ATVNLAAGESQETPLHVAAAARGLEQHVALYLEHGADVGLRTSQGETA LNTACAGAEGPGSCRRHQAAARRLLEAGADARAAGRKRHTPLHNACA NGCGGLAELLRLRYGARAEPNGAGHTPMDCALQAVQDSPNWEPEVLF AALLDYGAQFVRPEMLKHCANFPRALEVLLNAYPCVPSCETWVEAVL PELWKEHEAFYSSALCMVNQPRQLQHLARLAVRARLGSRCRQGATRL PLPPLLRDYLHMKRSRCRDRPQPPPPDRREDGVQRAAELSQSLPP RRRAPPGQRLEERTGPAGPEGKEQPPALASQSAEIAASARLPRLG SEERLCLAAHRLGCPEPLCLAAQSGNLGDNGLPAGRQELKQGTHEET TALAQVRAEGLPVLVWMETEDLQVMSFRISLSRHGPKPSHPKSDSFS LAGSKSLLPFKDLKHTVNDEEGRWSAIPDTDGPSARAGGQTDPEQEE GPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSL PLTTNYRDNVISPDAAATEEPRTFTFGKAEAPELSPTGTRLASTFV SEMSSLLEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSASG MKVQGDGPGKGTGTEKSRGSSSSSSSSSRCL
5004	A	227	2119	RCRKEMFSLCWAYYCI*KLQQIPMLAPLPTLDPV*SP/GGASTATN SGSSVTSSGVSTATISGSSVTSNGVSIVTNSEFHTTSSGISTATNSE FSTASSGISIATNSESSTTSSGASTATNSESSTPSSGASTATNSDSS TTSSGASTATNSDSSSTTSSEASTATNSESSTTSSGASTATNSESSTV SSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSESSTTSS GASTATNSESSTPSSGAGTATNSESSTTSSGAGTATNSESSTVSSGI STVINSSESSTPSSGANTATNSESSTTSSGANTATNSDSSSTTSSGAST ATNSESSTTSSGASTATNSESSTTSSGASTATNSGSSTTSSGTSTAT NSESSTVSSGASTATTSESSTTSSGASTATNSESSTVSSGASTATSEAK ESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAK PGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVVSACVPLCECRDALK MPGGLEQLLTESRIVHWGTEGRPIATAEGWVLLLAMKIRLAAEAKIK CFLDGMAGLRRSSLSRLGSQAEALPTSQTMGGQAEILLSSQTGSRP NRGLFSLRRAAGQRRSLTS
5005	A	124	670	FQRTKLLNGPGDVETGTSITVPQKKWLHVISPIFVQS\LTLPLAKW GDRLQLLQIELAAREVSDI*EETV*NETYLLLLCSRKTLDLTKWAHS IPSYARLFYI**FSCSLKLAFSQFLPA\DPYGVAVGGTVGHCLCTG LAVIGGRMIAQKISVRTVTIIGGIVFLAFAFSALFISPDSGF
5006	A	3	273	AAAPGNRASAPRLLLLFLVPLWAPAAVRAGPDEDLSHRNKEPPAP AQQLQPQPV\AVQGPEPARVEVSGPGWGERGCRAGCAEYQAPGL
5007	A	2	986	AAAAPGNRASAPRLLLLFLVPLWAPAAVRAGP\DEDLSHRNKEPP APAQQLQPQPV\AVQGPEPARVEKIFTPA\APVHTNTEDPATQ\TNL G\FIHAFVAAIS\VII\VSELG\DRTFVIAAIMAMRYNRPGPCWAGA MLCL/AGLMTCLFS/VLFGYATTVIPRGLYILMFQPVLFIFGIRML REGLK\MSPDEGQEELEEVQA\ELKKKDEEFQTK\LLNG\PGDVET GTSITVP\QKKW\LHFISPIFGQALTLTFLAEWGDERS*\LTTIVLAA REDPYGVAVGGTVGHCLCTGLAVIGGRMIAQKISVRTVTIIGGIVFL AFAFSALFIS
5008	A	2	439	GVEKLVLKLYEEGSNKRLFNVDHRVGMAGLLADARSLADIAREE ASNFRSNFGYNIPLKHLADRVAMYVHAYTLYSAVRPFGCRIYIVHDA VKDKAFELELSWVGELTNGRHEIVPKDIREAEKYAKESLKEEDES DDNM
5009	A	3	366	RDSVVEILFEQDNKEQSVATLILDSLIQCPIDTRKQLAENLEMMFDV

				GKTQPLLKRAFSTEK*KFD*/TINLASYQIFNQL*ANCTKYVGCVF IEDYSGSESILCLLFALIYNSFDFVSLV
5010	A	387	446	HLLQHLLYFKFLLQSNVTI
5011	B	16	348	MVLDCGYRESLVLPIYEGIPVLNCGALPLGGKALHKELETQLEQC TVDTSVAKEQSLPSVMGSVPEGVLEDIKARTCFVSDLKRLKIQAAK FNIDGNNERPSPPPKC*
5012	A	1	595	MGCRPVGQAGLELLTSARTCFVSDLKRLKIQAAKFNIDGNNECPID TRKQLAENLVVIGGTSMLPGFLHRLLAELIRYLVEKPKYKALGKTFT RIHTPPAKANCVAWL/GKVFVGI*QVEYAMKAVENTSSTAIGIRCKD GVVLGVRKISPF
5013	A	3	461	YIEDDMNPFQGNLE\EQRPKSKTFL*QGAAEQIKHILANFKNYQ\F FIGENMIS\DGM\VLLEDYVKGWVCPYMIFFK\DGLDMDKMLNKC KLFWIYHPVIHNWASALSSHTTTRDLRQNWTDCHPGALPFILDWGFY LGVGGHCFYEKPCPW
5014	A	3	325	RRVSSVTQAGVQWHGLGSLQPPPPGFKLFCLSLPRSQDYRCMPRPA NFC/IFLVETGFHPAH*DKLVSNS*PCGPPAPASQSAGITGVT/HRA HLPCNV/C*LDLFHHV
5015	A	1593	4449	PSGLGNTCIYRRGPHLPNSHRHAARGRISADRRFRHLGHRHLPAPC VPGRGEPHPAPCVPGHGLHPALCVPGRGQLHSVPCIPGRGEPH/RC TLCPRSWA/RCTLHPRDLRFNRIREIQPGAFRRRLNLTLLNNNQI KRIPSGAFEDLENLKYLYLYKNEIQSIDRQAFKGLASLEQLRLDSNT LHCDCEILWLADLLKTYAESGNAQAAAICEYPRRIQGRSVATITPEB LNCERPRITSEPQDADVTSGNTVYFTCRAGNPKPEIIWLRNKSLE HAAADTGSLSSRVDLTCLPNKGSLLCPQTCCGPVKAKTALAAAVRV TEGSPTADHYMRPGSEPHLSSSLTCRLALPNIQSHLQATLTCLWAVFL TGISVASNVTSLLFTCFIKGTKVKLQVGNELSMKTD SRLNLDDGT LMIQNTQETDQGIYQCMAKNVAGEVKTQEVTLRYFGSPGSFLGNVC TSSVSVCATSLQPQNTQEVLVGESVTLECSATGHPPPRISWTRGDR PLPVDPRVNITPSGGLYIQNVVQDGSGEYACSATNNIDSVHATAFI VQALPQFTVTPQDRVIEGQTVDFQCEAKGNPPVIAWTKGGSQLSV DRRHVLVSSGTLRISGVALHDQGGYECQAVNIIGSQKVVAHLTVQPR EEEAPLCFLLRESGSPQSLLSSVGPAAQHMPETAPPSFFDVIDSFSW ILYICLPVTPVFASIPSDTTVEVGANVQLPCSSQGEPEPAITWNKDG VQVTESGKFHISPEGFLTINDVGPADAGRYECVARNTIGSASSGVST CCKKMVQKGRVGPVITNSRRHLVVRANAFVGTLSVLSQTYRDA MRKFPAEEHLPDVS RNGDPFVAT'SIVEAIATVDRAINSTRTHLFD RGAVNTLTLSLFRVKGTSPMPVIVLGQGLQSQTEEIKTSALKDQT FQRNADGKPERGPCT
5016	A	1	3174	GPCVAVSVSWVCPSHAICEVWSSGLGFLHGHKNPSLGWSCGKLLVAG GPPFIQPSGSAGAGGEWVLVEWVLVERVLVESGCWWRVGAGGVGAGG EWMLVESGCWWSGCWWSGCWWRVGAGGAGAGGAGAGGEWVLVEWVLV ESGCWWRVGACGAGAGRV DAGGAGAGGEWVLVERVLVERVLVESGCW WRVGAGGAGAGRV DGGVAGGEWVLVERVLVERVLVESYHYNDLVS PQYLNLIANLSGCTAHRRVNNSCDMCFHQKYRTHDGTNNLQHPMWG ASLTAERLLKSVYENGFTNPRGINPHRLYNHALPMPRLVSTTLIG TETVTPDEQFTHMLMQWGQFLDHDLDSTVVALSQARFSDGQHCSNVC SNDPPCFVSMIPND SRARSGARCMFFVRSSPVCSGGMTSLLMNSVY PREQINQLTSYIDASNIVYGSTEHEARSIRDLASHRGLLRQGIQVRS KPLLPFATGPPTECMRDENESPIPCFLAGDHRANEQLGLTSMHTLWF REHNRIATELLKLNPHWDGDTIYYETRKIVGAEIQHITYQHWLPKIL GEVGMRTLGEYHYDGPINAGIFNAFATAAFRFGHTLVNPLLYRLDE NFQPIAQDHLPLHKAFFSPFRIVNEGGIDPLLRGLFGVAGKMRVPSQ LLNTELTERRLSMAHTVALDLAAINIQRGRDHGIPPYHYDYRVYCNLS AAHTFEDLKNEIKNPEIREKLRLYGSTLNIDLPALVEDLVPGSR LGPTLMCLLSTQFKRLRDGDRWYENPGVFSPAQLTQIKQTSLARIL CDNADNITRVQSDVFRVAEFPHGYGSCDEIPRVDLRVWQDCCEDCRT

				RGQFNAFSYHFRGRSLEFSYQEDKPTKTRPRKIPSVGRQGEHLSN STSAFSTRSDASGTNDFREFVLEMQKTIIDLRTQPRDQVYIPQAAVR VDSVWQVLLPPQPRDQVYIPQAAVRVDSVWQVLLPPQPRDQIKKLES RLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPAT CAVPVNI PGACCPVCLQKRAEEKP
5017	A	1	4759	SRPWLRASERPSAPSAM\AYRSRGPGRRCLLALVLFCAWGTLAVVA QKPGAGCPSRCLCFRTTVRCMHLLEAVPAVAPQTSILDRLFRNIRE IQPGAFFRLRLNLTLLNNNQIKRIPSGAFEDLENLKYLYLYKNEIQ SIDRQAFKGLASLEQLYLHFNQIETLDPDSFQHLPLKLERFLHNNRI THLVPGTFFNHLESMKRLRLDSNTLHCDCEILWLADLLKTYAESGNAQ AAAICEYPRRIQGRSVATITPEELNCERPRITSEPQDADVTSGNTVY FTCRAEGNPKPEI IWLRRNNELSMKTD SRLNLLDDGTLMIQNTQETD QGIYQCMAKNVAGEVKTQEVTLRYFGSPARPTFVIQPNTEVLVGES VTLECSATGHPPPRISWTRGDRTPLPVDPRVNITPSGGLYIQNVVQG DSGEYACSATNNIDS VHATAFIIVQALPQFTVTPQDRVIEGQTVDF QCEAKGNPPPVIWTKGGSQLSVDRRHLVLSSTLRISGVALHDQGG YECQAVNIIGSQKVVAHLTVQPRVTPVFASIPSDTTVEVGANVQLPC SSQGEPEPAITWNKDGQVQTESGKFHISPEGFLTINDVGPADAGRYE CVARNTIGSASVSMVLSVNVDPVSRNGDPFVATSIVEAIATVDRAIN STRTHLFDSPRSPNDLLALFRYPRDPYTVEQARAGEIFERTLQLIQ EHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCTAHRVNNCSYD MCFHQKYRTHDGTNNLQHPMWGASLTAFERLLKSUYENGFTNPRGI NPHRLYNGHALPMPRLVSTTLIGTETVTPDEQFTHMLMQWGQFLDHD LDSTVVALSQARFSDGQHCSNVCSNDPPCFVSMIPPND SRARSGARC MFFVRSSPVCSGMTSLLMNSVYPREQINQLTSYIDASNVYGSTEHE ARSIRDLASHRGLLRQGIQVRSQKPLLP\FATGPTECMRDENESPI PCFLAGDHRANEQLGLTSMHTLWFR\EHNR IATELLKLNPHWDGDTI \Y\YETRKIVGAEIQHITYQHWLPKILGEVGMRTLGEYHG\YDPGIN A\GIFNAFAT\AAFRFGHTLVNPLLLPGLDENF\QP\IAQDHLPLHK AFFSPFGIVNEGGIDPLLRGLFGVAGKMRVPSQLNTELTERL\FSM AHTAALDLAGINIQRGRDHGIPPYHDIRVYCNLSA\AHTFEDLKNEI KNPEIREKLKRLYGSTLNIDLFPALVVEDLVPGSRLGPTLMCLLSTQ FKRLRDGDRWLWYENPGVVFSPAQLTQIKQA*LARIYDNADNITRVQS NVFRVLEFPHGVDSCDEILRVDLRVWQDCCEDCRTRGQFNAFSNHFR DRRSLEFSYQEDKPTKNTRPRKIPSVGRQGEHLSNSTSAFSTRSDAS GTNDFREFVLEMQKTIIDLRTQIKKLESRLSTTEC\VDAGAESHANN \TK*KK\DACTICECKDGQVTCF\VEACPP\AT\CAVPVNI PGAC\C PVCLQK\RAEEKAPRLPGEAPSEFCLACAI VRSGGRWQGAADLQTRK HPELRDISLTTSKLGAVYRKAVQEGFPTRAFCGEGRHSRCWKGSRQBS S
5018	A	2	267	ADLSAEAL*TRREWDDIFKVLKTSS/LGQPKILYPSKLSLINEASSS SSSSSSS/REFTTRLVL*EMLKGILHMEAQQGYLPS*KHTKV
5019	A	1	164	TRVNNQIESKAAYALFYKRQDVARRLLSPAGS/SGAPASPACSSPP SSEFMDVN
5020	A	1	712	EILIIHLKRFSYTKFSREKLDLVEFPPIRSGARERMAGGRQGKEGVY QY*PSPHPQ\DLDFSEFVIQPNESNPELYKYDLIAVSNHYGGMRDG HCMCQAVGGACPGSGQGGDQDLPSE*LGM*ASGEGSSVVGK*TRS EIWTLSEEARKGRR*LSFPFR\TTFACNKDSGQWHYFDDNSVSPVN ENQIESKAAYVLFYQRQDVARRLLSPAGSSGAPASPACSSPPSSEFM DVN
5021	A	3	3090	IPLLQLLLRLWRRHGRWTEDEPQHEELPGLDSQWRQIENGESGRE RPLRAGESWFLVEKHWYKQWEAYVQGGDQDSSSTFGCINNATLQDE INWRLKEGLVEGEDYVLLPARAWHYLVSWYGLEHGQPPIERKVIELP NIQKVEVYPVELLLVRHNDLGKSHTVQFSHTDSIGLVLR TARERFLV EPQEDTRLWAKNSEGLDRLYDTHITVLDALETGQLIIMETRKKDG TWPSAQLHVMNNNMSEEDDFKGQPGICGLTNLGNTCFMNSALQCLS

				NVPQLTEYFLNNCYLEELNFRNPLGMKGEIAEAYADLVKQAWSGHHR SIVPHVFNKVGHFASQFLGYQQHDSQELLSFLLDGLHEDLNRVKKK EYVELCDAAGRDPQEVAAQWQNHKRRNDSVIVDTFHGLFKSTLVCP DCGNVSVTFDPFCYLSVPLPISHKRVLEVFFIPMDPRRKPEQHRLVV PKKGKISDLCEVALSKHTGISPERMMVADVFSHRFYKLYQLEEPSSI LDRDDIFVYEVSGRIEAEIEGSREDIVVPVYLRETRPARDYNNSYYGL MLFGHPLLVSVPRDRFTWEGLYNVLMYRLSRYVTKPNSSDEDDGDEK EDDEEDKDDVPGPSTGGSRLRDEPEQAGPSSGVTRNCPFLDNCLGT SQWPPRRRRKQLVQLQ\TVNSNGHNRLHHSPTKSNAPVHCYSTWK P\EMKK\RYYDE*EGEGLREGNAFRRGYV*RKAPVRLQECIELFTTV EPPPFGGK\EREKPW\YCP\SCKQHQLAT\KKL\DLWM\LPEILIIH LKTFPPYTQVLPEKKLEHPSWKFPYPGTLDIFS*/EFVIAHQNEVEI RELYK\YDLI\AVS\NH\YGMRDGTLTQHLACNKDSGQWHLLLDN SVFPLFN*GIQIRVPRAAYVL\FYQRQ\DTLARLLSPCRAHLAPSV LPLGHAPSPQLVSSCDVILRALGPAPEKKKKKALSAILLVSAPLL FVLGAPARHCRLSRGYCSVPVPLNRSPLPGKNRSCLLAVRAPPCVCS SSDPPF
5022	A	1	1584	MTISTAIPAPTDLKTQVTPSTLSAQWTPPNVQLTGVRVRVTPKEKT GPMKEINLAPDSSSVVSGLMVATKYEVSVYALKDTLTSRPAQGVVT TLENVSPRRARVTDATETITISWRKTETITIGFQVDAVPANGQTP IORTIKPDVRSYTTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTGL EPGTEYTIYVIALKNNQKSEPLIGRKTDELPLVTLPHPNLHGPEI LDVPSTVQKTPFVTHPGYDTGNGIQLPGTSGQQPSVGGQMI FEEHGF RRTTPPTTATPIRHRPRPYPPNVGEEIQIGHIPREDVDYHLYPHGPG LNPNASTGQEALSQTTISWAPFQDTSEYIISCHPVGTDDEPLQFRVP GTSTSATLTGLTRGATYNVIVEALKDQQRHKVREEVTVGNSVNEGL NQPTDDSCFDPYTVSHYAVGDEWERMSES GFKLLCQCLGFGSGHFR DSSRWCHDNGVNYKIGEKWDRQGENGQMMSCCTCLGNGKGEFEFTRNS GLGSSIWESLI
5023	A	1	3519	MLRGGPGGLLLLAVQCLGTAVPSTGASKSKRQAQQMVPQSPVAVSQ SKPGCYDNGKHQYINQQWERTYLGNALVCTCYGSGRGFNCEKPEAE ETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRC HEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCCKPIDRCNDQ DTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGWEWKERHTSVQTTSS GSGPFTDVRAAVYQPQPHQPPPYGHCVTD SGVVYSVGMQWLKTQGN KQMLCTCLGNGVSCQETAVTQTYGGNSNGEPCVLPTTYNGRTFYSC TEGRQDGHLCWSTTSNYEQDQKYSFCTDHTVLVQTRGGNSNGALCHF PFLYNNHNYTDCTSEGRDNMKWCGTTQNYDADQKFGFCPMAAHEBI CTTNEGVMYRIGDQWDKQHDGMHMRCTCVGNRGGEWTCIAYSQLRD QCIVDDITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQD SETGTFYQIGDSWEKYVHGVRVYQCYCYGRGIGEWHCQPLQTYPSSSG PVEVFITETPSQPNSHPIQWNAQPSHISKYILRWRPNKNSVGRWKEA TIPGHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSTNTVTGETTFFSPLVATSESVTEITASSFVSVWSASDVTSGFR VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDE QSLILSTSQTAPDAPPDITVDQVDDTSIVVRWSRPQAPITGYRIVY SPSVEGSSTELNLPETANSVTLSDLQPGVQYNITIYAVEENQESTPV VIQGETTGTPRSDTVPSPRDLQFVEVTDVKVTIMWTPPEASVTGYRV DVIPVNLPGEHGQRLPISRNTFAEVTGLSPGVTYFKVFAVSHGRES KPLTAQQTTKLDAPTNLQFVNETDSTVLVRWTPPRAQITGYRLTVGL TRRGQPRQYNVGPVSKYPLRNLQPASEYTVSLVAIKGNQESPKATG VFTTRHHSRPMKSGMNTPWRTLHMRCSLSHPGFITHSERLCVPKIH CEWLYVLITHYECTCPLPTMSGCACPSPAVGGCASVTCRGWLCMYVT RRGWLCVSVTCRGWLCVSVACHGWLCMFCPHHHLGLQHFALGHGG
5024	A	3	673	LDAPTNLQFVNETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYN VGPSVSKYPLRNLQPASEYTVSLVAIKGNQESPKATGVFTTRHHSR

				KMSGMNTPWRTLHMHRCSLSHPGFITHSERLCVPKIHCEWLYVLITH YEECTCPLPTMSGCACPSPAVGGCASVTCRGWLCMVVTRRGWLCVSVT CRGWLCVSVACHGWLCMFCPHHHLGLQHFGALGHGG
5025	A	3	2383	QTEMTIEGLQPTVEYVVSUYAQNPSGESQPLVQTAVTNIDRPKGLAF TDVDVDSIKIAWESFQGGVSRVRYVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFTQVT PTSLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSSSVVVS LMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRRARVTDATET TITISWRKTETITIGFQVDAVPANGQTPIQRTIKPDVRSYITITGLQ GTDYKIYLYTLNDNARSSPVVIDASTAIDAPSNLRLATTNPNLLVS WQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEY TIYVIALKNNQKSEPLIGRKKTDLPQLVTLPHPNLHGPEILDVPST VQKTPFVTHPGYDTGNGIQLPGTSGQQPSVGQQMIFEEHGFRTTTP TTATPIRHRPRPYPPNVGEEIQIGHIPREDVDYHLYPHGPGLNPNAS TGQEALSQTTISWAPFQDTSYIISCHPVGTDEEPLQFRVPGTSTSA TLTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPTDD SCFDPYTVSHYAVGDEWERMESGFKLLCQCLGFGSGHFRCDSSRW HDNGVNYKIGEKWDRQGENGQMMSCCTCLGNGKGEFKCDPHEATCYDD GKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCRPPGGEPSPEGT TGQSYNQYSQRYHQRTNTNVNCPICEFMPPLDVQADREDSRE
5026	A	2	2349	TFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPAVPPPTDLRFTNIG PDTMRVTWAPPPSIDLTNPLVRYSPVKNEEDVAELSISPSDNAVLT NLLPGTEYVVSVSVEYQHESTPLRGRQKTGLDSPTGIDFSDITANS FTVHWIAPRATITGYRIKHHPEHFSGRPREDRVPHSRNSITLNLTP GTEYVVSIVALNGREESPLLIGQQSTVSDVPRDLEVAATPTSLNIS WDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDY TITVYAVTGRGDSPASSKPIISINYRTEIDKPSQMQVTDVQDNSISVK WLPSSSPVTGYRVTTTPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEY VVSUYAQNPSGESQPLVQTAVTTIPAPPTDLKFTQVTPPTSLSAQWTP NVQLTGYRVVTPKEKTGPMKEINLAPDSSSVVVSGLMVATKYEVSV YALKDTLTSRPAQGVVTTLENVSPRRARVTDATETTITISWRKTET TITIGFQVDAVPANGQTPIQRTIKPDVRSYITITGLQPGTDYKIYLYTL NDNARSSPVVIDASTAIDAPSNLRLATTNPNLLVSWQPPRARITGY IIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIYVIALKNNQ KSEPLIGRKKTVQKTPFVTHPGYDTGNGIQLPGTSGQQPSVGQQMIF EEHGFRTTTPPTATPIRHRPRPYPPNVGQEALSQTTISWAPFQDTS EYIISCHPVGTDEEPLQFRVPGTSTSATLT
5027	A	1	7338	MLRGPGLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVSQ SKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGSGRGFNCEKPEAE ETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRC HEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFD HAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCTSRNRCNDQD TRTSYRIGDTWSKKDNRGNLLQCICTGNRGEWK CERHTSVQTTSSG SGPFTDVRAAVYQPPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNK QMLCTCLGNGVSCQETAVTQTYGGNLNGEPCVLPFTYNGRTFYSCCT EGRQDGLWCSTTSNYEQDQKYSFCTDHTVLVQTQGGNSNGALCHFP FLYNNHNYTDCTSEGRDNMKWCGTTQNYDADQKFGFCPMAAHEEIC TTNEGVMYRIGDQWDQKQDMGHMMRCTCVGNRGEWTCTIAYSQLRDQ CIVDDITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDS ETGTFYQIGDSWEKYVHVGRYQCYCYGRGIGEWHCQPLQTYPSSSGP VEVFITETPSQPNSHPIQWNAPOPSHISKYILRWRPKNSVGRWKEAT IPGHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTSTSTP VTSNTVTGETTFFSPLVATSESVTEITASSFVVSWSASDTVSGFRV EYELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGEQ SLILSTSQTTPADAPPDPTVDQVDDTSIVVRWSRPQAPITGYRIVYS PSVEGSSTELNLPETANSVTLSDLQPGVQYNITIYAVEENQESTPVV

				<p> IQQETTGTSPRSDTVSPRDLQFVEVTDVKVTIMWTPPESAVTGYRVD VIPVNLPGHEGQRLPISRNTFAEVTGLSPGVTTYFKVFAVSHGRESK PLTAQQTTKLDAPTNLQFVNETDSTVLVRWTPPRAQITGYRLTVGLT RRGQPRQYNVGPSVSKYPLRNLQPASEYTVSLVAIKGNQESPKATGV FTTLQPGSSIPPYNTEVTETTIVITWTPAPRIGFKLGVPSQGGEAP REVTSDSGSIVVSGLTTPGVEYVYTIQVLRDQGERDAPIVNVVTPLS PPTNLHLEANPDGTGLTVSWERSTTDPITGYRITTTPTNGQQGNSLE EVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPEVPQ LTDLSFVDITDSSIGLRWTPPLNSSTIIGYRITVVAAGEGIPFEDFV YSSVGYYTVTGLEPGIDYDISVITLINGGESAPTTLTQQTAVPPPTD LRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSISSPS DNAVVLTNLLPGTEYVVS SVSSVYEQHESTPLRGRQKTGLDSPTGIDF SDITANSFTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSI TLTNLTPGTEYVVSIVALNGREESPLLIQQOSTVSDVPRDLEVVAAT PTSLLISWDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISG LKPGVDYTTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQ DNSISVKWLPSSSPVTGYRVTTTTPKNGPGPTKTKTAGPDQTEMTIEG LQPTVEYVVSVAQNPSPGESQPLVQTAVTNIDRPKGLAFTDQVDSI KIAWESPQGVSRVRYTYSSPEDGIHELFPAPDGEEDTAELQGLRPG SEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKTQVTPSLSAQW TPPNVQLTGYRVVTPKEKTGPMKEINLAPDSSSVVSGLMVATKYE VSVYALKDTLTSRPAQGVVTTLENVSPRRARVTDATETTITISWRT KTETITGFQVDAVPANGQTPIQRTIKPDVRSYTTITGLQPGTDYKIYL YTLNDNARSSPVVIDASTAIDAPSNLRLFLATTPNSLLVSWQPPRARI TGYIIKYEKPGSPPREVVRPRPGVTEATITGLEPGTEYTIYVIALK NNQKSEPLIGRKKTDLPQLVTLPHPNLHGPEILDVPSTVQKTPFVT HPGYDTGNGIQLPGTSGQQPSVGQQMIFEEHGFRTTPTTATPIRH RPRPYPPNVGQEALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFR VPGTSTSATLTGLTRGATYNIIVEALKDQQRHKVREEVTVGNVNE GLNQPTDDSCFDPYTVSHYAVGDEWERMSESGFKLLCLGFGSGHF RCDSSRWCHDNGVNYKIGEKWDRQGENGQMMSCCTCLNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGQGRWRCNCRPG GEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPICEFMPLDVQADREDS RE </p>
5028	A	2	7106	<p> KSKRQAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLG NVL VCTCYGSSRGFNCE SKPEAEETCFDKYTGNTRYVGDTYERPKDSMIW DCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHETGGYMLECV CLGNGKGWETCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTC LGEGRITCTSRNRCNDQDPRASYRIGDPWSNKHVRGNLLQC\ ICT GNARGEWK CERHTSVQTTSSGSGPFDTVRAAVYQPPHPQPPPYGHC VTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVNQNYR\GN SNGEPCVLPFTYNGRTFYSCCTTEGRQDGHLCSTTSNYEQDQKYSFC TDHTVLVQTQGGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGT TQNYDADQKFGFCPMAAHEEICTNEGVMYRIGDQWDKQHDGMHMR CTCVGNRGGEWTCIAYSQLRDQCIVDDITYNVNDTFHKRHEEGHMLN CTCFGQGRGRWKCDPVDQCQDSETGTFYQIGDSWEKYVHGVRYQCYC YGRGIGEWHCQPLQTYPSSSGPVEVFITETP\ SQP\ NFPPIQWNA PQ PSHISKYILRWRPKNSVGRWKEATIPGHLNSYTIKGLKP/GVWVYEG QLISIQQYGHQELTRFDFTTTSTSTPVTSTNT\ VTGETTFFSPLVATS ESVTEITASSFVVSWSASDTVSGFRVEYELSEEGDEPQYLDLPSTA TSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTSQTAPDAPPDPTV DQVDDTSIVVRSRPOAPITGYRIVYSPSVEGSSTELNLPETANSVT LSDLQPGVQYNITIYAVEENQESTPVVIOQETTGTSPRSDTVSPRDL QFVEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPGHEGQRLPLSRNT F\AEVTGLSPGVTTYFKVFGQ*ATGRESKPLTAQQTTKL\ DAPTNLQ FVNGTDSTVL/VLRWTP\ RAQITGYRLTVGLTRRGQPRQYNVGPSV SKYPLRNLQPASEYTVSLVAIKGNQENPKATGVFTTLQPGSSIPPYN </p>

				TEVTETTIVITWTHAPRIGFKLGVPRSPNPGEAPREVTSDSGSIIVVSG LTPGVEYVYTIQVLRDQDRDAP\IVNK\VVTPLSPTNLHLEANPD TGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVHADQSSCTP \DNLEVPGLEYNVSVYTVKDDKESVPISTIIPAVPPPTDLRFTNIG PDTMRVTWAPPSIDLNTNPLVRYSPVKNEEDVAELISPSDNAVVL NLLPGTEYVVS SVSSVYEQHESTPLRGRQKTGLDSPTGIDFSDITANS FTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTP GTEYVVSIVALNGREESPLLIQQSTVSDVPRDLEVAATPTSLIS WDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDY TITVYAVTGRGDSPASSKPI SINYTEIDKPSQM QVTDVQDNSISVK WLPSSSPVTGYRVTTT\PKNGPGPTKTKTAGPDQTEMTIEGLQPTVE YVSVYAQNPSGE\SQLVQTAVTNIDRPKGLAFTD VDVDSIKIAWE SP\QQQVSRYRVTYSSP\EDGIHELFPAPDGEEDTAE\QGLRPGSE YTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFTQVTPTSLSAQWTP PNVQLTGYRVRVTPKEKTGPMKEI\NLAPDSSSVVSGMLVATKYEV SV\YALKDTLTSRPAQ\GVVTTLENVSPRRARVLDATETITIS\W RTKT*TI/TLGFQVDA\VPANGQTPIQRTIKPDVRSYITITGLQPGTD YKIYLYTLNDNARSSPVVIDASTAIDAPSNLRLFLATTPNSLLVSWQP PRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIY VIALKNNQKSEPLIGRKKTDLELPQLVTLPHPNLHGPEILDVPSTVQK TPFVTHPGYDTGNGIQLPGTSGQQPSVGQQMIFEEHGFRRTPPTTA TPIRHRPRPYPPNVGQEALSQTMSWAPALYAEYIISCHPGGSDEE PLQFMDTGTATSATLTGLTRGATYNMIMEALKQ\RHKVRREVTV GNSVNEGLNQPTDDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLG FGSGHFRCDSSRM/WCH\DNV\NYKIGEKWDRQGENGQMMSCCTCLG NGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLG\AICSTCFGGQR GWP/CVDNCRPPGGE\SPGT\TGQS\YNQYSQ\RYHQRTTHNFKL PQLKCSWP\LDVQADRRRFPEKSSFP IQRNQACLSAKIHLKLE
5029	A	1	389	SMAASRLRLGAASGLRYWSRRLRPAAGSFAAVCSRVSASKTPVGF LGNMGNPMAKNLMNLGIRLGLDPKLLAKILNMSGRCSWSDTYNPVP GVMDGVPSANNYQGGFGTTLMADLGLAQDSATST
5030	A	2	554	ADALGRPTRPASQSRCTRSQSVGPSGFGGHRGE/SGRAYVWQPPYG SSE/HASGLRYWSRRLRPAAGSFAAVCSRVSASKTPVGF IGLGNMGN PMAKNLMKHGYPLIIYDVFPDACEFQDAGEQVSSPADVAEKADRI ITMLPTSINAIEAYSGANGILKKVKKGSLLIDSSTIDPA\VSKELA
5031	A	1	1123	MGNPMAKNLMKHGYPLIIYDVFPDACEFQDAGEQLCPNLDVNHPFV QRLHAADTPWPI SHLLAASVIGCCDIACLFSGRVSISSLCVTISSQA DEVRAKENKPI PQHPTKIAEMLVVSSPADVAEKADRIITMLPTSINA IEAYSGANGILKKVKKGSLLIDSSTIDPAVSKELAKEVEKMGAVFMD APVSGGVGAARSGNLT\FMVGVEDEFAAAQE\LLGCMGSNVYCGA VGTGQAAKICNNMLLAISMIGTAEAMNLGIK/S*GFDPKLL\AKILN M\SS\GRCWSK*HFINPVP\VMGVP SAN*LFRVDFGTTLHLWKDL GLAQDSATSTKSPILLGSLAHQIYRMMCAKGYSKDFSSVFQFLREE ETF
5032	B	13	441	MEGVEEKKEVPAPVETLKKKRRNFAELKIKRLRKKFAQKMLRKARR KLIYEKAKHYHKEYRQMYRTEIRMARMARKAGNFYVPAEPKLA FVIR XRGINGVSPKVRKVLQLLRLRQIFNGTFVKLNKASINMLRDCRAIYC MG*
5033	A	1	775	RRVPA\VPETLKKKRRNFAELKIKRL\RKKFAQQML\RKAR\RKLIY EKAKH\YHKEYRQMYRT*NF EWARMGKKLANF\YVPAEPQIWR FVI RIRGI\NGVSPKGSERFFQLRLRQI\FNGNLL*KLNQGF RFNMAED F*SPYIAMGGTPNLKVKSMN*SYKRGWLAKSNKKR\IAL\TDNAL\I ARSLGKIRHILAWEDLIHEIYTV\GKRFK\EANNFLWP\FKLSFSTK VEMKKKTTHF\VEGGDAGR\EDQINRLIRRMN
5034	A	193	384	EQGFDGHLASWISLKD TAKWNGDELCSYYQSCCTDYTAECKPQVTR GDVFTMPED EYTVYDDG

5035	A	96	1636	ARSPAMAPLRPLLILALLAWVALADQESCKGRCTEGFNVDKCKQRDE LCS\YYQSCCTDYTAECKPQVTRGDVFTMPEDYTVYERLGEEKNNA TVHEQVGGPSLTSDLQAQSKG\NPEQTPVLKPEEEAPAPEVGASKPE GIDSRPETLHPG\RPQPPAEELCSGKPFDAFTDLKNGSLFAFRGQY CYELDEKAVRPG\YPKLI\RDVWGIEGPI\DAaft\RINLFRGRPYL FKG*\QYW\RAFEDGV\LGPWIYPRNISWTAfDGHSPGQTWD\AALG LPCPLAYSGRERV\YFFQRGKQYW\ESYQFPGTSPVQEECEGSSL\S AVF\EHFAMM\QRDSW\EDIF\ELLF\WGAERSGWVTR\QPQFHLG EW\HGVPg\QVD\AAMG\GRILHLQGMATRPLLWPKKK\RFRH\NRN \KGYRS\QR\AHSRGR*PETPRRP\SRA\MWLSFVLPSEESNLGA\N NY\DDYRMDLALCLPTC\EPIQECFFFSFGDKYYRVNLRTRRVDTVD PPYP\RSIAQYWLGC PAPGHL
5036	C	1	300	MRSFQQLTLCPRNGTVTGKWRGSHVVGLLTTLNFGDGPDRNKTRTFQ ATVLGSGMGLKGGAGSVWLQAAGLGLLPASLLWPSLLCHCYVLP PAP GVPLV*
5037	A	359	1229	MPQPPTLGQEMTGPSQPWTGKGGLPGP*QLRAKAEVDSHLGRKKIK QQNRSKSC
5038	A	2	311	VRWNSAAPLVTSRGAPASARPRGQALPGGSAPSAPHGQLPGRAQPAP VSGPPPTSGLCHFDPAAPWP\PGLGLGMLPPHPQDWPAP*HPPGLG LFFEIFSAS
5039	A	310	415	SQYFGTLRRVDHLRSGVRDQPGQLGKTPS*PQVIHPPQCPKVLGLQY YHFLFFLRSL/DSVAQAGVQWRDLGSLQRPPPGFTPFSCSLSPSSW DYRRPPRLANFFVFSVETGF\TVSARMVIS*PRDPPASASQSAGD TGVSQAPV
5040	A	1	114	ARAEMLIVQYILPRLTHCAIFTILFIFSLLT*VMLLSS
5041	A	335	478	TPASLKIPVE**NTLLAKMVIS*PRDLPASASQSAGITGVSHRARC
5042	A	135	804	GIDTILTLNQNSLKTQR*FTLIIF/IFFFLRWSLSPRDCGLQ WRDLGSLQAPLPGFTPFSCSLSPSSWDYRCPPRPANFFCNFFFSRD GGFTVLARMVIS*PQ/CDPPTLASQRAG\ITGLSHCTRLFFF*WME SPSVTQAGIQWHDLGSLQPMPPQFR*FSWLSLPSSQDYRCMPPCQAN F\CIFSRDEVSPC*PGWSGSPDLVIHLPWPPKVLGLHA
5043	A	63	363	TSQEPLRTSARLLWAHSTDGRGWSTRICTPSTDFPFMAIMASLASS MFSKVTNPNPRDLWSPCLSQPPLQRSVTRLRRPAPATAHWQNSASN KSLPS
5044	A	151	384	PRSPPLENPRPRPRPRPKPRPPAEPPRYPRDRLSDDLPAWSTRIC RPSTDFPFMAIMASLASSMFSKVRDGRGGR
5045	B	385	479	MAGAFRRRFASEVRAQGLESLEHGLRCAGSLRGGQSLPTTMWSPVK VGFE*
5046	A	3	698	VFFFFFFSGCTRGPLFESDFHRAPHRCGQGLAAP*AAGAPQPRAPGET RGPEPAPHWRSASGDKPPGQAA\PPALVPGEGPSWSDPRGHRCSQA TLPRVLGAPLQP*LS*LSL*DPPELRL*PPL*LRL**SLEPP*PP LLDSNRFP*PRSPPLENPRPRPRPRPKPRPPAEPPRYPTESVSD DLPAWSTRISVHLQTSWSWPSWASLASSMFFKVTKPNRELWSS
5047	A	138	550	FCCCFTSSEHSLAYGSCSPRTEVLCAQQNPSETQAAPLAS\YMWK *PCNSRLKGPGLGEGWPES\RMTSGVTVPGGTSPGTRAGGS\PCP GGLSPEALRQ*GAGSGPRVSPGA/PGCGAPAAAGAASPCPQRCGAL
5048	A	2	555	FFFFFFLGAHVALYSNPTFTGLHIVVGKDWPPP*AAGAPQPRAPGET RGPEPAPHWRSASGDKPPGASGCLQLLFQGEVPPGDS*PQRSSLALR PPFPRVLGPGFPQ\AKAKQYSQRPPQGSQAPP/GPPRKQPQPLR KVSG*SGGCDLRLRHRPACGRVCTLAQLEPATRMGWSYVGQCGL
5049	A	1246	1379	RCLFILSFFTGRRTHTP*PPLPGLRTGFPP*PRSPPSREPTGP/RP RPPREESPGPRQ*PPRVPHGIGLSDDLPAWSYSGS/GRPSTGLPI/P WPSWHP*RRQCSQR*QTQIPEISGSPCLSQPPLQRSVTRLRRPAPAT A/PLVSKLSPPTKSLPSSDAM\RPLSRAGP*RKQEDSAPQ\DPEPPR NRGPGN
5050	A	207	253	SASLRLPKCWDHRRG

5051	A	335	419	TFDFPNWRSYFSMSNWITSLPTLLSSWD\YRHVPLYPKACIFSRDR VLPYWPQ*SHDFTLFVSMITLTLOIYKMTKLDNYLETIYY
5052	A	68	399	WELLIYFSGHTCSNLSPLLSLSEFFFF*DSLAVSAPGVQ\WHDLC SL \RPLPPRFKRFWCLSLLSGWD\YRHVP\QYPAKICIFSRDRVLPILA KASRNVSLTLNMLGGFS
5053	A	2	322	AAAAFFFF*DGACSVT\RLECSGTITAHCNFRHLGSSNFPASTSRVV EITGTCHHT*LIFVFLVETGFHVGQAGLELLT*VIHPPQSTKVLG LQVVSHCTRPLSDF
5054	A	16	357	TITIGQNFFFFFLEMGSQSV\RLCSG\ISAHCNKLKGSSNLPTS TS*VAGTTGVCATIPSYFYNKISM*NQSLPMLPSLGLELLGLRPVFL PRPPKVLGITRHEPPHSALK
5055	A	2	346	LRWSL/DSVAQGGVQWHDGSLQPPPPGFKRLSGLSLMSSWDYRRPP PRLANFLHF**RRSFTMLARMVLIS*PHDPPASASQSAGITGVSDHA QSQIFLKLQMTKSMGFKTKFLN
5056	A	3	401	FFFWRQSLTLVTQAGVQ*LDHGSLOPPLPGPKGFSHLSPSSWDHKK APPHLANFLL*RHGFTM/RLVLTSLPQ/CDPPAAASQSAGITGVSHC AQPVIKCKLDFSSDIFTPSNLQPRGFWDLTAPQGEIVST
5057	A	142	250	PPTGSLTLPPLWDPQFASLFGTL*WERE*PLPQNV
5058	A	2	775	RCNSAQQMTSSQKALMLELKSLOQEEPVEGFRITLVDESOLYNWEVA IFGPPNTLYEGGYFKAHIKFPIDYPSPPTFRFLTKM\WHPNIYBEW EMYGISILHPPV\DDPQSGELPSEWRNPTQQCEGLILLRC*SHWLNE PQHLSPQMSDASVMFR\KWERQ*REKTKBYGLKFIRETKFSAT*GP KAGKGWVEGSPTNPGREYCIKTEVP\RNDEQVQSLLYDELGMMTDI DDER*GRRKAD\CYDDDEFWGMKRP
5059	A	1	571	ALGKAGYID/KYVTAMGIVAFVFF\RSGKYNLDFSRNDP/ARHI/T PEQLVALYKSFIREKH*VFPD*GLVQRTLSLVFLVCLKN/SFDCDD REVWKKFTANACLQEAGNDLTV\NLRHIAEAVDENS CNFLQLTVD*I \ACKLIQSNW*GIMVSHYSLT*NTFIALVKHCTG*/INTGAPC*SE PLARYKELSF
5060	A	32	534	GRERPLLSPYMETLYRVPFLVLECPNLKLKKPPWLHMPSTVYALV VVSFYFLITGGIYDVIVEPPSVGSMTEDEHGHQRPVAFGLQSKMDNN INGKGLCIQAS*FTMGGRFS*ILDPIECTKYPKTSI\DSFFCSIGI SSVVLLEFFPWARSNMRNGNCPGLI
5061	A	1	328	FLKRQRFGLVAQAGL*WHNLGSLQPLPGFK*FSCLSLLSSWDYRHL PPHPNPNLLFLVETGFYHFGQAGLKLLTD\SGDPPALASQSAGIIGV SHRAGPGLCTFSNHI
5062	A	2	687	GRVGFNVWRDRNDTNLIPNGSSITVNQTNKRDRYVSKYINYIFNDSVK AVYEEFRRGFYKMCDEDI IKLFHPEELKDV\MLGNTDYDWENI\EKN ARYEPGYNSSHPTIVMFWKAHKLTLLEKKKFLVFLTGTDRLOMKDL NNMKITFCPPESWNERDPIRALTC/YPVSLLPSPKYSYNGNS*KKRF KKPINNRGIWLTSLPCPNLILLLLSLLLLLLLLFLYFVLF
5063	A	1	527	ISHDAIAQESKRYWQNLNANVPGAQVLGNQIMPGLNMKIKFVCRPQ CPEKRSKSI EPDKNRKYCSAKARHSWT\KDRRAMRVMSY*\RKKWMN IRPLPTKKQMPLOFDLCNHIA SGKKCQYVGNC SFAHSPEEREVWTYM KENG IQDMEQFYELWLKSQKNEKSEDIASQS NKEN
5064	A	735	1517	SYSYFFIQLCNHIA SGKKCQYVGNC SFAHSPEEREVWTYMKENG IQD MEQFYELWAQESKK*KK*RHRPVSPNKGKWNQIHMNRIMAGRLQW DFSLAGMCGKGTGNSEKQWQGHISSEKHKEKVHTE\TDQYCWQHRF PTGYFSICDRYMNGH/AAQEGNSCK/CLHMGNARTFMEWGRKGRRLP LKVEASTKHKRDLHIGPK\DNDFGK\YSFLFKDLN*YAGFYGMIPNQ SIDQNLKCSAHSRGAARFPACIGVYRSS
5065	A	237	381	LHQPTTQTTLAFTSNLRGR*RSAALPDALDSSKVSEMRFLKRRGVN
5066	A	1	876	MVIMERSKLSLAASTSVQEQNTTDEEKTQPVSLLPITIKLLHDLSP LPLLRNILAPEFLLPGTHVAQPESL TESKELEDSRGFSSSLTAHPVLV WFPRGAFKTSASIFDGSALAA YDDVLVVVVQYRLGIFGF TTDGEH SPGNWGHLDQLAALHVVQDNIA SFGGNPGSVTIFGGSVGGESVSVLV

				MVWIHRGGLMVGTASTDGRVLAAHENVVVVTIQHCLGIWGFRRPN GEGPLHWPEYNQKEGYLQIGANTQAAQKLKDKVAFWTLNFAKKA KPPQTEHIEL
5067	A	1	78	LVRSGRKGRRRVFSLSEADSHGGHWV
5068	A	155	418	IILGEVTEQAPKSMKERLVLCLAGFAVAQCINQHSSPSLSSQSPPSA SGSPSGSGSTSHCDSSGGTSSSSTPRHSLSFPDTSFLAFLN
5069	B	40	411	MQVTGVRTDSGALNITIHKLASSPHSKPFPFIQATFIFSDHIRCIIA EQRLAKGRIPGKAHEDAENSCPPWTSQSSPPLKSWGLDSAPPPPLST CLSASTRGAGAAATPQCSAPCLHRWTRCQ*
5070	A	1	987	MVHGREGGMDPEKLERIQLPVPNAAEKTTYNHPLAERLIRIMNAA QPDGKIRLATLELSCLLLKQQLMSAGCIMKDVHLACLEGAREESVH LVRHFYKVIQRAQMDSSMGEDIFLDMFEDEYRSMTMKPMNVEYLMMD ASILLPPTGTPLTGIDFVKRLPCGDVEKTRRLLPRVDECGCEVTSPG PGRQQLAHAARKQEGENRAFPVPGQLVGSAAHHRCHPVVPARSVSSSIK SSSYNKVPTVPATPDYIEGHLILGDKVLADDDGCSVQAIRVFFMLRSL SLQLRGEPETQLPLTREEDLIKTDDVLDLRLSPGSGKMAFSSPKIC
5071	A	111	2187	DERRVGAADMFGRRSRVGGGHGKTSRNIHSLDHLKYLYHVLTKNTT VTEQNRNLLVETIRSITEILIWGDQNDSSVDFDFLEKNMFVFFLNIL RQKSGRYVCVQLLQTLNLFENISHETSLYLLSNVNSIIVHKFD FSDEEIMAYYISFLKTLCLKNNHTVHFFYNEHTNDFALYTEAIKFP NHPESMVRIVRTITLNVYKVDNQAMLHYIRDKTAVPYFSNLVWFIG SHVIELDDCVQTDDEHRNRGKLSDLVAEHLDDLHYLNDILIINCEFL NDVLTDLHLNRLFLPLYVYSLENQDKVFLIIHHAPLVNSLAEVILNG DLSEMYAKTEQDIQRSSVLPTLSSLWQGSLSLNQLQSGHLKCSSHL CGAQAAADSVTGEIPAIRSLEWLISAGSKARTFFFLKMLIGFWEKVD CEYQRRQVLSTRLQEALPSNRLTDVAHVSSCMLGFGSTAPRGSWIG DPAAVHLPLPGELAEHLGSKGTTTTVTKHQPAKPSIRCFIKPTETLE RSLEMNKHKGKRRVQKRPNYKNVGEEDDEEKGPTEDAQEDAERKAGT EGGSKGIKTSGESEIEIMVIMERSKLSELAASTSVQEONTTDEEKSA AATCSESTQWSRPFLDMVYHALDSPDDDYHALFVLCCLLYAMSHNK/G KSPEKEGLSGTQSHPGKAGTFGKEGAERKRAQV
5072	A	2	2774	RNLLVETIRSITEILIWGDQNDSSVDFDFLEKNMFVFFLNILRQKSG RYVCVQLLQTLNLFENISHETSLYLLSNVNSIIVHKFDSDDEE IMAYYISFLKTLCLKNNHTVHFFYNEHTNDFALYTEAIKFFNHPES MVRIVRTITLNVYKSLDNQAMLHYIRDKTAVPYFSNLVWFIGSHV IELDDCVQTDDEHRNRGKLSDLVAEHLDDLHYLNDILIINCEFLNDV LTDHLNRLFLPLYVYSLENQDKGGERPKISLPVSLYLLSQVFLIIH HAPLVNSLAEVILNGDLSEMYAKTEQDIQRSSAKPSIRCFIKPTETL ERSLEMNKHKGKRRVQKRPNYKNVGEEDDEEKGPTEDAQEDAERKAG TEGGSKGIKTSGESEIEIMVIMERSKLSELAASTSVQEONTTDEEK AATCSESTQWSRPFLDMVYHALDSPDDDYHALFVLCCLLYAMSHNG M\DPKLERIQLPV\PNCGREGPPYHNPLG\ERFIQGSWNNV\AQPD GKIRL\ATLGA*GCLVS*RQQLMSAGCIMKDVHLACLEGAREESVH LVRHFYKGEDIFLDMFEDEYRSMTMKPMNVEYLMMDASILLPPTGTP LTGIDFVKRLPCGDVEKTRRAIRVFFMLRSLSLQLRGEPETQLPLTR EEDLIKTDDVLDLNNSDLIACVTITKDGGMVQRFVAVDIYQMSLVEP DVSRLGWGVVKFAGLLQDMQVTGVEDDSRALNITIHKPASSPHSKPF PILQATFIFSDHIRCIH/IAKQRFAGRIQARRMKQRI AALLDLPI QPTTEVLGFLGSSTSTQHLPRFRYDQGRGSSDPTVQRSVFASVDK VPGFAVAQCINEHSSPSLSSQSPPSASGSPSGSGSTSHCDSSGGTSSS STPSTAQSPAVRSGRKGRRRVFSLSEADSHGGHWV
5073	A	2	1802	NYAYPGVLLIGTDSHTPNGGGLGGISIGVGGRRDVRVDMAGIPCELKC TKVIAMKL TGSLSGWTSPKDVILKVAGILTVKGGTGAI VEYHGPVGD SISCTGMATICNMGAEIGATTSVFPYNHRMKKYSKTGRADIASLRE EFKDLVDPDGCQYDQVIEINLNLKPHINGPFPDLAHPVAEVGT AEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQF

				TITPGSEQIRATIERDGYAQILRDVGGIVLANACGPCIGQRDRKDIK KGEKNTMVTSYNRNFTGRNDAFPETHAFVTSPEIVTALAIAAGTLKFN PETDFTLGKDGKKFLEAPDADELPRSSFDPGQDQTYQQPPKSSGQR VDVSPTSQRLQLEPFDPKWDGKDLEDLQILIKVKGKCTTDHISAAPF WLKFRGHLDNISNNLLIGAINIENGKANSVRNAVTOEFGVPVDTARY YKKHGIRWVIGDENYEGSSREHAALEPRHLGGRAIITKSFARIHE TIKKQGLLPLTFADPSYDKIHPVDKLTIOGLKDFAPGKPLKCIKH PNGTQETILLNHTFNETQIEWFRAGSALNRMKELQQ
5074	A	546	802	GQAGRARQVRSVPSSALITLPPLA*QKHG/ISRWVIGDE\NYGEGS \SREHAALEPRHLGGRAIITKSFARIHGELESVPRPSSSH
5075	A	3	2380	SLSVHKMAPYSLLVTRLQKALGVROYHVASVLCQRAKAVAMTHFEPNE YIHYDLEKNINIVRRLNRPLTLSEKIVYGHLD PASQEIERGKSY LRLRPDRVAMQDATAQMAMLQFISSGLSKVAVPSTIHCDHLIEAQVG DEKDLRRAKDINQEVYNFLATAGDKYGVGFWSPGSGIIHQIILENYA YPGVLLIGTDSHTPNGGGLGGICIGVGGADAVDMAGIPWELKCPKV IGVKLTGSLSGWTS PKDVILKVAGILTVKGGTGAIVEYHGPVDSMS CTGMATICNMGAIEGATTSVFYNNHRMCKYLSKTGREDIANLADEFK DHLVPDPGCHYDQLEINLSELKPHINGPFTPDLAHPVAEVGKVAEK EGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLCKKSQFTIT PGSEQIRATIERDGYRQILRDLGGIVLANACGPCIGQWDRKDIKKE KNTIVTSYNRNFTGRNDANPETHAFVTSPEIVTALAIAAGTLKFNPET NYLTGTDGKKFRLEAPDADEL PKGEFDPGQDQTYQHPPKSSGQHVDV SPTSQRLQLEPFDPKWDGKDLEDLQILIKVKGKCTTDHISAAGPWLK FRGHLDNISNNLLIGAINIENGKANSVG\NAVTOEFGVPVDTARYYK KHGIRWVIGDENYEGSSREHAALEPRHLGGRAI\ITKSFARDPRD EPGRKQGLLPFGPFA\DPADYNKIHPV\DKLTIOGLKDFTPG/RSPL KCIKHNGT\Q\ETILLNHTFNETQIEWFRAGSALQK*RNLOQ
5076	A	3	203	APRGSWMVVAEDPACSVTLCPESLSGYLPGGSGQGPSPAAGEACGTQ LGWQPLVGRCPHVSLSK
5077	A	52	393	EASAWPAPRGSMVVAEDPACSVTLCPESLSGYLPGGSGQGPSPAAG TSPSLPPRSLPGLEKLRSPPSGRESRLSSSAPRAPSISAKAQLQCQAE EEDPEIVNNV*FSSVTCLSL
5078	C	121	396	MALPGRLPHRKLAGGTLEAPWPGIPSGAVRRHQPPPTTLXXWLGV KKPLRKRIEAKFLCAEGPEHIRQGSAAVPGGGSRNCEQCLI**
5079	A	3	755	FVVDFDRPHETRVLQVSCGRAHSLVLT DREGVFSMGNNSYQCGRKV VENEIIYSESHTVHRMHDFDQVDQVACGQDHSFLTDKG\KVYSCGW GADGQTGLGHYNITSSPTKLGGDLAGVNVIVQVATYGDCCLAVSADG\ DIFGWGNLEYLQLA/APVTDSTQVNVPRCLHFGSGVGKVRQ/CLHAVA RAVQC*TGEHGVFWGYGILGK\GPNLSGKCPSLKMIPTLFGFDGF QPRNPGFPAFRCGIQATLLH
5080	A	1	446	MPILFTTVSSALSGAQHIADAQCDRKGHRRTTIQGSRVNLVQPSVGPK VEETQCWGPGRGMPGAPEAPRERRVRSGSRSGDPGVA/PRAASGVGG RYAITRGRASAAVPCRSGGARRGGAGQAADCGPGH*KESESRGPEG PAEGSQPL
5081	A	1	744	GGLIPRAQRESKRRSRGRARAASGV/VWALCYHPRQSECCGTL*KWR SSPRRCWRTSG\DCGPGH*KESESRGPEGPAEGISASLKM*WFGST CLSRCLTLRQRK*LKKIKIWIKK/SEK/PAEAT*SEGQPPF*GPRQ TGAEGF*LEPPQPGMSLKLKFKVILKG*DSRTKMGDQPPRVHGRTHG PLQPLTPVKGQGSCPVKGPSPSGIWP*KPLL*CLATL*WQEGTFSLS GLLPGTTPGASVGHKIY
5082	A	7	279	GQVCIAETGVQWYHLSSLQPLPPGFKRFL\CSASRRAPPCPANF\F LVEMGFHHVQAGLQLLTLGDPPTSASQSAGITGVSHHALPAWL
5083	A	5164	5586	FTAALNSWVILSSCFSLLSSWDCMYMPPCPASFFFFFLR*SPALVA QAGVQWCDLGLSLPPPPSGFERFSCGLPLSSWDYRRPP/PTPG*FFF VFLVEMGFHYVQAGLELLTSSDLPTSASQSAGITGVSHHALPSLYK
5084	A	2	5438	NMTPSELMDEIISIRVYNHSLRADCLMGEFKIDVGFVYDEPGHAVM

				RKWLLNDPEDTSSGSGYMKVSMFVLGTGDEPPERRDRDNDSDDV ESNLLLPAGIALRWVTFLLKIYRAEDI PQMDDAFSQT VKEIFGGNAD KKNLVDPFVEVSFAGKKVCTNII EKNANPEWNQVNLQIKFPSVCEK IKLTIYDWRDLTKNDVVGTTYLHLSKIAASGGEVEDFSSSGTGAASY TVNTGETEVGFVPTFGPCYLNLYGSPREYTGFPDPYDELNTGKGEGV AYRGRILVELATFLEKTPPDKLEPISNDDLLVVEKYQRRRKYSLSA VFHSATMLQDVGEAIQFEVSI GNNGYGNKFDTTCKPLASTTQYSRAVFD GNYYYLPAWHTKPVVTLTSYWEDISHRLDAVNLLAMAERLQTNIE ALKSGIQGKI PANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLD TQIRKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDII IWMIRGEKRLAYARI PAHQVLYSTSGENASGKYCGKT QTIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAEGTFTVF AEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREFFLPPKGWEW EGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYPGGDWKP AEDTYT DANGDKAASPELTCPPGWEWEDDAWSYDINRAVDEKGEWEYGITIPP DHKPKSWVAEKMVYTHRRRRRLVRKRKKDLTQTASSTAREMEELQDQ EGWEYASLIGWKFWKQRSSDTFRRRRWRRKMAPSETHGAAAI FKLE GALGADTTEDGDEKSLEKQKHSATTVFGANTPIVSCNFDVRYIYHLR CYVYQARNLLALDKDSFSDPYAHICFLHRSKTTEI IHSTLNPTWDQT IIFDEVEIYGEPTVLQNPVKVIMELFDNDQVGKDEFLGRSIFSPVV KLNSEMDITPKLLWHPVMNGDKACGDVLVTAELILRGKDGSNLPILP PQRAPNLYMVPQGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLV VECGGERVESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKV IDHRQFGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPP CRDIVIEMEDTKPLLASKLTEKEEEIVDWWSKFYASSGEHEKCGQYI QKGYSKLIYNCELENVAEFEGLTDFSDTFKLYRGKSDENEDPSVVG EFKGSFRIYPLPDDPSVPAPPRQFREL PDSVPQECTVRIYIVRGLEL QPQDNGLCDPYIKITLGKKVIEDRDHYIPNTLNPVFGRMHYELSCYL PQEKDLKISVYDYDTFRDEKVGETIIDLENRFLSRFGSHCGIPEEY CVSGVNTWRDQLRPTQLLQNVARFKGFPPQILSEDSGRIRYGGRDYS LDEFANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NISQGLQMWVDVFPKSLGPPGPPFNITPRKAKKYYLRV I IWNTKDV ILDEKSITGEEMSDIYVKGWIPGNEENKQKTDVHYRSLDGEGNFNWR FVFPFDYLPAEQLCIVAKKEHFWSIDQTEFRIPRLII IQIWDNDKFS LDDYLGFELEDLRHTIIPAKSPEKCRDLMIPDLKAMNPLKAKTASLF EQKSMKGWWPCYAEKDGARVMAGKVEMTLEILNEKEENRPAKGGRD EPNMNPKLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVI IGLLFL ILLLFVAVLLYSLPNYLSMKIVKPNV
5085	A	1	4294	WAVFDGNYYYLPAWHTKPVVTLTSYWEDISHRLDAVNALLAMAERL QTNIEALKSGIQGKI PANQLAELWLKLIDEVIEDTRYTLPLTEGKAN VTVLDTQIRKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKL MQLTEEPQNSMPDII IWMIRGEKRLAYARI PAHQVLYSTSGENASGK YCGKTQTIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAEG TFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREFFLPP KGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYPGGDWKP A EDTYT DANGDKAASPELTCPPGWEWEDDAWSYDINRAVDEKGEWEY ITIPPDHKPKSWVAEKMVYTHRRRRRLVRKRKKDLTQTASSTAREME ELQDQEGWEYASLIGWKFWKQRSSDTFRRRRWRRKMAPSETHGAAAI IFKLEGALGADTTEDGDEKSLEKQKHSATTVFGANTPIVSCNFDVRY IYHLRCYVYQARNLLALDKDSFSDPF AHICFLHRSKTTEI IHSTLNPT TWDQTI IIFDEVEIYGEPTVLQNPVKVIMELFDNDQVGKDEFLGRS IFSPVVKLNSEMDITPKLLWHPVMNGDKACGDVLVTAELILRGKDGSN LPILPPQRAPNLYMVPQGIRPVVQLTAIEILAWGLRNMKNFQMASIT SPSLVVECGGERVESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMP LVIKVIDHRQFGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASL LSAPP CRDIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKE EEIVDWWSKFYASSGEHEKCGQYI QKGYSKLIYNCELENVAEFEGLT

				TDFSDFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPPRQ FRGLPDSVPQECTVRIYIVRGLELQPDNNGLRDPYIKITLGKKVIE DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYDTFTRDEKVG ETIIDLENRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVAR FKGFPQPILSEDGSRIRYGGRDYSLDEFEANKILHQHLGAPEERLAL HILRTQGLVPEHVETRTLHSTFQPNISQ\YYLRVIIWNTKDVILDEK SITGEEMSDIYVKGWIPGNEENKQKTDVRYRSLDGEGNFNWFVFFP DYLPAEQLCIVAKKEHFSIDQTEFRIPRLIIQIWDNDKFSLLDYL GFLELDLRHTIIPAKSPEKCRDLMIPDLKAMNPLKAKTASLFEQKSM KGWWPCYAEKD GARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMN PKLDLPNRPETSF LWF TNPCKTMKFIVWRRFKWVIIGLLFLLILLF VAVLLYSLPNYLSMKIVKPNV
5086	A	444	797	FHSLSPGASKPMLPEGLDWEPCCKLNDVKRAKSVPLTRHLH*VYLLM LSLPPPTPQQAPVYDVPLPVSKCSHCQFPLWF*FAFL*WPVMSVF SCVCWLHKCLLLRSVCSYPLPTF
5087	A	489	611	SPCPCLCPEWYCLGFLGFLWFLV*HLSL*SILNYFLYKV
5088	A	1	336	MAVLPLPSNPHDQFQNSMPDIIWIMIRGEKRLAYARIPAHQVLYSTS GFLELDLRHTIIPAKSPEKCRDLMIPDLKAMNPLKAKTASLFEQKSM KGWWPCYAEKD GARVM
5089	A	1	1581	MDEAGNHHSQQTNTGTENQTPHVLPHKWELNNENAWTQGGHEHTLGP VGSVSSGQGNQARERNKDIQLGKEEVKLALFADNMIVYLENPIISA QNLLKLISNFSKVSGYKINVQKSQAFLYINKRQTEIQIMSLEPPTTA SKRIKYLGTQITRDVKDLFKEDYKQLLNKIKEDTNKLNIPCSWIGR INIMKMAILPKGPSCKGSKLHPYLPPLSQVALDLLGHMAQVABQLAQ EPGLVAEPSVPLSPTQNSGNFPGLHDEQEMEARSRCNHLACCVVN INPDYTNEHSYPRLDKEGSRSPFLKNCMQVLPVEAAEQSLLFVPSS GTFIPEGTHQVPAGAVLYEVSVPNCWEESPSQEAQGSRTHLRRDAMP REEESREAVWLQWLCGTAVSSARFKLPGSFVYTVRGKPPTQASVMVD ALPPAKLKCPRSTSDCCAGSENFKPVDSL L LASMGSIFTLTGCKKCF KVTTEGKQNCQWEKIIITISSPEECDVPIPVSPACESPECDVPLPVSM CSHC SIPTYE
5090	A	235	583	DSVGGFQIYNCELENVAEFGLTDFSDFKLYRGKSDENEDPSVVG FKGSFRIYPLPDDPSVPAPPRQFRELPSVPQECTVRIYIVRGLELQ PQDNNGLCDPYIKITLGKKVLV
5091	A	1	430	MKGDFMTKTPKAMATKAKIDKWDVIKLSFCTAKETTIRVNRQPTW EKFFATYSSDKGLISRIHKELTQIYKKKTNNPIKKWAKDMNRHFSKE DIYAANKHMEKCPSSLAIKEMQIKTTMRHYHLMVPRMAIIKKSCKNRW ELNNENTWTQEGEHHTLGPVVGWKGKGGKALGDTPNVNDLMAFSTT RPTFFPRSDPTTTRPMAVPPHEEKDDHLETHRPLRPRTTLPHAPDGR WLLLTLTHTSTPGKTGLRTPCLSRTEKVQTAGARPSHPHSSAAFT TWAKGPTGRRPGHMRSESATQKEVTMSPCTALRGQKADSKAHGQOGT WAARGMHTESGTCKASRGFPSSLSPRTRIPKFVFAERKGLRGFVLSL TLPFSCIQKHWEQTPMSP LVEDVSE* TGNLQNGRNFLQPTHLTGK* YPESTKNSHKFTRKKQTTPSKSGQRI*TDTSQKKTFFMQPTNTWKNAH HHWPSKKCKSKPQ*DTT*QLEWQSLKSQEKTTGN
5092	A	65	163	LEASKFSLVPTGPSV*CSPPCVHVFSLFNSHL
5093	A	175	495	PQFFGNVLGHLLYSFLGPFQCDENIRYLS*CSPPSCPPCTNRPPQYVM FPSLPCPCLMVQLPPMSSENMWCLVFCSCDSLRRMVSSFIHVPRFC YCNLVVYFEVRCH
5094	A	67	351	LHTRKSVFNCVKLFLHCISSVLINQLYDRPWCVMFPTLCPSVFIVQF PPMSSENMWCLVFCPCD TLLRMMVSSFIHVPPERHKS KHHDRG*CSN M
5095	A	2	432	QVFGSIVRIHQGEWFPLLYGILLPRVQNCLTN*LDLCWSQHQTPHVL THRWELNNENTWTQEGEHHTLGPVVGWEGGGIALGDI PNVDKLMG AAHQHDFLVSPKITGIVLSISQVRVPFIDHRRKARYSADLTSLIAI PG

5096	A	75	173	IPGFPPETCALHFLPHFCKWQPQSSSYSSKEH
5097	A	1	2349	MLEDREDEDEGEDRLDNAVRGPGPKGPVGTVSEAQLARRLTKVKN SRRMLSNKPQDFQVATAWRSASLFNLYIAHLLAIAMVFQWTYSNGQW LNRPALNDFIPTAALGLYNPTPVPILGMTLGGSTQLVAPGIAQSCPG LVLAILIGEGNEATPEDPKDPTCWERLGNHPPSVLQIRVRVIEGRQL SGNNIRPVVKVHVCQGQTHRTRIKRGNNPFFDEVWLWLPQGDHTPASYS RAGLNDYHNCCKNKMQQVVLTHKWEINNENTWTQDGEHHTLGPVVGL WPQCLTDPEGFGEETWASTQFFAGVTCKALYLLHFTPTAIGSHCLDH CFSDFLGIKNYRKEKVGLRDLGICRRPGEGRLGKHILNRNLGDDAEA ELIGTATVALKDLTGDQSRSLPYKLISLLNEKGQDTGIYNCELENVA EFEGLTDFSDTFKLYRGKSDENEDPSVVGEFVKGLQMWVDVFPKSLG PPGPPF\NITPRKAKKYLRVLIWNTKDVILAESITGEEMSDIYVK G\WIPGNEENKQKTDVHYRSLDGEGNFNWRVFPFDYLPAEQLCIVA KKEHFSIDQTEFRIPPR\LIQIW\DNDFKSL\DDYLGFPRLTLR HTIHFLQKSPGGNC/RGLDMISGTFKAMNPLKAKTAFLEQKFMN*W WPCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNPKL DLPNRPETSFLLWFTNP\CKTMK\FIVWRGFWVVIIG\LLFLILLF VGRAPLTLLPNYFVQWKIVKPNVLTGKGFISRVIOQ
5098	A	1	296	RRSAPSTSLRTTCVSSCCWPRRRAPSMTPGAGYPSGSSAGP/PTHSP *PPWTRPS/SAQRYLRK*QPQPGPPALLPLLPAP\PKAWLSGLGPVV LDSPGPQ
5099	A	26	253	RWLSWPWL/SCPQPGWTARNPQPTRELPPHPQAGKPFPLVPVPFQPT SPSLLPVMGGLSRPGSFSPVSVASLRCTH
5100	A	274	2462	RRSAPSTSLRTTCVSSCCWPRRRAPSMTPGAGYPSGSSAAHRCDGW ATTHSP*PPWTRPSWRSAYLRK*QPQPGPTQHCCPLPSQPPAKGVAV RAGPCSAGLSRATIGTGQG/PG/TSPGHTWGQORYHEATFWG*LLDC LVFKSEKPR*LILLITMF*STSVSLTMSLD*ARGREPAHPTPGP SPAATN*PGALLPTVQIS*KCSSLQAPERASPPPCSPR/PPATASFR PSLSDPGPS/APSFGKPSPHLKPNNSIFIFLPHYQLLSHL*VAQSMAT PCPQPGWTARNPQPTRELPPHPQAGKPLLPVPVPFQPTSPSLLPVMG GLSRPGS\SLPSQWLL*GAVHAR*PVPFSILPRGTELTWTPSAKGP GWAAGLAASGGCLHSSR*PTLVFRGWWEHIFVPLPHNRGDSGPRP* QGSSMVVRDSGEL*GLGDPGLPGFENKPCCPF*AEILKWNARLARN VLTQNAAPSPCPYWTWPCLMPSKDPYPEAYPPYVLRREACPLQAVMGP EAPPAPWPCSPVG/SVTVPF/TSVSRSPPPKLTCE*PWAS/SPNLL VPQFPHLEKMGPPPLASSSRAAHAPFSP/SPHPALGRMLPLQWALWE PTGSPALTPPEASEACVMSQLSSR*GPRVLCWGWGMPFSFLYLFHRK SPAGAEMQSGGLPSP*PVLL*GPEAGPGPVAEPPSQSEVKLVPSGR LPVRGLSPSPQSNRRGLQSPVRQTGPFKVKPCV
5101	A	1	545	DFPRQSS*NLNITGKCGISP/GTPLNA\AHFVPGQY/VDVTTKTMCK GFQGVMKRWGLKAQP\ATHGQSKSTGRPGA\VATGDIGRVWPGTKMP GKWGNIYRQEYG\LKVWRINTKPII\YVKWSGPGP*KWLR*RSKDF KLPA\FKDLGKNLPIPIYIFFLEGDEGGTAQKIGMDEKRVSSPGAPSN
5102	A	2	202	LFGYLPK*VDNMSTKKPCTWIFTLALCITARTWKQPRCPLVGKWI/Q LCCI*KMKYYSDFKKSCQAMK
5103	A	1	422	FFFFLRSFTLVA*A*VQWRDLNSLQPPPPRFKRFSCLSLPSSWDY RRASPCSANFLDF/HFLVETRFHHVCQAGLELLMSGDLPASASQSAG IIGVSHCARPLASLFLIHIFNKCISGVR LCSRPWRYSAAQKSLDLAY
5104	A	2	375	DGSCFVAQTGVQWHNLGSLQPLPPRFK*FSCLSLPSSWDLRQV\PPP HPANF*FLV*PGFHDVGQAGLELLTSGDPPTLATRSVGITGVSHCA RPGSIYKQRLDKKLRSVAARTNRCPLWSLPI
5105	A	1	293	RRLFFSFLRQSLVLVIQAGVQWGDLSLRPLPAGFKRFSCLSLPSPG* DYRHGPPRLANFWIFTREGM/FAMLARLVSNS*POGDPPASASQSSG DYRA
5106	A	3	305	ETETCSVAQAGVQWPILSSLQPLPPRLKRFSCLSLNSWDYRCLPPH AANF*FLVETGFPVHGQSGKLKLTSGDLPTSGSQAAGITGVSHCTW

				AGKSYIF
5107	A	1	487	ARRDAAEVFLVSDPSGRMVKFSLQRIILNSHCFAREKEGDKPSATIHA SRTMPLLSLHSRGGSSSE/SDDRILNVTEELTSNDKTRILNVQSRLTD AKRINWRTVLSSGSLYIEIPGGALPEGSKDSFAVLLEFAEEQLRADH VFICFHKNRREDRAALLRTFSFL
5108	A	1	506	FGVSVYLHDYNMRTNPGEMSESTVPTHADKGWPQGPDAQPRGGPTP PPLPKTLSTCRPMQASGLLGTTRGCPGLTISKPKLKVRSKAAAGE KPSEPLPTRTPRPHPPPPQGDRAAGLRMKGRRRHHPHAPYCCRYGSPT SVLAVLVEANEDMVGSQLLSELQENWQAVLAPLGQRAARDLDVEAA ATQHCSN\WRTVLSSGSLYIEIPGGALPEGSKDSLPLVLEFAEEQL RADHVFICFHKNRREDGR*PVSPAUGCVCVGPAPPLHSQAGTVSLRG WGVRAAGSGRQGF*RLLP\AALLRTFSFLGFEIVRPGHPLVPKRPD ACFM\AYTFERESSGEEEE
5109	A	1	996	MVKSSLQRIILNSHCFAREKEGDKPSATIHASRTMPLLSLHSRGGSSS ESESVMARDAPGEEAH/CRRHPG/PSPRGPPGSGWRTPTARQRP KTPAASREDASRFRGRCQLRLWGS/HAGSRSSFPDCVPRGRRSAP DREDDRLNVNRGN*RSNRQDGGFFNVQ\SL\TEAQTALNWRMNC*S GGSLEFNIPAGRRRWPEGSKGQLLQFLLEFAE/EKQLRADHV\FI\C SHKNRE\DRSCLAPKLSAFLGLKIL\RPGHP\LVPKETPDACFMAQ RSRESLPGEEEVGARLRGWAIPPPWGHFPVSRVGRNRRLAHLAWVC PHVVIVQINAHSQ
5110	A	1	125	FFFEMESHVIRLECSGVNSAYCNL/TLPSSSGSPASAPPPQVGGTT GTHHHAQLIFVFLVETGFHHVQDGLDLL/NLVIRPPQPPKVLG*QA VLLPQHRPPK
5111	A	2	280	FFFFGDRVPLHSAAQAGVKWCNLGSLQPPAP/GLKPFSCSLPSS*D YRSLPPCPTHFCIFSRDEVSPSWPGWSPTPDLNMHPPRPPKVLGIQV
5112	A	2	291	FLEMESHVAQAGVQWRDLGSLQPPPPGFKRFSCLSFPSSWDYRRPQ PRPA/NFFVFLVETGF\TILARLVSNS*PRDPPASASQSAGITGVTY RARP
5113	A	3	690	FFFFFLRQSL/DSVTQAEVQW/RRILGSLRP/LQLPGLK*CCCLSL SS*DYSYNPLPRLANFF/VFCIF**RRGFTMLARLLSNS*PCDLPTS ASQSAGITGVSH/HAPGLASPSLNNKVQSSVGAQRRHDEDNDSRA*V FFCFFFFKRFALVA*AGVQWRDLSSLQPLPLRFM*FSCLSLPSS*DH RCVPPHPANFFVFI*\RDGVSPCQPG*SRSPDLAIRPPRPPKVLGLQ A
5114	A	3	282	FFFFETESHSLSPRLECNGTISAHCNLRPLGPRDCPASAS*VAGIT GVCHHAWLI FVFLVETGFHHVQAGLELL/NLVIRLPQPPKVLGLQA
5115	A	3	198	LSLNWCIIILYIYICIYVV/CVVLFCCHSCLSNMGT*FFLAGLLLFRIC LCLFIFYFLL***LLFIMI
5116	A	1	854	MNKLFSILLGEKVDTPQNVLHNDPHARHSDDNQONHLEGQMNFNADS SQFKDENTDIAEK\LEEKVRLCWMTGPQ\NLEKKAKHVKATWAQR CNKVLFMSSEENKDFPAVGLKTEGRDQLYWKTIKAFQYVHEHYL*D ADWFLKADDDTYVILDNLRWLLSKYDPEEPIYFGRRFKPYVKQGYMS GGAGYVLTREPLKRFVDALKTVKCTHS\SSIEDLALGRCMEIMNVEA GDSRDTIGKGNFFHPFV\PE\HHFNLKGYLPRTFWYWNYNYP\PVE GPGLLL
5117	A	13	290	ECRRQRGVQ*CNHS*QQL*PP\GLMQSSLLSSPGSSDYRQVLLHSAE F*VFNLVEMGSYYVQAGLKFLASSDPPALTSQWARITGMSHITRA
5118	A	1	595	MGIHHVQASLELLTSGDLPASASQGRGVRLYYI\EGRSSQSASVTA LFLSSLPTVTSAMAGTRPPSARSHQTLQACRAQKTKTRMSSI*GTGA KHQASSPGKAPLSTPSPYFWKPSLQTSPCSGSRSLWASLPPLAALF LCFWQDAT*RSSTTRSSLPSWPSRSTRALRLSTS*PECAPSA*ASSK AGERSTGDRL
5119	A	3	496	FFFLRCSV/NSTAKAGVQCHNLSSLHPLPPGFKQFPFCSLPSS*DYG CAPHPANFYIPSRISQAWWRVPVIPATQEA\RQSFNFVAQGVQWH NLSSPQAFPAFGK*FSCLSLPTSWDYRHMPPCPDNFCIFSRGGVSPY

				WPSWSRTLDIMIHIPRPPNVLGLQA
5120	A	3	329	ETVSHSVAQAGVHWHVGSQQPPSPGSKQFSNLSLPGGWDIRHPPHP PAN\FIFLVETGSHYVAKADLQLLASNDPPTSASQHAGIIGRSHCTR PRIY*WSNKL*YKIT
5121	A	1	537	ERQSCSVARAGVQWHDLGSPQP/LPPRLKRFS\CLNLLSSWDYRRAL PHPG*FLYF**RQGFTMLVRL/VLNS*PCDPPTSASQSAGITGVSHR ARPVLRF*QNYYYFETGSGSAAQAGMQW\PIMAMQPQPPRLKQASNL SLLSSWDH\GMQPHPANTTVCKTERKQVFRMHLLNNTNYREQ
5122	A	1	197	EAGSHSVAHAGEQWCDYGSLOHQF\PVLKQFSHLSLPSS*DYRCVPP CPANFLIILMISVSIRGSV
5123	A	809	1472	KTLLLSCLYLSKLWPDYLRSSRLRRAASSFGSWRFALQRTPHHTRR LSRSSKAVQTAFFRRSPSSRHRCGSSSRATTTCRMFLSLLTTCAQQ LAGWVTLKRSIGLRKRSMSLMALKKWPCLMWKKRRSLPRYPQPQRT GKKRSGSKIMIRRLNGQMPRTVPAPAMKEVQI/TKLKKSKRRSCSH CSSKVCDSKS/VQEQGAP*VGGQQPPPRG*SYAWC
5124	A	1	504	DSEPCSVAQAGEQ*RDLSGLQPLSLGLKQFSCCLPSSRDYRRPPPC LANFCYF*YRWGFTTSARPV*NSWPCDPPTSASQSAGTTGVSHQA\R LLLFFKAFKVWGSISI*CVNEFNIISKISSFPSTSTPQSCPIHMS QIKYK*F*DYP*CSKQAGGISISDTYY
5125	A	2	351	KQGIIMTYVLRPPFFFRWSL/DSVSQAGVQWRVFGSLQAPPPGFLP FSCTG/RQPPSPANFFLYFLVETGFLF**RQGFTVLDRMVIS*PRD PPALASQSAGITGVSPRTRQEGHS
5126	A	1	1047	MVISISWPRDLPASASQSAGITGLIGALVLSVGIYAEVER/HEI*NP* KCLPGSSHHPPGRRHVHGLLHWCAGVPP*QPPELLASRLSRGYG LVLSWLEPRYKEMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKT RGIFETKFLSQIESDRLALLQVRAILQQLGLNSTCDDSIIVKTVCGV VSRRAAQLCGAMAAVVDKIRENRGLDRLNVTGVGDGLYKLBPHFS RIMHQTVELKSPKCNVSFLLSEDGSGKGAALITAVGVRLRTEASS
5127	A	116	498	YNFALKSELKFNQAIIVSLNKFFFFFLRWSLRPVAQAGVQWRDLGS LQ\PPPPGLTPSSCLSLPSSWNRPPPCPAKSFWIF/M*RRGFTVL ARMVIS*PRDLPASASQSAGITGVSHRTRQEGHS
5128	A	3	490	GIYHTLRTGQEGRSIKQORLLQRPYPFFLFIFPSFLYMIEIKH*L SFYILLFAFNIVS*PFSYFIFFF/RF*DSVLLCGPWSTVA*S*LTA ASTSQDQDSDPTSGPLKVTDRVCGHHT*ANFYIFCGWGGLTILLRR IPNSWAQGIFPPWPPKVLGLQA
5129	A	423	495	LLFPIRRPFATRSSQKESPPTP
5130	C	628	849	MCGSVYSTIWSLIASRREETIRVIVLYIQSPNINTRHISKRLNKG NQFHKEDWNLLKRVCSHSGAEAGIFS*
5131	A	350	412	NFELKLSPYQKSIYWGAQVMPVAVGKPSSEWPPGSHMDNSQIRGN PVCGIK*FSCPSLQCSWDYRCMTPCLANLFFPKLEGGFCHVAQTSK LLGSSSPFILASRSTGITGMNHA\RQLLN*SIRE*HSITHRLTHSR EKSCECNLYGKTLSSNFPPTKKKVSTGELPR
5132	A	3	189	HERKAQPAGEGRTHMTKSDSLPSFRVSTLPLESHHPDPNTMGASHR DRALSGTATVRDTRGIDPAPVHASPTRNR\NEGRHVFKRFPDTLTDR SISIYTDHSLQIRTLRALSQ*TTPTQTPWAGPATGTGLSRGLPPY GTPEG
5133	A	32	800	FKTIKVRFLCIRVYSLCKLLTYCDHFHSLDFEECAHKLLKMEFPE SQTKELCNMILDCCAQORTYEKFFGLLAGRFCLMKKEYMESFEGIFK EQYDTIHRLETNKLNRVAKMFAHLLYTDLPWSVLECIKLEETTS SSR\IFVKIFFQELCEYMGLF*/SLIARLKDGN\LAPFF*RI\FPRD DPRITRVAI\SFPPSIASGCLTYCPVSALSSIPLRPLVVALLLPIPI FHHDLLLELFRLPFFYNDTLVLPFV
5134	A	2	706	RCNSAQQOMTSSQKALMLELKSLEEPVEGFRITLVDESOLYNWEVA IFGPPNTLYEGGYFKAHIKFPIDYPYSPPY/TFRFLTKMWHENIYEN GDVCISILHPPV\DDPQSG\ELPSEWRNPTQQCEGLILLRC*SHWLN EPQHLSPQPMDSASVMFR\KWR\DSKGKDEYGLKFIRET KFSAT\K

				ARRQEKGG*RFPTTLGGNTCIKTEVP\RNDEQVQSLLYDELGMMTD IDDER*GRRKAD\CYDD\DDSGE*GSPQPWAGIPASKLRPCNDEQ VQSLLYDELGMMTDIDDER
5135	A	7	219	EGV*VSRDW*QWS/DIGSWRHSMTGSGDSLASF*VSGGTGESHHKQ LIAVNMVEMGSHRAGQAGNELSTL
5136	A	2	309	DGVSLLLSPRLQWHNLGLLQPPPP*FKGFSCSLPGSWDYRHV/PPC LANFVFLVETGFRHVGTGLELLTSGDPPASASQIRAGITGVSHRTWQ KMYFLSQKYF
5137	A	1	309	SCLSLSSWDHRRVPAHPANFVFLVETGFHHVSQV/GLELLTSSNPP ASASHSAGITGVNHRWLPLNLRF*KMIIRRLRLLKNKPHSTILR KSETSNSCE
5138	A	2	625	TYGEMAKIVDVPKQLRAPDPIDSMCHFCNVSPCTRNGCVDMEH FKVIKTHQIEDERERREKKLYFGYSLGAHPILNQTIGRMQRATEGR KEELFALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKP S*TF\VRILYNGVDVTFHTSFCQDHHKRSSKPMFPLENLVRFVKRDM FLALGGSCNTYDACHREGF
5139	A	167	688	VIKILGTEKGKQNRNLIFLSGNRVLKWMERSHGTEKALTALLKCGA EDHVEAVKKLQNSTKILQKNLNLRLDLAVHIPHSLREQSRLGRCGH ITQETLLFLTVDGDEKGGGLFLLAGPPASVETLGPRAEVLEGKGAGK KGRFQKATKMSRRMEAQALLQDYISTQSAKE
5140	A	3	1230	QRDSYAREFTTTVVSCSAELQT/GEGATARNIFLSGFQVVEEDTVL FPEGGGQPDRTGTINDISVLRVTRRGEQADHFTQTPLDPGSQVLVRV DWERRFDHMQHSGQHLIT\AVADHLFKLETTSEVGRFRSAIELDT PSMTAEQVAAIEQSV\NEKIRDRLPVNVRELSDDPEVEQVSGRGLP DDHAGPIRVVNIIEGVDSNMCCGTHVSNLSDLQVV\ILGTEKGKQNR TNLIFLSGNRVLKWMERSHGTEKALTGLLKCGAEDHVEAVKKLQNST KILQKNLKSQAQ/RT*AVHIAHSLKEQSRLGRCGHITQEGG*FRVHE YHCQ*RLGQRRPSLFLTCGR*ERWWTLLYWQHLRLWRPWGPWLRS WEGKGAGKKGRFQKATKLSRRMEAQALSPGLHQHAEC
5141	A	3	306	SRQWTLFADGQHSQPAAPCPGGEV*RTGALNPKTFQG/LPSAPGPCP VPHGASHP*TPQKLQPGNKSQMKPVKPGFPSPGAGGAWASL*PSSLP FPDLQYLL
5142	A	1	306	FFFFFL*QSCSVAQAGVQWYDPSQKPPPPRFRFSCNLNPSS*DY RRPPSLPA\IFVFLVETGFHHIGQDSLKLLASSDLPISASQSAGITG MSHCTWPV
5143	A	81	657	TAEKGGEEKSGELGRSQRTLSQVGATRGTSSEITLIVQMRDAGGSA LCSGIGGGEKWSVLGVILKKDDRIVLAYCMGHEIKRGIEDDSKVFFF FFLEMKSCSVVQAGVQWHDLSLQPALPRYK*FSCSLPGSWDYRHV LLRLVNF*FLVEIGFHHVVQAGLKLTTSSDLPHSASRSAGITGVSH RARPG
5144	A	3	494	ETEDLALSPQAGVHVAR/SLSSLQPPPGVFKQILCLSLSSWDYRG /PCHPHPAKFLAF*VETGVSPSWAR\LFLNS*PRDPPASASQSAGEP PRWASVCNSVKMLSSAFNWCVCRLHKEKWMRRQKTHTVMI PHSNRCS SRHFSRIPSSIETYNLRLHTLLAGRF
5145	A	3	123	ESGSHS\LPKL*CSGAITAHCNLKLGSRDPPPTSASGVAGT
5146	A	3	292	RQRL/NSVTHSGVQRNPGSLQPLPPGFKHFSCSLSSWDYRHTPQ CPA\IFVFLVETGFRHARLVNS*PHNLVPSAQ/SAWITGLSHHAR PCVSF
5147	A	2	303	FLGWSFTLVVQAGVQWRDLGSPHPLPPGFKQFFCLSLPSS*DYRHAP PHLANFVFLGEMDFLHAWQAG\LELLTSGDPPTLASQSAGITGVHRC SRPVSE
5148	A	2	613	PRVRTYRFGSVGHDTQLCLWDLTEDILFPHQPLSRARTHNVNMNATS PPAGSNGNSVTPGNSVPPPLPRNSLPHSAVSNAGSKSSVMDGAIA SGVSKFATLSLHDKKEKAPRERSQSRNHSMGHNF*QEASDKLESS/S PKPKPDPAKTLGTPLCPMEDVPLLEPLICKIAHERLTVLIFLED IVTACQEGFICTWGRPG

5149	A	2	395	IGFQPQLTEPQVSLQDLEKLSGLVFFPHLDRTSDIRNICSVDTCLL DFQEFTLYLSTRKIEGARSVLRDLKIMDHLKNV*NE\PYDYPMRRYY KKLQELTAIDLSTHISQPSLLSYTCLISGATPPFT
5150	A	644	962	NASSLAWTVLLKLLVGFAGQCMGNFFFCWGGAMESPSVAQAGVQWR NLGSLQPPPPGFKRFSCLSFPSSWDYRHVPPHPANF\CIFS RDGVSR CWPGWS*TPDLR
5151	A	3	321	RRCLCAGYFKNVARRSCWRTFCTMDGRGSPVHI\HPSSALHEQETKL EWIIFHEVLVTTKVYARIVCPIRYEWRDLLPKLHEFNAHGFEQCGP T*SERRCKKEMDK
5152	A	237	602	LLITGRQYSLTFRFYIHLRNKILNSGLGKPPKLHIFYTEAFFARNP DQMEFHSVAQAGVQWHDLG*LQPLPAGFKQFFCLRFLSSWDYK\GTP PCLAGFCIFSRDEVSPRWGWS*TPDLK
5153	C	166	417	MPPWDPCFPNHPAPKPHQPHPARLTDRHHPXFPPTHQLPCLLPAPSP GSLVVALSPQGHVYTINVEGTRSIRECSCTKNPPFGPI
5154	A	282	1112	FLKRENLLKNVCRNKLDLRPNRASPTGSQEWQHGQVQSEVQFVHSL KPGPPADSCRTAA/GDPGGTETADPGHTGLELRFPEPPKPTLPLALS EAPVP/PERGENTGPRSLPSTPMPSWGPLLSSPPRPATSPSPSQAN *PPPPRSSHPTTTPPTRPQWPQGCCAQPPRPCLH*RGGN*VY*G MQLHQKSVSWPHSQWPQKREGNGSSHEIHPSCPPSGFHVSPGGRMP TQAGALHSWVPGLSLSHGSGPHPPRWTATVQAARPPVPLTLNL
5155	A	69	734	SRLGRDHVGPGLGGVG/VRR/RENDIGEYEGGRNEAGERHGRGRARL PNGDITYEGSYEFGKRHGQGIYKFKNGARYIGEYVRNKKHGQGTFIYP DGSRYEGEWANDLRHGHGVYYYINNDTYTGEWFAHQRHGQGTLYAE TGSKYVGTWVNGQOQEGTAEIHLNHRYQKGFLNKNPVGP/AKVCIC WV*TTW*ISFNRYGKRRRGRGGRISNCCSKMESYPNH
5156	A	4	674	GVQRGHFQEAKGSGRCLSSLNVPHSPSPSAGMDPSSPVNPPEAGGP LAQVPSAALAQVAPGPVPISSLLEGPT\PSLPF*ERGNSSHQASGP ERGARPPALLGPQEIGGSSK/YPPPGPGSTLGKGLLASPRCGPPQVL GWGLRDPTRLEEGPWGSL/GNTPREPSIKCSP*MGRMGAQLPKAEG APPPTQLPPTHSPRRILGPLGASPERPPPRVPPGGE
5157	A	3	342	NFFFLRQSF/NSVTQAGVQWRDLGSLQPLPSGFTPFSCLSLLSSWDY RHPPPHPANFLYF*RRGFTLLARMVLIS*PHDPPTSASQSAGITGV SHGAWPKSIFFLNAEVMYY
5158	A	1	251	VCVCGFCFVLETESRSVTQAGLQRHHLCSLQPPPPGFKGFSCLSLPS SWDYRCPPRLANF*FLVEMGFHHVQAGLKLVASSDPPASVSQSA EMTGVS HALPG*SRSVTQAGLQRHHLCSLQPPPPGFKGFSCLSLPS SWDYRCPPRLANFCIFS RDGVSPRWGWSQTRGLK
5159	C	24	362	MGITVFRXX XX XXXXXXXXXXXXXXXXXXXX*
5160	A	1	287	FFFF*DIRVSAQSPRLECSGAILAHCNLCPLGSSDSCASTSPVAGIT GMCHHTQLIFFVFLVETGVVHV\RGLEL\RLQVIHPPQPPKVGL QA
5161	A	1	1672	QTGLQATTKHSGFPVRMDNAVPIVPQAPAAQLQIQSGVLTQGSCTP LMVATLHPQVATITPQYAVPFTLSAAGR PALVEQDCRCTAGVAWK LKQILLPSNFGQQLAWG*ALHNS\VOPTAMIEAMSGQQLADWRNA HSHGNQYSTIMQQPSLLTNHVTLATAQPLNVGVAHVVRQQQSSSLPS KRNK/QSAPVSSKSSLDVLPVSQVSLVG/SSPLRTTSSYNSL\VPVQ DQHQP I I I PDTPSPVSVITIRSDTDEEEDNKYKPSSSGLKPRSNVI SYVTVNDSPDSDSSLSPYSTDTLSALRGNSGVSLEGPRVADGTG TRTIIIVPPLKTQLGDCTVATQASGLLSNKT KPVASVSGQSSGCCITP TGYRAQRGGTSAAQPLNLSQNSQAAPTSSQERSNPAPRRQQAFA PLSQAPYTFQHSPLHSTGHPLAPAPAHLPQSAHLYTYAAPTSA LGSTSSIAHLFSPQGSRRHAAAYTTHPSTLVHQVPVSVGPSLLTSAS VAP\AQYQ\QQVATQ\SYIGSFRGSTIYTGYPSPKISQCYL
5162	A	1	111	ELRYKRWPGWKADTPQAQ\TVKWVGVGKSRESMIQLF

5163	A	2	1034	DRAHLVDFHQAVDGLQEVQRQAQEGKNIGTTKKGIGPTYSSKAART GLRICDLLSDFDEFSSRFKNLAHQHQSMPFTEIDIEGQLKRLKGFA ERIRPMVRDGVYFMYEALHGPPKKILVEGANAAALLDIDFGTYFPFVTS SNCTVGGVCTGLGIPPQONIGDVYGVVKAYTTRVGIGAFPTeqINEIG GLLQTRGHEWGVTTGRKRRCG\WLGS\MILRYAHMVNGFTALATKL DIL\DLGEVKVGV\SYKLNGK\RIPYFPG*PGRCFKKGRKLKYETL PGWK\ADTTGRPGRWEDLPPQAQ\TYIRFVENHVGSRSGYHYQSFL /VSVKVVGVGQVQESPMIQLF
5164	A	3	148	LLSSRDHRHVPHPANFFCRD/RGLAMLPRALNSWA*AIHPWP VL
5165	A	3	325	YVFSGLAHQILNVSLGIRRLHLADVSVGICLAKLRIAPVPPHNE SVFNRWRCP\YSSCSY\HHLITSHQFQPSSELIKYNHNLQHNKHNACANA A*EKAGMYRHRRLH
5166	A	373	950	SRGVFFFLRQSFTLVA*AGVQWCDLGSLOPLPPRFKQFSC\PASLVS WDYRHAPHPANFFIFLVEDKGFMSMLVRLGLELPTSGDLPASASQSP GITGVSHHARP*MILFIFMFSFGRRDGVSVTQAGVQWHDLSLQASP SGFMPFSCSLSPSSWDYRHV*PCQANFLYF**ANLSRVSPCWSGWSR TPNLK
5167	A	2	334	VRHRTLVPOAGVQ*CSLG*QQSPPWFVKQFSCSLSPRSWDYRHLPP HPANFFVF/VEKTGFHHVQAGLELLTSVDPASASQSAGLTGLSHH AQLSFNLSAKKSFTKTRS
5168	A	35	438	NSEAAQAFCKNGDPQTSIFDHLVAIERAGRAADGNYYNARKMNIKH LVDPIDDLFLAAKKIPGISSTGVSNWGGYALACALYILYSCAVHSQY LRKAVGPSRAPGDQAWTHALPSVIKEEKMLGILVQHNSRS
5169	A	1	1845	MAGELRPASLVVLPRLSLAPAFERFCQVNTGPLPLLQSEPEKWM LPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCS FSLEEALAKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVV TMRPIPKDKLEGLVRACCSLGGVSRGKGPEQGSKALAAVSGGLQ MPLRFKELLGIKELSKPAYGDAMVCPPEVPVFWPSPLTSLGAVSSC ETPLAFASIPGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLH YSIASVSASQKIRELES MIGIDPAKLESQWKRFDHLVAIERAGRAAD GNYYNARKMNIKHLVDPIDDLFLAAKKIPGISSTGVGDGNGELMG KVKVKEAVRRHIRHGDVIACDVEADFAVIAGEHSDGRFVRPATQGV SNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQAWTQALPS VIKVNPLSQPLAWKQLLPWMSSRPEVPSQQAPPPTPIPGSNPPPLG LLKEMGPAPLGGEGAGGPDLRDIHNASVLNGTPTWGIFFGQVLSTH GDMVEYAIISPGHSSHVEEKMLGILVQHKVRSVSGVIGMEVDGLP FHNTHAEMIQLVDVT TAQV
5170	A	1	212	LRAPGDQAWTQALPSVIKEEKMLGILVQHKVRSVSGVIGMEVDGLP FHNTHAEMIQLVDKQGHFSGAF
5171	A	371	915	NQPHFVNACCVPTLLSALLEEKMLGILVQHKVRSVSGVIGMEVDG LPPFHNTHAEMIQKAGGRHHGTGVTVHVPCEQSPYQAGLHPGRMQLL LATILLVNTGLRQPTWSPVRIFFSTVTYGDTCQLTARQSMRTNIPRP CRIRYSRLQSSSPIHGFCYSWFQLLIANCRPKILNEFKQ
5172	A	1	2460	MAGELRPASLVVLPRLSLAPAFERFCQVNTGPLPLLQSEPEKWM LPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCS FSLEEALAKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVV TMRPIPKDKLEGLVRACCSLGGVSRGKGPEQGSKALAAVSGGLQ MPLRFKELLGIKELSKPAYGDAMVCPPEVPVFWPSPLTSLGAVSSC ETPLAFASIPGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLH YSIASVSASQKIRELES MIGIDPGRGIGHLLCKDELLKASLSLHARS VLITGFPPTHFNHEPPEETDGPFGAVALVAFLQALEKEVAIIVDQRA WNLHQKIVEDAVEQVWGMTCRVFLAIRGSPGPPELGRVVEYEVAERL RQOSH LVVMGRAAPGAPSLAWRRLPDSTQSWVLSVLVLMGAQRVEFA ILDFTE LTLHLHEESVLKTQIPILTYQGSVEAAQAFCKNGDPQTPRFD HLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKKIPGISSTG VG

				DGGNELGMGKVKEAVRRHIRHGDVIACDVEADFAVIAGEHSDGRPV PATQGVSNWGGYALACALYILYSCAVHSQYLKAVGPSRAPGDQAWT QALPSVIKVTNPSQPLAWKQLLPWMSRPEVPSQQAPPTPIPGSNP PPLGLLKEMGPAPLGGEAGGPDLDRIHNASVLNGTPTWGIFFGQVLS THGDMDEYAIISPGHSSHVEEKMLGILVQHKVRSVSGIVGMEVDGL PFHNTHAEMIQKLVDVTTAQV
5173	A	1	933	LESMIGIDPGNRGIGHLLCKDELLKASLSLHARSVLITGFPPTHFN HEPPEETDGPFGAVALVAFLQAL\GRRSP*SLTREPVIHLHQKIVEDA \LSKVF*RRRSRY*LTKVDQWKLLRHSCAKIGDPQTLRFDLVAIER AGRAADGNYYNARKMEHQAL/RLTPFDDFL\SAKKIPGISS\IGVG DGGNELGMGKVKEA/DEEAHTARGCHRLATWKAFAVIAGVSNWGGY ALACALYILYSCAVHSQYLKAVGPSRAPGRFRPGLRPSRRSLRKKK CWASWCSTKSGVASRASAWRWMGCPSTTPTPR
5174	A	367	460	VTPEKQHEQWIPHSSIRQQNQPKQWS*YPAPQSG\SPLTIMEGTV VVQQLMSVMISKHDLFPKDAELQSKPDGVSNNNEIQKKATMGQLQ NKENNNTKDSRQCSWDKSESQQRNSMNGSPTALSGSKTNSPKNS GHKL
5175	A	96	403	IKSLYLLLRPHPPPPPNILCSLEQRNLTLETMMSLHDELDQERKK FTMIEIKMRNAERAKEDAERNDMLQKEMEQQFFSTFGELTVEPRTE RGNTIWIQ
5176	A	74	1506	QQIMRATSSWQAPRMIWKTG*SQSAESYGDLSGGGTVVVQQLMSVMI SKHDLFPKDAELQSKPDGVSNNNEIQKKATMGQVTEQGEQ*HQGQ P**AVLLG/PSLSH/HQRSSMNGSPTALSGSKTNSPKNSVHKLDVS RSPPLMVKKNPAFNKSGSIVTNGSFSSSNAEGLEKTQTTPNGSLQAR RSSSLKVSQTKMGTHSVQNGTVRMGILNSDTLGNPTNVRNMSWLPNG YVTLRDNKQKEQAGELGQHNRLSTYDNVHQFSSMMNLDDKQSIDSAT WSTSSCEISLPENSNSCRSSTTTCPEQDFFWGELLRTLFWMAPPQ\P DPFPTPRDYESKSDHRSVGGRRSRATSSSDNSETFVGNSSSNHSALH SLVSSLKQEMTK\QKIEYESRIKSLEQRNLTLETMMSLHDELDQER KKFTMIEIKMRNAE\RAKEDAERNDMLQKEMEQQFFSTFGELTVEPR RTERGNTIWIQ
5177	A	1	439	GNEFSILKSPGSVFRNGNWPPIGERIPDVAALSMGFSVKEDLSWPG LAVGNLFHRPRATVMVMVKGVNKLALPPGSVISYPLENVDDLFLSEL QVLHDISSLLSRHKHLAKDHSPDLYSLELAGLDEIGKRYGEDSEQFR DASKI
5178	A	1	553	GNEFSILKSPGSVFRNGNWPPIGERIPDVAALSMGFSVKEDLSWPG L\AVGNLFHRPRGYPSWVM\VKSGTKLALTPQAVVISYP\LENRVY MVGKANSVF\EDLSVTLRQLRNRLFQENSVLSSPLNLSLRNNEVDL LFLSELQVLHDISSLLSRHKHLAKDHSPDLYSLELAGLDEIGKRY
5179	A	3	1111	ILKSP\GSVFRNG\NWPPIPRE\RDPPDVAA\LSHGLPL*KKDLSWP GLAVGNLFHRPRAT\VMNVNGVNKLALPPG\GIS\YPLENAVPS LDVSANS\IHSF\SEET\PVVLQAPSEERVY/VKGRANSVFEDL S\VTLRHSRNLVFKKTLFLSFTPPQILLSRNNEVDLLFLSELQV\L HDISSLPSPKHL\ARDHSPDLYFTGSWAGL\DEIG\KALLGEDSEQ FRDASKILVD\ALQKFADDHVPVFMVGNPVVELVHCPSHLNTSPPLG KTRDLPLRPKQAQEPQVPYNLA\YKYNFEYS\VFNMVLWIMI\AL ALA\VIITSYNIWNMDP\GYDSIIYRMTNQKISEWIECYLWPRIRKR GFGNWLF
5180	A	18	595	NVAGTAICSFAPGRRQTPCHTREPQDGRPRARLTAWTRARGTCRVAH THTGRQNHMPPLWGFSRHHRAFSEHLSLGCAPPSATWT*TRSPAAAA AGP/PVPRKPNPSPSRSPAGLRPPGRAGPLTSRCPGPPASQASDT VGPVRHKQRGPTSDVSGAWDGPATAASGPVVRLYPSTLGGGRQITR SADKT
5181	A	68	446	RLTSELAQTLAVHPSKSARPRP*AGE\KPGKKPPLQVNGAWD**PRV GADPGHSPDSLDPST\GDVQGGSSYWEGRITIMPLWGF PDRAGLLG SPGSSGPGKRRPILAGQPYKLELQARFLGPGH

10382

5182	A	2	513	APPSATWT*TRSPAAAAAGF/PVPRKPNPSPPSRSPAGLRPPGRAGP LTSPRCPGPPASPGIGHGCGCRQTQAAWPRRRTYQGRGMGPRPRRRP VVPVGGERSHSHSPGPPLRSPGPEWGLTSSSSCPARG/PGGCLCPQNO LPNPGP/SGPASPNLPSRLHPTDTSGBPFPRA
5183	A	14	720	RNFDRPTPRTRGRTRGRTRVTRTFGPGPVASAGCSRGDGRFGEAGP TALDSGADSGVRDTLPVHEPGSCLRYRTPRPRSRHAHTPLIRPTSG PRCFGSDGTHSVRCFVNAGRPGHLGLGG/AKSSGFAGQKGRLLLAAG TCGVHVQGPLRAARPQEVLIQGGPLQPAAL\PEQPPATGAWLQPRLR CSEKAL*LP*GAP/SQSPPRPMQ\PITVPASG*NAGGPGASGGTRVP G*KLPDTGGP/SAQHPLSPTGLPHDARP/PSSCPTGRSCVHCPLNA VHL*E*PANSELSRPLSEDTP*AA*TRPGSAGPISDPHS\PPSSP SSSGTPALPGHMS/GGKWOHQPSACPVLGL/PPDPGAEKAGSQPS PGHLVQAPGHPGPPGPHTPAVTSPFNSRAALPSFSR*PCPQSPK QGS CDPRPPRKPWKFGSL*GLPLQKNRPPFSRTGATPGEPPGA L/PLSGNPPKSHRDSALPSMSMHPARPSVLGSKLSGFLPSSWGP CTF*WMKCGRTRSIRGHSCAWLKA
5184	A	2	1558	RRSRDSGYRAPPASHSRPGQAARAPAPRPARREVCCPRPGVPRRART TRKTPTWAAVATGTRGASAEAGGPTGLAHG/SGLAAAAGLM/GCEPAS GWGPGRQGSAGARTAGSSSGSSSGSGPSAPTSSSVLGSLVAPVSPYK PGQTVFPLPPAGMTYPGSLAGAYAGYPPQFLPHGVALDPTKPGSLVG AQLAAAAAGSLGCSKPAGSSPLAGASPPSVMTASLCRDYPCLSYHCA SHLAGAAAASASCAHDPAAAAAALKSGYPLVYPHPLHGVHSSLTAA AAAGATPPSLAGHPLYPYGFMLPNDPLP\TSATGCRPTGRATSASPR PKSC*AT/SRTHTAFFPGTDKLLSGYPSSSSLASAAAAAMACHMHIPT SGATGQPDAGAAQPPRGWDSAAATTPTPRA/ALPTGAPVVPVPA TGYYSPYALYGQRLTTASAAGVSVRGGERGERIGRKRGGVQGE AASRTRLLTPARGEGLGPRKERNVLPYISYPTAATETRWDTPLLPTF TSHTQTL
5185	A	6	56	VVAWRGSDSFGSLTSLVQVQVHHQLLKTVPQAHFY*LPRAALQQ IHRG*LPR/DTSQVAASLLASKSSSQTSGSLVSKSTSLASVSQLASK SSSQTSTSQLPSKSTSQSSESSVKFSCKLTNEDVKHEATFF/LIRLY KTVAWKLAVGGFSPNVNHGELLNAAIEALKATLDVFFVPLKELADL PQNKSSQESIVCELKCKSVYLGTCGKSKENAKAVASREALKFLKK KVVVKICKRKYRGSEIEDLVLLDEESRPVNLPPALKHPQELL*CVQN ITAYNIWYLRKRTDFCIV*N
5186	B	133	345	RLSERRNWTQAMLYLKGAQGRYLLRPEPANGPLRPAHCRIDHAPI STYYILRRPEPSYRSSSYFPDD*
5187	A	2	2168	KESRRTVRRMLRGRSLSVTSLGGLPQWEVEELPVEELLLFEVAWEVT NKVGGIYTVIQTKAKTTADEWGENYFLIGPYFEHNMKTQVEQCEPVN DAVRAVDAMNKHGCQVHFGRWLIIEGSPYVVLFDIGYSAWNLDRWKG DLWEACSVGIPYHDREANDMLIFGSLTAWFLKEVTDHADGKYVVAQF HEWQAGIGLILSRARKLPATIFTTHATLLGRYLCAANIDFYNHLDK FNIDKEAGERQIYHRYCMERASVHCAHVFTTVSEITAIEAEHMLKRK PDVVTNGLNVKKFSVHEFQNLHAMYKARIQDFVRGHFYGHLDLFDL EKTFLFLIAGRYEFFKTKGADIFLDSLSRLNLLRMHKSIDITVVVF IMPAKTNNFNVELTKGQAVRKQLWDVAHSVKEKFGKLYDALLRGEI PDLNDILDRDILTINKRAIFSTQRQSLAPVTTHNMIDDSTDPIILSTI RRIGLFNNRTDRVKVILHPEFLSSTSPLLPMDYEEFVRGCHLGVFPS YYEPWGYTPAECTVMGIPSVTTNLSGFGCFMQEHVADPTAYGIYIVD RRFRSPDDSCNQLTKFLYGFCNMSRRQRFIQRNRTER\LS\DLLDW\ RYLG\RYQ\HAR\HLTLRQSFSKINFHVG*HAPPTDRKDFKYPR\ PSCSYPPFSQGS SP\Q\SSDVEDEVEDERYDEEBEAERDRLN IKSPFSLSHVPHGKKLHGEYKN
5188	A	1	1347	MKRLLERRNWTQAMLYLKGAQGRFISDQSRKDLSDRPLPESVSS PERRGSEAPSDTVRPAARVGSSSSWMPSAGAGSSRVQPRANGGKGG PGWRCGSPSLIGLRLFSQPSGCQERRSPNPQLLTPEAATILLASLQ

				KSPREEQFSSKAIWEGAVEVQRKASESKQFEKCLHKEEQPKAVSEPEW REEGIRACEGVYGERLVTQKKIDPICKSLKVILHPEFLSSTSPLLPM DYEEFVRGCHLVFPSPSYEPWGYTPGGLGFPPLSAYKDIGAGLKPS FGLFPLAAECTVMGIPSVTTNLSGFGCFMQEHVADPTAYGIYIVDRR FRSPDDSCNQLTKFLYGFCKQSRQRRIIQNRNTERLSDLLDWRYLGR TEGFKYPRPSSVPPSPSGSQASSPQSSDVEDEVEDERYDEEEEAERD RLNIKSPFSLSHVPHGKKKLHGEYKN
5189	A	1	272	QTEGFKYRRPSSVPPSPSGSQASSPQSSDVEDEVEDERYDEEEEAERD G/RVY*ESPSILYAVPYSDSCCQVTPSLHCSHFFILFPKTDKSS
5190	A	2	603	PRVRERGVSDSCCQAPGQSEKEGQIPS\NPSGAS*HSLPMPRC*AT VSHRSLCPEWPAPRPCNSPSPSPQEPQPPPLWPLLGVILAPQNVTV SVWCAGSPTAVPGPCSWPASMPSAPSA*SSCCACRTTPGPSPARCA ARSPPSPGASSAACATMRRWWSWPSHAQRYRSVLRGWILLTWQQD TPAWWERMDRMK
5191	A	225	432	SNQIRQMEEVKISKKSKVGILPFVAFEEFAGLAESIFKNAERRGDL DKAYTKLIRGVFVNVEKVANE
5192	A	16	1420	PSVRRNQRF*SCKDFDYWHN*RKQEGCYT/VLEKKVLSNRKQRF/ DGSSGKLTGSTSSLNKLVSQSSGNRRSQSSSLDMGNMNASDLDVAD RTKFDKIFEQVLSELEPLCLAEQDFISKFFK\HSNIKVCLELWAGSR GPGMGGTIITAT*LLGTPLPVSEKDMIRQMMIKIFRCIEPELNNLI ALGDKIDSFNSLYMLVKMSHHV*LQQNVDPASFLSTTLGNVLVTVK RNFDKCISNQIRQMEEVKISKKSKVGILPFVAFEEFAGLAESIFKN AER\RGDLDKAYTKLIRGVFVNVEKVANES\QKTPRDVMMENFHHI FATLSR\LKISCLEAEKKEAKQKYTDHLQSYVIYSLGQPLEKLNHFF EGVEARVAQGIREEVSYQLAF\NKQELRKVIKEYPGKEVKKGLDNL YKKVDKHLCEENLLQVVWHSMQDEFIRQYKHFEGLIARCYP\GSGV TMEFT
5193	A	2	391	FFFFLRWSLA/SV/TQAGVQWRGLGSWQRPPPGFKSFSCSLSSWD YRRPP\HAQLIFVFLVETSFTMLAGMVIS*PRDPPASASQSAGITG VSHRARLTLLIFKRCSIRDESFEVFLYVYLFKTNILLKA
5194	A	2	302	KTLQSGCPRLEVQWCNLSLQPL/PFPGSK*FSCSLSPG\SWDYRSV PPRSANF*FLVETAFHHVGQAGLELSTSGDPPVSASQSAGITGVSH SARQ*RAF
5195	A	2	388	RATPRHIIVRFTKVEMKEKMLRAAREKGRVTLKGKPIRLT\ADLSAE TLQSRREWGP/IFNILKEKNFQPRISYPAKVSFISER*IKYFTDKQM LRDFTLSRPALKELLKEALNMERNNRYQPLQNHAKM
5196	A	1	578	VAACKMHKDAKKGFIRLDMS*FQERHEVAKFIGSPPGYVGHEEGQL TKKLKQCPNAVVLFEVDKAHPDVLTIMLQLFDEGRITDGKGKTIDC KDAIFIMTSNVASDEIAQHALQLRQEALEMSRNRIENLGDVQISDK ITISKNFKENVIRPILKAHFRRDEFLGRINEIVYFLPFCHSELIQLV NKEC
5197	A	3	1618	MKLLRTSEAKYQEQKQKREAEERRRFPLEQRLKEHIIGQESAIATVG AAIRRKENGWYDEEHPLVFLFLGSSGIGKTELAKQTAKYMHKDAKKG FIRLDMSEFQERHEVAKFIGSPPGYVGHEEGQLTKKLKQCPNAVVL FDEVDKAHPDVLTIMLQLFDEPLDGIQVHSYDQTRMCPLGALCLVDR WKGDMVVAGILHFVCHSLSSSEAYVYQFNPFNNPPKLAIITASIEQMW KLKQKSALWDQVEEDLGHALPGQSPWLARLKFFDHKGSSSGSGRGS SCCLDCKVIHLAKCHLLAVDVPSSAAWLQTLQCNPLRKGSWTLEPTN NPPELSALEMLENSLCSPTWEGSQFWVTVQRTAEVHCGLHASVYLR VEAERLTLLTMGAQSQTAQGNDIFQADETAIHRQKAQGKARQGHNA RADSHERKVVEGKFSSPPGPQELLESPPALYAEPLDSLHIASGPSQG SLYSDLLDGTLAGAGEGVQWKPLYWDLYEHEQQQLLAKLTDPKED PIYDEPEGLAPALPQGLYDLP
5198	A	495	653	MTLTSIDPVLTTFFNLECP/VFTATASSGLGEVE*AIALN
5199	A	1	1433	MPESNCSLTWRHSVGRAVAAQGGEHSSQGASLVLGEPGGSSWLLGL EGDTGLWGGLLKEGRLTDGKGKTIDCKDAIFIMTSNVASDEIAQHAL

				QLRQEALEMSRNRIAEN\LGDVQISDKITISKNFKENVIRPILKVRG LSWHFLLPEKAFRRDEFLGR\IGEIVYFLPFCHSELIQLVKNELNF WA\KRAKQRHN\ITLLWD\REVADVLVDG\YNVHYGARS\IKHEVER \RVVN\QLAAAL*SRTLLP\GGCTLRITVEDSDKQLLKSPPELSPQA EKRLPKLRLEIIDKDSKTRRLDIRAPLHPEKGRITDGGKGTIDCKDA IFIMTSNVASDEIAQHALQLRQEALEMSRNRIAENLGDVQISDKITI SKNFKENVIRPILKVRGLSWHFLLPEKVLTTFFNLVLYLHGNSIQR LGEVNLAVLPLRLSLTLHGPNMEEKGYRRARGHSLHQIEKYICE SDDIFRKYCNNQFL
5200	A	1823	4712	FFKKNLCASAHYY/TWCVPLPFFFFLQGL/NSIGQAGVQWCNHSSL QPCPPRLKLSLHLSLPSSWDHRHAPLRMT/NFFKYLRRLPVLPRLV SNSWAQVVLPS/SASQSIGITDMSH*PAQLPNSLPFFKRQFRSISP GLGMQ*CDHSSL*PQTLGLKQFSHQPPFYFFVQMGSCYVAPSW*TP KENTTIIQHPHMYTLKTTVTFLYTELYSDIA
5201	A	3	298	RQSCSVA*AAVQWRDLSSLQPPPLGFKRFSCSLSSWDYRRPPRS VNF*KIFLIETGFHHLGQAGVERLTS\DPGASASQAGIIGISHCTW PELKF
5202	A	1	422	APMPAATMTARSGPAAISTRCPWRPRSPSTPRPSWSGTCCAPTRSLR RAATASQGPSPATNTPSPRAASPP*RVWAPRTETIKGHTAHSRTGA TTGPKLSAP/VATESGHPDSQKPPTHPGTSD\TILPPETASHPSTRR P*LPPETASHPSTRRP
5203	A	123	201	KRGFCWVPQVGGQGHDFGLWQSPFGLRQFSGFFLWKSWDYGHPPPC *ISSSSSSSSS\FSSSSSSSLKLT*GDPLA*VSQRVGIPGLSHWP* PRLGGRGTILVYGNLHFRD
5204	A	88	167	KINMGILLKLVRFNINPVKTPAGLFSSSSHE/ITEIDKRILKFIWK CTEHRIAKQSLKRTKLEDLLNFKTYEATEIKTS*YRFNINPVKTP AGLF
5205	A	179	474	FGFQINVFKDPVADPNKRSKKGRLSLHRTF\AGNFVTL*GKGDLEE YG\QDLLHTV*KNGKVTKAYSFDEIRKNAQLNIELEAARSLGLMDW VCVVC
5206	A	195	351	LLPLQDKSEATRGALSQRPCRPRPNSLPLNLPEEETLRIRARIFSSQY SQKD
5207	A	1	1080	ERCTMPDEPLVRAPDKGTDSPPSPPLEETSNGGRMLHESLRHAVPIT RMQSSSEDTEAG\PAYSEDEYEDIEPRTLNEITVTDKTSPWSSVI SDTSEVISPPQDEVQREGPSCPSPGPFCEELMVKSSFLSSPERAVN PHLPRQD\SPSQSLVACECEASKARVGGESASANPQIPCPITLSGAQ QSSTFVGWSSPQTDQNKPEKSEAPA\EELKVATS*GSVDS\A*LAFK KLPLNLASQSRRENHKGPPIDSSDIRQRQVTTGSETSTKQSLLLPGP IVVPNFFLPPQLEASRLMLSLSATLPPAATTQDKSEATRGALSQR PCRPRPNSLPLNLPEEETLRIRARIFSSQYSQKD
5208	A	1	1140	AIVEDKHSGRSYDITSDLGNVLTSTSIKTVNG*AESSDGAESDEE DAQEDLMGAYHSDIDKMMKIVADHKNLEIVTNGYDKDGFVHDIQN DIHASSSLNGRSTVHVKPIDENLGQTGKSAVCIHQDINDDHVEDVTG IQHLTSDSDSEVYCDSEMEQFGQEESSLDSTSNMNGPFQYYLGVHSSPP MENSGFREDIQPPGNGNIGNMQVVAVEGKGEVKHGEGDGRNNSGAP \HREKRAGETDEFSNVRGRGRHMQHLS\EGTKGRQVSGSGDGERWG SDRGSRGSLNEQIALVLMRLQEDMQNVLQRLQKLEMLTALQAKSSTS TLQTAPQPTSQRPSWWPFEMSPGVLTFAI IWPPIAQWLVLVYQRRR RKLN
5209	C	68	331	MLKNVLMRCKGVHDREKFLVLDYFCQSSVLAVLYLILSLCYFPYQDV ASECEVKCMPTFQFFKKGQKVGEFSGANKEKLEATINELV*
5210	A	935	1036	QMFQFPPPKNPITTKTHTQITSQLHICISLTKQ
5211	A	1	3270	MRPKTFPATTYSNSRQRLQEIREFGLKQPSKSSVOGLPAGPNSDTSL DAKVLGSKDATRQQQMRATPKFGPYQKALREIRYSLLPFANESGTS AAAEVNRQMLQELVNAGCDQEMAGRALKQTGSRSEAALEYISKMGY LDPRNEQIVRVIKQTS PGKGLMPTPVTRRPSFEGTGDSFASYHQLSG

				TPYEGPSFGADGPTALEEMP/PAVRGLPFFRSRPPRARPPAPAPTQG LRCQRRGSRGTLPAAGRALRAAAPAGAWGTPGLRSAAQPLLPEQDAA GDRGLRQPA\PKGQGGPPGAGLAFPPAAGLYVPHPHHKQAGPAAHQ LHVLGSRSQVFASDSPQSLLTPSRNSLNDLYELGSTSVQQWPAAT LARRDSLQKPGLEAPPAHVAFRDPVPSRTNSFNHQPRGPPGK AEPSPAPNTVTAVTAAHILHPVKSVRVLRPEPQTAVGSPHAWVPA PAPAPAPAPAPAAEGLDAKEEHALALGGAGAFPLDVEYGGPDRRCPP PPYPKHLRLRSKSEQYDLDLSCAGMEQSLRAGPNEPEGDKSRKSAK GDKGGKDKKQIQTSVPVRKNSRDEEKRESRIKSYSPYAFKFFMEQH VENVIKTYQQKVNRRQLQEQEMAKAGLCEAEQEQMRKILYQKESNYN RLKRAKMDKSMFVKIKTLGIGAFGEVCLACKVDTHALYAMKTLRKXD VLNRNQVAHVKAERDILAEADNEWVVKLYYSFQDKDSLIFYMDYIPG GDMMSLLIRMEVFPEHLARFYIAELTLAIESVHKMGFIHRDIKPDNI LIDLGDHKLTDGFLCTGFRWTHNSKYQKGSVHRQDSMEPSDLWDD VSNCRCGDRLKTLQARQKQORCLAHSVGTPNYIAEVLRLKGYT QLCDWWSVGVLFEMLVGQPPFLAPTPTETQLKVINWENTLHI PAQV KLSPEARDLITKLCCSADHRLGRNGADDLKAHPFFSAIDFSSDIRKQ PAPYVPTISHPMDT\SNFDPVDEESPWNCQR/ EVSTKAWDTLTSPN NKHPEHAFYEFTFRFFDDNGYPFRCPKP*EQKLHKAESSDLESSD LVDQTEGCQPVYV
5212	A	3	274	LERLIFVGGGLGQFFPPPKLRFFPKIPQLVFFSPPPFRKKIFPCPPRLS LGPPRVLLKGPPSSSSSSSSSKKC*PLMFYCHRRWPTGVYVLP
5213	A	403	776	QGDHFSLSFWHLLQAPGLSPCLKWATALETPPSPNGLPIVPVFGSS RMAGMIE\SHIISEIGFLPNKEKKKGGCPLFPFRNFGFKFAPSGLKV G\YLVKFEPKLNYSDDHVIKWR*\IGR\SGIY
5214	A	165	440	PPRQAKMQNLAAAGSHSQSPW/TLRPKAL*LTPSQIFSA*RLKTDTA RSPRKPPSFQGPVSLASITVVGIDQASKPLKTPQLWCQLRQYSFK
5215	A	2	525	AAED*HCPIASETYKTIT\ELWVTLPEVEGKSVPLINTEATHSTLPS FQGPVSLASITVVGIDSQAYKPLKSSQLWCQLGQYSFMHSFLVIPTC PVPLLGQDILTCLASLTIPGLQPHLIATLFPKPPSHPLVSPHL NPHIWD MSTPSLVTDHAPLTIPKPNHPYPVQC
5216	A	1	425	PGNEIYR/KGTISFFEIDGRKNKSYSQNLCLLAKCFLDHKTLYYD TD PFLFYVMTEYDCKGFHIVGYFSKEKESTEDYNVACILTLPYQR/RG Y/GKLLIEFSYELSKVEGKTGTPEKPLSDLGLLSYRSYSQTINEIS EITS
5217	A	25	193	LGGCEDSRKGAAPRCFLSRGDHSWEPRD*PPPWLFPNSNC**LAAGR PSPVRSSPS
5218	A	1	1383	MAEVGEIIEGCRLPVLRRNQDNEDEWPLAETLSVKDISGRKLFYVHY IDFNKRLDEWVTHERLDLKKIQFPKKEAKTPTKNGLPGRPGSPERE VKRKVEVVPATPVPSETAPASVFPQNGAARRAVAAQGRKRKSNCL GTDEDSQDSSDGIPAPRMTGSLVSDRSHDDIVTRMKNIECIELGRH RLKPWFYFSPYPQELTTLPLVLYLCEFCCLKYGRSLKCLQRHLTKCDLRH PPGNEIYRKGTISFFEIDGRKNKSYSQNLCLLAKCFLDHKTLYYD TD PFLFYVMTEYDCKGFHIVGYFSKEKESTEDYNVACILTLPYQRRGY GKLLIEFSYELSKVEGKTGTPEKPLSDLGLLSYRSYSQTILEILMG LKSEGERPQITINEISEITSIKKEDVISTLQYLNINYYKGQYILT LSEDIVDGERAMLKRLLRIDSCLHFTPKDWSKRGKW
5219	A	1	1617	MAEVGEIIEGCRLPVLRRNQDNEDEWPLAEILSVKDISGRKLFYVHY IDFNKRLDEWVTHERLDLKKIQFPKKEAKTPTKNGLPGRPGSPERE VPASAQASGKTLPVQITLRFNLPKEREAIPEGGEPDQPLSSSSCLO PNHRSTKRKVEVVPATPVPSETAPASVFPQNGAARRAVAAQGRKR KSNCLGTDEDSQDSSDGIPAPRMTGSLVSDRSHDDIVTRMKNIEC IELGRHRLKPWFYFSPYPQELTTLPLVLYLCEFCCLKYGRSLKCLQRHLTK CDLRHPPGNEIYRKGTISFFEIDGRKNKSYSQNLCLLAKCFLDHKT LYD TD PFLFYVMTEYDCKGFHIVGYFSKEKESTEDYNVACILTLPY QRRGYRKLLEIFSE\YELSKVEGKTGTPEKPLSDLGLLSYRSYS\Q

				TILEIL\MGLKSKSERPQITSNDISEITSIKKEDVISTLOQLNIN YYKGQYILT\LSEDIVDGNERPMLK\RLLRIDS\KCLHFSQRTWSQ EVDSDQDTCPHCKCQRPASQDLGAD
5220	A	890	1537	MLLMFICDLLLLTSCSIALGYELSKVEGKTGTPEKPLSDLGLLSYRS YWSQTILEILMGLKSESGERPQITIK*AWRCLPGGTWHGLSVPGLSL SGLLGTDKGPQGT*PVLHSEISEITSIKKEDVISTLOQLNINYY/ KGREAGRGDRCVGCRCVQSSVG*PPAEPISQAQGYILTSEDIVDGH ERAMLKRLLRIDSCLHFTPKDWSKRGKW
5221	A	2	435	LRDGVLLCHPGWSTVAQS*LTAALNFW\VRGSSCLSL*LVLRNSPL HPANLFFYFCR/DKHLTILTRLVLNFWAQVILRPWLPKGLGITGMSH CTQPNFKNQKGYCQVNFNNQTKTSLAGNTYFTPILPFGNKHVTSY NFPSM
5222	A	3	384	VVAEVPSEFFFFLRTESCFVTQAGLQWHDLGSAISI/SPGSSDSPA SASQVAGITGRHHYALA*FFVFLVDMGIHHVSGWSRNSLNLVNLPC LGPPQYWGLOQMSPPMPRLKCPKSLKGMPSHP
5223	A	2	322	LYFFSFETESCSVTQAGVQ/WWCDLGSLAT\PPP\GSSNSCASAS*V ARITGVHHAQLMFVFLVETGFHHFGQSGLKPLSDPPASASQSAGIN RCEPPGTGHHYIFSK
5224	A	1	2535	MQPLDFSSGGSDPNISLSEKIRDQLVVGQLIPDCYVELEKIILSERK NVPIEFPVIDRKRLQLVRENQLQDENELPHAVHFLNESGVLLHFQ DPALQLSDLYFVEPKWLCKIMAQDVSSIFGLYIRDILTVKVEGCPKH PKGIIISRDVEKFLSKKRKFPKNYMSQYFKLLEKFQIALPIGEEYLL VPSSLSDRPVIELPHCENSEIIIRLYEMPYPFPMGFSRLINRLEI SPYMLSGRGICILLGQVVDHIDSLMEWFPGLEIDICGEGETLLKKW ALYSFNDGEEHQILLDDLMKKAEGDLLVNPDPQRLTIPISQIAPD LILADPPRNIMLNDELEFEQAPEFLDCFVCIHLYPSSDYISRHYM RTINIVQTGFAKCRWRVTVHGADHGDGSGSVYRAAYEGEEVAVKIF NKHTSLRLLRQELVVLCHLHHPSLISLLAAGIRPRLVMEASKGS DRLLQODKASLTRLQHRILHVAHGLRYLHSAIIYRDLKPHNVLL FTLYPNAIIAKIADYGIAQ/SLL*NGD*KTIQRTGTFRAPEVARG NVIYNQADVYSFGLLLYDILTGGRIVEGLKFPNEFDELEIQGLP DPVKEYGCAPWPMVEKLIKQCLKENPQERPTSAQVFDILNSAELVCL TRRILLPKNVIVECMVATHNSRNASIWLGCIGHTDRGQLSFLDLNTE GYTSEEVADSRILCLALVHLPVEKESWIVSGTLLVINTEDGKK RHTLEKMTDSVTCLYCNFSFSKQSKQKNFLLVGTADGKLAIFEDKTVK LKGAAPLKILNIGNVSTPLMCLSESTNTERNVMWGRMWHKDFLLF
5225	A	2	223	LGVAFCFCFFCFWFVLFVGLQLLSNLEKFQPLCLQIFFLSPCPIR SLYI/C*SSKVVSQTLVTLLVFPVFFSL
5226	A	236	1626	LAAAHPPLAGLVGGEAWIGGAKSWLSFSAGSSCMAEMATATRLLGWR VASWRLRPPLAGFVSQRAHSLLPVDDAINGLSEQRQLRQTMKFLQ EHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLG\ITAPVQYGGSGLG YLEHVLVMEEISRASGAVGLSYGAHSLNLCINQLVRNGNEAQKEKYL KLISGEYIGALAMSEP\NAGFWMVSMKLKAEKKGNHYILNGNKF NGPDADVLIVYAKTDLAAPPA\SRGITAFIVEKGMF\GFSTSKKLDK LGMRGSNTCELI FIEDCKIPAANILGHENKGVYVLMGSLDL\ERLVLA GGLLGL\MQAVL\DHTIPYL\HVREAFGQKIGHFQ\LMQGMADM\Y TRLHGLFGQYVYNVAKACDEG\HIIPKDCAGVILYAAECATQVALDG IQCFGGNGYINDFPMGRFLRDAKLYEIGAGTSEVRRLVIGRAFNA DFH
5227	A	1	867	MATATRL\LGWRVASWRLRPPLAGFVSQRAHSLLPVDDA IKGVLR/E SQRQLRQTMKFLQ\NLAPKA\REIDRSNEFKNLREF\WKQLGEPW AVFGASQPLVQYG\GFRPGAYLGSMLLG*WEEISPSFSGAVGL\SYG AHSNLHQPSLLRNWEFRAQKEKYLPEG*FSG\EYIGALAMS\KPHA GSDVVSMLKLAKEKKGEATLNLGAKMGRGNHYILNGNKF WITNGPDADVLIVYAKTDLAAPPASRGITAFIVEKGMFPGFSTSKKLDKLGMRGSNT CELI FIEDCKIPGK

5228	A	3	391	SHHHPLAAPSLGEEAISRSFQSLACSPGLPAADRISYSGRPGSRQAG LGRAGDSAVLVLPSPGPRSSRPSMDSEGGSLLLDEDSEVFKMLQEN REGRAAPRQSSSFRLQEALEAEERGTPAFLASSLPQSFLARLQG /GLATPPKLHTCEKCSSTIANQAVRIQEGRYRHPG\CYTCA\DCGLN LK\RRGHFWVGDELYCEKHARQRYSA PATLSSRA*APFGSCRKPWKL RREVARQPSWPAH
5229	A	2	384	FVHFQSKKTMRKICLFFFFSSETGSRSVSQAGVQ/WARVIAHCNKLK LDSSDLPALALAS*VARTVGMYHRGLACVYFIIQINLILYFLAQMNL KKHQTFLFYEMLNLIASQAGKIYSSNRNIKVFWPQ
5230	C	301	369	MPTLYNHCFLQLFTIISKLISY*
5231	C	210	329	MWNLCIWRVNTINNTMPTLYNHCFLQLFTIISKLISY*
5232	A	2	268	FFFLKRD\RVSFCHPGLSAVAQL*LTVALNS*\VKGSSYLSFQS/SW HYRYVLPYLANFKNFFFKRRELTFLRLILT SWAQVSFLLQPPK
5233	A	1	415	LFAGPSAMFYLA AAVSDFYVPVSEMPEH/KIQSSGGPLQITMKMVPK LLSPLVKDWAPKAFIISFKLETDP AIVINRARKALEIYQH QVVVANI LESRSQSFVIVTKDSETKLVSTHSFYR*QK LK*KALIGSKIVQGS
5234	A	3	705	PVRFLDNFSSGRRGATSAAFLAAGYGVLFYLRARSAPFYAHRFPQ TWLSALRPSGPALSGLLSLEAEENALPGFAEALRSYQEA AAGTFLA VE\FTTLADYLHLHQAAAQALNPLGPSAMFYLA AAVSDFYVPVSEM EHKIQSSGGPLQITMKMVPKLLSPLVKDWAPKAFIISFKLETDP AIV INRARKALEIYQH QVVVANI LESRSQSFVIVTKDSETKLLSEEKKK
5235	A	200	636	GPCAMFYLA AAVSDFYVPVSEMPEHKIQ\SSGGPLQITMKMVPKLLS PLVKDWAPKAFIISFKLET*PR/LIVINRARKALEIYQH QVVVA\NI LGVKDSPLCLL*PKDSEPKLLS EEEIEKGVEIEEKIVDNLQSRHTA FIGDRN
5236	A	17	424	LVVISPCGGIPGTAA AATMSDQQLDCALDLMRRLPPQ QIEKNLSDL IDLVP SLCEDLLSSVDQPLKIARDKVVGKDYLLCDYNRDGDSYRSPW SNKYDP PLEDGAMP SARLRKLEVEANNAFDQYRDLWRMMKL
5237	A	1	338	SDRQLDC/ALDLMR/RLPPQ QIGKNLSNLIDLVP SLCEDLLSSVDQPL LKIARDKV VAKDYLLCDYNRDGDSYRSPWSNKYDP PLEDGAMP SARL RK LQVEACFCHTSLSVLSTFP
5238	A	2	160	ENKIRSTLNEIYFGKTKDIVNGLRSVQTFADKSKQEALKN DLVEALK RKQCC
5239	B	46	426	MSDQQLDCALDLMRRLPPQ QIEKNLSDLIDLVP SLCEDLLSSVDQPL KIARDKVVGKDYLLCDYNRDGDSYRSPMEVTKYDPSLGRMGNAVKL RAEKSLEVGKANKWPFQYPKTLLLELLDPG*
5240	A	2	938	PRVR*APGPAAGGRATDAGTGTA A AATMSDQHLD CALDLKRRLRPQ QIEKNLSDLIDLVP SLCEDLLSSVDQPLKIARDKVVGQDYLLCDYNI DGDSYRSPWSNKDDP PLEDGAMP SA\RLRK\LEVEANNAFD\QYRDL YF*KVGVSSV\YLWDL\HGFGLS/VILHKRKGWEDGIKR RSKGCW\ DSI\HVVEVQEKSSGRTPHYKL TSTV MLWLQTNKSG\ SCTMNLGGSL TRQMEKDET VSDCSPQIS/ATIGRLVEDMENKIRSTLNEIYFGKNKG YRSMGLRSV\QTF\ADNSKQEAL EELTLVGGFERESKQC
5241	A	1	1911	MTLEDPPGFCERLLSRVAALFPALRSGGFQAHYRAHSSSLCPAENPW VLTCCLLN LDEDGDLVAFSSDEELTMAMSYVKDDIFRIYINDSPAV ENISSFCFVSLKSAGRADALKERQSGSTAHVQLRLQSGRGN SGHSQ RPSNYKVL AGSQ RDNFTDITAAAAAPSGLYLDNVVNKQSVSPPIPH LRALLSSDDPPAEVDIFELLKVSYEKFSSLRAEDIEQMRFKQRLKV IQSLED TAKRSVDRFSELQLSRQTQHEHFKELDNFYKISSHEQSYGS QPPILQPALGAAQHCASHSVTCQSTSFLQLKKGKTKLYAEKQLNSTW SRQTSGANLRVLHEAREAQSSGPAPSI SRMDARQWALVLLPSSRESSQ KRTRTCS PRGDEDPGKFKEAELKMRKQFGMPEGEKLVNYYSCSYWK RVPRQGWLYLTVNHL CFYSFLLGKEEKKRHL SICKIIPVCAKGWVQF SSEMLHQHRWVLRQCDPKHLGSLPDKSQAPPTLTHQDQKRPGLSLLG PGCCAGTLPLQLTGLPGCRFFFRSGNIEHPEDKLFNTSVEVLPFDN PQSDKEALQEGRATLRYPRSPDGYLQIGSFYKGVAEGEVDPAGGPL

				EALRLSIQTDSPVWVILSEIFLKKAD
5242	A	3	803	ESVAAALSPLG\IEVDIDVEHGGKRSR\LTPVS\PEVS\ATGEKSSS QPSSCC\SDPSKPGGVEGATQSLAEQMRKIALESEGRPEASLCFPF PPGTTGQPSDLWPAPPPHSQHLCSPYKPEGAGCWLAVDVCCHLKSR WEPARTL*LLGLCEWPLFPLDPCSLNCTCACVLPDCLPGARAMVRLG LLRVSPVCSW*VLFQEQMESDNCSSGDDDWTHLSSKEVDPSTGELQS LQMPSESEGPSSLDPSQEGPTGLKEAALYPHLPFGK
5243	A	2	1511	RGGCDRDGPFSSASSPLAMASLTVKAYLLGKEDAAREIRRFSCCSPE PEAAEAAAAGPGPCERLLSRVAALFPALRPGGFQAHYRDEGDGLVAF SSDEELTMAMSYVKDDIFRIYIKEKKECRRDHRPPCAQEAPRNMVHP NVICDGCNGPVVGTRYKCSVCPDYDLCSVCEGKGLHRGHTKLAFFSP FGHLESEGFHSRWLRKVKHGFGWPGWEMGPPGNWSRPPRAGEARP GPTAESASGPSEDPSVNLKNVGESVAA\ALSPLGIEVDIDVEHGGK RSRLTPVSPSSSTEES\SSQPSSCCSDPSKPGGVEGATQSL\AE Q\MRKIALE\SEGRPEEQME\SDNC/SQGGDDDW\THLSSKE\VDP\ STGELQS\LQ\MPSESEPKLSGTPPREG\PTGLERKLPYHPH\PE V\DPRLDLSPPFSQIACSMGLSS*LKGGLGSTRVPGRPKNY*HSERLW DTIQ\YSK\HPPAVVDHFLPTFFLRAPLLVFIUVFKLCVELAGLL
5244	A	24	493	HWQVLPRVKRLSPLKTHNCALPSTKLSAVRDYLFYSENLFNPQLNK DS*RGK*QALK/SPTAVVFLSLSHSFSFAVSEGCFHRERQVASTS MEQLLSLLAGIPFVEDSCPLQKELSKTLPLTLEVLGVSMFFKFSWLP VIWVFGFISQLSGLES
5245	A	1	4547	MRNPVHSHIGATVSHQTDGANGVNPMPALQSQLITSDTYSMQQMIP SNSTRLPVAYQGNQGLNQSFSEQQVDWTQCCISKGLTYPDYRPPPKL YRYSPPQSFLPDSTIQKQNFIPHTSLQVKNSQLHNSVLTLPSTQSAV PSQQYATQTDKRPPPPYNCRYGSQPLQSTQHITKHLMEVPPQSREM LSSEIRTSFQQWQNPENNVSTIGNFTNLKVNTNSKQPFNSPIRSSV DGVQTLAQTNEEKIMDSNPTSQVLDTSVAKEKLVRIKTLVEIKQ KFSELARKIKINKDLLMAAGCIKMTNTSYSEPAQNSKLSLKQTAKIQ SGPQITPVMPEAERQTPTVVESAEETNKTCMLNSDIQEVNCRFRNQ VDSVLPNPVYSEKRPMPDSSHDVKVLTSTKTSVAVEMTQAVLNTQLSSE NVTKEQNSPAVCETISVPKSMSTEEYKSKIQENMMLLLALLSQARK TQKTVLKDANQTIQDS/ITRQL*NESKYPNDW*PTEFEETWNSKYF* S/ILQILQKKRSVINSEQTQQQLEFQSLLTSTLRVLVQL/SGNSNSQ NKISNPSQQTALSM/VNAQL*VFRYKYNKGNRTSDSCSVTVSSVRGQ NIVCQRNNTCSVT*NSVSRY*RGQCLWFKYNWQKMQRQLLL*KL VDQ*QVQQHQPRFFH*LRRKSRMSQLMVIQKSHLMSIKESITN*SQ/ LIHSPMNDQQISQESRNSTVSSDTLQIDNICSLVEGDTSYNSQIAK IFSSLPLKMVEPQKPSLPNQOGIGCREPEKQLDNTTENKDFGQKDK PVQCTDVSHKICDQSKSEPPLESSFNNLET/QQSYSREK*FGACHLK KAQLTIRARQLAIQEDIYPQEIASSNYTPQDPARNEIHSKAPVLY LHDQSELLEKFPYGIEAVNTREGSVGQQTYYQTSQDQADKTSSDS KDPADQIQITILSSEQMKEIFPEQDDQPYVVDKLAEPQKEEPI TEVV SQCDLQAPAGQSRDSVILDSEKDDIPLLCIGLALHGLRRSTPVSV* FHQELI\LEEBKQKEQCSPLDTNSCKQERTSDRDVTVVQFKSLVNN PKTPPDGKSHFPELQDDSRKDTPKTKHKS LPRTEQELVAGQFSSKCD KLNPLQNHKRRKLRFHGNLSLQ**NDSIL*TSFS/EKPDRRNM*HR THVH*KQKQLFLPNKDVKHSSLGQSLSPKIKLKLKSVSFKQKRK LDQGNRIR*EVKKKKHDKQEQKGSVGATFKLSDSLSPNERAIVKE KMVSNTKSVDTKASSSKFSRIILTPKEYLQKQKHKEALSNAKSKKICV KNVPCDSEHMRPSKLAVQVESCGKSNEKHSSGVQTSKESLNGLTSHG KNLKIHSQSESETYNILRNVKEKVGKQPDKIWIDKTKLDKLTNIN EAQFSQMPQVKDQKKLYLNRVGFKCTERESISLTKLESSPRKLHKD KRQENKHKTFLPVKGNTKSNMLEFKLCPDILLKNTNSVE\NGRM*S LILGRSKPLCKFQE*KVQKKTG
5246	C	191	397	MLPRAGLLLCGLVPNNFSQPSRQILLCLGCDSPHLTVGHEGWKTTL

				PGAGATPYRIGPFSLLQRGVS*
5247	C	598	744	MSKVLNQSTYITVQCGYVSINSFYVSFYYSIKLAKRHLGTFFRVLV I*
5248	A	164	355	NGSTGCIGIQANQYFNYSLSSESGKFVKCTEQLELVPGENIH*L LEGSKKKLTLKNLFRNM
5249	A	1	308	KVQSFFIFYLFIYF*DGVLFRPGWSAVVLSRLTATSA\FRFKQFSC LSLPSSWDYRCPPLHLANFCIF**RRGFTMLARLVIS*PQVIRPPW PPKVLGLQM
5250	A	67	367	SDELRTPGRESLPAENISL*DRVNHQPAIESCTA*NYLYSINAKTKG EMLEAEGMRVVTNSVYHWRLECEKQQTVMKAGCWRTDKLCLPPEGML WAVMSR
5251	A	1429	1621	IPWIPPVSRSMVTHTRAPTRFVHLPFFQTDPFVVFISAFVLLRLV QKQP*QVVPDQGPGR
5252	A	180	411	IPWIPPV/CPFHGHTLE/VHPHGLSISLYSPPADSPVQGFVRLIS FTFSALADLPRSGPWSDTTCHGCFTVAASSEL
5253	A	288	532	FRNLPLPIPSQGTDLIFSAGRLSRPGVRSSDQFHFLCGRPSSFRS LVGHLSRMLHCGSLLREPSRPVIRAPVSDEISI
5254	A	9	257	IFTAVAFIISESWKQPQCL*TNE*/IKLWYIHTMQYSAIKRNEKLI HATTVMNSENVQW*KARHKKPHIV*LHLYEGSQKRQI
5255	A	6215	7038	RTVTTFLSKDSHGVCYCAQGGKIPDHQNPQCNRKQHPVSTILMLDKAS FCQLRKRKHNLVNCINRNPMSLKNTSWHSSLSVTQRHQQQSKLHF QGSILLH*PSQNIL/SNI*KCINYC*HCSSVLLSYLFIETESYSVAQ AGVQWHDLLGLLQLLPLRFKQFSCFSLPSSWDYRSAPSPANFCILVE MGFCHVGQAGLKLLASSDPPALASQSAGITGVSHYTQPCSPFLKSTG LFSCVKLSNPYHKGRIYLGRCFLNSTWHLVKSTLFCPLFI
5256	A	2	513	VLIQLVWIALLLVDPSRPVLTKEPASSTSSFTSQSQKKGQSGFL QSRN*GCIALCE/VFQREBIY*VGMD*DSFRIKWFFNFIHFLTIVITS SDLHIHGEIWVVPNTDHCVTRFFVYDDCLVVYAYINTLL*GFY*YI LLVIVNYTGSVHWFIYYLVNLVLCFLLYI
5257	A	1	274	STPPHSSQRACEPLPSFAQCPR*APSPAPHCALICPIPKMEERP/P M*IGR*RRHLLSTYCARSCTEQAPCIILLNPHNVLDLSRLVWKQ
5258	A	3	437	GYLSEVVEENTPPKMEKEGLEIMIGKKGIQGHYNKYLDSTLFCFLF AFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYGYVCATK IMKLRKILEKVEAASGFTSEED/PAGQKVQDCYFYQIFMEKNEKVG VPTIQ
5259	A	1	340	BELNTAPVQESPLPAMPPGNHGLEVGSLAEVKENPPFYGVIRWIGQ PPGLNEVLAGELEDEDECAGCTDGTFRGTRYFTCALKKALFVKLKSCR PDSRFASLARIWSYLLFSA
5260	A	215	385	LPYKEFFLCAIGGQNGFNIPQVTPCEVGEYLKMSLEDLHSLDSRI QGCARRLLC
5261	B	347	1742	MPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPLPAMPPGNHGLEV GSLAEVKENPPFYGVIRWIGQPPGLNEVLAGELEDEDECAGWYGNLQ EGTRYFTCALKKALFVKLKSCRPDSSSVLDTVLLRPKEKNDVEYYSE TQELLRTEIVNPLRISAGQKVQDCYFYQIFMEKNEKVGVPPTIQQLLE WSFINSNLKFAEAPSLIIQMPRFGKDFKLFKKIFPSLELNITDLLE DTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPK RLNHKYNPVSPLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFV KYGKDDSAWLFDSMADRDESNEFVQITGVIGKGKETEGRVLTLLH IRAGSSVHVHCRQWMSLW*
5262	A	1	1547	PVQESPLPAMPPGNHGLEVGSLAEVKENPPFYGVIRWIGQPPGLNE VLAGELEDEDECAGCTDGTFRGTRYFTCALKKALFVKLKSCRPDPSRFA SLQPVSNQIERCNSLAIWEAYLSEVVEENTPTQWEKEGLEIMIG\K KKGIQGHYNKYLDSTLFCFLFAFSSVLDTVLLRPKEKNDVEYYSETQ ELLRTEIVNPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEDPEE FLNILFHHLRVEPLLKIRSAGQKVQDCYFYQIFMGKK*GKLGVPPTI SGSC*EWSFINSNLKFAEAP\SLIIQ\MPRFGKDFK\LFKKIFPSL

				ELNITDLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTC NTQVHLHPKRLNHKYNPVSLPKDLP\DWEIARHGCI PCQNMELFAVL CIETSHYVAFVKYKDDSAWLFF\DSMAD\RDGGQNGFNIP\QVTPC PEVGEYLEDVSWKTLHSLGLPGESQGCARRLLCDIYVPCTQSPTMS LYK
5263	A	29	258	LRKYHATDLIS*GSVVGEF\DCCF\SFLDGSLEDAVDGLL\LALQPH KEQYKEFQDLNQEVMLDDILKVSTFSQKLD
5264	A	98	497	THENNYNEKKDEIKIFKISLQISAQEEFPFFRRWKSCLCCPRLGVQW HDLG\SLQPPTSP/GFKRFSGLKLP/RAAWIYRYVPITSG*FLYFQ* RRGFTHVG\QADLDLLTSGDPPVWASQSAGITGVSHHAQPPYC
5265	A	156	1047	VPAGEARVQWHDLSLQPPPP\GSSDSPASSSRVAGITGIKTNTICK KCAQNVQLYGTTPKPCQYCNIIAAFIGNKCQRCTNSEKKYGPYPYSC CKQQCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSQKTLSTSSIQNEIPKKSKFESITTN GDSFSPDLALDSPGTDHFVIAQLKEEVATLKKMLHQKQDMILEKEK KITELKADFQYQESQMRAMNQMEKTHKEVTEQLQAKNRELLKQAAA LSKSKSEKSGAITSP
5266	A	156	960	VPAGEARVQWHDLSLQPPPP\GSSDSPASSSRVAGITGIKTNTICK KCAQNVQLYGTTPKPCQYCNIIAAFIGNKCQRCTNSEKKYGPYPYSC CKQQCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFVIAQLKEEVA TLKKMLHQKQDMILEKEKKITELKADFQYQESQMRAMNQMEKTHKE VTEQLQAKNRELLKQAAA LSKSKSEKSGAITSP
5267	A	4	496	DGFPPSCCQAGVQ*HDLGSRQPPPP\GSSDSPASASRVAGITGMHH*S RDVLIRILELEEGLELCPHFVSRKLPKTGQILTLMLSLAPVKLAPQP KLSWMLTRTQQA VSPFGRWGGIGRRKVLVPIAADGWASGQARGLL GGSGKGEGKATGCEREGTCLLQG
5268	C	190	435	MFCYLGPLHSHDPILFAKVVRIGKSFMEKFQSDGSKQEDKEKTEVIL SCLLSITDQVLLPSLSLMDCNACMSEELWXMFKTF
5269	A	114	269	QLYINHTPPPLSKSKEREMDKKDLKSRTLKQKQKPLVNVVHNSWF* DHSN
5270	A	1	1071	MKGVMNVALVHSSQEPNGETPSSLYRVA VLLQFNLIDLDDLYVHLL PADNCIMDEHKREIAEAKQIVRKLTMVVLSSSEKMDEREKEKEKEEEK VEKPPDNQKLGLEALLKIGDWQHAQNM DMPPIYAASHKLIALAI CKLIHITIEPLYRSVTSWAVDHAGFLES DPCDSTVGHLLSRVGVPKG AKGSPVNALQNKRA PKQAESFEDLRRDVFNMFYLGPHLSHDPILFA KVVRIGKSFMEQSKKVGEKDCCVAAKLRAQATRGAGQSPDWVPRFA FSPVRCSDGLGLVGGGWYVAGEWGVGNKVDGEQYQIPETMGEIGTK TKDLKNGNVKIPTAYPFNWPWIMENAI
5271	A	1	1231	GRFLCCMLETVTRWHS DRATYEKECGNYPGFLTILRATGFDGGNKAD QLDYENFRHVHWHYKLTASVHCLETGEYTHIRNIIIVLTKILPW YPKVLNLGQALERRVHKICQEEKEKRPDLYALAMG\YKIF*CDLQD *MTEGF*RL*NVLQC*SLSSAFRRLWEIMRSCFHLVRVTTSDYQLP VYTG**FF*SHV*YFLIGRKYNFIIIVNRSSRVKKKKPS*FKD*FIG KL*FLRKLGV* KPSRTY*KWVFFNSLEPHSRMNNLILFLKTSCLC FLIWVCIFKH FVRLSSYSQQLK*EKSIP*YPENEFPSQRPPPRNA VA\SVQNGP\GGGPSSSSIGSASKSDESSTEETDKSRERSQCGVKAV NKASSTTPKGNSSNGSNSNKA VKENDKEKGKEK
5272	A	2	3383	ITDQVLLPSLSLMDCNACMSEELWGMFKTFPYQHRYRLYGQWKNETY NSHPLLVKVKAQOTIDRAKYIMKRLTKENVKPSGRQIGKLSHNPITIL FDYVCFEILSQIQYDNLITPVVDSLKYLTSLNYDVLACILSNCIIE ALANPEKERMKHDDTTISSWLQSLASFCGAVFRKYPIDLAGLLQYVA NQLKAGKSFLLILKEVVQKMAGIEITEEMTMEQLEAMTGGEQLKAE GGYFGQIRNTKSSQRLKDALLDHD LALPLCLLMAQQRNGVIFQEGG EKHLKLVGKLYDQCHDTLVQFGGFLASNLSTEDYIKRVPSIDVLCNE FHTPHDAAFFLSRPMYAHHISSKY\DELKKSEKG\SKQQHKVHKYIT

				SCEMVMAPVHEAVSVLHVSKVWDDISPOFYATFWSLTMYDLAVPHTS YEREVNKLKVQMKAIIDNQEMPPNKKKKEKERCTALQDKLLEEEKKQ MEHVQRVLQRLKLEKDNWLLAKSTKNETITKFLQLCIFPRCIFSAID AVYCARFVELVHQKTPNFSSTLLCYDRVFSDIITYVASCTENEASRY GRFLCCMLETVTRWHSRATYK\ECGNYPGFLTILRATGFDGGNKA DQLDYENFRHVHWHYKLTASVHCLETGEYTHIRNIIIVLTKILP WYPKVLNLGQALERRVHKICQEEKEKRPDLALAMGYSGQLKSRKSY MIPENEFHHKDPPPRNASVQNGPGGGPSSSSIGSASKSDESSTEE TDKSRERSQCGVKAVNKASSTTPKGNSSNGNSGNSNKAVKENDKEK GKEKEKEKKEKTPTTPEARVLGKDGEKPKPEERPNKDEKARETKER TPKSDKEKEKFKEEKAKDEKFKTTVPNAESKSTQEREREKEPSRER DIAKEMKSKENV*REEKTPVLGSLE\SPVSPGSDISQSLERGNQKR RKIDTHPSPSHSSTVKE\SFIEL\KESSAKLY\INHTPPPTVPRVRR EKMDKKDLKSRERSREREKDEK\DRKEREKGVHSGRQRPVKLPDDL /TPKRRKEENGTMGVSKHKSESPECSPYPN\EKDKEKNKS KSSGKEK GSDSFKSEKMDKISSGGKKESRHDKEKIEKKEK\SSGGKEEKKHH KSSDKHR
5273	A	442	1457	KHFLYIIYAQMNCFSRLKKKKKKQLLLQVFSSADE*GSSSSSSSSS GHKRHHKHKRNRSESSRRRHSSRASNQIDQNRER*VLPSSS*YF SIFSFNP*TRSGRKLKGQDRLQYEKTIKEKDRCPSSSSLEIPDD FGGRSEDPRDFYNSYKTQAGSSKTEKPYKSE\DIFFARRNSSDSFCR NSEAKIYGYRRFEKDIEGRKEHYRRWEPGSRVHSTSPASSEYSWKS EKYKKAHSGSRDFSRHEQRYRLNTNQGEYEREDNYGEDIKTEVPEE DALSSKEHSESVK/NKFTSEFTEYI*SDS*I*KRKRK*GQKINTPK DIGHPLPQNAH
5274	A	2	457	KLIFFP\KPSAPQEGRQFC*KIGNRPTQLTGVP\MPVRNVYK\KEK ARVITEKEKNFQSPCLVFMARAK\ARL\FGIRAKKSPRPQNQDVE KEKIKTLPGNFEISLAVMPGSPTWCVSVGTTWALGWGFTACDFLLPR GFGAFLKRQVQAPG
5275	C	27	158	MHSKPTGQVSWLGMTTASLPGTNASSMWPWRLEDHNSLDALP*
5276	A	1	320	FFPNGNAFATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSK SGRLLLAGYDDFNCNVWDALKADRAEITSYSCNHCGSVHFSLLLCT YRKQYSARLYTL
5277	A	100	659	CPLVIRSCSSALWDIETGQQTTFGTGTDVMSLSLAPDTRLFVSGA CDASAKLWDVYSQCFFLSVYMS*FAFSFQFFPNGNAFATGSDDATC RLFDLRADQELMTLTPHDNIICGITSVS\FSKSGRLLLAGYDDFNCN VWDALKADRAGVLAG\HDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5278	A	16	495	AFSAPDTRLFVSG\ACNASAKLWN\VEGEMCGQTFTG\HESDINA\I CFFPNGNAFATGS\DDATCR\LFDLRADQELMTYPHDNIICGITSVS FS\KSGRLPPGMGTTFNCNVWDALKSRTGQVFLAG\HDNPRQPAWG VTD\DGMA\VATGSW\DSFPQDLGN
5279	A	5	108	SRGFTLLARLVLS*PQ/CDPPLPLASQSAGI/TRLGMSYHA*PIII FETRSRSVTQDG/GVQ*CNHGLLPWHPGLKESSCLSLPG/GHAPPH LANFIFCRNRVSLCCSGWS*TSSDPPLPLASQSAGIIGWV
5280	A	1	458	PVARSWVCRKTYVTPRRPFESRLDQELKLIGNALLRRLVRIGVLDE GKMKLDYILGLKIEDFLERRLTQVFKLGLAKSIHHARVLRQRHIR VRKQVNIIPSFIVRLDSQKHIDFSLRSPYGGGRPRGRVVRKNAKKGQ GAGAGDDEED
5281	B	403	629	XVHLVKASCQACQQLDRVRKQVNIIPSFIVRLDSQKHIDFSLRSPY GGPRGRVVRKNAKKGQGGAGAGDDEED*
5282	A	1	637	PVARSWVCRKTYGDPGGPFKE\SRDQ\ELKIGVWGSCTKREVL \RVKFTLAQDSAKAAPGNWLT\LDEKDPTGVLFERQTPLLR/RGLVP QLGCWDEGQMK\L\DYIPGP*RLDFFRETQVFKLGLAKSI H\QPRFACLSRQRHVRK\QV\VNIPSFIVR\LDSQK\HIDFSLR SPYGGGRPA\RVKRKNAKKGQGGAGAGDDEED
5283	A	3	295	VCIGVLLCCLGCGVRWHDHASL*P*PPGLKRSSHLSLLSTWDHRHML

				THPLNFFI\VEPRSHYVAQTGLKLLGSSSPASASQSARITGVSHHT QSKK*FLFVEPRSHYVAQTGLKLLGSSSPASASQSARITGVSHHTQ SKK
5284	A	2	284	WFLTETSPFMWSNLGIGLSISLSVVGAAWGIYITGSSIIIGGVKAPR IKTKNLADAQNPSLFVKILIVEIFGSAIGLFGVIVAILQTSRVKMGD
5285	A	1	785	MTGLALLYSGVVFVAFWACALAVACWVNSGTDWAGGIWLERLLPRSRL GFGLAGGDPACAGVCYTIFDLGFRFDVAWFLTETSPFMWSNLG\IGL AISLSVVG\AAWGHISILTGSSIHVVEGS*KAPRDSKTKNL\VSIIF\ CEAVA\IYGIIMGNCSLSNMT\EPF\SATEPQGHRRQFGN*PWQGYSH GLGAGLHRKPCNLFCG\VCVGIVGTWGCWPQMPQNPTASLCKRFSI VEIFWQAPLALFGVIGRKFFKTSMSERWVTR
5286	A	2	351	DEDSLHSPVPAQMGNVQEYLKTLASPLREIDPDQPKRLHTFGNPFKQ DKKGMIDEADEFVAGPQNKVKRPGEPNSPMSSKRRRNATI IHDGHE EKMENGQITPDGFLSKSAPSEL
5287	A	1	999	NLLKTHKF\LLQDEDSLHSPVPAQMGNVQEYLKTLASPLREIDPDQ PKRLHTFGNPFKQDKKGMIDEADEFVAGPQNKVKRPGEPNMSYV\T KRRRSMSLLLRKPQTPPTCN\NHVGGKGPSPASWFPSPNLIKPTLV HTDATI IHDGHEEKMENGQITPDGFLSKSAPSELINMTGDLMPNQQV DSLSDDFTSLSKDGLIQ\NLVVTHL*EEPKAASP*MTKKTQ*HLLW ELCQIHYKSLLLWHKE/VNADIKHQLMKEVRKFRKYERIFILLEEV QGPLEMKKQFVEFTIKEAARFKRRVLIQYLEKVLEKINSHHLHNNIS HINSRSSC
5288	A	329	661	ITLSLLSFFNLRPSFALLAQAGVHWRDLDSLQPPPLRFK*FSYLKSP \RSWDYGHAPPRPANSVLLVETGSLHVSQGGILPTSGDPPASASQS AGITGVTNCARPPSLFS
5289	A	46	554	NKTRKDPFPYTPAHGHT\PTPSLPFG/CSAHGLKPRGSHCDQPP STCRPPVQSPVAHASQVAGRTWA*KRALHLPGGGVKRGKTGSPKAPR SGCGLPYKLGSTARAAGSCSPAE/EPETFSPQGQPLPVNKGKLRVVG QPSFQCAPRDCSRYPQFQGEQGRAIEHQIP
5290	A	228	388	VHYCDRQSGKECVTCLTAPVQMTFHAIGSSIEASHDQAALSALKQF SEQGLD
5291	A	3	257	GPRERETGRATAVEPDSCEERTYSNDTKRWCSSHPGGNGGVPERQH LG*ATGSWGAKPLRLAAATRASNPGHRSCLKCLETIF
5292	A	3	1379	NEFFGEGKTLQARHFAAMKALQALQNEPIPERSPONGESGKMDDD KDANKSEISLVFBIALKRNMPVSFEVIKESGPPHMSFVTRVSVGEF SAEGEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFPPKPKT IVKAGPEYQGMNPI SRLAQIQQAKKEKEPDYVLLSERGMP*RRFV MQVKVNEVATGTGPNKKAKKKK\NVAVAMLLQLGYKASINLQDQLE KTGENKGWSDPTPGFPEPTNNTPKGILHLSPDVYQEMEASHHKVTS/ GHYSRLFVTQRYEPTFKLFSSVYLPHRIVQSTFARHLLMNGTSSTAB AIGLKGSSP\IPLVPPVQPSKQLGIFSKGFAFRVHYCDRQKQWQVC DLSDISPCADGL/SHAIGSSIEASHDQAALSALKQFSEQGLDPIDGS MNIKGSLEKQAKHLIKKVDHNQAPPGSIAHDCKISNSAV
5293	A	7	351	SSTSLIRKMQIKTRYQNI PNMAKIKNADNTKL/WSRILTNYWWEY RHLHK*KYVHKKT CNFMLIAALFIKFLKWKFKHSSTGE*I IKL*DR HMTYYY*AIKKAQATDRMQHE
5294	A	3	1585	GEPLI/LHHTTCH/NSKALIAFLAFLIIVTSI\ALLVVL TNIDLHR KRSCNVDEQQELVERYDESNLMNVQPIHADIMLETYHRRIA\DEGR F\LAEFQSI PRVFSKFP I KEARKTH\NQKNRYVDILPYDYNRVELS EINGDAGSNYI\NASYIDGFKEPRKYIAAQGRDETVDDFWRMIWEQ KATVIMVTRCEEGRNKA EYWPSEEGTRA FGECCKDLTKHKRC P\DYIIQKLNIVNKKKATGREVTHIQFTSWPDHGVDPEDPHLLLKL RRVNAFSNFFSGPIVHCSAGVGRGTGYIGIDAMLEGLEAENKVDVY GYVVKLRRQRCLMVQVEVCSNL*\DYSHFGFLDLNLFQVIIMIFFKN PNSSQPQTVDLFLKTKTW*SPWPMLCIW
5295	A	1	1324	MEDSRKAQKRDTKIEREEQLYWP SRKSRGKSGKDLVLHTTYKPSHSG

				GRAVSGLFSGSPIPSLGSWTAFLDPPWARVEPIALKGLTQORSPNGGGH RVCVFI PPAPPDGSEQKKRLCSFRRKEQSLPGNLENSFGSCPRLSRQ YVYESARTTALMRLGCPKQIQLISQDLSPFEYRESLPMKDKQNKHQ RISLSINTIQETIISPNELSKSPGTNSGETEIHDLSDREFKIAVLRT LKEIQDNTEKEF\KLYQINLTKRIEIKKNQABEILELRNAIGIQKNA SQSFNSRNGREEEIISELENRLFENTQRRQNKRIKNNKACLQDLEYR LKRANLRVIGLKEEVEKAIGVESLFKGIITENFPSLEQDINIQQVQEG YGTSPSRFNPKKTTSRHLIVKLPKIRDKERILKVITRENKQVT*NGTHI CLAADFSVVAL*ARREWH
5296	A	1	868	PTPHRGAFGRLEPEGLVQPLVGP/ PGLGGPQRSTHPPDGPAPQG GPVPAAGAHPTHLHHLRGPEARPRRPGGPPAAPQRATW*PCCSGGP AP*LLPPIFGKKCSWRCRGKVQYRPVEGDPQTQLQDDKDPMLILRGP SP*GPGPGTSEVDPDF*RTTWVSGGLFLESHQAPP\PP\GGLAGREP EQRSGRLGSR/ PRETTVPRTDFYLPWCQRMNM*LPPQSGRIIGTAGA RAAASLLCSTGPQPLPAALGPCQQPWDPASSPGKRLWPQG\PPSARK *SPGKRLWPQGASQCQKIKSFWILKKKKK
5297	A	3	226	GSGCEQGCPPGRYGPCEQLCGCLNGGSCDAATGACRCPTGFLGTDC NLTCPPQGRFGPNCTHVCGCGQGAACDPVTGTCLCPPGRAGVRCERG PQNRFGVGCHEHTCSCRNGGLCHASNGSCSCGLGWTGRHCELACPPGR YGAACHLECSCHNNSTCEPATGTCTRCGPGFYQACEHPCPPGFHAG CQGLCRCQHGA PCDPISGRCLCPAGFHGHFCERGCEPGSFEGGCHQR CDCDGGAPCDPVTGLCLCPPGRSGATCNLDCRRGQFGPSC TLHCDCG GGADCDPVSGQCHCVDGYMGPTCRE\VGPSGSPRTRP*PRGPAAAPL GSSGRTATS PVRRAASAPTAPTCTVGVGRGRPATL
5298	A	152	990	LLLIHSEEKPFEDNLYGKALSSNSHLHGPRRLCT/GENPEE/CEQL* KAFSAISRDCDSSH*GRKPVKVSEGFSDSHPLRHTGNHTMEQHSEM RNTLQKCSHY*ANYSVVFC*SWESLECSIGF*GDLRINS GENAPF EHHQYWRAFWFSTFVKET/W*SIHTEK/PWK*EEKAFSDASVLG K/HMELLPGCKTYEYINIGKFFSDSSLSCI/WRELTRWNP*ECNQ* DA/FSLNSSLG/HQFSLGTTKYNHCFECGISFIQCLICRLDCWLIN FFSLFFF
5299	A	1	181	EIEDLN*TITQLYLT*HLYRTLHRTPPAYKFFSSVHETFSRIDH\VL EHKTSLNEF*RLK
5300	A	1	170	PPPPFFPLIPD*G*\PPSPLSPGQLQLSAPPP\PLPCPDITLSYGR RPVLGLSLMD
5301	A	846	1094	IPAL/P*FYFIFVYLNILKYLFFFFD/DGVLLCCPAWSAVA*SRLTA TFASQV\KRFSCSLSSWYRSVP/SSLANFCIFSRDG/SFIVLAM LVLNS*PQVILLPWPPKVL*LPIMECSSLTIAHCSLNLPGTSNPPAS ASK
5302	A	19	391	AYPLRGGRDFLRGGPSRSVSLLSVVPARV*RRRRRLREEARGAMTSA STKVGEIFSAAGAAFTKLGE LTMQLHPVADSSPAGAKWTETEIEMLR AAVKRFGDDLNIHISCVIKGPDKGHCETQGI
5303	A	1	338	SLIFSDSLSSISGNTLAFLSWMLPYIPWILQARPALGLLHLLAA CNVVGQSAT*PSPSLPLGLCSSSHSQ*GLF*PPVFKISPLITDNPNP FDLHLMDFIQTKIKISL
5304	A	3	180	TVKRKYEDSGIPLPAESPKKGPVKVASGVLSPPPAAPPSSSSVPE AGGPPHKETEG
5305	A	1	518	RAAQSPCSPWSRLACSGGGGVIREEARGAMTSASTKVGEIFSAAGAA FTKLGE LTMQLHPVADSSPAGAKWTETEIEM/PEGCCEAIWGRS*SH QLCHQGTDSGPDKGHC*NARYIEDFWASPPA*V/IPRKGPRRWASG VFVHLLQLAPPPKQLPVFPEGRGSPPIKETERLM
5306	A	1	705	GAKFQRTSRVPRTTGPGQLKCLEDKVSRLETDELDEEKNTVELLTDR\ LNRGRDQVDQLRTELMQERS/SSGRTWKCDKISLERQNKDLKTRLAS SEG/SPESLVPASLSLSPRISCCRERLPAEQRVKTVLRSTNRKLERK VN*LSLQIEDERHHVSDT\KDQLSLRVKALKRQV\DEAKEEIERLDG LR\KKAQREVEEQHEVNEQLQARIKSLEKDSWRK/GFPLSC*VSSQK

				RRaelR
5307	A	831	1159	DVKSksFFFFLrWsl/NPFAQAGV*WHDLSsLQPLPHrFKQFSCLSL LSS*DYRRVPP*LANFLYF**RQGFTMLARLASNS*PHDPPASASQS AGITGMSHRTQKKQIS
5308	A	296	527	FNCCEEEKFKKKPCFVSFLEGLERG*VKCQEHIPDTH***LLGLSEQ INSDSRLRKELNHFILFLEQLTCPPHSRER
5309	A	5424	5957	YNFFLNEMGSCSVAQAGVQWHNHSSLQP*TLG*SSYHPASAS*VAGT VCTCHHVQLVF/IFFFLR*SFALVAQAGVQWCDLGSLLPPPPSGFERF SCLGLPSSWDYRRPPLHLVNFFFLYF**RWGFTMLARLVNS*PHD\ HPASASQSAGITGMSHHVWLNFFFNCKSLIFSNVFRN
5310	A	2	237	IKRFSYLSLPSNSWDYKVPSSMPG*FLYF*LR*GFTNVGQAGFEIP*P QNDSNPLSSQSAGITGMSH\HNRPPLFYFLK
5311	A	36	386	LNiHRKFMlLYYH*LLLFL\FHF*DRVSVCHPGWSTVVNSQGFT\AA LTYW\VK*SSCFNPPCVSWEPRGACHAL\ANFLIFCKNQVSLCLPR LVNS\WVQAILPSW\PPRRAGIYGV
5312	A	1	310	FFFFET/ESHsVAQAGVQWDLGLL*SS\PP\GSSDSPASAS*ASGT TGA/QHHAQLIF\VFSVETGFHPVSQDGLDLLTS*SARLSLPKSWDY RHEPLAPGLGFTF
5313	A	598	884	LIFFLFsFFFFSFFFFFFFFFFFFFFFFFFFFFFFFLLLLLLLLLL LLLLFFFFFFFFFFFFFLRQSL/DSVAQAGVQWRHLGSLQALPPRF AP
5314	A	439	1169	QSGHRYLYNIIQVLCFTIFLFLRQDLAVL/TQAGVQWC/DSWQPR PPGLK\GTPTSAAQVAGTTGMCHH\TR*FFFFFFFFFFFFFFFFFFFF FFFFFFFFLRLQSL/DSVAQAGVQWRNLGSLQPLPPRFKRFSCGLPSS WDYRNAPPPANCCIF/M*RRGFTMLAKLVNLSGDSPASASQSAGII GVSHHARPPRYFKYIFCRDGGTMLLGWS*TPGLKQSSHLGFPNFW DYRCEPPCLATLFI
5315	A	1	222	ETGSHFVTQAGV*WCNLGLLQPLTPGLKQFSHLSPSSWDHKCVPS PANSFCTLGK*RRVSTMLPPGWS\QTP
5316	A	1	234	LRQSFAGWPRLECNGTIPAYCNLHLGSSNPPASSPR\RLIFVVLVE MRFLYVA*AGLELLSSSDLPPWHRKVLGLQA
5317	A	1	196	FFLINLTLIIVTAQFIN*LDFIDSYSTICPKPPEYTFFSRA/PNGTF TTKDHILGFKISLNKYKSI
5318	A	1	477	SCWSPV\WGHPDRDREPPPS*LGIOSSPGVPQALPPWPSPASHQAS ATWAVLPLPPLQGPAREPPCPPHLRRHVQPTKTSAVSILSAPPLPPP G*DLPEASFSQWACKGINKCLQGLGLVCRRTHEKDLGLGLFGPLVLA MVEVRGVDLTENNSGASVPRGR
5319	A	139	398	FYFFYFYFLRQSCSVNQAGVQ*/HCLNSLQPPPPGKFRFSCLSLPSR WDYKCPPPCTPNFCVFS/EMGFLHVGQAGLELMTSGDPPGFG
5320	A	11	137	RWGFTKLRLVNSNSWPQAILSPWLPKVLNNHREALYFSLYYISKYTE GQFRNRLYPGTICQDYLWRYLLFLFIFETESCTVIRLECSGSLQPPP PRFKQFTCLRLHSSWDYR\RPP\WPIINFCISRVQTGFHHVGQ\GL DLVDLCDPPASASQSAGITGREHPAGTYLWEGFKKSFKSRA*RTL FFPLLH
5321	A	1	293	LERMSFGHIQTKEDILQENTIFIATEVQIQPNPD*TPEAKAFI\RR LSYRKEDRIDVHQLTCDPYLMPHMRMSVSTCSPAGAAIASTSGASS SSSN
5322	A	3	291	RKPFHGNQSQQDILQENTILKATEVQFPKPVVTPEAKAFIRRCCLAY RKEDRIDVQQLACDPYLLPHIRKSVSTSSPAGAAIASTSGASNNSS N
5323	A	14	943	HRILEPLIFHFFFFFFSSAPPQPELly/PASLTLPASPGREEVYPLP ARLPSLPRWEPLQVWLALGAVKLPLSPWSPG\NGLGKPPGTPKRRG ALFCHMPGILTP/WMPGARWTKPPANPPST/TSPVPPKDG*KLQPGG LRGKPGPERGWNPPCP/RSRPPYLLC*PQTLPR*CFPIPKMSFTG HSPCRASLGHE/VGHGIPLWPRVCQRRKSRAFFVLFFFKGACLFNV

				NNRKP*YLCNTE*YFNHVLDVHNIFITKQQUEST*PWLPRGVSWLG AGGGYQGAWDREAPPPRPIPKLPPTLASRMRSCHL
5324	A	12	486	GPRPAVVKRQNRQVPSTQDPLFPGYGPQCVDLAGPPCLRPLFGGLG GYWRALQREGRETRMTSRASELSPGRSVTAGIIIVGDEILKDWTYRD IWDFLRQLFVPYCILYDRGYTSLGSRENTVRNPALKCLSPGGHPTYR PAYLLENEEEERNST
5325	A	51	390	DGVLPSLLGWEVMCGSSAPLLRSPVDRDLGMWGVCHP\GWSIVAQS\ QFTAASNLLASRAT/LSLPSSWDYRRVPPHSAHFKFLL*KWGLAMLP RLVLNSWSQVILLQPPKVLEL
5326	A	279	380	ASHPLQGLLCGPSLLDEHHPLLHGAQSHRPPKG
5327	A	618	818	GILALVPAECDADVPWTEIRRNLDKLQRGAPIPLASRSLSRNPFLT SAGPDHWSILHELSPGGW
5328	A	1	197	LHFYQONYDNPSDFTFLTTLGIVNSFNNIHSNVYVVVRGDSVLAVLT ALTRSQRLLCLGSHFGGT
5329	A	2	498	CPRMTPKDFQ*PVL/VVTNLLGHVIDIKWMSIAFINDRAWPSAFVSD ENHARIQCDGQHRFEVSVSELPDETVDVSTVLDLDHQLGPPPPPAE PDPLQLLLQQLFGLQLSCVVGPGPWRGLSSARDKQNMVSIHKKVK RPQSPLRVYWPLRYCILPSRRATVN
5330	A	600	811	PIWLSLSPWHFINQRKEKKK*DIVKREKPLMGLSTLTSI*MQSKPR KEHQINLKSEIK*LQDLSQYFGR
5331	A	1	75	FFFFFFFFFKLAMFVILFFIFSK*KEIVLSQFLFVFL/IYLFYVF TSLKVALKISRDIKSTFLRVALFFFLNNSWEFCGSTAFPSVSMCMF *LLL*FFFFFFFFFKLAMFVILFFIFSK
5332	A	949	1711	VTIPLIPDLKGSSCVGPPKP*DCRHWTCLTLIYFFFFFKVESPSVAH AGVQWHDLSLLTLSPDQV/HSPVSAF*VAGIQG/MHHHARL/IFFF FFFFLRQSL/SSVAQAREQWCYHGSQPPPSGFKRFSCLSLPSSWDY RCPPPHLA/DFVFLIEMGFTMLTRLVSNS*PQ/CDLPASASQTAWI TGLSHRAW\LNFFCIFSIYGVSPCWGWSLTPDLK*SACLSLP*CWD YKCEPPCPAQFTFIRKDSFADVYCSVS
5333	C	11	154	MESRSVARLECNAGISAHCNLHLLGSNDSPASASRVAGTTGTATTPG *
5334	C	163	270	MNMESLIFYCFNADILIKQDYFHHQHLYIYTKPV*
5335	A	92	404	WLQICVSGCICT*\MALYICIN\VVVKVVLFYEDVCIAVK*AFHF IHNLMCVYICMVCVWNIEGLYIPPQRYIHMAVLLHRSNSQTPGSIR YKFKISFIGFI
5336	A	2	1100	FALAARLQEFGRKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKV LPIIHEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFGTYFRVGF YGTKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIK DSNPVDKCKLDPNKAYIQITYVEPYFDTYEMKDRITYFRQKLQSSVR FMYCTPFTLDGRAHGGTSMEQFQKGRPI\LDYVSCFLFPYIKTRG/PM SLIKKRSSLHPFEV\AIEDMQKKTQELAFATHQDPADPKMLQMVLQG \SVGH\QVNQGGLGSCPGFFCSGNT**PKALSDIH*\KLATLAFKDF TKRCEDALRKNKSLIGPDQKEYQRELGEKLSSALKRALPAT
5337	A	48	1057	RCWENCTSTCKTMKSDPYLR/PYTTINSKWIKDLNVRPETIEENIGE KFLD\MTLGNDFLDITPKAQSTTK/DKWDYIKPKSF/CTVKETVNK MKQ*PTD\W*KIFVRHIYKGGLVSKIYKEFIQLNF*KWAKDLKRHFS EDDTQMANRYIKGCST*LIIEKMHFKNHSKYLLSPVRLAVIKKN\N NKC/W*WCGIKGTL/LHCWWECLVQPLWKTEWKFL\RKIKLPYDPA IPLGIYSK*MKSPCKYICS/RVFIAALFIVA/K/TWRQLKCPLT/ V*IRKLCTIYMPYTPMEYYPPLKTKKNPTISCHLLPTWMGLKDTVINE ISQTEKKILHNFTIYVESKKKI
5338	A	2	409	PLALALAMAYPSCPGDAHGPPRPGPLSPPS*PASVP/TSP/PQSSA* FLCPQSYPVGELTPRILPAGGGHVPCSRPSSSPGLASVSAPRWGALL LPGPCPTSLSSGCRKGRASPRAHPPPTASLCTALWPPCFSP*PGVG LGNGLSLLPRRCTWPAAARSTVSSLLACLCPNSPLNLLRDSSVLSHT QLRGSPHGFYPLEGAMFPAPALPPHQAALPRYQPPGGELCCCLDHALL

				PSPRDVGKGGPALELTHPPQACVLRSGHLASRLHNL
5339	A	32	323	KFHLGGGGWFPPLPFGPGGARGVGS*VRGFRPPWAPPLNPPFFPKPQ NSPGLVVFAFRPSSSGG/PGPGNSPHPGGQGG*QKFRPCPSAWGTK GGFP
5340	A	2	570	LKILSKMKIHOQGYNSDENACVHQHVRALTGSMCKSKPGSPAPGGR *NLPSREPGAPAGIGGSFLASAAVSPSPSPH*CPLE*EPVAEAGL LGELSKVWKEGPPERAPG*P\PRGPPGLHQLHASQMLFIGRPG\GPG QISPAPGCGGLEGLSRHCAIAGAGERISETTFGSNALYHRSPNRLG QGL
5341	A	4	329	IIAHCKLKRPSNDPPQPPSSWDCRHAPPHAN*FFF*EMGSCHVAQ TSSQTPALNPSRYPPTSASQGAETVMISHCAQLYPCFLTKEK/FSHS *IRRTLSETSNGEY
5342	A	3	274	FQSQNIKLNLGMVLFCEFEAHSVT*AGLQWLDLSSLQPPPPGFKQ/ FSCLSLSSWDYRSPRGPVNFICIFSGDEVSPYWSGWSQTSDLK
5343	A	1	1075	MVDGTLTLLLLSEALALTQTTA\GSHSLKYFHTSVSRPGRGEPRFISV GYVDDTQFVRFDNDAASPRMVPRAP\WMEQEGSEYWDRETRS\ARDT AQIFRVNLRTLRL/Y*QSERRPGSHTL\QWMHG\CELGPD\NASFR GYEQFAYDGKDYLTINEDLRSWTAVDTAAQISEQKSNDAEADHQR \YLQATFVDSFPK*LYEGKETFLHLEPPKTHVLHHPIS\DHEATLRC WALGF\YPAEITLTWQDGEHTQDTELVETRPAGDGTFO\KWA VPSGEEQRYTCHVQHEGLPEPVT\LRWEARFSPPI/LPSWASLLGL VLLGSVVSEAV\VAAVIWRKSSGHFLPTGGKSSGYFKG
5344	A	58	426	KLQLL*FFWFF\FCLFTYFLETVECSGAI IAHCSLKLGGSSHPAS ASLVAKITGACHPAWLI*VVLIVLFKRKWQSHLKLMEKRFLESGQI LSVYHFRVPLQLQNDRLAQIILGRKREMY
5345	A	3	284	KKILRKKILRKSSV*I*D*SSQPEN\IP*KQFLSNHPKCTITLSMRN MSIMKKGGRISE\DFIKLFFPSLLSHLLVIEWGLYIEIYLTPPNNT F
5346	A	2	225	TLPCTLSTSSTPWSASSQEREMSFQDG*PVG*PPLTAVP\CCSVWGL RRL*GERTKLIGAGGFHSYDGTQT
5347	A	3	104	WSTVARS*LTATSCFCLSPSSWDCRRVPPCLA/SFHFQYIALNN* A*AIILPQPSKVLGL*ASALQVAGTAGVYHHAW
5348	A	2	392	TGKNEIYCICFIDLEYQ*KIGLLHIGDKEEYS/WNSGYFIGYCLEL PCPVVKVSGN*NDSEAAVMTTPSKI*VTLQSKEASPIKVLTVQV IGDIKIGILENGHYKYQL*QFFKLQKGNNDH
5349	A	2	67	AAED*HCPIASETYKIT\ELWVTLPEVKGSPFLINTEATHSTLPS FQGCVSLSITVVGIDGQASKPLKTPQLWCQLGQHSFMHSFLVIRTF PAPLLGRDILTNLASLTIPGLEPHLIAAFCSSSKPPSHPLVSLHL KPQV*DRLGNLQDHHRCFG
5350	A	2	275	ETESCSVA\RLCSGMISAHCNLCPLDTGNSPASAS*VAGIIGACHH AQLIFVFLVETEFHHVFHHVGQASLEFL/NLVIPPPRPPKALGLQG
5351	A	3	1031	SSAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEY PDLFEWFCVKTLLKCCV\PGT\YGPDCCLACQGGSORP\CSGNGHCS\ GDGSRQGDGSCRCHMGYQGPLC\IDCMDRLQLRNRNETHSI\CTA\ CDESCK\TCFGP*PT\GLRRSCEVG\WVLDEGACVDVEKCAAQT\PP CSAAQFCKNANGSYTCE\EGDSSWVGCPG\KGPGNCKQCISGYAREH GQ\CADVERVPH*PEKTLCEEKTKTCYNTPG\SY\VCVCPDGFET/ RRCLCAAGRRLKPQKGESPTQLPLP
5352	A	206	330	KMLQLALQSCIKVRTLSNRHLGAGVTAHEE*CPCCHPMIKQ
5353	A	1	8271	GEFGSEKKTALHEKEETLRLQSAQAQPFHQEKESSLQLOKKNHQV QQLKDQVLSLSHEIEECRSELEVLQRRERENREGANLLSMLKADVN LSHSERGAQDALRRLGLFGETLRAAVTLRSRIGERVGLCLDDAGA GLALSTAPALEETWSDVALPELDRTLSECAEMSSVAEISSHMRESFL MSPESVRECEQPIRRVFQSLSLAVDGLMEMALDSSRQLEEARQIHSR FEKEFSFKNEETAQVVRKHQELLECLKEESAALALELHKTQGT

				EGFK VETADLKEVL AGKEDSEHRLVLELES LRRQLQQAQEQQAALRE ECTRLWSRGEATATDAEAREAGFFRVFSGTSLTSCIALSIFALAVLL HLGVRRCRCFSDAFSACPLLSSGSLMCLRAQPAGAGPHPAGGDHLVVFH HLEPLDFSQSLRLSGLRADKGVCGLSVERPALRKEVEDLTKEQSET RKQAEKDRSALLSQMKILESELEEQLSQHRGCAQAEAVTALEQQVA SLDKHLRNQRQFMDVRI LNNTFFCITKSCRYSMNFFPDRIEQAARE HEREEFQQEIQRLLEGQLRQAAPQWPGRDQSVELLQQLREKLDEF NELAIQKESADRQVLMQEEEEIKRLEEMNINIRKKVAQLQEEVEKQKN IVKGLEQGGPLSITCTWSGVVPLAGHCTHFS DSCSRAASPLLP SLSE RLLSLVDARDKEVLKKQOMSSLLLASTLQSTLDAGRCPEPPSGSPPE GPEIQLEV TQRALLRRESEVLDLKEQLEKMGDLESKNEEILHLNLK LDMQNSQTAVSLRELEEENTSLKVIYTRSEIEELKATIENTLQENQK RLQKEKAEEIEQLHEVIEKLQHEL SLMGPVVHEVSDSQAGSLQSELL CSQAGGPRGQALQGELEAALEAKEALSRLADQERRHSQAALQQR LQGAEEAAELQLAELERNVALREAEVEDMASRIQEFEAALKEATI AERNLEIDALNQRKAHSAELEAVLLALARIRRALEQQPLAAGAAPP ELQWLRAQCARLSRQLQVLHQRFLRCQVELDRRQARRATAHTRVPGA HPQPRMDGGAQAQVTGDVEASHDAALEPVVDPDQGDLPVLVTLKDA PLCKQEGVMSVLTVCQRQLQSELLLVKNEMRLSLEDGGKGKEKVLED CQLPKVDLVAQVKQLQEKLNRLYSMTFQNVDAADTKSLWPMASAH LESSWSDSDCGEEDISP HIDTCDANTATGGVTDVIKNQAIDACDA NTPPGVTDVIKNWDSLIPDEMPDSPIQEKSECQDMSLSPTS SVLGG SRHQSHTAEGPRKSPVGMLDLSSWSSPEVLRKDWTLPEWPSLPVTP HSGALSLCSADTSLGDRADTSLPQTQGPGLLCSPGVSAAALALQWAE SPPADDHHVQRTAVEKDVEDFITTSFDSQETLSSPPPGLEGKADRSE KSDGSGFGARLSPGSGGPEAQTAGPVTPASISGRFQPLPEAMKEKEV RPKHVKFSRSFYGKTIDKNLAKQALLQMVRDESHQILALSEGLAPPS GEHPHPRKEDEIQDISLHGGKTQQALVVCERQPGWHSGGSLVLHAAP GDQREVPTACPDWRGDLQVVQEA FEKEQEMQGVLEQRLSGSDLGG HSSLLERLEKIIREQGDLQEKSLHLRLPDRSSLLLEIQALRAQLRM THLQNEKQLHLRTALTSAEARGSQQEHLRRQVLD SVKGNGLAVQP TALVPAPMPFVLSGAGGRRCAHALELLAYKVEQEKCIAGDLQKTLSE EQEKANSVQKLLAAEQTVVRDLKSDLCE SRQKSEQLSRSLCEVQQEV LQLRSM LSSKENELKAALQELESEQKGGRALQSQLEEEQLRHLQRES QSAKALEELRASLETQRAQSSRLCVALKHEQTAKDNLQKELRIEHSR CEALLAQERSQSELQKDLAAEKSRTE LSEALRHERLLTEQLSQRT QEACVHQDTQAHALLQKLKEEKSRVVDLQAMLEKVQQALHSQQQL EAEAQKHCEALRREKEVSATLKSTVEALHTQKRELRC SLEREREKPA WLQAELEQSHPRLKEQEGRKAARRSAEARQSPAAAEQWRKWQDKEK LRELELQQRDLHKIKQLQQTVRDLKDEVP GSRHLG SARRAAGS DADHLREQQRELEAMRQRLLSAARLLTSFTSQAVDRTVNDWTSNEK AVMSLLHTLEELKSDLSRPTSSQKKMAAELQFQFVDVLLKDNVSLTK ALSTVTQEKLELSRAVSKLEKLLKHHLQKGCSPSR SERSAWKPDETA PQSSLRRPDGPRLPPAASEEAHTSNVKMEKLYLHYLRAESFRKALIY QKKYLLLLLIGGFQDSEQETLSMIAHLGVFP SKAERKITSRPFTFRFT AVRVVIAILRLRFLVKKWQEVDRKGALAQGKAPRPGGTAAVDRWTH KPFFLLLLFFIHFSGFFSV DGDVIKHVYICGFTGRSLGPVDRRRKNTG LFYQRIHTALNQLPRPSSIAHGSMYILTLGYFFHKKVDDQELCLKFC LLRGYALITIFQEWFLQKQTLRLSLGYEDVDMVSTPVKGRGRKQDWA EEEGYAPRAATKQPARLKPATLKQAQRACRERRSPASPNGSPERHR RVFGANGSEALVLLGGAGRAARARDPLRTRARYPPFPTRSRGRPG AQERAGQRRRGGAIRARARAASARTLAGLAMADRGCPLEAAPLPAEV RESLAELELELSEGWKKKLN SDKDAVFNRNW
5354	A	2	10028	LCVSPVTAGRPARSLREMEVEQEQR RRKVEAGRTKLAHFQRKTKGD SSHSEKKTAKRKGS AVDASVQEE SPVTKEDSALCGGDI CKSTSCDD TPDGAGGAFAAQPEDCDGEKREDLEQLQKQVNDHPPEQCGMFTVSD HPPEQHG MFTVGDHPPEQ RGMFTVSDHPPEQHG MFTVSDHPPEQ RGM

				<p> FTISDHQPEQRMFTVSDHTPEQRGIFTISDHPAEQRMFTKECEQE CELAITDLESGREDEAGLHQSQAVHGLELEALRLSLNMHTAQLELT QANLQKEKETALTTELREMLNSRRAQELALLQSRQQHELELLREQHAR EKEEVVLRGQEAELKEKLQSEMENAQIVKTLKEDWESEKDLCLE NLRKELSAKHQSEMEDLQNFQKELAEQRAELEKIFQDKNQAEALR NLESHHQAIEKLREDLQSEHGRCLEDLEFKFKESEKEKQLELENLQ ASYEDLKAQSQEEIRRLWSQLDSARTSRQELSELHEQLLARTSRVED LEQLKQREKTQHESELEQLRIYFEKKLRDAEKTYQEDLTLLQRLQG AREDALLDSVEVGLSCVGLLEEKPEKGRKDHVDELEPERHKESLPRFQ AELEESHRHQLEALESPLCIQHEGHVSDRCCVETSALGHEWRLEPSE GHSQELPWVHLQGVQDGDLEADTERAARVLGLETEHKVQSLSLQTEL KEEIELLKIENRNLFEKLQHETRLKDDLEKVXHNLIEDHQKELNNAK QKTELMKQEFQRKETDWKVMKEELQREAEKLTMLLELREKAESK QTIINKLELREAEMRQLQDQQAQILDERSLTEQQARLQQLQEQDLT SDDALHCSQCGREPPTAQDGLAALHVKEDCALQMLARSFLEERK EIAEKFSAEQDAFLQLLQERHQQLLSVTAELEARHQALGELTASL ESKQGALLAARVABLQTKHAADLGALETRHLSTLDSLESCYLSEFQT IREEHRQALELLRADFEEQLWKDSLHQTILTQELEKLKRKHKGELQ SVRDHLRTEASTELAGTVAHQLQGVHQGEFGSEKKTALHEKEETLRL QSAQAQPFHQEESLSLQLQKKNHQVQQLKQDQVLSLSHBIIECRSE LEVLQQRERENREGANLLSMLKADVNLSHSERGALQDALRRLGLF GETLRAAVTLRSRIGERVGLCLDDAGAGLALSTAPALEETWSDVALP ELDRTLSECAEMSSVAEISSHMRESFLMSPESVRECEQPIRRVFQSL SLAVDGLMEMALDSSRQLEEARQLHSRFEKEFSFKNEETAQVVRKHQ ELLECLTEESAAKAELALELHKTQGTLEGFKVETADLKEVLAKGDS EHLVLLESLRRQLQQAQAEQAALREECTRLWSRGEATATDAEARE AALRKEVEDLTKEQSETRKQAEKDRSALLSQMKILESELEEQLSQHR GCAKQAEAVTALEQQVASLQKHLRNQRFMDQAAEREHEREEFQOE IORLEGQLROAAKPPQWGPRLDSQAPLDGEVELLQHLKREKLDEFNE LAIQKESADRQVLMQEEBIKRLEEMNINIRKKVAQLQEEVEKQKNIV KGLEQDKEVLKKQMQSSLLLASTLQSTLDAGRCPEPPSGSPPEGPEI QLEVTQRALLRRESEVLDLKEQLEKMGDLESKNEEILHLNLKLDQM NSQTAVSLRELEEBENTSLKVIYTRSSIEELKATIENTLQENQKRLQK EKAEEIEQLHEVIEKLQHELSLMGPVVHEVSDSQAGSLQSELLCSQA GGPRGQALQGELEAALEAKEALSRLADQERRHSQALEALQORLQGA EEAAELQLAELERNVALREAEVEDMASRIQEFEAALKAKEATIAERN LEIDALNQRKAHSAEAEVLLALARIIRRALEQQPLAAGAAPPQLQW LRAQCARLSRQLQVLHQRFRLRCQVELDRRQARRATAHTRVPGAHPQP RMDGGAQVTDGVEASHDAALEPVVDPQGDLPVLTCLKDAPLCK QEGVMSVLTVCQRQLQSELLLVKNEMRLSLEDGGKGKEKVLQEDCQLP KVDLVAQVKQLQEKLNRLLYSMTFQNVDAADTKSLWPMAAHLLSS WSDSDCDGEEPDISPHIDTCDANTATGGVTDVIKNQAIACDANTTP GGVTDVIKNWDSLIPDEMPDSPIQEKSECQDRSLSSPTSVLGGSRHQ SHTAEAGPRKSPVGMIDLSSWSSPEVLRKDWTLPEWPSLPVTPHSGA LSLCSADTSLGDRADTSLPQTQGPGLLCSPGVSAALALQWAEPPA DDHHVQRTAVEKDVEDFITTSFDSQETLSSPPPGLEGKADRSEKSDG SGFGARLSPGSGGPEAQTAGPVTASISGRFQPLPEAMKEKEVRPKH VKALLQMVREDESHQILALSEGLAPPSGEPHPPRKEDEIQDISLHGGK TQEVPTACPDWRGDLQVQEAFAFEKEQEMQGVLPRLSGSDLGGHS SLLERLEKIIREQGDLQEKSLHLRLPDRSSLLSEIQALRAQLRMTH LQNQEKLQHLRTALTSTEARGSQQEHQLRRQVELLAYKVEQEKCIAG DLQKTLSEEQEKANSVQKLLAAEQTVVRDLKSDLCESRQKSEQLSRS LCEVQQEVLQLRSMSSKENELKAALQELESEQKGGRALQSQLEEEQ LRHLQRESQSAKALEELRASLETQRAQSSRLCVALKHEQTAKDNLQK ELRIEHSRCEALLAQERSQLSELQKDLAAEKSRTELESEALRHERLL TEQLSQRTEACVHQDTQAHALLQKLKEKSRVVDLQAMLEKVQQQ ALHSQQQLEAEQKHCEALRREKEVSATLTKSTVEALHTQKRELRCSL </p>
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				EREREKPAWLQAELEQSHPRLEKEQGRKAARRSAEARQSPAAAEQWR KWQRDKELRELELQQRDLHKKQLQQTVRDLKDEVPKSRHLHG SARRAAGSDADHLREQQRELEAMRQRLLSAARLLTSFTSQAVDRTVN DWTSSNEKAVMSLLHTLEELKSDLSRPTSSQKKMAAELQFQFVDVLL KDNVSLTKALSTVTQEKLELSRAVSKLEKLLKHHLQKGCSPSRSE AWKPDETAPQSSSLRRPDPGRLLPAAASEEAHTSNVKMEKLSLHYLRAE SFRKALIYQKKYLLLLIGGFQDSEQETLSMIAHLGVFPKSKAERKITS RPFTRFRRTAVRVVIAILRLRFLVKKWQEVDRKGALAQGKAPRPGPRA RQPQSPPRTRRESPPTRDVPKSGHTRDPARGRRLLAAASPHSGGRATPS PNSRLERSLTASQDPGHSLEYIHHLEVIQORLGGVLPDSTSKKSCR PMIKQ
5355	A	2	5217	APLDGEVELLQKLEKLEDEFNELAIQKESADRQVLMQEEBIKRLEE MNINIRKKVAQLQEEVEKQKNIVKGLEQDKEVLKKQMSLLLASTL QSTLDAGRCPEPPSGSPPEGPETQLEVTQALLRRESEVLDLKEQLE KMGDLESKNEEILHLNLKLDQMNSQTAVSLRELEENTSLKVIYTR SSEIEELKATIENTQENQKRLQKEKAEEIEQLHEVIEKLQHELKSLMG PVVHEVSDSQAGSLQSELLCSQAGGPRGQALQGELEAALEAKEALS LLADQERRHSQALEALQORLQGAEEAAELQLAELERNVALREAEVED MASRIQEFEEALKAKEATIAERNLEIDALNQRKAHSAELEAVLLAL ARIRRALEQQPLAAGAAPPPELQWLRAQCARLSRQLQVLHQRFLRCQV ELDRRQARRATAHTRVPGAHPPQPRMDGGAKAQVTGDVEASHDALEP VVPDPQGDLPVLTLDAPLCKQEGVMSVLTVCQORLQKLELLLVKN EMRLSLEDGGKKEKVLDCQLPKVDLVAQVKQLQELNRLLSMTF QNVDAADTKSLWPMASAHLESWSDDSCDGEEDISPIDTCDANT ATGGVTDVIKNQAIACDANTTPGGVTDVIKNWDSLIPDEMPDSPIQ EKSECQDMSLSSPTSVLGGSRHQSHTAEGPRKSPVGMLDLSSWSSP EVLKRDWTLPEWPSLPVTPHSGALSLSADTSLGDRADTSLPQTQGP GLLCSPGVSAAALALQWAESEPPADDDHVQRTAVEKDVEDFITTSFDS QETLSSPPPGLEGKADRSEKSDGSGFGARLSPGSGGPEAQTAGPVTP ASISGRFQPLPEAMKEKEVRPKHVKALLQMVRDESHQILALSEGLAP PSGEPHPPRKEDEIQDISLHGGKTQEVPTACPDWRGDLQVQVQEA KEQEMQGVLEQPRLSGSDLGHSLLERLEKIIREQGDLOEKSLEHL RLPDRSSLLSBIQALRAQ\LRMTHLLN*EKLQHLRTGLRSAEARGSH HEHQLRRQVELVAYKVEQEKCIAGDLQKTLSEEQEKANSVQKLLAAE QTVVRDLKSDLCESRQKSEQLSRSLCEVQEVQLRSMLSKENELK AALQELESEQKGRALQSQLEEEQLRHLQRESQAKALEELRASLET QRAQSSRLCVALKHEQTAKDNLQKELRIEHSRCEALLAQERSQSEL QKDLAAEKSRTELESEALRHERLLTEQLSQTQEAHVQDTQAHHAL LQKLKEEKSRVVDLQAMLEKVQQALHSQQQLEAEAQKHCEALRREK ERELELQQRDLHKKQLQQTVRDLKDEVPKSRHLHLSARRAAGS DADHLREQQRELEAMRQRLLSAARLLTSFTSQAVDRTVNDWTSSNEK AVMSLLHTLEELSDLSRPTSSQKKMAAELQFQFVDVLLKDNVSLTK ALSTVTQEKLELSRAVSKLEKLLKHHLQKGCSPSRSESAWKPDETA PQSSSLRRPDPGRLLPAAASEEAHTSNVKMEKLYLHYLRAESFRKALIY QKKYLLLLIGGFQDSEQETLSMIAHLGVFPKSKAERKITSRPFTRFR AVRVVIAILRLRFLVKKWQEVDRKGALAQGKAPRPGPRARQPQSPPR TRESPP\TRDVPKSGHTRDPARR\RLA\AAASP\HSGGRATPSPN LERSLTASQDPEHSLTEYIHHLEVRPPKNCGEAYPHSTSKKSCHPM IKQ
5356	B	224	326	XSSSDGNLRPEAITAIIVVFSLLAALLAVGLALL*
5357	A	87	558	STFFPAIKHWVDLTAQRGHCLSPRSHSNEGRQMQRGPRWAGSPAPS PWSPEGPGPRLHGRTERKERGLWGLLDLQKVGSAASRGVGPPEQHT* AAGTAKQRQHAASQSPPHGCPQLPTSPPEPSEAGVSAAAVYKPTR SPGQCWWLQQAFAFR
5358	A	3	713	TDRGCRGRDTFHEPELG/PKTPGPGAPLQVPLAGDAVGASARSFPL GAGNPPPIPWRT\AGAASGAGPAAPAGPLGPSLG/RKYRPLLMRI

				ALFCLHPPAPAPMATCVHKPSLLSSRSSTS/SAALLLAVGAGTVGAE /RFGRRRRRAPTPGVARSSSPMQPRPGPLRTPRRRCRAACPSRSP LHLSPPFIIV*PWGKAVPSLGSQIHPVLNSREEGTSKTLPLRSREDGA IHFYIFI
5359	A	2	807	RPQGFPAWRLPSRRGATPGRLP RS*PRPHRPEPGVRVGPWVIESV R/HQDCSGRSPGQTPTCEDRAPSGKGSALGRGSLGPWTLIGSGRG/R SPGKLGSPSPGPAKAF*RRR\RASKVAPGPLDGPWRIAQAWAREKGL AWGTGGSWPPSHAPGHQLGFQKQPLGNQREWGQNLGIQDL*QGVDP N\RPPPLSGPDRHLTGKPSGREGALSQGPQGRHSPGRPQQQASSC CERSHPGLPPVTTHCPGVQWASCPGWGCLARCSRPRA
5360	A	1	412	FFFFLRWSL/NSV/SQAGVQWWDLSLLQPLLPQFKQFSCLSLLSSWD YGCPPRPANFLHF**RQGF TMLFRLVNSNS*PHDSPISASQSAG\IIG VSHRARPSCLLLAYFSEFVSKWKQSSTKALPCGFRMLCPVLTPEVK
5361	A	3	886	YLSIHQVYGKEACIPCGPGSKNNQDHSVCYSDCFFYHEKENQSLHYD FSNLSSVSGSLMNGPSFTSKGTYFHFFNISLCGHEGKMMALCTNNIT DF\NVKEIVAGSDDYTNLVGAFVCQSTIIPSES/TGVSEKPYHHNPI ILADTFIGVTVETTLKNINIKEDMFPVPTSQIPDVHFFYKSSSTATTS CINGRSTAVKMRNPTKSGAGVISVPIKCPAGTCDGCTFYFLWESAE ACPLCTEHDFHEIEGACKRGFQETLYVWNEPKWCIKGISLPEKKLAT CETVDFWLKVGAGV
5362	A	3	2697	CSVKECLQASAKLPSAPASVSLCLLVAKVWRRRLRWQEAFAFSCASGE YLEMKNQVCSKCGEGTYSLGSGIKFDEWDELPAFNSNIATFMDTVVG PSDSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKSAGYVFFE YQYVDNNIFFEFFIQNDQCQEMDTTDDKWVKLTDNGEWGSHSVMLKS GTNILYWRRTTGILMGSKAVKPVLVKNITIEGVAYTSECFPCPKPGTFS NKPGSFNCQCKIIDPFLKRFFYVAEESSECTERPPCTTKDYFQIH TPCDEEGKTQIMYKWI EPKICREDLTDAIRLPPSGEKKDCPPCNPFG YNNGSSSCHPCPPGTFSDGTKECRPCPAGTEPALGFYKWWNVLPGN MKTSCFNVGNSKCDGMNGWEVAGDHIQSGAGGSDNDYLI LNLHIPGF KPPTSMGTGATGSELGRITFVFETLCSADCVLFTMVDINRKSTNVVES WGGTKEKQAYTHIIFKNATFTFTW\AFPEN*FRVQDNRRFINDMVKI YSITATNAVDGVASSCRACALGSEQSGSSCVPCPPGHIYEKETNQCK ECPPD TYLSIHQVYGKEACIPCGPGSKNNQKMMALCTNNITDFTVK EIVAGSDDYTNLVGAFVCQSTIIPSESKGFRAALSSQSIILADTFIG VTVETTLKNINIKEDMFPVPTSQIPDVHFFYKTIYRQIIDIKCPAGT CDGCTFYFLWESAEACPLCTEHDFHEIEGACKRGFQETLYVWNEPKW CIKGISLPEKKLATCETVDFWLKVGAGVGAFTAVLLVALTCYFWKKN QKLEYKYSKLVMTTNSKECELPAADSCAIMEGEDNEEEVVYSNKQSL LGKLSLATKTAIGVFGGPWSLGYVISCQYSETRSSCIISVHAKNEI LAIEE
5363	A	1	1146	NFDSKRRTVNRNLRREDIAKYLRNLDPNSAHYDPKTRAMRENPYAN AGKNPDEVS YAGDNFVRYTGDTISMAQTQ\LSVSSMSSHFI SAHKT GIV*SLFSRSIQ*CSQ LTKMFRITLVFAWEA\YDKGSE\VHL\QAD P\TKLELLYKS\FKVKK\EDFKEQQKESILEKYGGQEHL DAPPAELL LA\QTEDYVEYSRHGTVIKQERAVACSKYEEDVKIHNHTHIWGSYW KEGRRGN\KCCHSFFKYSYCTGEAGKEIVNSEECINEITGEESVKK PQTLMEHLHQEKLKEEKKKKKKKKKKHRKSSSDSDDEKMGHVKSNAK NA*EA\RLHVKET\MQI\DERKRP\YNSMY*TSRP\IEEEMEAYRM K\RQRPDDPMASFLGQ
5364	A	3	1589	APALKVILRYT*TDAPAIWWLDPELTGCAKPFVFTQGHSVCNRSFF PCFDTPAAKCTYS AVVKAPSGVQELMSATRSAYMEEEGVFHFHMEHP VPAYLVALVAGDLKPGDIGPTSRVWAEPCLLP TATSKLSGAVEQWLS AAERLYGPMWGRYDIVFLPPSFPIVAMENPCLTFI ISSILESDEFL VIDVIHEVAHSWFGNAV TNATWEEMWLSEGLATYAQRRI TTETYGAA FTCLETAFLDALHRQM KLLGEDSPVSKLQVKLEPGVNP SHLRNLT YEKG YCFVYLSQLCGDPQRFD DFLRAYVGE\YKFTSVVAQDLLDSF

				LSFFPELKEQSVDCRAGLEFERWLNATGPPLAEPDLSQSSSLTRPVE GLFQLWTAEPDQAAASASAIIDISKWRTFQTALFL\DRLLDGSPLPQ EVVMSLSKCYSSLLDSMNABIRIRWLQIVVRNDYSLT/FHRVRRFP GRARCHACYTIPLYEDLCTGALKSFALEVFYQTQGRHLPNLRRAIQ ILSQGLGFQHRAR
5365	A	1	418	FMGGVNRADENIDKYRASIRGKKWYSSPLLFCFELVLQNAWQLHKTY DEKPVDFLEFRRRVCHYLETHGHPPEPGQKGRPQKRNIDSRYEGP* IQVDSNPQ GK\QTRC\AECHKNTTF\RCEKCDVAL\HVKCS\VEYHT E
5366	A	1	205	KKFSCGLKKIFHEKNCQST*QISLLSYFKKLQPPQLSSTTL/SQQP STLRQNPAPAKRL*LIEGSADG
5367	A	1	389	CRFNAISSKITADFTVFGGFLLEVHKVILCKWKYY\KSRIVKTGFK KTQLS/GLILHNKNT*YTSIIKTELTKYRH\RMENPEIDLHRFDQM IFDEGIKVIQ*GKERLFNQWCWSRLRCICLKFSITNGQ
5368	A	2	300	TFPNLMTNMNLQIQEAO*IPSWKNSE/RSQ/SRHLIILKLIKGKER ILK\EQKLITYKGCSIRLRGDFSPETTEARK*WDDIFKVLKEQVSTK NLIFSCTVL
5369	A	199	494	CSKGMPCSSKRNFRCQTMPFSFIHEDDKNGRLIEKASVNRKPQLPQHF VDAYLDEMDQ GKNDPSSSTFSKENLIFSVGELIAGTETTTNVLRWAI LFMA
5370	A	256	514	ELHNNLNTFSLTGQVQKEIDLLMGPNGKPSWDDCKCMPYTEAVLHEV LRFCNIVPLGIFHATSEDAVVRGYSIPKGTTVITNLYSV
5371	A	2	1340	SDDLGGISTVVVNGYDVVKECLVHQSEIFADRPCPLPFMKMTKMGG LK\SRYGRGWDHRRRLAVNSFRYFGYGQKSFEKIL/EKETKFFNGC YWKHTKVGPFDF*TV**RMLFSNITNLIFWEERFHFMOGHRFFRHM DWSYFRWKMN*AAASVFLYNAPW/IWA/FLPFGKHQQLFRK/WT AVVYDFLSRLIEKASVNRKPQLPQHFVDAYLDEMDQ GKNDPSSSTFSK ENLIFSVGELIAGTETTTNVLRWAILFM\ALYPNIQGGVQKEIDLI MGPNGKPSLGR/RNAKCPYTEAVLHEVLR\GNIVPLGIFHATSEDA S\LRGYSIPKGT\IITKP*FLYHLGWKKVPGEDPQKVFPPIPERFPG TSSGIFWPQEGKLWVPFFPLGRRHCPWENTLARMEMVLFSSIASEV SFAFSHMN*FQI*SPRLGMTLQPPYLYICAERR
5372	A	135	273	SPLVLVSHFHLHDITRRWWGAWFPALPPSPSSPVCLPYPHFPNL
5373	A	1	344	LNTLPEVPFTPLSCLPSLSLSS*LAPSPFICICYAIVP/PPFLLPS DLADPSSHPGLPFLFPPHSPRHAPSAPPSKKKKKKKKKKKTAPVQ ASLGTSSLYPLGGSETGPTWS
5374	A	1	724	GRRGRGRAGSRAGRRGGAQAAL\VNRGGGPIRNY\SDVAGGAAGG\ GGR\NRPA PYSRPKQLPDKWQHDLFDSGFGGG/AAGVETGGKLL\VS NLDFG\VS\DA D IQE\LFAEFGER*RAAVHYDRSGRSLGTADVHFE RKADALKAM\KQYNGVP\LDG\RPMNIQLVTSQIDAQRPAQ\SVN\ RGGMTRNRGAGGF\GGWVDGTRKGT\RGA\RGRGRGAGRNSKQQLS AEELDAQLDAYNARMDTS
5375	A	37	331	GLLCQASGPQAPGWPA GLRRGQGSPLPVPPRPVPA*/APGHTCHA L/GKIPF*VPLPLQ*GPPETHLREPPPGPCPPS/PVPSPYQGFLLQG GRAGGDRD
5376	A	1	385	FFFFFFFFETETCSVA*AGVQWRDL*LOPPPPGFKRFLCLSRPSSW DYRCTSPYLAHF*FLVETGFHHVQAGLELLTSSDPPI SASQSAGI TGVSHCTWPKLTSTLMNVFPLNIILLYLVILAK
5377	A	21	352	PTHPWPPTVLEATAPGSEYFFF*DAVLLSSRRLECSG/SISAHCDLH LPSSSDSPSSVPQVAWIIGVRHHVQLIFVFLVEMGFRHVDQAGLK/I A*PQVIHPPRPHKVLGLQV
5378	A	2	545	TCLGFFQMFFLGSLIFVCYILLKFDVFISSNLGSLIFVCYILLKF DCVFISSQLPFFTFYMDYSNPLGLSMSSLRIS*KTF*MYG*VLYF\ FF*KRNSQCFPPFNRDYFWIVCSSVDLFTLFTTSCPHQQPSCSP PPGNKGPA PLPTVTLEALKMMMVFFIGLSSRIRGRSWKSP
5379	A	545	1462	GYFPCFI FVATS*QSIGVVNF*LFYFVYIYIFEGFWGGLICLKVS

				SVCLFQVYFSFAKIIIEPPGFKTTLPPSTLVNNWELTSLHQPK/RPAN FVIFGKRQGFHVGPGLN SGPHAIRPASASQSTGITGVSHCACALNF ITEP
5380	A	2	243	GFKQFSCLSHPSSWDYRCAPPHPTNF*FLVEPGFHHVQGAGLELPT SGDLPALASQSAGITGVSHHPWPM SALNSKNVR
5381	A	1	328	SPETGSCSGAQAGVQWHDLGSLQP*LGLK*SSYLSLLSNWDYRCA/P PRLANFLFFVQAGSCHLAQAGLELLSSCHLPALVSQNA GITGVSHHA RAGSCMEENTSLWLT
5382	A	2568	3052	RGTEGRRVKSSKAGFFCFVLFCFVLRWSLTLLAQAGVQRHDLSSLP PPPTFK*FSCSLSPSSWDYRRPPPSRG*F/SFVFLVETGFHQVQAG LELLTSGDPPASASQSAGITGVSHHAQPQLDLEPPVCGQORDMALLL ERLPETVTCFLFPSELRRAR
5383	A	2	306	FFEMESCSAAQAGVQWHPSSLPPLPGFKQFSCSLSPSSWDYRRAP PHPANF\EFLVDARFYHVGQAGLELLTSSDLLASAS*SAGITGMSHH GWP*ATF
5384	A	141	415	IRITEGGAQASVVKTPQV/WLGTVAHTCSPSTLRSRGWIT*VQEF KTSQSNRNQRGCNLVWSLKLTSILLTFELDSIRQEEGKLVRRWGR
5385	A	2	287	GRVGNKKFGGRISLC/QPGWSAVTQLQLIVTLNSWAERFSQDLPS S*DYRCTCLANFLTFCDECLAMLLRLVLNSWPQGIPLPQLLKVLEL QV
5386	A	663	1014	ILKHYPSSQISSILQRKHTRQLSASLITNAKVFFQASRFNVSSHILAL LQENIFYFNTKPVICKPG/CVIRITF*KL*IASQVRWLTVPVIPALWE AEAGRSRGQIKTILANTVKPRLY
5387	A	3	208	EDVNRWRDIPSPWIGRVIRVMSVL\PNPINNTYINTEFLILI*Y*Y RNTSIPIKISGRFFVLLRENN
5388	A	190	261	ISIF/CFFKTDSSCVAQAGVQ**NLGSLQ/PCNLQPLPPGFK*FSC LLSNWDYRCAPP/HPNFCIFSRDGISP*LSILPTTFFIKVARKILI
5389	A	31	1431	RETRSCWAHYHAESSKHQKAKLKDSRKARRSIELIGPSSQKGGDIC SLIHLSSKLGILCYSKTGNMGGWEGGMQLRVSSSENSMGKSSRERAAA DLPQGSCHWELPGRLINTRISLKPRHVWNLSSVLCQVVKVKSQMFM HMPITSAMQGDRLGICVTQFDPKLLERGLVCAPESLHTVHAALISVE KIPYFRGPLQTKAKFHITVGHETVMGRMLMFFSPAPDNFDQEPILDSF NFSQEYLFQEYLSKDLTPAVTDNDEADKKAGQATEGHCPQQWALV EFEKPV/YLPSAVPGDWLQARCGHS\PNTCRLAFHGQSCSTG*RTGT /NADSFLPRLKVYKLKHKHGLVERAMDDYSVIGRSLFKKETNIQLFV GLKVHLSTGELGIIDSAFGQSGKFKIHIPGGLSPESKDPDTPPSKT GPGWPVGGQPGRRRSPSGANPHKMGWLTRPFKRYVFDTHKRMVQSP
5390	A	1	421	FFF*GTESQLLPQCSGAI TAHC SL*LPGSSEPPTSAS*VPETIGTY /RHAWLFFFNLFVETGSHYVAQAGFEPLGSNDPP\POPPKLLGIT GMRHHSRPELLPLTVPM SWESQDGETEDFCAMETWKVNITCLAQTPR L
5391	A	1105	1497	LFRTSLLVIAFLPKKNFFF*HYA*SYNVHPNTARKIKPEFRAVRVSF LLSERMSNIFFFFDTEFHS\VT\RLCTG/T*SSTHCDPRLPGFEQ ILPASASQSSWDSPACATHARLIFVFLVETGFLHVGQAG
5392	A	109	695	LLIPSAVTSYPPKDLPWGGMILSKPPLGSM LANNCIVAGGCS*SS TLPS*LSSWRVGPQHLPRHARPPHQVQYIISQDGVQHLLPQYVW\ VPEGHHIQGQGRITHIQYEQGAPFLQESQIQYVPVSPGQQLVTOAQ LEAAAHSAVTAVADAAMAQAPGPVWLQDEDKCPKHNSNKLQHPRASK YDVITPGR
5393	A	1	405	YAPSDLPVKAERSTYNYSLPITVKKTS SQLVTMHD LKQGLGPSGTSG ARKPASSKYKLKVS LQTLRVTRVQSPRAVCVGD IWRRGDKSQGSL APAAACGCPSRALWEPGPPLSHVTTPGMIGIGHTQEDRARA
5394	A	203	459	DDASGEGARND SFAERLRRLWEYFVGRTL AGPARRTGMAAEADLG LGAAPVELRRERRRMVCEYPGVVRDVAKMLPTLGEE
5395	A	2	1185	LILNKKSRTRRSFFRRHGSPHGPAPWRPSRLAEPGELG*REREGYN NPPISGENLIGLSRARRPHNAIFVNFEEDEVPKQPLEAAAQ\TWRRV

				CT\NP\VDRKVEELRKASPALRLAPLFDIRPIWSRNAVK\ANITVH PNRFKAWLPFIAYMI\TGPWRSWIRFGYDP\RKNPDAKDL/YQVL DF\RIRCGMKQGY\APSDLPVKAKRSTYN\YSLPITVKKTS\SQLVT MHDLEAWPWPRRGRSGARKPASSKYKLKVSLQTLRDSVY\IFREGAL PPY\RQMFYQLCDLNV\EELQKII\HRNDG\AEDFLAQERGWWGGCLP QGGPDEF/RGDTMSPMIRE\TIGSKRPALFSSSAKADGGKEQLTYES GEDEEDEVEEEEEEDFKPSDGENEMGNQNF
5396	C	95	295	MSTIKAPXXXXXXXXXXXXXXXXXXXXXXXXXXXXLSSLRIILFQNI YLYWDKITFLYCEHTVGAQ*
5397	C	262	390	MLVARMNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
5398	C	118	132	MGVGD
5399	A	109	559	QFLHRLVHDSGEVWMKLVE**NTLLAKMVISISWPRDLPASASQSAGI TGLIGALVLSVGIYAEVER/HEI*NP*KCLPGSSSHHPHPPGRRHVHG LLHWCAGVPP*QPGKH
5400	A	1	362	FFFFFLRRSL/SSVPQAGVQ*HDLSSLQPP/PPGFTPFSCSLSPSSW DYRCPPPRPAKFFLYF**RRGFTMLARMVISIS*PRDPPASASQSAGI TGVSHRARPPPPQFFIQLPLYNIHTLEGR
5401	A	2	462	NPPTSAS*VAGTTGACYHTRLILVCRDRVSPCCP/VLVFFFFFF*DRV AQAGVQWHGLGSTCQSPCPGFKRFLLPSPSPSSWEYRHPPP RP\ANFFCIFIVETGF\TVLARMVISIS*PRHLPALASQSAGITGLSH CARPVDNFLATSIY
5402	A	3	352	SSRPGSCRRGAVRAAIRYVRLRAVPSGGGEPPSGAPLQPSWK*AFAR PGMLRCSPMSQAPSRSAAVLFEPLAEWMLHCA*QDEVRLGGH*GRRG PILLDRSRA*RESPAEVRPARE
5403	A	3	286	SVAQVGMHGSLSGLQPLPPGLK*SSHLNLPSSWDYRHAPPHLANFC IFFVETGFRHA\SQAGLSLSSSNWPTLASQSVITGVSHRAQPC*T F
5404	A	73	542	VLIFFFFLKLSSL/DSVA*AGVQWCNLSSLQPPSPGFK*FSCSLLS SWDYRCVPPSPANFFIFLVETGF\TVLARMVISIS*PHDPPTLASQSV GITGMSHCPWTDLIF**CKRDTLCIPMSLS**FKVPKGNLIWKLLG KFGGLPLGIQNAFWIV
5405	A	1	397	EMESSSVTOA*VQWHDLALLQPPPPRFNRFSCLSLSSWDYRCPPLS PANFCIFSRD/MGFIVLARLVLS*PNDLPASASQSAGITSVTHRIW SKIFFRVDNDHYIILFSSMELNVPTIVLCYHPQSSNMYS
5406	A	72	243	EPMTPOVSMFSLRQPMKTTGMRIAMQEKVTQNTQSS*KIFRFPSTYL IGVSLVISI
5407	A	34	420	MLYSHDPELS*QRVLTALYAVFPFVVPVDFL*I*FPSALVSIGGSRL L/PVLSHWFLDLRV\FH*FEKAHL*KLCGNP/WLSALLSTFKVM*ER LVDQ*LSMAKTTE*EPMTPOVSMFSCGRVEEFRHHP
5408	A	3	316	FFNFSTRQGLCHPSWAVTQSRRTVASIFR\VQGSSHLSSLGSW/DA RHVPPCLANF*FFCRD/RGLVMLPMSVSNWAQAILPPWLPSIGIT GVSHHVWLASLFVF
5409	A	905	1291	RGADTCLGFQVSADLHHLFSFLFCSVAQAGVQWRNLGSLQPPPPGFK LFSCSLSSWDYRHAPP/RPG*FFVFLVETGFT\RVGQAGL*LLTS GDPPA\SASQTA/RGL*GMSHLASPIYLDYFK*NFNKP
5410	A	2	308	FLRHNLAVTQPGAQWRLLSSLQPLPPELKPSSHFSLPSSWEYRCEPP HPANF*FLVETGFHHVAQAGLEFLASSDPPTSAPFLNAGVTGVNHSA WLCFSYLL
5411	A	3	368	HRGESVWNICRWGTLR*GKIGKMTTRAHCLEFIGALIVFSITSPAPFE AEPKWKNLDL*TLTHGRPVSVLLAKKCDHG/KDECRNSSLKMGQIY MEHSFVG*IETSAKENVNFDEASRCLDAK
5412	A	73	380	GQALQWCVSVMCSCIHSHPCV*VLWVCV\CLCISM\CMYSYACVLG YTKFGVCTEKNKQCTGNRSTQGLPLNRHTGSFRFWLDFHPLASPK GTLRSLSP
5413	A	1	400	NSEGAAWIQPPAGEPTWQSGGTQORAGAMPPGDYS*SQGHPFLH/RA

[illegible]

				VEPETSSDEHPVQCQENSDEAKAPQTPSALLGQKSNTDGALQKPSNE GVIEIKATKVCQDQRTKCKSRCNEMLPGTSTGNNQSTITLSVASQNL FTSSSSPPNGDSINKDPKLCCKSPRKLSSSTLQETQVPPVKKPIVEQ LSAATIEGQKQGSVKQDQKVPKSGKTEGSTAGAQIPSKVSVNVSSHI GANQPLNSSLVISDSALEQQTPSSSPDIKVKLEGSVFLDSDSKS VGSFNPNGWQQITKDSEFISASCEQQQDISVMTIPEHSDINDLEKSV WELEGMPQDQTYSQLHSQIQESSLNQIQAHSSDQLPLQSELKEFEP VSQTNESYFPFDELTDQDSIVEELVLMQQMSMNNSHSYGNCLGMTL QSQSVTPGAPMSSHTSSSTHFYHPIHSNGTPIHTPTPTPTPTPTPT PTPTSEMIAGSQSLRESRCSRLAQTPVDSALGSSRHTPIGTPHSN CSSSVPPSPVECRNPFAPFTPISSSMAYHDASIVSSSPVKPMQRP HPDKTKLEWMNNGYSGVGNSSVSGHGILPSYQELVEDRFRKPHAF PGQSYQSQRHHDNFGRLTPVSPVQHOGATVNNTNQEGFAVPAPL DNKGTNSSASSNFRCSVSPAVHRQRNLGSGTLPVSNIPRSNVTPF GSPVTPEVHVFTNVHTDACANNIAQRSQSVPLTVMQTAFFNALQKQ ANSKKITNVLLSKLSDNDDAVRGLGMNLPSTNYTARMNLQILEPS TVFPSANPQNMIDSSTSVYEFQTPSYLTKSNSTGQINFSPGDNQAQ EIGEQQLDFNSTVKDLLSGDSLQTNQQLVGQASDLTNTASDFSSDI RLSSELSGSINDLNTLDPNLLFDPRQGGQDDEATLEELKNDPLFQQ ICESMNSMTSSGFEWIESKDHTVEMLG
5421	A	288	668	VEKRQFLNSTADPECIRYPLTYFVLGQSLALVTKAGVQWRNLSSLQ PPPEFKRFSCLSLSSWDE\RHAPPCPS*F/CVFFLVKTGFHRVSQD GLDLLTSNDPPTSASQSAGITGVTLAPSLFVLIH
5422	A	3	288	STFFFFFK*NLARLSRLECHGTISAHCNFRLLGSSDSPALASQVA\G LRGTCHHT*LIFVPTVETGFRHVQAGLELLA\WVICPP*PPKVLRL QA
5423	A	1	782	MVHITGLCADNLQYQAGARIISVPEEDNSKSLENIPGGIIEENFPSL ARDLDIQIEAQGTGPKCITKRSSPRHIVIRLFVKTKERILRAVRQ KHQVTYRGKPIRLTADFSEETLRARRDWGHIFSLKQNDYQPRILYA AKLSIIYEGKIQSYSDK\QMLREFTITNGKLLKGAVSLVVALNR*NK SWKHIKTHQNRSLKHKSHRTYKTKIPLHDEYNDLRSALRPASHTAY GSMLMILKSSLTLFKHGDEVVGRRAK
5424	A	2	392	KTKIIQMANKHRKRH\QSQ**VRLMQKKIIMIHYYIPQWLKTSKSDM IKCCSGYGTTEIFTHYLWECKLLHLLWRMVWL\ILLKFKTDTPHDPA IPLLGTYPAEC\CTCTPKAHTAALSIIIVPSWEQPKYPQ
5425	A	1	181	VSHVITNVLQPPANRPQERGDELADSALEIFKQASAFSRASQRSVRL APVYQKLLERMKH
5426	A	1	2162	MALFVRLALALALALGPAATLAGPAKSPYQLVLQHSRLRGRQHGP VCAVQKVIGTNRKYFTNCKQWYQRKICGKSTALGTADVKGVSSLA VSDLGGEQMRKLPRREMMKLAEDGPAALPLSNLYETLGVVGSTTTQL YTDRTK\LRPEME\GGPGSFTIFAP\SNEA\WAP\LPAEVAGTPLV SNVNIELLNALRYHMGRRVLTDELKHGMLTSMYQNSNIQIHYPN \GIVTVNCARLLKADHHATNGVVHLIDKVISTITNNIQQIIEIEDTF ETLRLA\VAASGLNTMLEGNGQYTLAPTNEAFEEKIPSETLNRILGD PEALRDLLNNHIL\RSQAMCAESIVAGLSVETLEGTTLEVGCSDML TINGKAIISNKDILATNGV\IH\YIDELLIPD\SAKTLFELAAESDV STAI\DLF\RQAGLG\HLSGSE\RLTLG\PLNSVF\KDGNP\PID \ALTRDLLWNHII\KDQLASKYLYHGQTLETLGKK\LRVFVYRNSL CIENSCIAA\HDKRGYGTFT\MDRVL\TPPMGTVMVDVLKGDNRFS MLVAAIQSAGLT\ETLNREGVYTVFAPTN\EAFFRALPPRERSRLGD AKELANILKYHIGD\EILVSGGIGALVRLKSLQGDKLVS SA*KTNV SV\NKEP\VAEPDIMA\TNGV\HVH\TNV\LQPPANRPQE\RGIDLA DFAV\EIFKQAFSVFPGASQ\RSVRLAPVYQKYL\ERMKH
5427	A	1	410	FFFLKRRDLAVAQGTGVQWGDHGSQLPQIPGRRQSSDLSFLNS*DH ILSCSATFTSF*RSHSAAQAGLEILATSNPPA*ASQGP I*\GVSHH TWQKATFCICLPANNILSCLNIYSFFYHKTNNHFMIMKTNNHKQI

5428	A	3	404	RLFYNFTIEMRFSLFVQGCL/INSLG*SDLLVFASASAGIT\GVSYPHALASIVFVCVCV*WGSALVAQAGVQ*RNLSLQPLPPEFKQFSFLSLPSSWIYRHPPPLSFYLPKLKSCGLCTGIWAWRLFIFIGS
5429	A	2	240	TRSAVV*SQLTAALTS\VKQLSQLSLPRSWDYTHVPPCLSIIFYFL*R*GLPMLPGLVSNWTOAIFLPQPPKVLGLQA
5430	A	3	468	RWSFTLVAQAGVQRVILAHQAQPPPGFKRFSCSLSPSS/WDYRLAPRLANF*FLVETGFLHVGQAGLELPTSGDPPASASQSARIIGVPLCPGISRIFVQQMALEDSDISLRLWFLSRHANLQCVTLWACQLLPCCTWRARETKANTLPAVP
5431	B	151	344	YENESALNLYETCKVRTVKAGTLEKLVEHLVPAFQGSDSL SVTIFLC TYRAFTTTQVLDLLFKS*
5432	A	1	439	PSASSGQAGGFWSQLFKQESSGFVRTSAESVLRQESLRGVLGVLLEYWRGSEVCGSRQSLYGLSSGRGILQGPQEH*SPLCPSPPPELKIPENANVFYAMNSTANYDFVLKKRTFTKGVKVKGASFTLP\RMKQKGLKIAKGIF
5433	A	77	444	GLGVPSELQEIRVPLPLTVCPSSVPPQYENESALNLYETCKVRTVKAGTLEKLVEHLVPAFQGSDSL SVTIFLCTYRAPASQVLDLLFKR*A*ALHCTGCTRGPRPHPLAAGLNAESPL
5434	A	1	3190	MVQRMWAEAGPAGAEPLPFGSRRSRVWDAVRLEVGVDPDSCPVLHSFTQLDPLPRPEVGGGRGLLQKSASRVGSGGCRRAPSNSRDHGWGFAPLNTVPGPAVTKAAAAQVDLFLRHCPCLHRWPVPYFTQFPFPRARSASLAFTMQAVGLCSRQSVPYLGNRLHRCIPCTVARQALDVPAPGCRA LSSQSSTQEI GEELINGVIYISILRKVQLH\ PAGNKGQRDKKGKELLAPT\IRATVTQFNSVANI\ VITTC LGNRSTKAPDRARVVEHWIEVAR ECRILKNFSSLYAILSALQSN SIHRLKKTWEDVSRDSFRIFQKLSEI FSDENNYSLSRELLIKEGTSKFA\ TLEMNPKRAHKRPKETGIIQGTVPYLGTFITLDLVM LDTAMKDYL YGRLINF EKRRKEFEVIAQIKLLQSA CNNYSIAPDEQFGAWFRAVERLSETESYNLS\ CEL\ EPPSESASNTL RTKKNTAIV\ KRWSDRQAPQH* AQLPVGSSSHFQVPVDQFRC/SGPYFSSGDIADALS VHSAGSSSDVEEINI\ SFVPES\ PDGQ\ EKKKFW/ENSAFKSYSPETSGISS\ ASSSTS\ SP*ASTTPVAATRTHKRSVSGLCNSSSALPLYNQVGR LVV IIRVSWDVGQWATCYKSIL\ VVTSQDKAPAVI\ RKAMDKNLEEEPE\ D\ YELLQILSDDRKL\ KIPENANVFYAMNSTANYDFVLKKRTFTKGVKVKGASSTLPRMKQKGLKIAKGIF
5435	A	1	436	EKINKIRWLPQONAAHFL LGTNDKAIKLWKISERDKKAEGYNLKDDEGRLRDPFRITALRVPI LKPM DLMVEASPRRIFANAHTYHINSISVNSDHETP\ NIVDIKPANMEELTEVITAAEFHPHQC NVFVYSSSKGTIRLCDMR
5436	A	204	397	VPILKPMGSYG*EASPR\ RIFANAHTYHI\ NSI\ SVNSDH\ ETYLSADDLRLNLWHLEITDRSFNIV
5437	A	1	1463	PLRSWLPRLPDSQADIISTVEFNYSGLLAT/GDKGGRVVFQREQEVLAQPRRPALP*SVSSFLSTSCREWQGEFSLPFRERIK/GRPHSRGEYNVYS/TAQSHGTGGFDYLSLEIEEKINKIRWLPQONAAHFLSTNDKTIKLWKISERDKRAEGYNLKDDEGRLRDPFRITALRVPI LKPM DLMVEASPRRIFANAHTYHINSISVNSDH\ ETYLSAR*PGGINLW\ HLGNRH*EAFNIVDI\ KPANMEELTEVITAAEFHPHQC NV\ F\ VYSSSKGTIRLCDMR\ SSALCDRHS/ KSFFEEPEDPK/SSRSFFS\ EIISSIS\ DVKF\ SHSG\ RYM\ MTRGLPVRWKVWGPSTWEEAGPVGGPTRVH EYL\ RTKL\ CSL\ YENDCIF\ DKF\ ECCWNG\ SDSAIMTGSYNFFR

				MFRDRTRRDVTL\EASRESSKPRASLKPRKVCTGGKRRKDEISVDSL DFN\KKILHTAWHPVGQCYLPWLATN\NLYIFQDKIN
5438	A	3	392	FCACFIGSKTPASCRAQGRPPGEFSPGSPSGPAGGKGVLEKEPSEM /PP/PEAGERKLERKTVPGRGAEYGPPLRLSYQAVNSHPLPSSVN GGGDSNNSSQLPESHCPFFSPKEGPRKGEVPCLHATRA
5439	A	1	298	SLLGPPEPTTWT/PAPQDR*HGPC*GR*RKRRPSL*T*QWELASPP/ REPMFVPPKKEMVAIQPLQEEASVGPTPELLSGSCRSPISGISILGNC PSLAPLT
5440	A	3	11	HELILSPGPTQGQTPDEAGVIIRVLKNVPDLAILNSKDALDPRQPGY QPPNPHPGPSSPPAAP\RPRGA*GNPQLENASRSDRNPSQGLRTRIR RPETPDGPPSPAGSS\PAPPPDPVPPAFHSSGPPEPTTWT/PAPQD R*HGP*GDKRGAPGVAGEDPDQP*GTS
5441	B	1	513	MEVAVSRIMTLHSSLGDRARLHLKKKKEEEEEKEEEEEEEEEKKKEEK EKEKKKEKMMRRRKTKNNTKQNKTC SKQALLRKEKNFHKRWPA PGVTARYATSKGDVSAASTLPVKTPAPIQRRGEVSTIHLSSQVVQWQ WGPHALYTVVLLLEEGLSPGDLGTGFI*
5442	A	2333	2633	GGTPISLLFLFCFETQSHFITQAGVQGTILAHNNLHLPGSSDSPASA S*VAGIAGAHHCWLI FVFLVEMGFLHVGQAGLELP/NLVIHPPRPP KVLGLQA
5443	A	1	704	MVAASAAIKFTNMSLAIAIAGEHVEFALIPVTAVKYTYTVIPALVM TWCLSYIERWVDSITPAVTKNFLKPMILIVLIAAPLAILLIGPIGIWI GSAISALVYTIHGWLVSVAIMGALWPLLVM TGMHRVFTPTIIQTI AETGKEGMVMPSEIGANLSLGSSSLAVAWKTKNPELHLDTPHTESPT PHDSNSHRP/PTAGVYNRSKAKSTDKNNDQTRWGNWRWSQRKYCLPL
5444	A	195	524	RALTFRHLPCTSQVASCNLCCLFLADLDTL\HTESPTPHDSNSHRP/ PTAGVYNRSKAKSTDKNNDQTRWGNWRWSQRKYCLPLIVLSFFQTKQ NTGTFRNFLSPFLMYV
5445	A	2	884	VPQFKPKLHQENGPGGLARCDHQGAQPTRETWLQDRDREFQSQTFL LRSRV*LVLQQLQESQHSLERLREGQRLVEREQARMRAQSSLGHWKH GRQRS LPAVLLPGGPPEVMELNRSESLCHENSFFINEALVQMSFNTFT KLNPSVIHQDATYPTTQSHSDLVRTSEHQVDLKVDPQS\QPSNVSHKL WTAAGSGHQILPFHESKSDCKNDLDTSHTESPTPHDSNSHRP/PTA GVYNRSKAKSTDKNNDQTRWGNWRWSQRKYCLPLIVLSFFQTKQNTG TFGRNFLSPFLMYV
5446	A	269	484	DKTSRGTIRQHSRFTKIRCSAATAADTQANRVWSGPLANSNRPAE GPRDPPASASQSAGITGVSHRAWP
5447	C	5465	5719	MRLGKTHSTAGAWKMGLLRQADSTRGEKRGKKAAIICVKSPPGYQV VAVWKYHSSLGVEFFKKTCSMMGRHDTEKKMSWERP*
5448	A	57	102	MEFCVNSQKCDINS
5449	A	3	287	RALYYFL*FALFGLT*M*LVS*KLQIIIEYEKKQTLGQNDTGFI CDGT ANTFRVMFKEPIEILPNVCYTACATLKVRVMHYVPDGFLLNVAECVF
5450	A	1	594	MAVHPVVITVIIISILGIISSVPHTERQQRQEGCLHVRQLDLGRRGG HAAVEHGVKDGAAGRQHEAVGGDALRAPSGGGAATLAQYEAHIAQQL RVEEEGEALLQRRLLGRLPVVERFPLQGEQGPQRGRPLITKSSAPIVY LGHVPRPVPRSVLP GSGGAGKYQGNTVSRVRSFWWVRGLADFKNGA VDLPDEFYSS
5451	A	1	768	SVEFPCLRLSGAVVRWAAEACQRQQLPVTFGNKQKVLGKALSIRFPL MTIEEFAAGPAQSGILSDREVNLFLHFTVNP KPRVEYIDRPRCCLR GKECCINRFQVESRWSYSGTSDRIRFTANRRTSIVG\LGLYGS\IH GP\TDY\QVNIQIIIEYEKKQTLG\QNDTGFS CDGTANTFRVMFKEPI EILPNVCYTACATL\KGPDSHYGHKRI*RKVVHGGHLLASKDCFFLF *F/ALGINNGTSIEDGQIPEIIFYT
5452	A	1	491	LKDVTILRRHVETKVRKIRKRVTTKINRHDKINGKRKTARKQKMP QRAQELRRRAEDYHKCKIPPSARKPLCNWVSLFVFLAFEHSLPGQDM DTFFSLQLCAQALQREMAERKAAYSITVPSLLVTVLCKNTFIPTQWA PDLNSKCQRFHICNSKWALTVN

5453	C	175	324	MKVFLHNTVTNRDGTVMVLVGSPLPLCHLPLQGLSTEPVAKRLSCKGGD FAF
5454	A	3	190	RAAYKPHSPIPVGTIPNEGLK*CSAKLVLVWPLYLQKLPSPMITRDG TCTLEVJHSHFKTCFV
5455	A	1	716	MVKLSIVLTPRFLSHDQGLTKELQQHVKSVCPCCEYLKRVINTLAD HRHRTDFGGSPWLLIITVFLRSYKFAISLCTSYLCVSFLKTIFFPSQ NGHDGSTDVQQRARRSNRRRQEGIKIVLEDIFTLWRQVETKVRKIC KMKVTTKVNHRDKINGKRKTAKHLRKLMSKEREHGEKERQVSEAE NGKLDMEIHTY/MITPSARKPLCNVRVMAAAEHRHSSGLPYWPLYT AETL
5456	B	1	387	MRVRWLLFWLLFWLLLGFIHQSTCVINTLADHRHRTDFGGSPWLL IITVFLRSYKFAISLCTSYLCVSFLKTIFFPSQNGHDGSTDVQQRARR SNRRRQEGIKIVLEDIFTLWRQVETKVRKIRKMK*
5457	A	1	435	MFQRGQELRWRAEDYHKCKITPSARKPLCNWVRMAAAEHRHSSGLPC WPYLTAE TLKNRMGRQPPPTQQHSITDNL SLKTPPECCLLIPFP PLPPSVDDNLKTPPLATQEAEEAKSLKPKRQRLSKLRTGHCTQAWAI RRNL
5458	A	1	4798	MGSTGVYKVTPRSCHRFEQAFYTYDTSSPSILTTLAIRHHVLTGTTT DKMMDVTVTIKSSIDSEPALVLGPLKSVQELRREQQLAEIEARRQER EKNGNEEGEERMTPPVQEMVDELQGPFSYDFS YWARVLCFVGTGPA KLKYINIFRSGEKITVTPSSKELLFYPPSMEAVVSGESCPGKLEIH GKAGLFLEGQIHPELEGVEIVISEKGASSPLITVFTDDKGAYSVGPL HSDLEYTVTSQKEGYVLTAVEGTIGDFKAYALAGVTLHSQDVLMLPG DLVGLQHDAGPGALLHCSAPGHPGPQAPYLSANASSWLPHLPAQLE GTWACPACALRLLAATEQLTVLLGLRPNPGLRPLGRYEVRAEVGNV SRHNLSCSFVSVVAGLRVIYPAPRDGRLYVPTNGSASVLDVDSGA SATATARWPGGSVSARFENACPALVATFVPSCPWETNDTLFSVALP WLGEGEHVMDDVVENSASRANLSLRVTAE EPIGLRATPSPEARVLO GVPVVLLAGSSGYLVGFKFLESHGSDSGSANSFHLISRNEFKTPLP DLTRVPRYSPPVEAGSDMVFRWTINDKQSLTFQNVVFNVIYQSAAVF KLSLTASNHVSNTVNYNITVERMNRMQGLRVSTVPAVLSPNATLAL TAGVLVDSAVEVAFLWTFGDGEQALHQFPYNEFPVPDPVSAQVL VEHNVHTHTYAAPALGGGAVLTRQPSVLLHLCSPHVAWEPGLKAG PQVSTVLTVLASNAPENRTQQVPVSVCASLPSVSVCAWYPR VLIRSGRVPISLECVSCKAQAVYEVSRSSYVYLEGRCLNCSSGSKR GGYTFTLTVLGRSGEEEGCASIPLSPNRPPLGGSCRLFPGLGAVHALT TKVHFECMGWHDADAGAPLVYALLLQRCRQGHCEFCVYKGSLSGY GAVLPPGFRPQFEVGLAVVVQDQLGAAVVALNRSIAITLPEPNGSAM GLTVWLHGLTASVLPGLLRQADPQLVIEYSLALVTVLNEYERALDVA AEPKHERQRRARIKKNITETLVSLRVHTVDDIQQIAAALAQCMRKL EQDIAQGSYIALPLTLLVLLAGYNHDKLIPLLLQLTSRLQGVGALGQ AASDNNGPEDAKRQAKKQKTRRTLATSINTSREPSTDDQLPAHNQTM PQRHARSAPPRAYDRKTRQENPHQTRSHAAAKRRERP PHDLQKQA TTRLIPAGPRRRDGTSPRRTPQPPNTRRPAAAGHLARFRRAAPGARG ARPPTARRGREELDPAHIYAAAPGLPTPPRAGRTPPTPERRDRNTRR RRTREEGEGERPVSFLKTIFFPSQNGHDGSTDVQQRARRSNRRRQEG IKIVL\EDIFTLWRQVETKVRKIRKMKVTTKVNHRDKINGKRKTAK EHLRK\LCMKEREHGEKERQVSEAEENGKLDMEIHTYMEMFQRAQA LRRRAEDYYRCKITPSARKPLCNVRVMAAVEHRHSSGLPYWPLYTAE TLKNRMGHQPPPTQQHSIIDNLSLKTTPSERLLYPFPFPPSAPP SADDNLKTRAVCLLHPLPPSAPP SADDNLKTPP/EVCLLTPLPPSAP PSADDNLKTPPECVCSLPFHPQLHPQRMII SRHLPVSVAHSPSTLSS TLSG
5459	A	2	568	RRQEGIKIVLEDIFTLWRQVETKVRKIRKMKVTTKVNHRDKINGKK KTAKEHLRKLMSKEREHGEKERQVSEAEENGKLDMN*IHFYMEMFQ RAQALRRRAEDYYRCKITPSARKPLCNRVSLVFLAFGHSLPGQDMD

				TFFSRLRCASSPAEGDGREEGCLQAFVPSLLVTVLCKNTFIPTQWG P
5460	A	69	419	LKSKLSDYKINL/QKSVTFVYTNSN*SEK/QFKKEIQFTNSCKDN*K NYLGINVIKEVK/DLYN/ENY*ILIKNEKNPKK/WRAIPCSWFGRIN IVNKF\ILPKVGYRSNAIPMKMPVTSRTRG
5461	A	2	216	YLFYIYLLPRLKCSGVITAHCSLYLPGSKYPPHSAS*VAGTTGPATMS S*YF*FFVETRFFLCSPGWS*GSSSDPSASASQSIVKIGVSHCT\CP RNFRNRLAQSLHFTGEETVPRKKGDLPWVYRQTQG*IPGPHRCQVLA F*PKDFLLSPHIYVSTSILWPPPA*AQAEVQWCDHSSQLPLPRFKI SSPLSLLSSWNHRSCHHVQLIFLIFCRDKVLPVFPRLVLRQLQ
5462	A	59	405	KRGFNFGAPDKREWGEFG*LKPWLPG*NNFSGQTLRRSGD*RKTPH GGVNLVF*EKTGFSNLGRGGLKPPPSGNTPAWPPKGVGITGGASSP PVFCFLGFCEINTLRAKKKFI
5463	A	1	242	STFFFFCETESSSVTQAGVQWHNFSSLQPPPPRPFKQFSCLSLPSSWD YRCAPPCPSNFCVFSRDGDSRWPWPGWSPTPDLK
5464	A	15	276	ASVTQAGVQWHNLGSLQPPPPRPFKQFSCLSLPSSWDYRRPPPCPTNF LF\LVLARMVISI*PHDPPASASRSAEITGVNHARPGFLFL
5465	A	2	309	EQKFNKQKGRALRCRGLSGLLSCSKDVKSFFSVARLQCSGLILA HCNLHLPG\SDSPASAS*VVGTPG\QRHHAQLGFVFLVEMGFHHVGP GMVFDLLTSG
5466	A	1	1209	GGIPALDKNVAELTVMDVYDILSLVGHEVERVIDQHGCETARLMPK VVRVLEILEVLVSRHHVAPELDELRLLE\APLR\RVRMDLIEKERKH QKELELVEDVWRGEAQDILLSQIAQLQEENKQLMTNLSHKDVNFSEEE FQKHEGMSERERQVMKKLKEVVDKQDEIRAKDRELGLKNEDVEALQ QQQTRLMKINHDLRHRVTVEAQGKALIEQKVELEADLQTKQEMGS LRAELGKLRERLQGEHSQNGEEEPETEPVGEESI SDAEKVAMDLKDP NRPRFTLQELRDVLERNELKSKVFLLOEELGLL*E*RNCRGKPNTP TPTHRPPEDGPPSRESGIKATCLASFFPEVKKRLGQTHRGVHIQGV PLDKLGKHPTAMTGYTEQRTGSPCSIC
5467	A	1	388	FKDPEAVRALTCTLLREDFGLSIDIPLERLIPTVPLRLNYIHWVEDL IGHQSDSKSTLRRGIDIGTGASCIYPLLGA TLNGWYFLATEVDDMCF NYAKKNVEQNNLSDLIKVVKVPQKTLLMDALKGSI*V*SMTFCM\CN PPFFANQIGSQVE*/YSRNP RRPPSSVNTGGITEIMAE GGELEFVK RIIHDSLQ LKKRLRIDMAALLIGVCSEVSGRKDWIQQLAPRWYSCML GKKCSLAPLKEELRIQGVPKVITYTEFCQGR TMRWALAWSFYDDVTV VHEGR LAVGGVTSDSQNKGSASPPSKRRKLEKPRKPI TFVVLASVMK ELSLKASPLRSETAEGIVVVTWIEKILTDLK\ASINEFPVEKRKSA FS*RP*KTPGFI*GERKESV*SDSKSTLRRGIDIGTGASCIYPLLGA TLNGWYFLATEVDDMCFNYAKKNVEQNNLSDLIKVVKVPQKTLLMDA LKGI
5468	A	72	680	LEEPRQSLEGHTEGERAALPGKAKVVEGRVADDGVPGQPAWPGAPP HTAAFQPVHALGSTRASQQGSLGDC*AACR*Q*KAP*VPKQGT*QER SSTK/PRAVPSGHWAGGSGCRCSE*RAALG*TTEPQQSGELPGPPWP LEGAHPLSAETGSCVPPRAFSGQKQPRGPG*AAEGPHGDFPQTGD RHCPPSSSTEPSGMTGR
5469	A	259	373	FSGLFLDFISFLGPMGSMGMNMGMDGQWHYMYPPSSCKA
5470	A	1	336	MEVGKLSKGVVEEPALPDERKTFASARGPVRKADTPVHRAAAGTAWR KVQCLTKDDAVWCVKENGLDISSGLIPAQTTCVILHPYPSEEQKKQ LAQDTGLTILQVNNWKAH
5471	A	1	1396	GAHAPHNPVMPASMGSAVNDALKRDKDAIYGHPLFPLALVFEKCEL ATCTPREPGVAGGDVCS SDSFNEDIAVFAKQVRAEKPLFSSNPEDN LMIQAIQVLRFHLLLELEKGHELCDNFCHRYISCLKGKMPIDLVIDER DGSSKSDHEELSGSSTNLADHNPSSWRDHDDATSTHSAGTPGPSSGG HASQSGDNSSEQGDGLDNSVASPGTGDDDDPDKDKKRQKKRGILPIV FP\NIMRAWLFQHLTHP\YPSEEQNIQLAHDGTGLTIFQVNNWFINAR IGIVQPMIDQSNRAGFLLDPSVSQGAAYSPEGQPMGSFV\LDGQOHM

				G\IRPAGTYEWDGA*IWAWMGNGTTC*PSSC*RHSQSKGEVCRAWPG DYVSQGGPMGMSMAQPSYTPPQMTPHPTQ\LRHGTPNAFHILPSLPH HPGLD*LHGGTPYPTWD*LC*AQSPTMLNSVDPNVGGQVMDIHAQ
5472	A	3	862	TMRPDIDNSQAAHQPPGRLPNSRKLKKTRRQMCVQTKKRIARLPPC CRNTPPTARSHPGRDCAKPNT*SLRSPGGDCH*QGNTTWMPMAR*L SGDSESGRSPVRTIICHQPSRSQSPVDRLQQLLPASQSTQLPCSSSP QETTQSRPMPPEARRLIVNKNAGETLLQRSARLGYEGS\VLYCLENK ICDVNHRDNAGYCALHEACARGWL\KFVRHLLLEYGADVNCSAQDGTR PLHDAVENDHLEIVRLLLSYGADPTLATYSGRTIMKMTHELMKFL TDLFK
5473	A	1	444	KLLRWLRQE\NCL\NLGGGSCSELKSHHCTPPWMIEGDSI*KKQNK KTRKRKPQGSHTLSGGPDWV*QNCEVSQVLPISHFPLQDILPPL PYLGANGQAGEQGATDGH*/RTTESHRAVGCRIWLCQRPLALAL SFFLCERMRTIP
5474	A	2	330	EMSFAVAQAGVQRHNLGSLPLPPGFK*FSCSLSPSSWDYRYAPPT P\AN\FAFLVETGCLHVGQAGLKLPSGNLPTSASESAGIIGVSHCA QPGTATHSNTVLSGLFC
5475	A	2	363	ELDTLCDLYEP*PSPSIIFINTRRK/VDWLTEKMHARDFTVSAMHGD MDQKERDVIMREFRSGSSRVLITTDL\RIGRGRFRGRKGVAINMVTE EDKRTLRIETFYNTSIEEMPLNVADLI
5476	A	112	434	ARGIDVQQVSLVINYLPTNRENYIHR*A*IWNTPPLHTWPSLGLK LLIFLIPFLVFQ\IGRGRFRGRKGVAINMVTEEDKRTLRIETFYNT SI\EMPLNVADLI
5477	A	3	724	NSNVEREEWKDLTCLDYETLTITQAVIFINTRRKVDWLTEKMHARD FTVSAMHGDMDQKERDVIMREFRSGSSRVLITTDL/AE*RELIKA EGRIQGDLSKGTSVPLRKVAAWNIWHA*GLWGTGMLISSAFLGCP HGCLSVFPPG*SVLRAHAEELSFLTHARGIDVQQVSLVINYLPTNR ENYIHRIGRGRFRGRKGVAINMVTEEDKRTLRIETFYNTSIEEMPL NVADLI
5478	A	1	1274	MSASQDSRSRDNGPDGMEPEGVIESNWEIVDSFDDMNLSESLLRGI YAYGEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQOI ELDLKATQALVLAPTRELAQQIQKVMALGDYMGASCHACIGGTNVR AEVQKLQ\MEAPHI\IVGTPGRVFDMLYRK/YTLSPKYI\KMFVLDE ADEMLSRGFKGQIY\DISKRLNSTTK\VVLLSATMPFD\VLEVTKKF MRGPPFRILVKKEELTLEGIRQ\FYI\NVEPEE\FNLDTLCDLYENL DHHPRQVIFHQPPGGKVDW/LSPEKMA\RDFTV\SAMHWRFWTQKE RRT*L*REF\RSGS*PEF*ITPLTLPAQRAFDVASRVSF*SPKLMTL PPPTRGKLLIHR\IGSRVDRFRGRKGVINMLTE/EKTKRNLEDIETF \YNTSI\EMPLNVA
5479	C	114	302	MKEELKKTAELYKRAMXNKXKQKHHSWVXKAPSRPFIKWETRGLK TAHSPNVFLQQGQR**
5480	A	1	2043	MPEISLSVHAQRRDHVS IWCDSAYTPRETKENE IQDLLRAKRELES KLQRLQAQGIQVDPGESDSDDNCTDVTAAQTCEYWTGGALGSEPS IGSMIQLQQSFRGPEFAHSSIDVEGPFANVNRDDWDIAVASLLQVTP LFSHSLWSNTVRCYLIYTDETQPEMDLFLKDYSPKLKRMCMETMGYFF HAVYFPIDVENQYLTVRKWEIEKSSLVILFIHLTLPSQDRVTWRSAD ELPWLFPQQGSKQKLHDCLLNLFVSQNLKRGHFAELLSYWQFVGKD KSAMATEYFDSLQYKCEGEDNMSCADLYETLGRFLKDLGLLSQ AIVPLQRSLEIRETALDPDHPRAQSLHQLASVYVQWKKFGNAEQLY KQALEISENAYGADHPYTARELEALATLYQKQNKADQFLKRSLEMR ERVLPDPDCAQSLNNLAALCNEKKQYDKAEELYERALDIRRALA PDHPSLAYTVKHLAILYKMGKLDKAVPLYELAVEIRQKSGPKHPS VATALVNLAVALYSQMKKHVEALPLYERALKIYEDSLGRMHPRVGETL KNLAVLSYEGGDFEKAABLYKRAEIKEAETSLGKGKAPSRHSSGD TFSLKTAHSPNVFLQQGQRFVMTVYLENAVVSQNLKLI SNFSKVS GYKINVQKSQAFIYTNNRQRAKS

10410

5481	A	153	332	QTFVLAEGKH*ENE/PVFCLNVSPLEDEWREGAFPPKSDVSASFISIAL LLYNSAAFSSKSPPS
5482	A	2	904	HILLVNLKHLQLCTRNRNIFKLFHFRKKSFMGHQRAIKKKGNLYGFL ALLRRRALQVEELTLGKOTPDNARTLNLGGLYYLQNNLETADQVLK RFL*MRERVLPDHPDCAQAL\NNGAGSYAMKKNQYDKPEDLYKRAL DIGRRALAPDHPFLAYTVKHLAILYKKMGKLDKAVPLYELAVEIRQK SFGPKHPSVATALVNLAVLYSQMKKHVEALPLYERALKIYEDSLGRM HPRVGETLKNLAVLSYEGGDFEKAELYKRAMEIKEAETSLLGKAP SRHSSSGDTFSLKNQLHFS
5483	A	2	331	PGQHGETLPLLKIQK\LAGQGGTSL*SEPLRRLRQENCLNLGGRGCS ETRSCHTLVWVTGRDSISKQKTAVDQAEERVSELEDRLFENTQSEK TKEKRIKISTLRGFRK
5484	A	26	117	AKGQVALGRPGARMQGGSKVVGVLAGPGSRSEAGTVPSYPAAQTRPH PPPQPLLI FRSPGVVPNGHQGPPNSTASSKQCNLRWGLPTVARHPK SGQRPO/PRPTR*PGSPQGPPTGRKNPERP*LVQQ*PCWAREPV
5485	A	111	270	LFQTFEDVSGFGAWHRRWCVLSGNCISYWTYPDDEKRVIIYVLFSS GESPD
5486	A	240	408	TDPSPQASDYETMETVVOIQEEKSESQSLVSPGKNQSESEAGELSHNQ LSSPLGFQ
5487	A	128	657	ESESYWAICSRKRSPLVSSYGGHIYLRKIRCPVDS\SVGRRGFLTIFB DVSGFG\AWHRRWCVLSGDCISYWAYPDDEKRNPIGRINLANCTSR QIEPANREFCARRNTFELITVRPQREDDRETLSVQCRDTLCVTKNWL SADTKEERDLWMQKLNQVLVDIRLWQPDACYEPIGKP
5488	A	1076	3513	IKALSSSAEDASLVNASISSSVKATSPVKSTTSITDAKSCGQNPEL LPKTPISPLKTGVSKPIVKSTLSQTVPSKGELSREICLQSQSKDKST TPGGTGIPFLERFGERCQEHESKESPARSTPHRTPIITPNTKAIQER LFKQDTSSSTTHLAQQLKQERQKELACLGRFDKGNISWAEKGGNSK SKQLETKQETHCQSTPLKKHQGVSKTQSLPVTEKV TENQIPAKNSST EPKEVIREIEMSVDDDDINSSKVINDLFSVLEEGELDMESQ/AGD GSSISR/TAANKRMH*ISPQCLYLHHWHKQLV*V*CPHLDWN*KTP AEVMKVQNQENSKELVS/RAESGDSLGSERDRLLYRSQRFKETERP SIKQVIVRKEDVTSKLDEKNNAPCQVNIKQKMQELNNEINMQQTVI YQASQALNCCVDEEHGKGSLEEAEERLLLIATGKRTLLIDELNKLK NEGPQRKN*G*S/APSEFIAIPKQFTLSEIRLP*KADFCVSTVQKP DAANYYYLIILKSRS\ENMVATPLASTSNSLNGDALFTTTFTLQDV SNDFEINIEVYSLVQKKDPSGLDKKKKTSKSKSNIHSSVMASPGGL SAVRTSNFALVGSYTLSSLSSVGNTKPVLDKVPFLSSLEGHIYLIKIC QVNSSVEERGFLGCPGGRLQPKRQTFEDVSGFGAWHRRWCVLSGN CISYWTYPDDEKRNPIGRINLANCTSRQIEPANREFCARRNTFELI TVRPQREDDRETIV\TNAGTHSVFTKNWLSADTKEERDLWMQKLNQV LCDIRLWQPDACYKPIGKP
5489	C	135	206	MFIFAFGKSIFKITTTTFQSTIVG*
5490	A	67	388	DAVFA/GAMPTMASVKLSTLHPIVNHPHYEDADLRPGCSMLEIWDVE DPSNAANPPLRSILLEDA\PKMPVFQNSVYRVLKN*EGNYPLHYG TMPCVKNNHPLAYLH
5491	A	3	107	SIKLSTLHPI\VNHHYEDADLRARTKIVYSTYSRTSAKEVRDKLLE LHVNYVLEEAWCVVRTKFI LQDGPVQLQAAEK*QCMVTQIYKKYSN ALEM\PGCSMLEIWDVEDPSNAANPPLCSVLLEDARPYFTTVFQNSV Y\KVLKN*EDADLRARTKIVYSTYSR
5492	A	3	289	YYLSPPEMGAIFEDP\AHVVVYIIFMLGSCAFFSKTWIEVSGSSAK DVAKQLKEQQVMRGRHRTSMVHELNRPKVKLRRWKGEGRHFTKRIL FY
5493	A	2	652	RVDLPIKSARYRGQYSSYPKLFYTSNIPILQSAVLSNLYVISQML SVRFSGNFLVNLGQWADVSGGGPARSYVGGGLCYLSPPEMGAIF EDPVHVVVYIIFMFGSCAFFSKTWIEVSGSSAKDVS*TA*KEQQMV\ MRGHRDTSMFHELNRYPITAAAFGGLCIGALSVLADFLGAIGSGTGI

				LLAVTIIYQYFEIFVKEQAEVGGMGALFF
5494	A	58	596	KFIFRDGSLCCPSWT*TLGLQQSSHMSLPSDWDSDRVRATKPNFPFS S*HSFSALY\MHLPRSPLNFIQPCRKYKGPAGLSRGGRE*HGL*SDF SVANLWQLGFLWQALTDYRAELPGMDPIISTHLAKLYDNLLEQNLIR VIEPFSRVQVRTLWGLHFWPGILTATSLPHLSRMGTHF
5495	A	2	951	PRVRPRVRPRVRSSRPSRSDPSPRRARLRWQLRWKPRWCPRPPKTPG VWKRPRTRPRSSAGGSTGFPSSPILRRSPSTRRRSSRKASPTATRAT GTPPRQAQRKTARAAGRRRASPGIATAGTRSMISM\RPGRKPSNPSPW EGRTNEETSSLSRLKPVSPGTITCPLRTPGSLKDSKIPISIKHLTN LPSSHPVVHQPPSRSEMPRTKIPVSKVLVRRVSNRGLAGTTIRATAC HDSAQKVVRSSRPRWMGPMRNTTFPWETTKVSAFPKESLL/WTPP VPRPAPERGPRLSLCPE*GPDNTRKRDATRGFLLSR
5496	A	1	279	VQWHDLG*PQPPPPGFKRFSCLTTP/RSSCDHRCP\PTTPD*FLCFL VETGFHYVGQAGLELLTSGDPPTLASQSAGIAGVSHHARPNFLIFFF N
5497	A	2	291	FLVARVAGSGGDGLTLFPRLECTSVITAPASISWAQGDLPASASQVA QTAGACHHSWPVFTSCVEMGFPCVP*AGLELLGSSPP\QPQPMFRL QA
5498	A	2	345	SHSVAQIGVQWRDLGSLQSPPGFKRFSCLSLPSS*DYRHAPVHPAN FF\FLVEMWLPRVSQDGLDLTS\DLPSASQSTGITGMSHRARPNE CIFSRDRVSPCWVWSQTPDLR
5499	A	2	311	QVLENPHFPRG*APPPSW*YPSGFYKSNRPRACFNPRSLAPRGPHQG FFFPFGPL\FPPPPFLGPPYGSRRFPSEHFQKVQPLNQPPFLSLKNP P*RFPPFFP
5500	A	1	2500	MEDAWGIRKETGRVKEAEKVGTGWGNNWRNVEKSSMSRKVKAARPGF KKLPMTSDIPPCKTIKDLLPKEKSSTEAVFHTTVLERHESPDIEDFS FKEPQKNVHDFECQWRDDTGNYKGVLMAQKEGKRDQRDRRDIE NNQLGVSFHSHPQLQFQEGKMYECNQVEKSTNNGSSVSPLQOIP SSVQTHRSHKYLHNLHFSLLTQRRKANSCGPKYKNECGKAFTQNSN LTSHRRIHSGEKPYKCECGKTFTVRSNLTIHQVIHTGEKPYKCHEC GKVFRHNSYLATHRRIHTEKPYKNECGKAFRGHNSLTTTHQIHTG EKPFCNECGKLFTQNSHLISHWRIHTGEKPYKNECGKAFSVRSSL AIHQTIHTGEKPYKNECGKVFRYNSYLGRHRRVHTGEKPYKNECG KAFSMHSNLATHQVIHTGTKPFCNECS\QVFTQNSQLANHRRIHTE EKPYKNECGKAFSVRSSLTTHQAIHSGEKPYKCECGKSFTQKSHL RSHRGIHSGEKPYKNECGKVFAQTSQLARHWRVHTGEKPYKNCDCG RAFSDRSSLTFHQAIHTGEKPYKCHECGKVFRHNSYLATHRRIHTE KPYKNECGKAFSMHSNLTTTHKVIHTGEKPYKCNQCGKVFIQNSHL ANHQRTHTEKPYRCNECGKAFSVRSSLTTHQAIHTGKKPYKNECG KVFTQNAHLANHRRIHTEGDKPYRCTECGKAFFRQGVTPGPSLECNGT ILAYSSLKFVGSSDTHISLLRSQDDRQVPLPHLANPNFREGLLPAFLL LCSDSHFLQFCSQFAPRKTQSGSVNNIQANI IAK
5501	A	1	2508	MPHQLGPNLVDPDIPPCKTIKDLLPKEKSSTEAVFHTTVLERHESPDIE EDFSFKEPQKNVHDFECQWRDDTGNYKGVLMAQKEGKRDQRDRRDIE NKLMMNNQLGVSFHSHPQLQFQEGKMYECNQVEKSTNNGSSVSPL QQIPSSSVQTHRSHKYLHNLHFSLLTQRRKANSCGPKYKNECGKAFT QNSNLTSRRIHSGEKPYKCECGKTFTVRSNLTIHQVIHTGEKPYK CHECGKVFRHNSYLATHRRIHTEKPYKNECGKAFRGHNSLTTTHQI IHTGEKPYKNECGKLFTQNSHLISHWRIHTGEKPYKNECGKAFSV RSSLAHQTIHTGEKPYKNECGKVFRYNSYLGRHRRVHTGEKPYK NECGKAFSMHSNLATHQVIHTGTKPFCNECSKVFTQNSQLANHRRI HTGEKPYKNECGKAFSVRSSLTTHQAIHSGEKPYKCECGKSFTQK SHLRSHRGIHSGEKPYKNECGKVFAQTSQLARHWRVHTGEKPYKCN DCGRAFSRSSLTFHQAIHTGEKPYKCHECGKVFRHNSYLATHRRIH TGEKPYKNECGKAFSMHSNLTTTHKVIHTGEKPYKCNQCGKVFTQNS HLANHQRTHTEKPYRCNECGKAFSVRSSLTTHQAIHTGKKPYKNE

				CGKVFTQNAHLANHRRITHTGEKPYRCTECGKAFRVRSSLTTHMAIHT GEKRYKCNCEGKVFRQSSNLASHHRMHTGEKPYK\ECGEVIRYNSLL SHQLI\HS*QNPYKCSDSGQSLMS*SINRYERP*ARD/YHVNICGRG SIQASQVTRHQDFISLMKRKNKCNMHPEAITQ*PMVSEDS
5502	A	3	361	PKKNYFPLHLKGPKTGVFFYSSSSSSQKGVSLCNPRWNAVGPFGFP STPPS\LVK*FLCPNPWS*CDFRPPSPRPGYFCFFNKNKALLARVVF NS*PQVIPLEFQPPKMVGFGQGLTLAG
5503	A	32	392	FLFLSFPPLSFKMTLNDAMRNKARLSITGSTGENRRVMTPEFP\KAV HAVPFT*SPGHGNGMSSVTESLGGLIRTLTLLSALPQWFSCVFIVQSGE RHPSILEDFSFPQKNSLNMWSSILKL
5504	B	473	524	MGEAKKTGEQVRRLPRTX*
5505	A	1	627	LVSSFFFFFFFCRDVSPCCLGWSPTWSPGLKRSARLGLPQCWDSRRE LPRPAYLLFLLSWGSPSPSAWQEGG/WCKKKRGTEHPEVPSIPSTC PSPTVQQ*S/GEKQVQETGRQS/LGEAKKTGVQWHDQGSLOP*SGLK *SSYLSFLSS*DHRCAPTTPD*FL*R*DPTMLPRLVLNSWAQ/CDHP ALA\SQSTGIIGLSHRAWACDQNSHFF
5506	A	3	649	RVSSVMSTSLLEIFNCIFDAHVPPPLWGKAYPSQKPLAAWTRDLAMRV EQFELWASRARPPVIFWLSGFTFPTGFLTAVLQSSARQNNVSVDLS WEFIVSTVE*QAT*VYPPKDGC\WVRGLYLEGAGW/DPEELLGGRQ SPCKLVWLMPTIHFPAESRKKSPKGMYSCL\YYYPNAGSSDRAS FVIGIDLRSAMTPDHWIKRG TALLMSLDS
5507	B	167	377	XKLIQFGLMKNLIRRLQKYPVRVTRREEQSHPARLYTGCHSYDEICCK TGMSYHELDERLENDPNIIICWK*
5508	A	2	1247	TPLREERGATGLGPVIAMGSGCRIECIFFSEFHTLGPKITQVPEP FISRELFDTVQVYIITKPELQNKLI/VLESSFVSMEEKQKLVPI TILLEELNASGRCTLPIDESNTIHLKVIEQRPDPVQAEYDVPVFTK DKEDFFNSQWDLTTQQILPYIDGFRHIQKISAEADVELNLVRIAION LLYYGVVTLVLSILQYSNVYCPTPKVQDLVDDKSLQEACLSYVTKQGH KRASLRDVFQLYCSLSPGTTVRDLGRHPQQLQHVDERSEENLLGHL GVT*GKLDPLCLSGALDHGALPIQAGFLEMMGYRDKIEGRLOQERVGL PERRPGQGVTPSSDPHPRKLIQFGLMKNLIRRLQKYPVRVTRREEQSH PARLYTGCHSYDEICCKTGMSYHELDERLENDPNIIICWK
5509	A	1	512	CTLPIDESNTI\H*KVIEQRQTPRVAQEYDVLVFTKDKEDFFNSQWD LTTQQILPYIDGFRHIRKISAEADVELNLVRIAIONLLYYGVVTLVLS ILQYSNVYCPTPKVQDLVDDKSLQEACLSYVTKQGHKRASLRDVFQ\ YDEICCKTGMSYHELDERLENDPNIIICWK
5510	A	1	474	HTIHLKVIEQRPDPVQAEYDVPVFTKDKEDFFNSQWDLTTQQILPY IDGFRHIEKISAEADVELNLVRIAIONLLYYGVVTLVLSIL\RKLIQF GLMKNLIRRLQKYPVRVTRREEQSHPARLYTGCHSYDEMCKCTGMSYH ELDERLENDPNIIICWK
5511	A	199	562	KESPGGRHPVPLIPHP*ES*IPVRAL*KNLIQATYRKYP\VRV\TR EE\RAHPARLYTGCHS\YDEICLQDRWRQAGSQGGFRAGCARPRPLT SPPPPHPGMSYHELDERLENDPNIIICWK
5512	A	1	1224	EFGTRPLREERGATGLGPVIAMGSGCRIECIFFSEFHTLGPKITQ VPEDFISRELFDTVQVYIITKPELQNKLI\TVTAMEKKLIGCPVCIEH KKYSRNALLFNLGFVCDAAKTCALPIVKKLAGYLTLELESSFVS MEESKQKLVPIMTILLEELNASGRCTLPIDESNTIHLKVIEQRPDP VAQEYDVPVFTKDKEDFFNSQWDLTTQQILPYIDGFRHIQK\ISAE DVELNWVRI\AIQNLLEYGVVTLVLSILQYSNVYCPTPK\Q\DLVD DKSLQEACLSYVQK\GHKRASLRDVFQLYCSLSPGTTVRD\LIGRP PPSSCQHVDE\RKLI\QFGLMK\NLIRRLQKYP\VRVTRREE\RAHP R\LYTGCHS\YDEI\CKCTGMSYHELDERLENDPNIIICWK
5513	A	2	313	FETESYSVAQAGVQWDLGSLQPPPPGFKRFSCSLSSWDYRRPPP RLANF*FLVETGFHHVGQAGLDLLT/S/GDPLASASQSAGITGLSH CAWQTTYITFNHK
5514	A	731	1156	SVLGLISDTSNTFLSFFFFFFEMESHSLAQAPLQWHYLGSLQAPPPCK

				LRLPGSRHSPASASRVAGTTGARHHARL\IFGFLVEAGCHRVSQDSL DLLTS*STCLKP/AQSAGITRREPPTPGLFFFLKMESCSVGPRLGVQ SW
5515	A	3	365	LLNSRPVDFFFFFFFFLSHSL/DSVVQAGVQWHNLGSRL\LSPPPGS MPFSCSLSSWDYRHPYPYLANFFFCIFSRD/MGFTMLARMVISI *PCDLPALGSQSAGITGVSHHAWPAYFYPO
5516	A	400	619	MPEQICPLETSQS*INNLPKKFFFMISI*CPGFERSYFFF*CC
5517	A	274	693	KYQILLYNGDVDMACNFMG\DEWFDVSLNQ/KGKVEIPGPGIEPAGE EWGAGMPGSGQLAAWLWAHRGQVWRNSQP*GLAGSCEQGCSCCRLMS FLVGQMEVQRRPWL\VKYGDSGEQIA\GFVKEFSHIAFLTIKVTGPAE R
5518	A	3	766	NRLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARI/VGNISGLNIY NLYAPCAGGVPSHFRYEKDTVVVQDLGNIFTRLPLKRMWHQALLRSQ DKVRMDPPCTNTTAASTY\LTNPYVRKALNIEQLPQWDMCNFLVNL QYRVFLPSQNSR\YLKLLSSQKYQILLYNG\DVDMA\CNFMGDEWVF VDSLQK\MEVQRRPWL\VKYGDSGEQIA\GFVKEFSHIAFLTIKAG H\MVPTDKPL\AAFTMFSRFLNKQPY
5519	A	2	279	FLRDVILL/C/HPGQSVVV*S*LTVSPTLPGSSDPSSAFNCSEWY RCVTPCQLMF*FTLLSIGIGSTLPRPVLNSSPQVILAPWP\PKVLRL QE
5520	A	2	1045	CPSRPCRRRPPPPRGPKPRASYPGGPAP/PGDKKKRPPQ\GPRGSSP APGPPP\POEAAAGPARPRPGQDAAAGPSGR\PPQALPS\PRGPQRA PRPGRQAPATAQRGPPMRRPRRRGRGPPPRAPP/PGAGPC/PRLRCAL LPESHPRGRPGHPEASSGEAAAGAAPQALPLTLGRTQAPTRPVSPG* GRGPAEGRPRQR/PPTHPPPPA\GPPRASARRPAAARRPAGSPAQA ARGPAADAQGVAAQRAAQVRRRGVRRGGARGGRGP/RGPRGRP/PGS SGRQRPLSG\PSAQAGPRGAQPDSPDGHGPPPALASRQPGPFSFTPV VSTPDACLCPHSGLLLASPSIHAVRGELSN
5521	A	84	202	SYWLFTLPGCKPLQGRGLSRVQCCIPAAGHGTWSMAFNK
5522	A	3	576	ILGFPPFVRWGSHTVAQAGVQWCDHGSLLQPRSPGVK*SSHLSLLGSW NHRHATTTTPG*FCFFSRIRSHCVAQAGL*LLTSNHPPALASQT\VGI TGVSHWTWPNTGFSVLATNKNLKFHYAISKCLVRACLSSRLKIE ERNKALSAPVSVSIFDRVLRLLGYSASDWQPEFVETAVSNFVIYGI FRGQ
5523	A	177	904	ESHLQNDTAAHPLLNGTECGVSPPLTSRQGVRRRTQSSTSRTC/S PVIPKQTFPQPVLMHSAAGVAL\DSPAPPPRPWQPPPGGAHT*DRKE EGDPIGIWAPEGKSCTPKPPPSLPRTSPGWKRALQKGDTCGPGPST ASTPHPLILGPSQAPPKPKPP/PSPGVPACAPS/YPALPAPISLITE KEQARAPGGQDGAGHTVGGGGAAGRREGQNKTFSGFFFSFFFLPFT LWVVLFLSFL
5524	A	1	173	FLGPSKFPPPGFPPFPPPPPRERGNQRSSSPSSSS/P/PSQKKTGV PPG*PGGFFPPPP
5525	A	1	392	LILNTRKPAFIFDILLHNLDPKQAYADLV SAYTLNSMFWLYLATQGV NPTDHPVKHELDTT/RACMNRSSSPTDKKAGLLYRGAASKFVKNAL WEPKSKNA*KVGNKGKSPTSLFGFDVHIFKKNMLPPP
5526	A	1	1548	MPERDSEPFNSNPLAPDGHVDVDPHSFHQSCLTNEDFRKLLMTPRAAP TSAPPSKSRHHEMPREYNEDEDPAARRRKKKSYAKLRQOEIERERE LAEKYRGRAKERRDGVNKDYEETELINTTANYRAVGPTTKADKSAE KRRQLIQESKFLGGDMETHLVKGLDFALLQKVRAEIASKEKEEEL MEKPQKETKKDEDPENKIEFKTRLGRNVYRVLFKN/KAYKRNELFLP GRMAYV\KVDCTMEAQTILTNDIVISKLTQLLSYLRQGTRNKKLK KKDKGKLEEKPAEADRSIFEDIGDYTPSTIKTPWDKERERYRERER DQ/RDRDRDRERERERDQERERDRERERDRER\GPSAKELIKSINE KFAGSAGWEGTESLKIAEDKKQLRDFGMSNSYAECYPATMDMAVD SDEEVDYSKMDQGNKKRTLSRWDFDTQEDYSEYMNNKEALPKAAFQY GIKMSEGRKTRRFKETNDKAALDCQWKISAIIEKRKKMEADGVEVGR

				PKY
5527	A	1	3162	MEQFLWQELFAEYNRQASAQVDLGEDRTEYYDQFCKDVPPKNEETEE VLVNGPTWSARTVDSHLGQKDL SRLQKVFDGFGSSDLQSIFFSSL NIQLTDATQKEPLCKKIATLHSESKLNSFEKDYIYIGASRNLCGSAK IDEGLLSKVYSSLNSELGSSQEIFYRVVTHKVLGVEINEATQEKLVK RLQELLKKDDTL SGLGYAFNVAPLLGASASF IANRVEDAIVQADEVD GKLLQFEGGLSITSLIINGAFGVSKTFNKPVPITADQAVKFANYFLS RRSVQTAKGAHVLI EALKTISGADKIAPVCVQLIGNGQLDAQSPTLN VAVVDLLGKPLSPAPKVINAKVIRKKDSSVLADKITVASKSSDKTTY VADLASLKPARGVYQAELSADGVYTQTLQFVLRVVKVQSLEVGIAE SDASAATRKQSVTPGKLQEVLSADSTQKLLKAVLVDESTSKPLAV HQA FVRLYNKKTDEKII FVAEQDSSKAYKFDMDVGNNGKNFNYSQSGT YSIYLTVGDDSSLSNSFEWLVAEVQLKFNEDEKVKPKNTSGPLPEIIH QFRVPDKRPPRIVSDIFTGLCITPLVLLFVFWGKLGINVSNLTAPS TIGFHLGFGGILVLFVFWLQLNMFQTLRLLIPIAVFTFLAGNRLLR RLYAQRNSKASASYNTDVLEQELKEIKECAQTTLTNDIVISKLTQI LSYLRQGTRNKKLKKKDKGKLEKKPPEADMNIFEDIGDYVPSTTKT PRDKERERYRERERDRERDRDREREREREREREREREREREREREEKK RHSYFEKPKVDDEPMDVDKPGGSTKELIKSINEKFAGMDDMAVDSDE EVDYSKMDQGNKKGPLGRWDFDTQEEYSEYMNNKEALPKAAFGYGIK MSEGRKTRRFKETNDKAELDRQWKISAIIEKRKMEADGTLAWCSS LGVTTASWLDATLPLSTLSPRFVASPDRKLESHLSHYLVFDYIHLV LLSMDRTCEERPAEDGSDEEDPDSMEAPTRIRDTPEDIVLEAPASGL AFHPARDLLAAGDVGDFV
5528	A	2433	2540	QRKNDNKMPPERDSEPFNSNPLAPDGHVDVDDPHSFHQ
5529	A	1	1739	MPERDSEPFNSNPLAPDGHVDVDDPHSFHQSKLTNEDFRKLLMTFRAAP TSAPPSKSRHHEMPREYNEDEDP AARRRKKKSYAKLRQOEIERERE LAEKYRGRAKERRDGVNKDYETEELINTTANYRAVGPTTKADKSAAE KRRQLIQESKFLGGDMEHTLVKGLDFALLQKVRAEIASKEKEEEL MEKPQKETKKDEDPENKIEFKTRLGRNVYRVLFKN/KAYKRNELFLP GRMAYV\KVD CPTMEAQTILTNDIVISKLTQLLSYLRQGTRNKKLK KKDKGKLEKKPAEADMKYVS*PLASDQREGVCTFLVSGILGRC*HE NLEKWSGGVKVYV*IW PASDLHFPSIFEDIGDYVPSTTKT PRDKERE RYRERERDRERDRDRERERERERDR*\HERERDREREEKKRHSYFE KPKVILLGPWTFDKPGGSTKELIK\SFIEKF\AGSAGWEATES\LKK PED\KKQLGDFLGMSNSYSECYPATMDMAVD\SDAEVD\YSKMDQG NQEGGP*ARW\DL*FPQEEYKRVFVTTKEA\LPRVAF\QYGIKMS\E GRKT\RRFKEPQ*PKQSLIRQWKI
5530	A	93	547	YNCRPTLGVSGCAGLDAQVVCQDCAFELGKKP/PSGGEQYPSSSAIK QGPKEPYADFIARLQESLKKVIADLAAQDIVLWLLAFDNANPECQAA LRPIRGKAHLVDYTKVCDGIRD KLHKATLLAQAMAGLRMGKGNTPFP GACFNCCKHGH
5531	A	1	541	MGQVWALVRSTLEL FHTDDEEGEYDEVTEEVTEQVYLPKAKVAQE EEVHPYPSAPPHYFEEKEWDPDPDLSFLED TGRKVAPVTEQHLE LLSVLFRQEF SRLDERGPKELYADFIAWNLLRQESLKKVISDSAAQD IVLQLLAFGNVNLDCQAALRPIRGKAHLVDYIKACDGIG
5532	A	365	661	SESMT PVCICTPFKFKLDLPRSNPIVPAGKGPQTPVGTFCRGSPGRR LTAFVQHKSTTALPAVAGDRHCPGVREWPEPEMLPFGMGPEIGFPSL SKLE
5533	A	3	74	RMGPRTGP*VFPETGFPPLSNLE
5534	A	83	262	CTVTPPPQDTGQSKS*STRVSSSLVPRSPTVAPVTLRPGFEPP*WTP LAKTSSVLTQWC
5535	A	636	698	PVVHLNQPSRRPPKAGLQLY
5536	A	125	340	SESMT PVCTCIPFKFKLDLPRRNPIVPAGKGPQTPVGTFCGSPGRR LTAFVQHKSTVALLAVMGTDIVQG
5537	A	81	1007	QPKAEHAALNLRKTFQHASHTPPFSAAQ*NPHRPHQPWL*HALVQHC

				SCSDMQRPSASGP*/PPGTFSRWSSCKMPVPPPAQVPKSLCGVLSSS C*PGRRSPGPAEPPSRACRPCRQDSG/PAQAGGPCRQDSG/PDPAGG PRDK*ASQGPLPAGERAI PAGGPCRQDRGQPRLASSAGGHCRLRG /PTPAGGPCRL/PQRAAPAGGPCRQDSEQLRLAGPAGRLAGRHGRRS PGPAEPPSRACRQESG/PAQAGGPCRQHSG/PDPAGGPRGQLSLPAG PARRRAGNPGRQPLQTGQRAAEAGEPAFATAVSGRD
5538	A	1	766	MGQVWALVRSTLELFTDDEEEGEYDEVTEEVTEQVYLPAAKAKVAQE EEVHPYPSAPPHYFYFEKEWPDPPDLSFLEDTGKRVVAPVTEQHLE LLSVLFRQEF SRLDERDDAVEQLRGVCIRAWEKITSGGEQYPSFSAV KQGPKELYADFI AWNLLRQESLKKVISDSAAQDIVLQLLAFGNVNL CQAALRPIRGKAHLVDYIKACDGIGAKQDSEFAFTIPVNNLQPAK HFHYFTDGSSNGKASYSGSK
5539	A	74	1178	WLRRTPVTSTNRLTQPPTWGQIKKLSQMAEENLRKAGQVPTMNNLM VAMIVVITTTTEEQYSEVTEEVTEQVYLPAAKAKVAKEGEVHPYPSAP PHYFYFEENDPPNLSFPEDTGKRVVAPVTVRAAPRGTA LSSIQAGIQ ARQEGDLEAWQFPVRIHPPDQGNIIATFEFPFKLLKEFKQAI SQY GPGSPFV MGLLNVTVSSQKIPTDWDTLTRACLT PAQFLQFKTCAMK QGPPEPYVDFIARLQESLKKMIADSA AQEIVLQLLAFD NAHPDCQAA LRPIRGKAHLVDYV KACDGIGEYTPSTYEKKVNCKTASCRSFRYP EGIVITGDDSSMRVVVPEDLPVGDVEVEDRDIDDPDPV
5540	A	1	857	MGQVWGLVHFTLELFTDDEEEQEYNKVTEEVTEHVYLPAA*PDVHLN QPSHQPPKAGLQLY
5541	A	518	578	PFVHLNQPNQPPKVG LQLY
5542	A	750	797	AVLWHHPAGGPWLAK
5543	A	2073	2846	IVRSLRTAQKIRSGCPCQSW*RRGRPVGSPSQSTEGPGQVRLRT*P LPFHTHPEGPGAGRRSRSSLERPTSQPHRSQSGRC PAAPATPLPSP GPQA\PLGAPFERG/PRSRSA/QGAPGTGVRFFSMAQFPFPCSTSQ LKPCSPQELKMLR LPKGA\PDSSAPGRTAGTPPCLRCWAGSVEPLRR VRGPRRCGRGPAAATQWARPLCRARRGT LGGIA*PRSV AARGSAPA PAAPGAARPGPGMGPPAAVA AIAGRP
5544	A	3	611	SLPPRASRLPPGPSFGSWSPGDNRLPNTPPPPRAGPRPPSRAPPA* TPGPPSAGSWP*PPGTGSAPRG PAPSAPGARRPGRPGCP PAPAGRPR VPTAGAGACSAASRPGTRPRCTRPGAPRSRRRGCGPGA*PGARRP PRPRPPATRAPRSPRSPRGAA PPPTPRTARGAAARELRVQRGP/APL HAPQOHTPAAIVPYKM
5545	A	3	42	HEEPPSSNSPK
5546	A	1	160	SMQQTLLLSYF*KLP*PPQPSATMTQISQQPSTSRQDPPPTK/RL*L VEGSNNH
5547	A	298	421	LHPHILPIDKLLHQ*KVVS VSEYRQNOEVPLYSISSNLVHS
5548	C	598	762	MNSMIQICQDRAEIISSYCNLKIHQRLQNLISFLQSLK LKNVNL S FINKNLK*
5549	C	138	296	MNLEVTVARDYLS PVLADLAQRRGNIQEIQTRQDNKV VIGFVPLAEI MVGTL*
5550	A	2	1575	AMLGTRVERCLRVLDGAVAEFDASAGVEAQT LTVWRQADKHNI PRIC FLNKMDKTGA\NFKYAVESIREKLKAKPLLLQLPIGEAKTFKG VVDV VMKEKLLWELQFK*WEKTLRRKAPLGK*MIPEFAGRETT*R\KECL* LEQVADL DDEFADLVLEEFCE NFDLLPAEKLQTAIHRVT LAQTAVPV LCGSALKNKGIQPLLD AVTMYLPSPEERNYEF LQWKDDL CALAFKV LHDKQRGPLVFMRIYSGTIKPQLAIHNINGNCTDR TQIALSVNHEV HIYKNGRQCVKAHELKEHNGHITDIDWAPKHDHIVTCGADHNAYVW SQKDG VWKPTLMILRINRTATFVKWSALENKF AVGSEARLISVCYFE SENDWWVSKHIKKLIRSTVLSLDWHPNNVLLAAGSCDFKHRVFSSYI KEVDEKLASMPWDSKMLFGQLMSESGGGGTGGVWHGLDIPKQSIQRN MSAMECF CNTDKRATTEGSNMAL KMLRQNSITQVSIYEVDEKDCRKY CTTGIDGEP
5551	A	1137	1288	RTLNL LKAMASRVLRRIILTGR*CLDVSIKIPL*ENLGESIMVDSL MV

10416

				KVP
5552	A	1	1851	MALKKADKQVLEPLMNLEVTVARDYLSPLVLADLAQRRGNIQEIQTRQ DNKVVIGFVPLAEIMVADLDDEFADLVLEEFSENFDDLPAEKLQTAI HKSDTKLRQQLPVL\CGSALKN\KGIQPL\LDVMTYLPSPPE/L*P MEFLQWYKDDLCALAFKVLHDKQRGPTGFYAPFNSRPL*KPQLAHSI ILMETATERISRLLLPFADQHVEIPSLTAGNIALTVGLKHTATGDTI VSSKSSAL\QLVEPNGREKRSTDKTMKAERLLLAGSGRFQEPVFFC TIGTPITV*GSQIWEHAFEMSFSVRIPVLKVRLLDPSGQTVLCGMGE LHIEIIHDRIKREYGLETYLGPLQVAYRETI LNSVRATD TLDRTLGD KRHLVTVEVEARPIETSSVMPVIEFEYAESINEGLLKVSQEAIENGI HSACLQGPLLGSPIQDVGNLYIP*QIHPWAPSTTYDFCLCLKMPCK KALERKADKQVLEPLMNLEVTVARDYLSPLVLADLAQRRGNIQEIQTR QDNKVVGIFVPLAEIMGYSTVLRITLTSQSATFALELSTYQAHESSRS KYTAQPEKWFDLNVLVFGRGNSGRHPRLLHFSVRNNFYCLYLLGRNK GTVSGTFRGT
5553	A	2	499	RCQKAKFTPVNRRHCRKCGFVVCGPCSEKRFLLPSSQSKPVRICDF CYDLLSAGDMATCQPARSDSYSQSLKSPINDMSDDDDDDDM/TVTKD TFGSI*SGEAL*EINFGGNARL*ALSLDCS\TMNLPEKLGTYVPQYI P*KEGAPAFCHSSHSSSTGIGFCKYIR
5554	A	147	315	LIPQPWGQHLPLPPNISNYD*RPQKFLGLPHPCSFGRALTPHWSTG LRLTPSAQ
5555	B	105	508	XPGTREVEELNALQEELAPFGLVILGFPCNQFGKQEPGENSEILPTL KYVRPGGGFVFPNFQLFKGDVNGEKEQKFYTF LKNSCPPTSELGTS DRLFWEPPQESSRHPLELWKFLVGMQMDTHALHHRPRQQR*
5556	C	4	165	MCLSGNVYHLCA CSCVVPQCCTTSLQFSTPMIIVHLHLNPKKEPAL GPIVLL*
5557	A	1	1803	MARLLQASCLLSLLLQAGFVSQSRGQEKSKMDCHGGISGTIYEGALT IDGEEYIPFKQYAGKYVLFVNEELAPFGLVILGFPCNQFGKQEPGEN SEILPTLKYVRPGGGFVFPNFQLFKGDVNGEKEQKFYTF LKNSCPPT SELLGTS DRLFWEPMKVHDIRWNFEKFLVGPDPGIPIMRWHHRTTVSN VKMDILSYMRRQAALGVKRKKVTSQYQDRDNKFQONVERIPLSGSHRT VCMMGVKGKVKQTQAKPLSGEESLELEQSGSLAMAAGADNHFLAEVPAK AVALVLT TTESQQGLQEVS GGVT LAEAE SRALGPLPREDGNLMLHLQ RLETTLSEPDHGQLFTHLGRMALEFNRLASKVHKNEQRTSILQEYKD VQSTLLPQEVPSQMGNARTSQTHAVPGGKPRRGYPYRIYDPGGSVPSG EASAAFERLVKENSRLKEKMQGIKMLGELLEESQMEATRLRQKAEEL VKDNELLPPSPSLGSDPLAELTGKDSNVTASPTAPACPSDKPAPV QKPPSSGTSSEFEVVTPEEQNSPESSSHANAMASPHSLGKSLARRGK EQRPSLTVASRLQRNGRAGRGHKEEGVEDKEEVVP
5558	A	2013	2024	KVAGSAGHLRRTVARDQAAAQRDPECAPTPSLARLLQASCLLSLLLA GFVSQSRGQEKSKMDCHGGISGTIYEGALTIDGEEYIPFKQYAGKY VLFVNVA\SY*\GLTGHVHLN*TAL\QEELAPFGL\VLG\FP\CNQ F\GKQ\EPGENFRRSFPNPSRYGPTKVGGFCSLNFALLRKGDVNGE KEQKFYTF LKNSCPPT\SE\LLGTS DRLFWEPMKVHDIRWNFEKFL VGPDPGIPIMRWHHRTTVSNVKMDILSYMRRQAALGG*RVGCPPFSFK ILYFPSSRVYSLGGGWSILFPPQNKGSFPKFPSPRFLGPP
5559	C	2	226	MLLPLPPSPSPSTALPGLGEMGRRPPPPYMLSVAPQTF CFISHSSPS SHRVSFSAFPCSVLPPPSQKFLHRTSF*
5560	A	2	1308	ALSLALPPASPP/AGRGRPAGPGPAPLPWHQGLPLTRPGPEG/PLP QGRLPSPPLQPTPAQPLLLPAFPLLPAPGPRRVGF AFWCP*SPGLS PPGLPSPDFQTLPCGISFL\PEMRKLESWSPAGEPSPPPAPPATRV SRMQLPDPLTLLPPAGPKATFNSYGV/PPPAPPE/PSQGRVRGHPEPT GPLLHSSQGQEAAPLPPGPCCYGD TAF/PRTEGPPSLPPTTRARLSS PPPRFPADVVCVLSVSLVLC TPSLLVPM*/PHPCCTGSLSSWLPL LMMLLPLPPSPSPSTALPGLGEMGRRPPPPYMLSVAPQTF CFISHSS PSSHRVSFSAYPCSVLPPP*APAWAQDPILPARVSPGPRVFPFPC/P

				PPSHPTPGSEAPHS*PSVFLRKWLKATGPPAQPSAPPKPGNLGPHKP LWKLFSKASHSFPRSFCTELPF
5561	A	3	259	FLFWVFQIPAPFPEYVTDLCICTPTSASPNGYLLA\GRDKAQL\WE RLRVVF\QRALRDGA*AGEAGG\STPNTVTMEMQCPCPGNAS
5562	A	2	329	AGVQWRNLCSLQAPPPGPRSFRLSLPSSQVAGTYRRPPSPANFLY V**RRGFTTVNQDGLDLTSGS\PASASQSAGISGVSHRAQPSFTFF RLACHVFVRHCHLPT
5563	A	3634	4389	LIQFLLLSIGLYSYTTICLFILLMEYWLFVFSYYYYYFFFFLRRS LALSPGWSAVVQSRLTATSASQVQTILLPQPPE*LGLQVCATTPS*F LYF**RRDFTMLARMVLIS*PRDLPTLASQSAGITGVSHRAWSFLFV LFFF*TESHSVAQAGVQWHDLGSLQ\PAPLRFK*FSCSLPSSWDYR RPPLRPANFFVFLVETGFCHVGQAGLELLTSSDLPALASQSVGITSV SHHTRPGMSFFITSHKL
5564	A	1	369	LQPQP\PGLNQSSLLSLLSSWDYRHMPYPANF*YFPETRFCHVAQ TGLELLSSSDPPYSASQSAGITGVT/HRA*PRFTLCTGLIRGQHGEK GLAQGHNVRASSSIQGSVVTWGLRGLFFPHH
5565	A	161	231	LLQPRTCLFFEGVDLNGWASLFL
5566	A	1	1401	MQIFDYNSEITDPGIQQAAGLEGTRKPWNISMLLTTNLSLCQWFS KCGPEPDTSTSWGTPQKEHCHLVNKVGVDSLRRMGYMHGIIQPLNLF QESQLMPQTLFFPHNFQNCFFBELHKWRCPDYENNVRKMQLPFSSK LLGSTLTSEEKQERRQQQLRRLQELNARRREEKLQDQERLDRLLYV QELLEDGQMDQFHKALIELNMDSPHEELQSYIQKLSIAVGAG*AENPP SGSQPR/EWDVV/TTASQRPLTWEQLEPSLEDVESMNDFDPLFSEE/ D/TLEWRSRSP/RVQPVFNLAAYHQLFVGTERIRAPEIIFQPSLIGE EQAGIAETLQYILDYRYPKDIQEM\LVQNVFLTGGNTMYPGMKS\RME KELV\G*DPSRLSFKVNLASNPCAGM/DWYGGVLVNWALNHLDDNEVW ITRKEYEEKGGEYLKEHCASNIYVPIRLPMSCLPLLRCPRHPSQGS AGGGGAG
5567	A	2	131	SSCLSLSKCWDYRHNPQLNKKVFKNFQSSYLIQLGFYPALQPE
5568	C	170	394	MKTNGYQGRVQWLTDLVNLKSRPVQSSRPSLGNMVKPPSIQKLGKA WVACTCCPSYSAGAGGWHEPRSLRLQ*
5569	A	2	583	DRKGLESSPEPPSDCRRPPGMDLLAIS\PVLLAPSPQVPVQSWPSPG* CGRQAPCVLESQHSAGAGVSSWDGPPVPCCKPPHPGLSQAHPGKTFG PKNLHMVPSGGAQAPGPHKANQSWPSCPPVPRSRPPTFSHIAENPM ERKSFAQSGGAGNWQRKVSNPHWPWELQVFESPSRPCVKNGRAAGLVT GGFREG
5570	A	3	312	FFLNRRQGLALLLKLEYSGLMIIDHCKPQISGAQVILPVASWVARPTG VYHHA*LIFFKWGREVETESCYVAQAGLELLASSDPPTSTSQRW/I TGLSHCAWPA
5571	A	1	121	IFHVLKNCQTRSIIYLALMSFKNEGEIKMFSNIQKLKEFITDRSK/LQ EMLKNAL*AERIYY
5572	A	2	228	FETGSHS\IFWAGVQWYNHSSLQPRLPGLR*FSHLSLPSSWDHRCPT PRPCNFSIFSIRDGFSSC*SGWSQTLGLK
5573	A	1	1896	MVSQGCRRSREMRDAHAGWDSPTALHMARGLGRRVFSAPRHTEGGTPD GNSHLSPNQKMEKLTEKGCKQLRQGGLCVRVSDRTVRSVQETTAITA TLKGSGLGTYCRGTRNLLTAEGFMPHASVCIQSKSGKVARNTVQGFTA HGKAVLEAAVSASGPAGTWGCLRIKWPRSVSWLLKPERAATLVGHGC RKSGCPPGLGSSAKM/PPRHQSAAPAGRGRCPGWGPEPTSGSLSNQQ WLPQ\ALHAPPLPSAPLLGPPLLSRTVDTGPGGSGREVEATTCGRRL KDKDSEHAGAGSRHHQSQVTGSLGEERAVRAESPGEGPAEFLRRIQG AVQTRAVTAGSSVEKINTKLETCDASEEEVLGGDNVETEERSVCV PEPVKMTLFEKRVFADIIRCLARWAPATNRRDLVNTLI PGHGPSCS LVAFL/APPSRPYP*PAARCWWASDFPERGKRLRAHSSFPVPAPP CVPVQSQSGPLPCTPRHFPLPFPAPAFGICRGPRAPGG/SKAVATQ RPWWLYAPGTAPGGLPW*/AVPGHNKSIPPQPVSNLTETPLNAPQSS WAALGSKRLQGCGSHGFFAFSFTADVCTNDDTLNANSLTEVLATEI

				KHDINLANEGLAWDRGWDYQGDMLSL
5574	A	1	475	FWKSPYSVQPRTEARAQGNKQKEFRETAPGSSSKADTKSEHLWALLP SRRWGGSTQHPPLAREPQFLACGPMKDIRLADWSTPLLSNPS*KLP *ICQSCPLEQEGKQKA*DARGVPSFPELQPPSGLTAQGGTHRPHFDL RMTCGRTWHFFLAKTLH
5575	A	2	468	SRGILADPPRPGGQPDFLQP*PTRVAALSGLSNQDSDLGHLMRQRPQ VPAGPEAETAASRTALPCAVNPWTVLRATLPDLDCIQTEACGMKPSA VSKFLVPRQYVPRLPFKVAVMAVVSCTLRVTLSLTTHSPPCRSLQ PFSVSFSIFWFGDK
5576	B	90	1686	XWWEPSFPQQRDSLKVTGLQRAAFNPVAPTHSFKDQHPMPFCHFL SGVPVSSRTTLATGRAAPHSSPLKSLVQGYAPWQTSMSCDYQPPRRQ EHKETSRRNSEKQLQAPARPTPKANTSGRSLQEDLLPEAQPGLSV PVCHPCPLLHAARLAVSAAAAIRGLEVAEAAALVCAQKLLAACSSHS ITVWSRGKVKTGLPSTVQAVSELLQVLLCKQKAGGCTPDQGPHTSK VLTEASSLPRIARMCLLQPGPFSDNIPLGATLTTPAATAATPQPLLP CTKHGNPLGHGLTCHYPLAPLPLPPAPHVRFAALSCLERSAGCCLCT PSCRITTVGGSVGSCASELNHRACFSLPLMLGFQAPIATHQWLFSVR NDKNTLDTPRSAGCDGAHRPRQEPAPDGPVLLCLEPMPAPGSYPGG APVSGHRQVHPQQWQVQHLGQSGGIRTGLGANCCKSHDSAYKKGGDV CFPGEMVPVHQILKGVQHPNCKRGHWGTLVQQKQPWTGSRGPTADQ LHPKNSSLTLVFPSSR*
5577	A	171	1631	GLPQAGADSDPRTRPFLLLGGLPGLPSRPYP*PAARCWWASDFPER GKRLRPAHSSFPVPA/PPMRPRTVPVRAAPHPSPSPTSVPSTGIRH LPRAEGW*TGQ*RNTPNKSRRLSPLVTPGSCRSSPTQSPGSGTTV EMPARRWCAGATGPGATSP/SSLKVKETGLPSTVQAVSELLQVLLCK QKAGGCTPDQGPHTSKVLTEAS/SSAPHLQNVLAARSI\SDNIPLG TATLTAPAATAATP/EASPPLHQAWQPS/TAMASPAITPWPYPQQL RMSGLLPCPA*NAPQAAVSVPPEAE*RLLAALVWHVLRN*TTGPASH CH*CSASKPPSPPTNGYSVSAMTRTPWILPDRLAVMLTGPQKSGPQ M/RPIVLLCLEPMPAPGSYPGGAPVS/AA*AGTPPAVAGAASRAVGG HPIRPGCKLRQIP*FCIQEGWGRVFSRGNGPCRASDSQRGPAPKQVQ GSLGDTGATEAALDWESGPHCRPAPP
5578	A	718	2209	IPSACFLVLLPSWWLVVAHGSPLGRVALDQAFQWTRVRGCSACGKG CPAAG/PQAQRGSGRSWAWDAGP*RSVWGPLG*TPPAAAL*P*VSPF VAGKGLAPTT\LVGTAIQSILOGLILSWNPGGEPAG*RNDLGAGGRA CCPEDDDQIRGGAVLAEVT*QCSCSPMPDAAHHRHRVRVGVSGAAVC PQWELGGHGGNARPDAGRGVLRSCRGRNLLTAEGFMPHASVCIQSK SG/TSQTQHCPCGVHCTWQSCPLPSAPLLGPPLSRTVDTGEEGHPVD ASWTPSTPREPGRWAHCLPQRKP/PLGPPEARASVPPAHSGTVAGEA PPVISHFR/SPAPAFGICRGPRAGATEALPAPRADAPVKAAP/PAHT GAAS/EPARHVRPFPTATAPFTFPSAVHKGSGFSTSLQTLVIFCCVL MVAIPMGVRWHLTVVLWNLAVISRVPISVCALDLSFISVPCPLRCW CWWNRVSPKLASPGCSECDLGGQMRVMVSSHFSVE
5579	A	2	354	LPSSWDYRRPLIFVFLVET\GFNMLARMVISI*PLDPPDLASRSDEI IGVSHRAWLILS**KGERKSTNVSHKEGLG*WSRATVLQVYSVGFWE VPFQGCQSQSYFHNNTNMLFAF
5580	A	1	1263	MAEEQGRERDSVPKPSVFLHPLDLGVGGAERLVLDAAALQARGCSV KIWTAHYDPGHCFAESRELPVRCAGDWLPRGLGWGGRGAAYVVRM VFLALYVFLADEEFDVVCDQVSACIPVFLARRRKILF\YCHFA DLLLTKRDSFLKRLYRAPIDWIEEYTTGMADCILVNSQFTAAVFKET FKSLSHIDPDVLYPSLNVTSFDSSES*KAGMT*SPRGKNSWLLSINR Y\EREGKIWTLGTGKALVQLRGRILTSQDWERVHLIVAGGYDERVLEN VEHYQELKMMVQQSDLGQYVTFLLRSFSDKQKISLLHSTCVLYTPSN EHFGIVPLEAMYMQCPVIAGNSGGPLESIDHSVTGFLCEPDVHFSE AIEKFIREPSLKATMGLAGRARVKEKFSPEAFTEQLYRYVTKLLV
5581	A	200	705	LSQTL/TVLYPSLNVTSFDSVVPEKLDLVPKGGKFLLSINRYERK

				KNLTLALEALVQLRGRILTSQDWERVHLIVAGGYDERVLENVEHYQEL KKMVQSSDLGQYVTFILRSFSDKQKISLL/RQLARVCFYTPRQ*GTLG IVPLGRPCYMAVPQFICCLIRVGPFGSSI
5582	A	1	259	ERGSRSIARLEC/SG/AISAHCNFRPPGSSDSSPSACRVAGITGTRH HPQLFFVFLVEMGFHVA*DGLKLL/NFMIHLPPPKVLGLQV
5583	A	94	395	PIIITYFEFLNGYIISQKIKFSHHQLQKIDFLP*TWHLFLIEQR*NI LMEGNQFSVTDDVKILFSGKLYSHSKIQSMML*LVTRE*CYMFNCNI CLLSFSSLSVIINDLQNP
5584	A	3	270	FFEAGSHSGCPGWSESGAIIAHCSLDLPGSSNPTSAS* IAGTRSMHH HAHLIFVFLVETGSPYVVPQSLKL\RVQAILPPRPPKVLGLQA
5585	A	13	775	YSVRGLVPAERTTPYPGSIAPADGMVYALEGMGPDAPQAQVRVYE PRRDCWLSLPSMPTPCYGASTFLHGNKIYVLGGRQKLPVTAFAFD LEARTWTRHPSLPSRRAFAGCAM\AEGSVFSLGGLQQPGAPQL\YSR PHFVNTVEMFDLEHGSWT/I IAPQPAHEG*EGQTLWLGLGATLWPL GALETSHVLWALLESFSLARRRWEALPAMPTARCSLQAGPRLFV IGGVAQGPSQAVEALCLRDGV
5586	A	1	936	MAALYACTKCHQRFPPFEALSQGOQLCKECRIAPVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPSSSDSPASSSRVAGITGIKTNTICKKCAQ NVQLYGTPKPCQYCNIIAAFIGNKCQRCNTSEKKYGPPYSCEQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSRAGH QEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFV IIAQLKEEVATLKK MLHQKQDMILEKEKKITELKADFQYQESQMRAMNQMEKTHKEVTEQ LQAKNRELLKQAAALSKSKKSEKSGAITSP
5587	A	1	1023	MAALYACTKCHQRFPPFEALSQGOQLCKECRIAPVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPSSSDSPASSSRVAGITGIKTNTICKKCAQ NVQLYGTPKPCQYCNIIAAFIGNKCQRCNTSEKKYGPPYSCEQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSRAGH QEKEQYSRLSGGGHYNSQKTLSTSSIQNEIPKKKSKFESITTINGDSF SPDLALDSPGTDHFV IIAQLKEEVATLKKMLHQKQDMILEKEKKITE LKADFQYQESQMRAMNQMEKTHKEVTEQLQAKNRELLKQAAALSKS KKSEKSGAITSP
5588	A	3	345	LNLLMYFRDNVSFCHPGWSTVM*S*LAAASNSW\VT*SSCFS/LPSS WD*S*LPPCPANFFFF/CQ*RQNLIMSSRLVSNL/QPQVMLLPQPL KALGLYRVSHHASVKFVNLINM
5589	A	1	430	GDGVLLCRPG*STVALSQFTAISASWV\KRSSCLNLPSSWDYRCAPP CPAKFCIFSRDGGFTMLARLVNS*PQMIHPPWPPKVPPLPACVWYF SMACNFLYTPSFRLFCQQPKMEKAALCQGSPTVKSCSQMFTFN FF
5590	A	3	389	GVSPCWPGWS*TPDLK*STRLGFPRCWDYRLLEVDPTGHSLYL*KD PPVLPLPAEGCDYQKEYALSSCCDKSYLLPDYRTKFLCCHPERGTW KLGTVGGCYAPIQSFGLADEQAWLQHGSGAVYLC
5591	A	3	53	GVSPCWPGWSQTPDLK
5592	A	363	777	DMPQLCSVDNHREQRAEFINIYQHQQFFLRQSLTSVAQAGVQWCSL SSLQPLPTGFKPFSCSLSSWDYRHMPPSLANFFCIPSRDRGFTML ARLVLS*PQ/CDPPALASQONAGITGMSSHAWPTPTFSYLLNTQD
5593	A	3	85	FFFFLMLHNNVYLVHLFTISYKHFI IIVLYKQQFKFTYVY/TFIC LLVFQFQIILLESFPFLKIILL*SL
5594	A	1	281	FFFAPETESYSVA\RLECSGTILVHCTLCLPGSSDSPASASQVAGTT GACHHTWLILVILVEIGFHHVGQAGLG/IS*LQVIRPPWAPKVLGII G
5595	A	2	369	FFLRWCFALVAQAGVQWQDLGSLQPLPPGFKRFSCSLSPSS*DYRCP PTRLANF/SVFLVEMGFHVSQAGLELLTSGDLTTLASQSAGTTGVS SRAWPDLYLFSYLIKTSPPKFSIPFHLEI
5596	A	432	1492	KKGCGKPGELCGMPSSWKNAYCPTAQQTAEYLSSPCGSAAPCLP/ DRASSSSRSVEASSLDSAPGT\SAAGSPSPRPFGEYHHPGPGANNE PTPPAESIVVPSWP*GCHSSVAVEKLSLAPGTPT/SDLPLLDSSMNR

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				KAPIPVFGLSASSLLPLKDARASET\SSR*THQ*FFGKDVH*TQNSL AQLQHQSSGPQLLWGKTGNSQSSFPQAG*HSRHKEGCWREPSHKPLE PHSLSQHHGTASSARIPEVPPPHSLGHSPACAWRSSSPRPPRPLAAL PGCRRRRGAGSSHKAPDRSTARPGRCGRRRRRGARRGCGGSGRGPS HSGPQRSESAPPAGAHLRLQPLRSHSLH
5597	A	1	2163	MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPO STYREATTVCNDLRLTRIPSNLSSDTQVLLQSNNAIAKTVDLQQL FNLTELDIFSQNNFTNIKEVGLANLTQLTTLHLEENQITEMTDYCLQD LSNLQELYINHNQISTISAHAFAG\LNLLRLHLNSNKLKVIDSRWF DSTPNLEILMIGENPVIGILDMNFKPLANLRSVLACMYLTDIPGNA LVGLDSLESLSFYDNKLVKVPQALQKVPNLKFLDLNKNPIHKIQEG DFKNMLRLKELGINNMGELVSVDRYALDNLPETKLEATNPNKLSYI HRLAFRSPVPALESMLMNNALNAIYQKTVESLPNLREISIHNPRLC DCVIHWINSNKTNI RFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQC LPMISHDSFPNRLNVDIGTTVFLDCRAMAEPEPEIYWVTPIGNKITV ETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNVQGADTRVATIKV NGTLDDGTQVLKIYVKQTESHSILVSWKVNNSVMTSLNKWSSATMKI DNPHITYTARVPVDVHEYNLTHLQPDSTDYEVCLTVSNIHQQTQKSCV NVTKNAAFAVDISDQETSTALAAVMGSMFAVISPAS\IAVSFPKRF \RRKNYHFIKKVLWQKTS\SIPLNEL\YPLI*PLGKVDSEKDKDG SADTKPTQVDTSRSYMW
5598	A	50	824	SLLKPYVRIFTKEKSYKCEGKFHKSCSRH*NHKIHTGEKHYKC EECG\KVFNHC*QLIAQKKIHAEKNSDFKECGKAFNNYYELTHQRF AR*KQCKCNDTHYIYLWKDVT*KP*STQGMVIVIHICTWKDFKNI SLRVHKSFYTEEKHYKYKDCNTFTYVTFVHRRRIYTER*PSNSCS NFIPP*IIYIGKKPYNCNEYEKNCLKSTP*KTLV*GRARWLTLII PA PWE\AKAGSGRQEIETTMKPCLY
5599	A	1	2043	MVSI SRPHDPPASASQSAGITGVSHRLRFYFDHQDVAPECGAYFFHE LAKEKRKGVERLLKMQNQRGGPAVFQDILKPGQDEWGKTEAMEAAM APGKNLNQSLDLHALGSAPTDPHLCDFLESHFRDEEVTFMPRKSAD LHAAGEAASLGGVSLNVMKGASLHALCLRLNSFGPGVATLCGERV HKNNRASALRKCFIWPVSLNSSRARPRQRTTAGGAVPTAALQRVIPA SSQCLFPAPMGTTTEATLRMENVDVKEEWQDEDLPRPLPEETGVELLG SPVEDTSSPPNTLNFNGAHRKRKTLVAPEINISLDQSEGSLLSDDFL DTPDDLDINVDDIETPDETDSLEFLGNGNELEWEDDTPVATAKNMPG DSADLFGDGTTEEDGSAANGRLWRTVIIGEQEHRIDLHMRPYMKVVT HGGYYGEGELNAIIVFAACFLPDSSLPDYHYIMENLFLPPGQQTTPGP VGLTQPAAGVEAGRVGTAGVLTLDPSMLGPCLLCPVSRVVISLELL VAEDYMIVYLNATPRRRMPGIGWLKKCYQMIDRLRLKLSLIIHV PSWFIRTVLAISRPFISVKFINKIQYVHSLEDLEQLIPMEHVQIPDC VLHQRQIILTTLCAYGEALASHLPHVILPFHIHSCFPSSTETSDP PCGPGLDLAYTTPFSTHFAQRGK
5600	A	18	403	FCIFSGDGVSPCWGWSRIPDLR*SACLSLPSSWDYRRPPPSANFF *FLVKTGFHHVGQAGLELLTSGDPPASASLSAGITGVSHCTRPMYA FLKQLNFHIIDKSDYRLYRKLYLKATTMVFRYAPL
5601	A	2	497	ETESHVTVQAGVQWCDLGSQPPPPRLKRFCSLSLPSGWDYRHVPPH LANVCIF**IWCFTMFARLVFNSRRTPSDLITSAS*SAGITGVSHRA \RLCIFYFFFAEMVRMSCFVTQVGLEFVALSD\LPWPVPKVLGLQ A*ANSAPVIFYCNSFFHSHLNAPN
5602	A	3	303	LSCFPQATFFFFIF*DRVLL\CPGRSTVVQSQLTAALTSRAQGSSCL SLPTKWDRHVPPYSAFFLVLDKSLALLPRLVLNSWAQAILPPQPP KVLRLLA
5603	A	122	525	QFFFFEIGSLVAQVGAQWR\STSPLQWPSPGFK*FSHLSLPESWEH RMPQGLDNFCI\FVETGFRHVAQASIKLLGSSDLPALASQSAGMTS MSHAWPIVKNFVCIYYVPDIVLSMLSVKSIHINHVRGLQ
5604	A	1	198	LTGRL/SKCEVVSWRFDVQLKDLKRWNHLLLSQQLACIVLTSAGIM

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				DHKEMR*KHTGGKSLGFFF
5605	A	156	1047	VPAGEARVQWHDLGSLQPPPP\GSSDSPASSSRVAGITGIKTNTICK KCAQNVQLYGTTPKPCQYCNI IAAFIGNKCQRCNTSEKKYGGPYSC EQ CKQQCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSQKTLSTSSIQNEIPKKSKSFESITN GDSFSPDLALDSPGTDHFVIIAQLKEEVATLKKMLHQKQDMILEKEK KITELKADFQYQESQMRAMNQMEKTHKEVTEQLQAKNRELLKQAAA LSKSKKSEKSGAITS P
5606	A	156	960	VPAGEARVQWHDLGSLQPPPP\GSSDSPASSSRVAGITGIKTNTICK KCAQNVQLYGTTPKPCQYCNI IAAFIGNKCQRCNTSEKKYGGPYSC EQ CKQQCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFVIIAQLKEEVA TLKKMLHQKQDMILEKEKKITELKADFQYQESQMRAMNQMEKTHKE VTEQLQAKNRELLKQAAALS KSKKSEKSGAITS P
5607	A	1	354	ETEFPSCCQAGVQ*HDLGSRQPPLP\GSSDSPASASRVAGITGMHH* SRDVLIRILELEEGLELCPHFSVRNLPKTGQILTLMLSLAPVKLAPQ PKLSWMELTRHSRLWAALS GGGQV
5608	A	3	403	YIFSRDRVLPFCFPGWSQTPGLKQSARLCLPKCWDYRREPPQLAED/S YFQFRASLKMTL*GIVSMV/PLLQKLLWMCKAQGNQAEEGTGVALPE REASSWSCLLQLPFPVDEPCSSFKRRESEKEPSNGFPNLNI
5609	A	340	1015	VGSVEEFQGGERSVILISTVRSSQS FVQLDLDLDFNLGFLKNPKRFNVA VTRAKALLIIVG\NPLLLG\HDPDWKV*APPPHSPS*WPQPLPRAGG SFLSACLSLS*SSDVSI FTASLLYL*VK*HPEVEQVQLRWDRVA*P PVSAGHSSVPHRFL\EFCKENGGYTGCFFPAKLDLQQGQNLQ/LW SKLSPSTSG\PHSHGLTSPREREGERGPVFCWEPWEWRNEL
5610	B	769	809	GFPIIFHGMVKDEREGNSPSFFNPEEAATVTSYLKLLLAPSSKKGK ARLIPRSVGVISPYRKQGASEDLEDIKDFEGGFSKKNKAQERSVIL ISTVAKRPRALLQLDLDF*
5611	A	99	341	SELGTVAHCTNLIILPSSGDYRRPSPHLANF*FLVEMGFHHVQGSGV ELLSSGDSLALASQSPGITGVSHRAQVPPPPFFFF
5612	A	1	1795	MRQSHQLPLVGLLLFSFIPSQLCEICEVSEENYIRLKPLLNTMIQSN YNRGTS AVNVVLSLKLVGIIQITLMQKMIQQIKYNVKSRLSDVSSGE LALIILALGVCRNAEENLIYDYHLIDKLENKFQAEIENMEAHNGTPL TNYQQLSLDVLALCLFNGNYSTAEVVNHFTPENKNYYFGS QFSVDTG AMAVLALTCVKKSLINGQIKADEGSLKNISIYTKSLVEKILSEKKEN GLIGNTFSTGEAMQPSGVLPLNGCSTTTTAVACSTGHRKCAASRALEN RCRSPA AKVTKNKRLSNCQTGQRKLRRCDNRMQCGVLDRILEQKEDI SGTTSEIQIKWGVELHSVSRWRLGKVAMEMVQCQKAGYPERGDGVA VAEGPNIKVAGGLRELETRKTALPENESSQEHAFITITLQHLVQGLA HSGYSVL SKLLNENRAMQKHGTVWTQQIQSSAAEKSEKTMWDRLG RGTASWQACPVSLKKQAVEGAHQEEQCKRRDEMPPGESDLVTMASG RDALLCGRCCQQA KTEELTITVPRLGQEAPLPCSTPPGSTPPAAK \PRPSAAPDGPSS*SPGARRQVARPRRGQAPENK
5613	A	12	367	LGGASEATGASAAQPPPPPPAPRAPNPAPGPAPAQR* SALDPPLPGR APRSFLKGPRPATARPPG/WRLQSPLP*PESPPDTRGVRGEAPAPAD PAAGPRKSKSDCLAAVIRCLCRAPR
5614	C	231	302	MNSFLVFFPLYVQMYMLRLNFCA*
5615	A	194	737	EGGVCLSWCGWFGPVCCDYTPPLPEPRDGCLC/PLPKMPPAPPMLPI QQSFQPFQERPGSPVPETASPPAGN*ISHLSEGPPNTQWSPGFKPW GVCHL*/CGHVGVPLPKPAPCPL/CCPSGCVDSGAFFQKHSPSGSG PETAAGPSHLNDNWQRLGFYELLSGIFCRAPNKCICYVSIFVLK
5616	A	2	360	PRVRDPRVRPRVRRRIYKPLRTRDELQFLDKMDDPDY/WPAVDFFS GDVMIHPVTNRPADKRSFIPSLVEKEKVS RMGHAIKMGWIQPRRPRD PTPSFYDLWAQEDPNAVLGRHKMHVPA
5617	A	1	2072	DSGSDSSDEDDDEGDEEGEDGALDDEGHSGIKKTTEEQVQASTPCPRT EMASARIGDEYAEDSSDEEDIRNTVGNVPLEWYDDFPHVGYDL DGR

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				IYKPLRTRDELQFLDKMDDPDYWRTVQDPMTRDRLRLTDEQVALVR RLQSGQPGDVGFNPYEPVAVDFFSGDVMIHPVTNRPADKRSFIPSLVE KEKVSRMVHAIKMGWIQPRRPRDPTPSFYDLWAQEDPNAVLGRHKMH VPAPKLALPGHAESYNPPPEYLLSEEERLAWEQQEP\SERKLSFLPR KFPSLRAPVAYGRFIQERFERCLDLYLCPRQRKMRVNVPEDLIPKL PRPRDLQFFPTCQALVYRGHSDLVRCLSVSPGGQW\LVSGSDDGSLR LWEVATARCVRTPVPGGVVKSVAWNPSPAVCLVAAVEDSVLLLNPA LGDRLVAGSTDQLLSAFVPPEEPPLQPARW\LEASEERQVGLRLRI CHGKPVTVQVTHWGRG\DYWPLVLA PRGHTGVLIHQLSRRR\SQSPFP CTHV*VHRVAFSPARPFL\LVGPQRSVRL\YHL\LRQELTK\KLMP\ NCKWVCQPGGCNPAGDN\VICGSY\DSKLWVFDLST\KPYRMLRN H/HRRALLAVAF\HPRYPLFASGSDD\GRVIVCHGMVYNDLLQNPLL VPVKVLKGVHLTRDLGVLDVIFHPTQP\WV\FSSGADGT\VRFLT
5618	A	1	214	QDSALLQLL*I IYPVYNLSPAGQGRDLFSCLLRHLKLPTSEGVRT \QSALQAFKGPNAQTQWIYGHDPN
5619	B	58	280	IHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMD KERRKSLKPKLLRLQRDIEKASKDKEX*
5620	A	2	785	HFNMRDPLTDCPYNKVYKNLKEFSQNGENFCQVTSVLQQRANLEIS YAKGLQKLASKLSKALQNTKSCVSSAWAWASEGMKSTADLHQKLGK AIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQOIKAKK KLMVSTQET*STFPSL*ESS/ARQSMTEKEKRKLLNKLTKSTEKLEK EDENYYQKNMAGYSTRLKWENTLENCYQSIL/ESWRRKEFNFYAITL NQYSQHISLFGQTLTTCHTADSLCHQQD
5621	B	13	543	MFLAPIAVSVRRFFXVKASVYAYTMFFSTFYHACDQPGEA VLCILSY DTLQYCDFLGSGAAIWVTILCMARLKTVLKYAYRCGHRRCYPTLWQ RWAFYLLPGVFMASVGA IYTSMTSDNYYYTHSIWHILLAGSAALL LPPPDQPAEPWACSQKFPCHYQICKNDREELYAVT*
5622	A	1	1798	MLCFYAGSCRHFRSGAPPVINPLGTSFPDDTAVQPSFQVGVPLSTTP RSNASVNVSHPAPGDWVFAAHLPPSSQKIELKGLAPTCAVVFQPELL VTRVVEISIMEPDVPLPQTLLSHPSYLVFVVPDYTRELLLELRDCVS NGSLGCPVRLTVGPVTLPSNFQKVLCTCTGAPWPCRLLLPSPWDRWL QVTAESLVGPLGTVAFAVAALACRPRSVTVQPLLQSSQNSFNAS SGLLSPSPDHQDLGRSGRVDSPFCLTNYPVTREDMDVSVVHFQPLD RVSVRVCSDTPSVMRLRLK\PGMDSGGSLTISLRANKTEMRNETVVV ACVNACLALPLALILSLNCTTAFFQGYPLSLSA\GSRRANLI I PYPE TDNW\YLSLQLMCPENAEDCEQAVGPRWEDHLCTWGALF*TDGCPYG QC\SLLRRHSYLYASCSCKAGWRGWSCTDNSTAQTVAQQAATLLLT LSNLMF/LGPPSPSSVRRFFLVEASVYAYTMFFSTGCGVGGQDRAHG ASPQFYHACDQPGEA VLCILSYDTLQYCDFLGSGAAIWVTILCMARL KTVLKYVFLFLGTLVIAMSLQLEPQGHVEHLGGPASLPS
5623	A	121	291	AFCFPKYELTINFKNFQLGVVTHACNPSILGGRGGRIT*AQEANLAN MAK\PCLLNK
5624	A	571	690	CQQGFSLQAYGPAQHAIS\MRKFKAKYPDYEVTWANDGY
5625	A	130	943	TGEAEHLGLARADTWLGEEGPRDGAFFPGGSLEGKAWCEQPRGPPNCP VPRVPPDPAGEELLRWLISSPPIADSTFPLSGAGGAARRQGTGLRLV STCLGPRYNWLRRLWALGSI PRDWSSLSQSPPPAVQAAPGWGWEAGD SGRRNMAVADLVLPDVIDSDCVFKYVLIRVHSAPRSGAPAAESKE IVRGYKWA EYHADIYDKVSGDMQKQGCDCCLGGGRISHQSQDKKIH VYGYSMVSRSPVPPCRRPQYQLRGPPEPAALTRGPS
5626	A	45	473	GIPGRRNMAVADLALIPDVIDSHGVFKYVLIPSPGLPAPGIRPAE SKEIVRGYKWA\GHHADIYDKSVGATCRKQGLRTVSVWTAGPHLPTK SPGQERFT*YG*FHGPMVLPKNANFNLRKSKAKYPRLTEVTLGLNRP AT
5627	A	3	348	TLRLTHLHTDTHQ/HSHSYTHTEIHTPHTPHTETQTH*YTYALQ/PL RSHLIFLRQSRPQNGNAPLCEFSPHSPDVLQTLHLTSVVVKIPSTS LLMCRSSGGAQCRESLDQHEGVGP

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5628	A	3	331	FFEMESPSV/SQAGV*G\PNLGSLQPPPPQFKQFFCLSLPSSWDYRR TPPCPANFWIF*\KDGVSPPSWP*WSQSLDLGLFKFIYFFKETLILCT QSSTTTTTTKRTTRSSHR
5629	A	3	336	SHSVAQAGVQWHNLGSLQPPPPAFK*FSCLSLPSN*YRRP\PPHPA DF*\FLVETGFSHVGRAGLKLLTSSEPPACASQSAGITSVSPPCRAH TFELIPLCPFLFWPLFCP
5630	A	1	267	EMESCSVT\RLECSGAILAHCNLCLLGSSDSPASAS*VAGITGMCHY TRPTFLFLVEMGFCHVGQAGLELLT\QVIRPPRPPKVLGLQA
5631	A	3	521	FSFFFFPAFKMSNRGRGGSLL\GRKFPDFPLGPSGRLL*SNWCLTNT RSPKTLYIHL*RGNGQDRLDQTSPLLGVGDMVMAHS/VKKGKPELR KK\VHPSSGSFRQPKVHYP*EKMGVFLLFFEG*LGQVIVEPFGKRGD KVSCHLPGTQLGKGSFADFVAPGICIPMPWQPLH
5632	A	3	216	DRSHSVTQAGV/Q/WCDLSSLP PPPPGLK*FLCLSLSSWDY\GAPP HQTNYIFIIRDGVSPYCPGWP*TPSLG
5633	A	1	412	IIRSKNI*YLEINPTKHTKTFSKTLTK\EMKEDLN*WQEI\PCS\WI GSVSIKMSVLSKLIHTEIQCNRNKYPQIGLLLLPLLLFLLDRLVL KFTWKGTGPRMAKAILRKS/SEDLTLTYINTYYKATVIKLVGAKPD
5634	A	276	2589	NKHFSFQTPKKSHQKSLSFSTTPRRIHTPQTPLYTPERLQKSPAK MTPTKQAAFKESLKDSSSPGHDSPLDSKITPQKRHTQAGEGTSLETK TPRTPKRQGTQPPGFLPNCTWPHSVNSSPESPSCPAPPTSSTAQPRR ECLTPIRDPLRTPPRAAFMGTPQNQTHQQPHVLAARAEPAQKLK DKAIKTPKRPGNSTVTSSPPVTPKKLFTSPLCDVSKKSPFRKSKIEC PSPGELDQKEPQMSPSVAASLSCPVPSTPPELSQRATLDTVPPPPPS KVGKRCRKTS DP/MKEAS/SECQLDASATPGVGTADSPAAPTDSDDD QKGLSLSPQSPERRGYPGPLRSDWHASSPLITSDTEHVTLLESEA EHHGIGDLKSNVLSVEEGELRTADAESLSLHPIPPSPSCGPGS PLMPSRDVHCTTDGRQCQASQAQLDNLPAASAWHSTDSASPQTYEVELE MQASGLPKLRIKKIDPSSSLEAEPLSKEESSLGEESFLPALSMPRAS RSLSKPEPTYVSPPCPRLSHSTPGK\TGKPT SARVPVPPT/SPSST PSPFQTDGVPWTPSPKHSGKTTPDIK\TGPGGRGRWAVAPAPLPGG ARSVQ\PSWEPVTA*VRGQGPRP*TQHPQDAHLGGF*ARGSVAPARP VASQE/PACLRPRKPLPGDSL*VPGRESCWPRKLTVEPKGSVT*E KIQKLVRVKRGLQGVHGSYPPRETKRCLFPAPPHLPAVPCGAPSPA SALQALTQSPLLFQGKTPSSQSKDPR
5635	A	29	268	ILINHFFLESCSVAQAQVQWHNLSSLP PPPPGFK*FSYLSFLSS*DY KHAP\PRPANFCIFSRDA\VSPMLASWSQTPDLK
5636	A	2	118	WSPSPDLVIHPPRPPKVLGLQALHWVLKVNHGSTDIGL
5637	A	1	262	ETDLALSARLECSG\TILAHKRLRLPGSRHSPASASQVGGTTGARTT PG*FFVFLVETGFHRVSQDGLDLL/NLVIHPPWPPKVLGLQA
5638	A	3	309	IDTTFEEEEEEFFETESLSVT\RLECSGAILAHYKRLRLPGSRHSPA SASRVAGTTGARHHARLIF/VYFLVEMGFHHVSQDGLDLLTS*SGPP RPPKS\LGLQA
5639	B	49	754	MAGAAPRLPWSRPHGSCGWPMQPLQGPGRRAVAAAWEVATPVFMPV GTQATMKASRPNSWTLWVAASAWEYLP SGSKAGGTAAFPDGVAGVSV RGDGGGLRFRSPYDGNETLLSPENPCRSRMRAWPGVVTGALLQVNPL AGPVHAAHQRPDKQNLFAIIQVGWTQISGPPALKRFGSAWHSRAFLT HCCTVTTRPRCTTSRPHRLPAELMSAVRTSIVEKRFPDSCGTSWAP X*
5640	A	3	906	TVKMAGAATQASLESAPRIMRLVAECRSRRAAGELWLP HGT VATPV FMPVGTQATMKGITF\EFLDALGCRICLGNTYHLGLRPGPELIQKAN GLHGF MNWPHNLLTDSGGFQMVSLVSLSEVTEEGVFRSPYDGNETL LSPEKSVQIQNALGSD\IIMQLDDVVSSTVTGPRVEEAMYSIRWLD RCIAAHQRPDKQNLFAIIQGGLDADLRATCLEEMTKRDVPGFAIGGL SGGESK SQFWRMVALSTSRLPKDKPRYLMGVGVVDREARALPVGSG FLGTPYPAWGGGIWKGRTQV
5641	A	379	677	EGLRP/ELQNLFAIIQGGLDADLRATWP*RDDQARNVP GF AIRGALS

				GE*EQSREF/CAGWLAAEHTLG*PKDKPRYLMGVGYATDLVVCVALG CDMFDCVFPTRTARFGSALVPTGE\LQLRKKVFEKDFGPIRPG\CTF PHVPKAPARAFHATAAQ*QHGPRTTLLTVHN\IAYQLQLMSAVRTS IVEKRFDPDFVRDFMGPMYGDPTLCPTWATDALASVGITLG
5642	A	2	335	AGVQWPDLSLQPLPPGFKRFFHLGLPSSWDY/RVHEAPRPANFL\K FLVEMAFCHVGQAGLELLGSSDTPVLAFAQSGITGESHLAWPVFNF*N GSFNVFSLRVINEHLALHL
5643	A	56	571	YYQNPPKKLAASCGLSPLVLQVLKSLKGEVLPLGETQHYFPLNREL LLTQHFLLLMPLSQ/QTSKAGTIIARLIDPDYQGRTKFKIRNGKKIL NGRRKEIAWNVGFSIT/PCLLWKVIGILEQSNMAIYWYIHPMKV*A SPPGKEQRPFEVTPEGQRNMEWLEERNGRCLP
5644	A	2	1085	AERQIEENREREREWEVLGIKRDKSDSPAQLRLKEPMDVDVEDYY PAFLDMVRSLLDGNIDSSQYEDSLREMFTIHAYIAFTMDKLIQSIVR QLQHIVSDEICVQVTDLYLAENNGATGGQLNTQNSRSLLESTYQRK AEQLMSDENCFKLMFIQSQQVQLTIELLDTEENSDDPVEAERWSD YVERYMNSDTTSPELREHLAQKPVFLPRNLRRIRKQCRGREQQEKEG KEGNSKKTMEVDSLDKLECRFKLSYKMVYVIXSEDMYRRRTALLR AHQSHERVSKRLHQRFOAWVDKWTKEHVPREMAAETSQWLMGEGLEG LVPCTTTCDTETLHFVSINKYRVKYGTVFAP
5645	A	387	533	RWSDYVERYMNSDTTSPELREHLA\QKPVFLPQGE*AMSIQCVHTV HD
5646	A	1	169	VFLVETGFR\LLARLALNS*PCDPPASASQSVGITGESHCARPGLTIL MKHRGQLCT
5647	A	2	369	FLRWSFTLVAQAGIQWCGVSSLQPLPPGFKQFFCLSLPSSWDYRCPP PCPTNF*LLVEMGFHHVGQAGLELLTSGDLPASASQSAGITGISHR ARPGTLFF*AVNGGNGVFLFLRVNLGL
5648	A	1	340	FRPQSC*CPPADSRFPATPEAVLSLLVKASPPPELPRSPPEKPTGL SGGALG*QRFSAARNRGDPLTRKNSKITSLLSFLQELTKALEQKPD DAHILSSKSLSSHSSWELL
5649	A	2	660	RPPPAPAPGPQGPWPQGPYP*AESPPARSRTPHASQLPRCGPRPTAD PSSAPSRRLRPTSRSRHCFPAAGS/PGTPPQPPSADVRVPPFSPLS SRWW*PFPQSC*RPPADSR\RSRPLRPSFRFL*KPARPQSSSVASR EAKGPLVERQVDSVLGAPRETASSFATRPCATLPGKVTANCKPPQKT SGQLLVRLGSRSAAYSSPFFGAPEIGEEMPI
5650	C	19	153	MKMTSNFLLFSSGIFSSTFQIHLDPLELQNTVMGCLMRIHP*
5651	A	2	306	ETKSCSVA*AGVQRRNHGSM*RQPPG\SSNPPISASRVFG/ITGICH RTHLIFLFFVETGSHYVAQGSS*TPEAQVIRLHQPPKL\VFFYIFQL FLCFLLCY
5652	A	2	760	FFFFFFSENDGHLDTGARFAPDRRHTGVGRTKDQTQVGYRCHTAPARA RGGWGEDGCLAS*PGVRVKSRWSVPGAPGRGGQCHNPSPGFPT*PGGR HRKQPRPGARVLQAGGQQAFLPLAGWHLSGPGYWLSTPWACKGLGV VLSVTPLPPRSPWVG*GLGSR/QAVEGRAAQGRYLSFCPGTQW*WPP SAPIPTGT*SEVAHTKGVPGPGEPPAARGRLRTLAVGPGPLPGSRLV QHPKRYRALQALTSCFCSA
5653	A	1	834	MVSI SRPRDPPASASQSAGITGPALGAEGERAHRHRVMIIVTEGAPG GLSSGHLRDAMDSEAGTDDGCASHVRVVRDLKPSNILYVDESGNPE CLRICDFGFAKQLRAENGLLMTPCYTANFVAPEVLKRQGYDEGCDIW SLGILLYTMLAGYTPFANGPSDTPEEILTRIGSGKFTLSGGNWNVTVS ETAKDLVSKMLHVDPHQRLTAKQVLQHPWVTQKDKLPQSLSHQDLQ LVKGAMAATYSALNSSKPTPQLKPIESSILAQRVRKLPSTTL
5654	A	674	1269	PRDLPASASQSAGITGVSHRLRFYFDHQDVAPECGAYFFHELAKER KGVE*NTLLAKMVIS*PRDLPASASQSAGITGVSHRLRFYFDHQD VAPECGAYFFHELAKERKGVRLKMQNRGGPAVFQDILKPGQDE WGKTEAMEAAMAPGNLNQSLDLHALGSAPTDPHLCDFLESHFRD EEVTFMPRKSADLHAAGEAASLGGVSLNVMKGASLHALCLRLNSFG PGVATLCGERVVKNNRASALRKCIFWP

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5655	A	2	612	RYDFFFFFFFVTESSRG*LQSQAGVQLRDLGSLQAPPPRFTPFSC\ PASPSSWDYRRPPRPANFFLYFYS/MRRGFTVLARMVVIS*PRHLPALASQRAG\ITGLSHCTRLFFF*WMESPSTQAGIQWHDLGSLQPMPPQFR*FSWLSLPSSWDYRRPPRPADF\CTFSRDGVSPC*PGWSRSPDLVIHPPWPPKVLGLQA
5656	A	140	261	RAEPPHLANHILFF*DRVSLCRPGWTAMA*TW\LTVASTSRAQAVLP PSASPNS*DYR\HVSHPHLIFVFSFLIMLSRMVNSWAQGILLPWSP KVLELQA
5657	A	79	358	AGVKWGDLSL/QPPPPRFKRFSCSLPSSWGYRHAPP/*PG*FSVF LVKTGFLHVQGAGLELLTSGDLPVSASQSAGITGMSHCWPTKALIS K
5658	A	2	350	SQVDR*QSEPEIRICREDHMERLQAFDANSRKQEAWEKEKAIKELE EWYARQDEQLQKTKANNRVADEAFYKQPFADVIGYV\EEAFVNDIDE SSPGTEWERVERLCDFNPKSLD
5659	A	3	752	HRCGVGSSVGFCITVGVRAVQLPAMAEIDPFGAPAGAPGGPALGNV AGAGEEDPAAAFIAQQESEIAGIENDEAFAILDGGAPGPQPHGEPG GPDVDGVMNGEY\QESNGPTDSYAAISQVDRLQSEPEIRKWREE QMERLEALDANSRKQEAWEKEKAIKELEEWYARQDEQLQNTKANNRV ADE\AFYKQPFADVIGYVYVAKLIPFSTSDSFYFCLEMLLLCHKLL CFLNYFKLALWGLPKN
5660	A	1	348	NSLGESANALGNQ/QPITQNVCPRLF/MQAPGMAPSPSFIMNTLE\R KAPLKRFP\WMSAP\IQVGLVGFCLVFATP\LCCALFPQKSSMSVTS LEAELQA*DPKRAHP\ELRRVY\FNKGL
5661	A	3	430	LRQSL/DSVAQAGVHWRDLGSR*APPPGFTPSSCLSLPSSWDYWHPP RRPAVFLYF*ERRGFTVLARMVVIS*RRDPPASAPQSAGIIGM/SHR ARPQILFFIHFSTVSAGINES*VCFYCIILEVPSKEGILES*CIS EAAH
5662	A	3	756	GAISAHNRRLFLGSSDSPASASQEHWTETLAH*RSQLTATSASWVQ VILLPQPPKNTGAQKHWPTEGEAKEHCVSDDSESTLKAGGQHRIKQG GNSSSGAREPAPNILNSRRSWWTLVAKAAAVTVIIRVILMAAILRGT LAKEVNWVLDLTDKNEAADPRARHKDSPSPHQTQEPSWLHSDPT PGPQVELPASPTMCAGTSQPLVSRWDWSPWSRKRHIIFAPSSHNKYA GESFPGIYDAIFDIENKANSRLAWKEVKKHISIAAFTIQAAAGTLKE VL
5663	A	2	774	LANFCIFSRDGVSP*WSGWSRTPDLR*STRVGLPKC*DYRREPPHPP GLLPVFSSSHFAFLFQRRRLFVCFFA\FLRQSLALVTQAGVQ\WHD LGSLLQPPPPGFK*FSCLSLSGWNYRCVPPRQANFCIF/M*RRDFTM LARLVNS*PQ/CDPPTSASQSAGITGVSH/H/ARLAFVS/CYTHTH THHTLA*IPFSPVFPNSLSPPLQQGFPCPHCTELTSYLIKITNPV HVIRPNHGSALCILVQVSAPLHWSLSPLE
5664	A	2	417	LDPGSLAGFTSYIQFMYDEFVEEYEPTKADSYRKK/VAQDGEEVQIY IINTAGQEDYTAIKDNYFHCVSITEMESFAATVDFKEQ/ILRVKQD ENIPFLLVGNKSDLEDKRVSIIEAKNRAD*WNVIYVETSPKT*AN
5665	B	151	1312	MMGGRLLTGGIPGEAAVWGCSRPTAPSVFPPPPAAAAAAAVSSGN LRLHPGQVPRVLSREGGLAPRRGCPSKSGGSESTRVPRAGPRGEST GDRDPAPPPGPPSSSHFSPPLRIERKADKPPENSGESSHDVASREQP LVLEAHFRWAILLACHSMPTVGRKQVNNEIKTEIKKFFETSENKDT TYQNLWDTAKISFFPDFSYNFFMPISVLDAGGGSETAKHHHQDVHEI QPHIEPQISLGSFEHPIFGSCTIKEGTYRKRVLGDGEEVQIGILETA GQEDYAAIRDNYFRSREGFLCVFSITEMESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRPVSVKEAKNRADQWNVNYVETSAKTQLML TRHKPGTSSQX*
5666	A	3	955	LLLLLLLLLLLLLQPPRLPRHPSDSSFDRSRGAFQATRTEYPPGGAT QPRLEPSGRRGTGRCKFFLILWRKL RHKMAANKPKGQNSLALHKVI MGGSGGVGKSALTQFMYDEFVEDYEPTKADSYRKKVLDGEEVQID ILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQIL

				RVKEDENVFLLVGNKSDLEDKRQVSVVEAKNRAEQWNVNYVETSAK TRANVD/KEWPFLKTRWNTCKYISSHCPRPAPVSRKTAHWAEEVFFD LMREIRARKMEDSKEKNGKKRKSIAKRIRERCCIL
5667	A	1	635	MAANKPKGQNSLALHKVIMVSGGVGKSALT\QFMYDEFVED*E\P TKADSSRKRV\VLGEEV\QIGYPLDTAG\QED\YAAIRD\NYFRSG EGFLCVFSITEMESPAATAE\FREQILRVKEDENVFLLVGNKSDLE DKR\QVFSRKQKNRAEQWNVNYVETSAKTRANVDKVFDFLMREIRA RKMEI\YYLNGTKNTKRLAERIREGGCIL
5668	A	2	178	WGFTMLARLVLS*SQVIHPWPVKVLGLQALGSGSLHRSFFISVKG SSGFTAPSRRL
5669	A	208	339	RGQRLPVSRLKLLGTEAWALR*STRLSLPKCWDYRHEPPCPAH
5670	A	73	269	DKIFFFFF*DRVSLCRPGWSSVARSRLTATSASQFKQFSCLSRPSSW DYRHVPPRPANFCIFSRDR/SFTMLVRLVLS*PQVIHLPRPPKVLG LQA
5671	A	1	586	KKPYECKECGKAFSSGSNFTQHRIHTGEKPYECKECGNFSSQSSQL IKHQRIHTGEKPYECKECEKAFRSGDLTRHQRIHTGEKPYECKICG KAYSQSSQLISHHRIHTSEKPYEYRECGKNFNYPQLIQHQLY** NRIYEMCREAFNYGSKQNLSC**FL*IE*C/SKHFICGLQLIQPGKN NVGEILYE
5672	A	2	355	LFLSFLFFSFFFFFETGPHSVAQAVVQWLNHGSLOPQLSGFKQSFRL RLLSG*DYRCTPLRLASF/*FFVEMGCHYVAQAGLQLDSDGLPASA SQRAGITDVSPCIWPPMSCYVKRT
5673	A	921	1086	TQPWYRHGGGPKTLRQSWSPCQAYHVPACPSHHKQLSSRPRPWC PPNATNMLLSLKALQPPTLLSPLP*QVCRQGNPPKQRCRGP GATHH IPVHLWHSWPLLHTLPAISAVQPSFFPKETLGQALQNRWVPLG PGKQVLRERPLSHQREKREAQLTPRLLARRPQAGEAAARRQKGTAE GERG*DGPSKPSLVRARVRKRAGPKQGPSASA*PGP\STPNPPTTQ GSHWPREQAPATPMSEEPNVLSQQTARP/RPSPGTGMGVGVLPKF VSVPGALAKLTMCPMHVLHITKTCPAAQGHGVHRMPQTCC
5674	A	2	70	WSRSPDLMIRLPRPPKVLGLQA
5675	A	2	118	WSPSPDLVIHPPRPPKVLGLQALHWLVKNHSTDIGL
5676	A	446	756	ISFFLSFFLSFFFFFFEASRSFTQIGVCSGTISAHCKLCLPGSHSP ASAS*VAGTTGARHHTRLIFLYF**KTGFHFRSRDGLDLL/NLVIRP PRPPKVLGLQA
5677	A	2	276	LRWSFSLVVQAGVQWCDLGSLOPPPSGFK*LSCLSLPSSWDYRSAPP CPANFVFLVETGFLHVGQA\CLELLTSSDLSTSAS\QSAGITRREQ
5678	A	60	235	VRVLQIYHSLRPLPGSHHPPRGDRLOQGRGFLTACQPC*STYC*TFPPG VLGNTGRDLLL
5679	A	1	2059	MSSQEVTFEQRPEGEDEGGAVELSRQQTQERRRQLGQTQLMYKWAKP KICSEDLLEGAVKLPAAGVKTCPNPGFFKTNNSTCQPCPYGSYSN GSDCTRCAGTEPAVGFEYKWWNTLPTNMG/TRPFVSGSTSSTR/CM TGWEVAGDHIYTAAGASDNDFMILTLVVPGRPPQSVMA DTENKEVA RITFVFETLCSVNCELYFMVGVSRTNTPVETWKGSKGRQAYTYIIE ENTTTSYTCAFQRTTFHEASRKYTNDAEIIYSIICHPCY*MPWASYA GPCAQKASEEGSSCTSPAGYYIDRDSGTCHSCPPNTILKAHQPYGV QACVPCPGPTKNNKIHSCLYNDCTFSRNTPTRTFNYSALANTVTL AGGPSFTSKGLKYFHFTLSLCGNQGRKMSVCTDNVTDLRIPEGESG FSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLD GITSPAELFHLES LGIPDVIFFYRSNDVTQSCSSGRSTTIRVRCSPQ KTVPGSLLLPGTCS DGTCDGCNFHFLWESAAACPLCSVADYHAI VSS CVAGIQKTTYVWREP KLCSSGISLPEQRVTICKTIDFWLKVGISAGT CTAILLTVLTICYFWKKNQKLEYKYSKLVMNATLKDCDLPAADTCAIM EGEDVEDDLITSKSLLEDQI IYLQEDS
5680	A	1	1098	MGFHHVQAGLELLISSDPPALASQAGITGSWKWILAPVILYICER ILRFYRSQQKVITKVKNMHFPLAVIRVIFYRTTELNFYVVTLKEEL GNWAQWVVMHPSKVLELQMNKRGFSMEVGQYIFVNCPSISLLEWHP

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				FTLTSAPPEEDFFSIHIRAAGDWTENLIRAFEQQYSPPIRIEVDGPF TASEDVFYQYEVAVLVGAGIGVTPPFASILKSIWYKFCADHNLKTKKI YFYWICRETGAFSWFNNLLTSLEQEMEELGKVGLNRYLFLTGWDSN IVGHAALNFDKATDIVTGLKQKTSFGRPMWDNEFSTIATSHPKSVVG VFLCGPRTLAKSLRKCCHRYSLLDPRKVQFYFNKENF
5681	A	143	571	KYCSQIYYLNRAAVRCRQKGLIAQVDLFLVGGCSSLWASYFTQML TQTATTLVHGNVLSPPSLYANTEAMATRRSQTWSFGSRSACERC RSMSSSLTRSSAVTARGSAKPRCSCCWPLRSRTSRRCWVPSGATG G
5682	A	3	355	FEIGSCSITQAGVQRHD\LCSPPLPPPGFKQSPRPSLPSS*DHRCAP PCPASFCIF**RQGFHHVGGAGLELLTSGDPPALASQSAGITGVSHQ AWPPFGFLDRTLISIVSQKTNTNRP
5683	A	1	2472	RYDLALWPRLECSGAITARNLKLGGSSNSPTSTSCI/C*GYRLIFF KFFVDTGSCYVAQAGFKLPASSDPPPKMLR\YRP\GHAR/LCLTV NRTNVP
5684	A	5	298	TGSRVAQAGVQ*H/DYQGSLOPPPRPM*SSHLSPRNWDYSHTAP HPAKLFFFLDTGSHYVAQAGLKLGGSSDPSTASQSAGITGMSHRIQ PHISF
5685	A	9	320	FIIYLF/RDGVLLCCPGQSAVAFLRLTVTST/FL*SPDGELLTL*STR LGLLKWWDYKGEPPRPVFLFCFLNV**RCSLAMLRLVLNS*AQAIF LPQPSKVLGLQG
5686	A	2	438	FFFFFSRLNFEFYKNPFCTNPGPRGPPRVGPPFAPRRGAFSLPQGG PF*SLLFSRPNP/SGPLVRPGLPPTGALPCSVR*VDRSPLPYMVSP GPPGGLRGAGPGPVHPRGPEAPPRARGRGREGGPAESVTRFPWQLR GGHFQP
5687	A	243	379	PASLSTNEAEHEMSLFSFQKPLNVTVIRRGKHLRLVPTRWAGK
5688	A	1	867	EYVDYNGGAGVQHIALKTEDIITAVRTPFPVRIPLSFRARDDLCKIE RAGGGSPGPVSLGWETDRTPSLLLATHGQAQPHPPPESSVSTEPLGF GGLQNDHKAVMKQVEEALHQLHARDKEKQARDMAEAHKEAMSRKLGO SESQGPWAFKVNISIPGSPASIAKTQRGSKSKLSLQLEDAETDEL LRDLSTQIEFLDLQISPEEQIISPERQPSGELEKTDMPQDELG QERRDLEPENREEGQERRVSDIQSKAGISRESLVSTTEDILFQKDK STPVYPL
5689	A	1	874	TVLAFADGCGVLAHGRSRSYGRLGRRPYSREPGLWSRGPFTMSDEE ARQSGGSSQAGAVTVSDVQELMRRKE\EIEAQ\IKANYDVLESQKGI GMNEPLVDCEGYPRSDVDLYQVTRARH\NIICLQNDHKAVMKQVEE\ ALHQLHARDMEKQA\RDMA\EAHKEAMSRKLQSESQGPRAFPAKVN SISPG\SPASIAGLQVDD\EIVGVSGSVNTQNFQSLHNIGSVQHS/ EGGPGTHHPTFCLYFDYSRDLI*KPLNVTVIRRGKHLRLVPTRW AGKLLGCNIIPLQR
5690	A	30	512	TPVRDMAEAHKEA\MSRKLQSESQGPRAFPAKMN\SIEPRLPQPSI AGLQVDDEIVEFGSVN/TPQDFQSLQ\NNGNVVQ\HSEKPPCEDQ* SARGEKH\QLKLVKNAAGPGKG\LLGC\NIIPSAKDELSRPGNSKQE KHPSPCPRTWLGDFTCPSSPLKA
5691	A	945	1358	KKQNFYITVHGFSCCLGRGKGQDRDGWESRDGRFLSRSLTFPQFAII RLVGQKEFSMLPKSFTLQILPRGSLSLPDPQEQLSK*SMPHRAVQSP SRHALGNPKTAREGSAPRSPLTGRPRPPVAAG*CRACRGAPQVARPP QGDQHRGFRGAHSDWRVWRGWASPSLLPRSSSSSGIANQAS\VPPE PGERS/RPALGGRSGSSPCRPP/PPKPPWRGA/GS*SGTWRRWLAGW RTRRPAPGRCARPARPGPPSWPSRPQTGLAAGLSGAPSVPSRRCRTP RRSRPPLPARWTPGAPACRRRPWS*SPGSTTAA
5692	A	3	316	FFFFFLRQSL/DSVAQAGAHNPGPLQAPPPRFTPFSSRLSLPSSWD HRRPPPCPTNFSAPPVETGF\TVLARMVSI*PCDLLTSASQSAGTT GTSHRARPIIFK
5693	A	2	769	LAITYKHAGGVFSFILLQTLNTYGGQDTKGSVLAYWRLPGLCIIY VKQSAKOFFSYDINRQSVSKL\QNVQLPP\DEIKELRQT\TMPAG

				VDKSSTDQKYVQAGRRLGKVIQQSRLNCFPLVSYIET\CLFILWRH LEYL\LHCMPD\SQKSLFASR\TLF*KQKDCQGFSPQETQS*DF *KVGLAYSEANHGF*TQLSGLMPINGFLENHYPKRNFLDIEGL/YIS KVRFFGYSFIALVRRIRGLLRISRN
5694	A	189	426	TLPISIYQSSPSGFHNYQFLASGVGATLPITPHPTS/ELPYRVPSPP SPSPRPPS*FSRTFQPP/V/PGPAH*PPDEIVEPG
5695	A	243	1660	AEPDTSPI*TPGQSGSS*GNTS/EPWTVTPPGLKMQQRVLCCTL*PP /RRLPVCRAAG*TRLDRA*ESGHPGPAVPREATGVPGALPAQASVR SIWPALATCVATTVQTST/DAEVARQG/ICPAPHPAYPPA*PALCCP ARADPRGRVLQ**ADAVPGPPAI*AVHRAVSHPGGAQCPHPNPPAPQ ARVPRETCLPALQLAAPVLRGAGATAASAPT\EEEEEEACLEEEEEEE DSDEEDQSRSGKSEAWVPDSEERLILREEFTSRMHQRFLDGKDGDFD YSTVDDNPDPDNLDIVARDEEERYFDEEPEPADAPSPELDGD*WPPFP PPPAPSPSPTRQLIPGLLSDPFSRGTS/AAVPHNPHTPPSHWV*SHL RQPPPPPLFLGFPFSSLPCLLPLSFLSVSWASFCLFLSFCLSPYPRS LFPVLWLAVSPFLPLSLCLRLCLHRRAGGESPPLAGGQLAGPFVAGS GQFGSGADP
5696	A	7	558	GWLDLGLTKVCV*NAEVPTCEWVRLMCMSVCASK/CGGGCGCLC/MA SGHCECLGMCWSL*ACVFLSKNECLCVS\LGTCQCLCLCVPVSHHLC IRVAHAASLCAMVCQCLCVDGWPMSPDPRQGRPGWLDPAHLPSGSLAL WVRVTEAFCLGKTGCSGSALRVAGGLPSLLPFLRVKRTPGGQGA
5697	A	272	1146	GFLGLEGLPLSSSPQVAWATVPLWAQLQGGLAGSCLGQILAPGPSEAR DWWASLAGP*ERVEGADRPWRFLSTPEALVLAAGR/SKARASDPGR SSTLSLLHVL\KVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCEL SPGYLAVPSTFLKDAPGEFLRVFSTGRVSLSAIRAVAKNTTPGAA LPAGEWGTGPIPG/CSWKFG\QTAGGHKNF\ASYPTNP/CVPLFGSP KGPGRVCVRITLHQHCRA\SDTEFHPIGFHIQVPEGGRSQDAPPLL LQDPLLSCVPHR\TPRR
5698	A	281	535	DSSKYRLFYIDAFSPAPAGNQPPPMGMNMNRRATIPGPPMGPGPA MGPEGAANMGTPMMPDNGSSCTMTDFLKGPPSQMGFT
5699	A	1	1014	MEPEMELISITTGKTACEDLTTESKMNSVFWKIRFTYSSSRISSEY TTSWASVFNRLKRRYDVHIAHIIHRHLHASYSNCLSEKDYIF PSFMKLQGESHLIQLRHGKVIWSTLDMGREEREQPPRFAQPGTYAS RWKALEEMEKQOREQVDRNIREAKEKLEAEMEAAARHEHQLMLMRQAN QMVKCDPRHGKYMCCMLYRGDVVPKDVNAAIATIKTKRTIQFVDWC PTGFKVGINYQPTTVVPGDLAKVQRAVCMLSNTTAIAEAWARLDHK FDLMYAKRAVFHWYVGEEMEEGEFSEAREDLALEKDYEEVGVDSE AEAEEGEY
5700	A	155	2916	QQKAAGVLPKGYGTVPWQQRAGQQFQTDKAKGLTFLGGKAVHLS*/ HLEREQPPRFAQPGTYASRWKALEEMEKQOREQVDRNIREAKEKLEA EMEAAARHEHQLMLMRQDPGLALVSCMQQGQSMSRSPKKVFKHLYELN LTKLQSLGSRSLRWKDSPPFWGEEAGGKRPLVSLALHRSPLSLLLF VPKHPSKGRPDCTVQSRSPKPTKSQLLDLRECISIHVGQAGVQIGNA CWELYCLEHGIQPDGQMPDSDKTIGGGDSFNFTFFSETGAGKHVPRAV FVDLEPTVVDVVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKE IVDLVLDRIKRLADLCTGLQGFLIFHSFGGGTSGSFASLLMERLSVD YGKSKLEFAIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNE AIYDICRRNLDIERPTYTNLNLIGQIVSSITASLRFDGALNVDLTE FQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPANQ MVKCDPRHGKYMCCMLYRGDVVPKDVNAAIATIKTKRTIQFVDWCP TGFKVKQGFLLGLDPLLLPSSATSLHGGTGDVCRVLWCDLSSSLPPV DNSTCFSGGGRGVKQTLWESLVVVLFSALALLNAGYARSEADWGHSS DAFSPAPAGNQPPPMGTGMNMNRRATIPGPPMGPGPAMGPEGAANMG TPMMPDNGAVIMASMSFQCCLEAFGVTLDSAFSPYPCLLNSIFSQOM LSALSSKICPITSVKVLNDWVPTAPTSPVPTSPAPTFFVPAPSAL LTSTAPTSPALLTSTAPTSPAPTFTPAPSALLTSTAPTSPAPAPSA

				LLTSTAPTSPAPTSPVAPSALLTSTASTPPAPILSASTSAAPTSPA PTLSAPTICCTYIICTYTLCTYILRIYTL
5701	A	37	1542	PREPTPPA/PPRLQRTTRTRRCGFTIDIKSFLKPGE\KTYTQRCRLF VGNLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRL\ESQNPWA EIAKAELGRAPFLKSRP\LRICFRLHMGAAFDCSRNLFSLLFFQLSC LEQ\AFSQFGS\VEKAGVVDDGR\PTGK\GFVEFASKNLPATKRL WKRCCDGAFL\LLTTTPRPSPLWKPMEQFDDDEDGLAQRLLMHKTQQ\Y HKER\EQPPRFCSTWGHLLKFEYQSRWKA\LDEMEKQQREQVDRNIRE AKEKLEAEMEAAARHEHQLMLMRQDLMRQEELRRLEELR\NQLQKR KQIQLRHEEEHRRRE\EDMIRHQ\KQEGLRQQEGFKPNYMNREQE MRMGDMGPRGAINMGDAFSPAPAGNQGPPPMGMNMNRRATIPGPPM GPGPAHGTRRSRKYGNSQ*CQIMEQCTNDRFPQGPSPMGSPMGSR RF*NPLKHPMSGVGPVSGGPGGFRGSP\GGNFEQPNRRRY
5702	A	81	334	HNVHC*VPCGEVGSVHCWW\NGDNLI*PS*KVSWKYESRAFKTSRP LDPTPLLLGIQSK*/YNKGHKDLDIRILITALFVVTKKL
5703	A	3	449	WGPEP*/PTRPTLDEGPGCPGCGCSPSLPMGPPRGRGPPTSMSLLCR WPGVPLGSPPGCPPRARVKLFPHPGPDVSTSPPWAGHGAHQDP*GPV SGSESP/PPAGHWAPPASTSSPKIQAGL*PE\GMRTAQPPSVAVGSP QGSFRHKEGWG
5704	A	1	206	GSL*SPSPRFKRFSCSLSSWDYKHVPPHLANFCIF*\RDWVSPCW LGWSRTDHLHLSWPPKVLGLPS
5705	A	32	401	AFPDKLPWNFRLCQVNRGISEWAGMSEMMSDIQLSVGKLVAR/CW LQAEI*G*QFTKQER/CPSLTRSRWHGQPREGQAERPFLCAPPEGAP IGFLR*HHLRVQLAMAWIKFKMLGQSPLPYI
5706	A	252	416	PFCRPPRADSVTKQER/CPSLTWIRWHGQPOGGQAERPFLRAPPEGA STGFLRQHH
5707	A	2	164	FFLYLFLFLFLRWSL/DSVIQAGVQWHD\ICSLQPLPPGFK*FSDCS TVLQPGRQSETGLKYFFITV*EMESCSVIQAGVQWHDNLFPATASW VQVILRLLHCTPAWATE
5708	A	1334	1707	VRPHEGARAGPGGRGRGDPGLGARALPQPRVAVAGAACQPPSRLRHA GHRGPMVHAVGGSTFLGFRQ*LSSHSTTRQCPSRDSVWGLQPHISL LHCPSRGSP*GPHPCRLLPGHPGISIHL
5709	A	57	376	KRGSLSGCPRRVQW/RKTALQLOPSKLPGLK*TFP/CLSLLK*TGT HTCAPLCPNFFVFLTYLIEM\GLTMLPRLVSYFWPQV\PSLASQST GITGVSHHALAWWSMQ
5710	A	9	264	PCPNTIN/CPLGLRLPC/PPHLCPSLCLGKVGGP*KVPQTPSLGET ELEQKKPPVPMASGWTGGRNGGWEKSLRGKERRVFSQEGFP
5711	A	124	770	QYFPTATHGNVKKSLLSGKASLKRHRVCCSCLFYIVQKQPKLNKTL FRQSYICDQTTFRKSKGIINIKFIFFFEMESRSVQAGMQWRNLGS LQ/PPPPGFMPLSCLSLSSWDYKRPPPCPANFFVFLVETGFTVLAR MVSIS*PCDLPASTSQSAGITDVSHHAWHIKFKPEVTWRERGREENHV DRHIFRLLDIRFTDTHFIKKELMRSDTL
5712	A	2	232	CLSLSS*YYGRMSRPRANF*\FLVETGFHHIGEAGLELLTLGDPPA SASQAGITGVSQRGQSLFAFLMSSTSFCK
5713	A	1	242	QAGVQWHDLSLQPPPLPGLKQFSCSLSPSSWDYRRVPPRLANFC/DF LVETEFHHVQADLELRTSGNLPTSASQSAGITGVSHHA*PKVLGLQ V
5714	A	1	133	ERLRYFRVEHLDQRLKAAENKFSY\CLMTWLKCGFWCLEKFIKFLNR NAYIMIAIYGTNFTSARNAPFLMRNIIRVAVLDKVTDFLFLGKL LIVGSGILAFFFTHRIRIVQDTAPPLNYWVPILTVIVGSYIAH GFFSVYGMCDTLFLCFLEDLERNDGSAERPYPMSSTLKKLLNKTNK KAAES*RLRYFRVEHLDQRLKAAENKFSYVPHDLAQMRLLVPGEVHQ IP
5715	B	166	969	MGSACIKVTKYFLFLNLIFFILGAVILGFGVWILADKSSFISVLQT SSSLRMGAYVFIGVAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLL ILIAQVTAGALFYFNMGKLKQEMGGIVTELIRDYNSSREDSLQDAWD

				YVQAQVKCCGWVSFYNWTDNAELMNRPEVTYPCSCCEVKGEEDNSLSV RKGFCCEAPGNRTQSGNHPEDWPVYQEGCMEKVQAWLQENLGIILGVG VGVAIIELLMVLSICLRHVHSEDYSKVPKY*
5716	C	300	347	MIHLPRPPKVLGLQA*
5717	A	316	797	APALPQPTGLAASSHMVQVPLWICLKLSHKSRSNPQLFF*VFQFLR RSL/SSVPQAGVQ*HDLSSLQPP/PPGFTPFSCSLSPSSWDYRCPPP RPAKFFLYF**RRGFTMLARMVSI*PRDPPASASQSAGITGVSHRA RPPPPQFFIQLPLYNHTLEGR
5718	A	2	519	WHPQSDVQAEVQWRDLGLLQSS\PP\GFTLFSCLSLSSWDYRRPPP RPG*FLYF**RRGFTVLARMVSI*LHDPPALASQSAGITGVSHRTR PGADL*PRVQKPRASLGG*NHMCNMKSLPTGQTRLNKGRRLGHPDH WRWKETPGL*CFHGNFCGALKAGRAHLDDGQGR
5719	A	1	663	MISPFINENTRRKFLIYSGSNYQGPGLVDYLDREVI PDFLGGESVL GLNYLRSFRLAGWRAVLVMLTFYLQVWGDTRGQASPFSSSTVKLSGL GLSPFFDPCSFSPTGRCPGCDNKLYGQLANVKKVRTGYKYIGMRK ARNNVEESQEITTAWLALTLALAFLLLISTAANLSLLSRAERNRRL HGDIAYHPLQEMNGEPLAAEKEQPGGAHNPFKD
5720	A	1	1561	MATSTGRWLLRLALFGFLWEASGGDLSGASRDDDLLPYPRARARL PRDCTVRAGNREHESWPPPPATPGAGGLAVRTFVSHFRDRAVAGHL TRAVEPLRTFVSLEPGGPGGCAARRRATVEETARAADCRVAQNGGFF RMNSGECLGNVSDERRVSSSGGLQNAQFGIRRDGTLVTGYLSEEBV LDTENPFVQLLSGVVWLIRNGSIYINESQATECDETQETGSPSKFVN VISARTAIGHDRKGQLVLFHADGHTEQRGINLWEMAEFLKQDVVNA INLDGGGSATFVLNGT\LASYPSDHCQDNMWRCPRQVSTVVCVHEPR CQPPDCHGHGTCV\DGHCQCTGHFW\RGPGCELDGCGPS*LAAQHGL CNGSTGLSAVD\AGW\TGSNCSEECPLGWHGPGCQRPCKCEHHPCPD PKTGNCSSVRVKQLQPPEATLRAGELSFFTRTAWLALTLALAFLLL ISIAANLSLLSRAERNRRLHGDIAYHPLQEMNGEPLAAEKEQPGGA HNPFKD
5721	A	1119	2008	ALHPPAQGELFCDFYKDPWSWSEGPSPPLTRLAPHQQTCTELSGGR RGSVLEECVPTPASAHLAASPAEAGTAGVWR*RHHF/HSTGLLGPR *LSMSLLMS*CKAGRCPPGEDCPRPLPGCSLSPLERKLCFSSA*GPA SFLGGLTAKASGCSLSLRP/HSHIQGHGLWEKL*VPARRAGGGVCFK SA\PHLQSL**KPSSKASKREG*Q*TLPSATIGELPFK*HAPKHLN AQGFLCKIH*HHK/QTANAIA*GGPGSLEGTLLRRPGSPSSSLGVGS GKTEVNSQNCRLGREGVS
5722	A	3	444	FFFFLQSL/NSVI*AGVQ\QPLPPEFKRLSCLSLSPSSWDYRCAPA HSANFCIFSKD/MGFTMLTRLVSNWQQ/CELPTLASQSGITGVSHH TQPIYH\FIFVETEFHHVAQAGVK/PPSLK*SSRLSLPKQWNYSH LYPALFNETFFFK
5723	A	1	6738	MRGAQKATNVNKLSEVIQKKEESPAQFYQRLCEVYRMYTPCDPDSPE NQHMIHMAVLRQSPEDMRRKLQKQAGLAGMNPSQLLEIASQVFNVD AVSRKENGKENGQARRYADLFSPVEPDCVEVLDSIHSSRPDLRDQP WPSGDWELYVDGSSFFNPQGERGAGYAVITLDTVVEATSLPQATSGQ KAELIAFIGALELSEGETVNIYTDSRHGTEEGQILKQPVSERLDFV CSFLQRRNSFYMGTCQDEPEQLDDWNRIAELQQRNRVCPHKLKTCYP LESRPSLSLGTITDEEMKTGDPQETLRRASMQUIAEGTGITTRQQ RKRVSLEPHQGPPTPESKKATSCFPRPMTPRDRHEGRKQSTTEAQKK AAPASTKQADRRQSMASFILNTPKKLGNSLLRRGASKKALSASPNT RSGTRRSPIATTTASAATAAAIGATPRAKGLGQDDVTLDNLFRVH EHTGEVGAQVGRGQLLQHQGLAQLRTCAPTFPAGAEGKERYGFQEVH PVFYVVVIAENRKHPSSPECLVSAQKVLEGESELELAKMTMLLLYHST MSSKSPRDWEQFEYKIQAEALAVILKFVLDHEDGLNLEDENFLQKA PVPSTCSSTFPEELSPSHQAKREIRFLELQKVASSSSGNNFLSGSP ASPMGDILQTPQFQMRRLKKQLADERSNRDELELELAENRKLKTEKD AQIAMMQORIDRLALLNEKQAASPLEPKELEELRDKNESLTMR LHET

10430

				<p>LKQCQDLKTEKSQMDRKINQLSEENGDLSEFKLREFASHLQQLQDALN ELTEEHSKATQEWLEKQAQLEKELSAALQDKARAKGDLGNKMMGPMF ADVYEGLCGNLKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVL GDVLQLETLKQEAATLAANNNTQLQARVEMLETERGQQAELLAERGH FEEKQQLSSSLITDLQSSISNLSQAKEELEQASQAHGARLTAQVASL TSELTTLNATIQQQDQELAGLKQQAQKEKQAQLAQTLLQQQEQASQRLR HQVEQLSSSLKQKEQQLKEVAEKQEAQTRQDHAQQLATAAEEREASLR ERDAALKQLEALEKEKAACLEILQQQLQVANEARDSAQTSTVQAQRE KAELSRKVEELQACVETARQEQHEAQAQVAEELQLRSEQQKATEKE RVAQEKDQLQEQLQALKESLKVTKGSLEEEKRRAADALEEQRCISE LKAETRSLVEQHKRERKELEERAGRKGLEARLQQLGEAHQAETEV RRELAEAMAAQHTAESECEQLVKEVAAWRERYEDSQEEAAQYGAMFQ EQLMTLKEECEKARQELQEAKEKVAGIESHSELQISRQONELAEHLA NLARALQQVQKEVRAQKLADDLSTLQEKMAATSKVARLETIVRKA GEQQETASRELVKEPARAGDRQPEWLEEQQGRQFCSTQAALQAMERE AEQMGNELERLRAALMESQGGQQEERGQQEREVARLTQERGRAQADL ALEKAARAELEMRLQNALNEQVFEATLQEAALAHALTEKEGKDQELA KLRGLEAAQIKLEELRQTVKQLKEQLAKKEKEHSGSGAQSEAAGR TEPTGPKLEALRAEVSKLEQQCQKQEQADSLERSLAEERASRAERD SALETLLQGLQLEKAQELGHSQSALASAQRELAAFRTKVQDHSKAED WKAQVARGRQEAERKNSLISSLEEEVSILNRQVLEKEGESKELKRLV MAESEKSKLEERLRLQLAETASNSARAAERSSALREELEHTSTQAL VSELLPAKHLQQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQLRRAEKASYAEQLSMLKKAHGLLAE NRGLGERANLGRQFLEVELDQAREKYVQELAAVRADAETRLAEVQRE AQSTARELEVMTAKYEGAKVKVLEERQRFQEEQKLTAAEQVLEVFQ REQTKQVEELSKKLADSDQASKVQQQKLKVGQLGEVWVPLDKGGKLF SKLWGRGGLVYKWFLLIYKISYATGIVGYMAVMFTLFGNLFFKIKP EDAMDFGISLLFYGLYYGVLERDFAEMCADYMASTIGFYSESGMPTK HLSDSVCACVCGQQIFVDVSEEGIIENTGAQLPRVLHPWLVRHGKEAN VSLQREGRPQEDVQQSVSFIGVVVGSGLWEESTGQCDLHLGPPGAL TSAPNQNMNSNHEQKDYEGDDEDKEDDDRHHGIMNPY</p>
5724	B	107	467	<p>MRLHETLKQCQDLKTEKSQMDRKINQLSEENGDLSEFKLREFASHLQ LQDALNELTEEHSKATQEWLEKQAQLEKELSAALQDKKCLEEKNEIL QGKLSQLEEHLSQLQDNPPQEKGEALX*</p>
5725	A	149	579	<p>GLLSTRPISCRHTL*GPLQSSWEYMDVPWDLRASEGNGLLYSARDC TLQQIHSVFQKLDVEEPDSANSSFYSTRSAPASQASLRATSTQSLA RLGSPDYGNSALLSLPGYRPT\TRSSARRSQAGVSSGAPPGEGETTGT YY</p>
5726	B	24	219	<p>MPRSSRTKSCRSSCGAWSSCMKENKELRAEAERLGHELQQAAGLKTKE AEQTCRHLTAQVRS LGGTX*</p>
5727	A	272	683	<p>REGLYLSRFPFHSKLPRTPDGTSPGEPASPISQRLPPKVESLES YFTPIPARSQAPLESSLDSLGDVFLDSGRKTRARRRTTQIINITMT KVRLLGQGLQGSNSHFLSRASLHWALSQEQGGMSSQSMQWES</p>
5728	A	1	406	<p>QELQEQLRSLEQLQKENKELRAEAERLGHELQQAAGLKTKEAEQTCRH LTAQVRSLEAQVAHADQQLRDLGKFQVATDALKSREPQAKPQLDL DSLDLSCEEGLTSLITRSGGSLPPYVCLWSACCLSGCILVR</p>
5729	A	211	5508	<p>IWCLFPLSVHMGLIYSQKCLEEKNEILQGKLSQLEEHLSQLQDNPPQ EKGEVLGDVLQLETLKQEAATLAANNNTQLQARVEMLETERGQQAEL LAERGHFEEKQQLSSSLITDLQSSISNLSQAKEELEQASQAHGARLT AQVASLTSELTTLNATIQQQDQELAGLKQQAQKEKQAQLAQTLLQQQEQ ASQRLRHQVEQLSSSLKQKEQQLKEVAEKQEAQTRQDHAQQLATAAE REASLRERDAALKQLEALEKEKAACLEILQQQLQVANEARDSAQTSTV TQAQREKAELSRKVEELQACVETARQEQHEAQAQVAEELQLRSEQQ KATEKERVQEKDQLQEQLQALKESLKVTKGSLEEEKRRAADALEEQ RCISELKAETRSLVEQHKRERKELEERAGRKGLEARLQQLGEAHQ</p>

				<p>AETEVLRRRELAEAMAAQHTAESECEQLVKEVAAWRERYEDSQQEEAQ YGMFQEQMLTLKEECEKARQELQEAKEKVAGIESHSELQISRQONE LAELHANLALALQQVQKEVRAQKLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARAGDRQPEWLEEQQGRQFCSTQAAL QAMEREAQMGNELERLRAALMESQGGQQEERGQOQEREVARLTQERG RAQADLALALEKAARAELEMRLQNALNEQRFATLQEAALAHALTEKEG KDQELAKLRGLEAAQIKELEELRQTVKQLKEQLAKKEKEHASGSGAQ SEAAGRTEPTGPKLEALRAEVSKLEQQCQKQEQADSLERSLEAERA SRAERDSALETLQGQLEEKAQELGHSQSALASQRELAARFTKVQDH SKAEDEWKAQVARGRQEAERKNSLISSLEEEVSILNRQVLEKEGESK ELKRLVMAESEKSQKLEERLRL\QAETASNSARAAERSALREELE HTSTQALVSELLSA\KHLCCQLQAEQAAAEKRHREELEHKSQAGGL RAELLRAQRELGELIPLRQKVAEQERTAQQLRAEKASYAEQLSMLKK AHGLLAEENRWLGERANLGRQFLEVELDQAREKYVQELA AVRADDT RLAEVQREAQSTARELEVMTAKYEGAKVKVLEERQRFQERQKLT AQ VEQLEVFQREQTKQVEELSKKLADSDQASKVQ*QKLVAVQAQGGESQ QEAQRLQAQLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQONQ* LQEQRLSLEQLQKENKELRAEAERLGHELQQA GLKTKE\AEQ\TCRH LYLPRLRSLE\AQ\VAHARPSSFRDLGKFQVAT\DALKSREPQAKPQ LDLSIDSLDLSCEEGTPLSITSKLPTQPDGTSVPGEPASIPQRLP PKVESLESLYFTPIPARSQAP\LESSLDSLGDVFL\DSGRKTRSARR RTTQIINI\TMTKK\LDV\EEPD\SAPNLSFY\TRSAPASQASLRA T\SST*SLTRLG\SPDYGNSALLSLPGYRPTTRSSARRSQAGVSSGA PPGRNSFYMGTCQDEPEQLDDWNRIEL\QQRNSELWPPNLKNWLS WESRP\SLSLGTITDEEMKTGDPQETLRA\SMQPIQIAEGT\GIT RQQRKTGLP*EPHQGPEN*VLKKATS\CFPRPMTPR\DRLEGAQT EHLLEAQKKAAPAFLLKQA\DRRQSMF\SILQPHRSLG\NSLLRR GASKKALSASPNTSGTRRSPIATTTASAATAAAIGATPRAKGTA NHLKGQVPVSGPTLCPRLPSPGPPPTVPLSAFSQLPRPNSSLTS</p>
5730	A	111	407	<p>NLLRTMIFWFGFEDRVWLCCPVLTATSVLTATS/TFPGFKQFSCLSL LSSWDYRCIPPHPGNLWYF**RQFTMLARLDSNSGPQAIHPPQPPK VLGLHV</p>
5731	A	3	615	<p>GLRALRRGQGLPGL*CCSRPQPS PRAQGHPSMGGPMQVRTPPRGMAS VGPQSYGGGMRPPNSLAGPGLPAMNMGPGVRGPWASPSGNSIPYSS SSPGSYTGPPGGGGPPGTPIMPSPGDSTNSENMYTIMNPIGQAGR ANFPLGPGPEGPMAAMSAMEPHHVNGSLGSGDMDGLPKSSPGAVAGL SNAPGTPRDDGEMAA</p>
5732	B	134	471	<p>MYAKGGKGSAPVPSDSQAREKLALYVYELLHIGAQKSAQTFLSEIRW EKNIMPSPGDSTNSENMYTIMNPIGQAGRANFPLGPGPEGPMAAM SAMEPHHVNGSLGSGDMDG*</p>
5733	B	223	692	<p>MEPS PRAQGHPSMGGXMQRVTPPRGMASVGPQSYGGGMRPPNSLAG PGLPAMNMGPGVRGPWASPSGNSIPYSSSSPGSYTGPPGGGGPPGTP IMPSPGDSTNSENMYTIMNPIGQAGRANFPLGPGPEGPMAAMSAM EPHHVNGSLGSGDMDG*</p>
5734	B	228	292	<p>XLARDDHERVMGRQPRASLRA*</p>
5735	A	1	1753	<p>MYAKGGKGSAPVPSDSQARENLSAFQAATELTSLDRLALYVYELLHI GAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWYGLGCCGVFWDLYC AAPDRREACEHSGEAKAFQDYETPERPAHRHGNAGRAGSSSGMIDVG GSSDPQILRPTTPVCSLTNASSLSHGAGHLQRGGGTPQSAAPSPV MGSMAPGDTMAAGSMAAGFFQGPQSPSPHNPAPMMGPHGQPFMS PRFPGGPRPTLRD\GSQPPAGPPWVPSPPSPG\AMEPS PRAQGHPEH GRPNARGVTTPRG/MGPAWGPRAYGGMRPPNSLTRPACLPNMNG PRKFVGPPWAQPPVEYSIP\YSSSSPGSYTG\PPGGGGPPGTP\IMPS PGDS\TNSENMYTIMNPIGQAGRANFPLGPGPEGPMAAY\G\GM EPHHVNGSLGSGDMDG\LPREFPQAPVAGLSNAPG\TPRDDGEMAAA GTFHAPSSQSE\NYS\GMTMSRVNWAAPGALCGPRLLPFRPCLRA</p>

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				KGLKVTPSGTLDLANQGLPMLGGPTRKTLTILLKTQGPRETFFSVW TLPAICILVPERKALWGGPSSPGRQGGGAH
5736	B	315	458	NGPSRTQQPSLTDVLYCPEAIVSLVGLRRLAACQEHKRAPEVYVAF T*
5737	A	202	402	RRVLHTHTGCFTVFCKISRSSSEDESINFASKLWQERRGFQHGDP RLPLDSREPRGPLRS PAATK
5738	A	1	3156	LLLWDWVICQLSKELAENRCNQSEPRSRSAACVEIAAFTFNMAKMF NDSNAARIHQDTQELMCFGRWCWKDGPGLCIPCSQPMISISTVQQG KKAASSHYSRGGAKYEGEAVKRSLVESYTHPNSNETERRENIDTVMN CFSTEDFDVTLYYREPDNVGHRFGPEAEKRKLMIQIGRTIVYLVG ATEKHSLSQTSAPWGDHREETQRQQDPLTNYIKFRVWVKFDIAGYG GFGPLPLKLGQEEALYQALKNAHPHLQVYKKEEFPEHFHLAKHDRV LPIVIFQRIIMCFNKGSHGFDNVLMDMNIIFRAFGPDFKRNRLAEPFN SIHIYPFVSPGSHPQTHNGSLAVTQEMLMNSYDQPGRELIKTAKAK QCPGPVLKPTFLNHPDPSQSRLGFRPVSRQCGPAPVLVPEENAGTE LLLQSFERRFLAARALRSFPWQTVKHPVCVKHRLSVKYARCFELSELT KKHEAVHTELLDKLYEDLAETLMAKESTQGHPSYLLNSVSGMFDEW NPVWPEMSVFHATTVLELGSASLTGLAICKMCRLOAYIPSDCHSQV LEKLRGNVLLNGLSLEADISANLDSPRVTVAQLDWDVATVHQLSAIQ PDVVIAAGNAQPRALCAGDVLYCPESIVSLVAVLRLAAYREHQRAP QVYVALIVRNPETCQLFTTELSFAPDHPEHSPSWQPCAMHAQQPLP AHRDVGPMPVHVQQRVNYRANKQASTRRHTGFHDHFLCANKNVCIK YDVPPNVDTLGSSQSQAARCSCHICGHTRFLTKPSPLQLPHRWTHSVP HKAKPAAAATSLDTLGSSQSQAARCSCHIPGHTRFLTKPSPLQLPHRW THSVLHKAKPAAAATSVDTLDSSQSQAARCSCHIPGHTRFTTKPSPLQ LPHPWTHSVLHKAKPAAAATSLDTLGSSQSQAARCSCHIPGHTRFLTK PSPLQLPHRWTHSVLHKAKPAAAVTSVDTLGSSQSQAARCSCHIGGHT RFLTKPSPLQLPHPWTHSVLHKAKPAAAATSLDTLGSSQSQAARCSCH IPGLMVQQVLF SRQESKC
5739	A	1	1470	MAPEENAGTKLLLQSFERRFLAARTLRSFPWQVGGGASGEACGACGS PGADGMGLPAETPGAPATEGSHSALPTHSIACFNVPVNAPLRFLSLP STRSLEAKLRDSSDSELLRDILQKHEAVHTELLDELYEALAETLMAK ESTQGHWSYLLPRYPSCDTKVKTPRKARSHSPSTAIISHGTTGLVTW DAARYLAEWAIKNLAFTNRTVLELGSAGLTGLSICKM/WPPPDH L\HDCHSRVLEQLRGNVLLNGLSLEADITANLDSPRVTVAQLDWDVA TVHQLSAFQPDVVITADVLYCPEAIVSLVGLRRLAACWEHQWAVEV YMAFTVRNPETCQLFTTELAPSTCEGVLSSHLDKNTRTHRGQETP ELPQIAARPPGFSAFTVHPSPLPPDFAPAPPEHSPSWQPCAKMHPQ QPLPAHRDMDDPVVHVGPVNYRANKQASTRRHTGFHDRVPHNLAQ EAGQAWGSGSLSSQHFRRLRQED
5740	A	2	414	PWGDHREETQRQQDPLTNYIKFRVWVKFDIAGYGGFGLPLPKLGQ EALYQALKNAHPHLQVYKKEEFPEHFHLAKHDRVLPVIFQRIIMCF NKGSHGFDNVLMDMNIIFRAFGPDFKRNRLAEPFN SIHIYPFV
5741	A	3	233	QARLPPGLPATLRPRPRLGARGERGDRTLAEEFRAPLPGGARTAF LADCEASCVCCEAPAVSQVCPVLSLRTHQK
5742	A	83	1503	SWNTPYNHWATKQ/LSSHYSRGGAKYEGEAVKQSLVESYTHPNSNET ERSANIDTVMNWFTKEDFDVTLCYREPDNVGHRFRPEAENRKLMIQ QIDRTIRPWDDHREETQCQQDPLSNYIKFMDLVKFDIVGYGGFGMP LPKLGQEEALYQALKNAYPHLHIYKKEGFPEHFHLAKHDRVLPVIMY ANFGYSINGISLLYFYTHLCDKYFNVHFFHEPLSLWRAQTTPSLSHR YISLVRHMDATNLDASEAQLPGSPYPDSAPGPANLDSTQDLPQRRLS WPYPRPRPPNAHPGPAALQAPRTLLLTLP GPAPSLPRTALGPPL QSRPGFRPVSRQCGPAHFMAPEENAGTELLQSFERRFLAARTLRS FPWQGGGGRAERPAGLAGVQGTGWVSVLKPPALLPREFLGSPRS RDPVPVPGAWPKSLAPLLPRELAAEDEGVSTALGGQTRARCGVQFTI IFTTF

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5743	A	266	477	DFSLSRPHGA*KQN*ETHQILSCC/GDILHKTUVK/HSCVCEAPAVRQ ICPVLSLRTHQKARGCPHRAFGRAV
5744	A	148	592	SHVALGQLGLWLTAVRSSWRWELCVSSTGSGLPASFSLKQPKSCRCW* EEVKTGSCVGIHWTST/VFPQAVFHLPPVLLPRSLACLSCPRGCA QIR\CQ*TPPYPLFPILTYSGMLSSSTVLIRHILETNKKEKSLAA EGVRHLQVS
5745	A	164	667	ERGTYICQITTSLYRAQQIIQLNIQASPKVRLSLANEALLPTLICDI AGYYPLDVVMMWTREELGGSPSPSLW\SSFSKPQAKALAGTYSISSS LTAEPG/RLQVPLYTCQVTHISLEEPLGASTPGCPTRAENSLGSHLC QQSLPSCTDVWPWGFRDQAPNRTWAASG
5746	A	1	790	VEELSKKLADSDQASKVQQQKLKVGQQLGEVWVPLDKGGKLFSLWGR GGLVYKWFLLIYKISYATGIVGYMAVMFTLFGNLNLFKIKPEDAMDF GISLLFYGLYGVLERDFAEMCADYMASTIGFYSESGMPTKHLSDSV CAVCGQQIFVDVSEE/EDH*EHRCS/CFHEFCIRGWCIVGKKQTCPY CKEKVDLKRMFSPNPYPPLGSLGSGGKVLASVTCIWVLLGPSLLP PTRTCQTMNNKKIMKVMRIKRMMDTDMAS
5747	A	1	1005	FRGRAVKMAAVVEVEVVGGAAGERELDEVMSDLSPEEQWRVEHARM HAKHRGHEAMHAEMVLILIALTVVAQLLLQVWQKQHRPSYNMVTLFQ MWVVPPLYFTVKLHWWRFVILWILFSAVTAFTVFRATRKLPLVQTTPL VYKWFLLIYKISYATGIVGYMAVMFTLFGNLNLFKIKPEDAMDFGIS LLFYGLYGVLERDFAEMCADYMASTIGFYSESGMPTKHLSDSVCAV CGQQIFVDVSEEGDH\ETTYRLSCNHVSHEFCIRGWCIVGKKQTCPY CKEKVDLKRMFSPNPWERPHVMYGQLLDWLRLVAVQPVIIIGVVQGIN YILGLE
5748	B	99	236	XTTSTSSSTVTVTAPGPAATGSPVKKHRPLLPKETAPAVQRVVWNSSX *
5749	A	1	783	MAEMRQSLEQERDLIAEVKKQLELEKQQAVIDETKKKQWCANCKKEA IFYCCWNTSYCDYPCQQAHPHMKSTQSATAPOQEADAENVNTETL NKSSQSSSSSTQSAPSETASASKEKETSAEKSKESGSDSIVHDGYFS SSLLCFGPCCISPCVTIPGRSGLLLCPLQGLRVSKRCDKQPAYAPTT TDHQPHPNYPAQCKYEPVLRKLPGLLPDHSRSNKSSWSSSDEKRG TRSDHNTSTSTKSLLPKESRLDTFWD
5750	A	1	1626	MDLKELESVQQQSTPVPLISPKRQIRSRFQLNLDKTIIESCKAQLGI NEISEDVYTAVEHSDSEDSEKSDSSDSEYISDDEQKSKNEPEDTEDK EGCQMDKEPSAVKKKPKPTNPVEIKEELKSTSPASEKADPGAVKDKA SPEPEKDFSEKAKPSPHPIKDKLKGKDETDSPVHLGLDSDSESELV IDLGEDHSGREGRKNKKEPKESPQDQGTPTPSTTVGSHSPPETPVL TRSSAQTSAGATATTSTSSSTVTVTAPAPAATGSPVKQRPLLPKET APAVQRVVWNSSSKFQTSSQKWHMQMQRQQQQQQQONQQQQPQSSQ GTRYQTRQAVKAVQKQKEITQSPSTSTITLVTSTQSSPLVTSSGSMST LVSSVNADLPIATASADVAADIAKYTSKMPFFRVYLLKHLESWGSV IPGLEATAMHLASSVMQEQLGWGRRPACRWLWAPHWLTWPVLSPLW EWREGALEVFGANVYIADTISHLLKPCPYGPVVGSRHCGNQEDSQMS PEEGAVPPLVKNLCSRELQNSLDYG
5751	A	1	542	CGWNTGYCD/YPCQQAHPHPIKSTQS\ATALQQGADVEVNTPELN KSSQSSSSSTQSAPSETA\SASKEKETSAEKSKESGSLDLGSRRET PSSILLGSNQSVSKRCDKATLLCPNHHRPPAAPQLPRPEVPFPEL* NSRLSPPVFKKKGIRRVPIPTSTSTKSLLPKESRLDTF\WD
5752	A	1779	3628	MEISEDVYTAGHSDSEDSEKSDSSDSEFISDDEQKSKDEPEDTEDK EGCQMDKEPSAVKKKPKPTNPVEIKEELKSTSPASEKADPGAVKDKA SPEPEKDFSGKAKPSPHPIKDKLKGKDETDSPVHLGLDSDSE\NEL VIDLGEDHSGREGRKNKKEPKESPQDVVGKTPPSTTVGSHSPPET PVLTRSSAQTSAGATATTSTSSSTVTVTAPAPAATGSPVKQRKL\I PKE\TAPA\QVRVRVELIK*SFKRPPKSGTCRRCSVSSSSSSSKTSS SSHQSSQGTRYQTRQAVKAVQKQKEITQSPSTSTITLVTSTQSSPLVT SSGSMSTLVSSVNADLPIATASADVAADIAKYTSKL\MDAIGTM\T

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				EIYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKNLELTM AEMRQSWEQERDRLIAEVKKQLELEKQQAVIDETKKKQWCANCKKEAI FYCCWNTSYCDYPCQQAHWPEHMKSTQSATAPQOEADAENVNTETLN KSSQSSSSSTQSAPSETASASKEKETSAEKSKESGSTLDLGSRETP SSILLGSNQS DSHRSNKSSWSSSDEKRGSTRSDHNTSTSTKSLLPK ESRLDTFWD
5753	A	2	1711	RSEDSEKSDSSDSEYISDDEQSKNEPEDTEDKEGCQMDKEPSAVKK KPKPTNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSEKAKP SPHPKIDKLKGKDETDSP TVHLGLSDSESELVIDLGEDHSGREGRK NKKEPKESPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQTSAGA TATTSTSSSTVTVTAPAPAATGSPVKKQRPLLPKETAPAVQR\SCGTS STVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSMSTLVSSVNADLP IATASADVAADIAKYTSKMDAIKGTMTETIYNDLSKN\TTWKAQLAE DSQGLRIEIEKLQWLHQQEL\SEMKNLELTMAEMRQSLEQERDRLI AEVKKQLELEKQQAVIDETKKKQWCANFKKEAIFYCCWNTSYCDYPCQ \QAHWPEH\MKSTQSAYCSSSRKADAE\VTETLKLSPSQGSS\SS TQSAPFRKRPPAPSKEK\ETFSLRKAKESGSTLDLGSRETPSSILLG SNQGS DSHR\SNKSSWSSSDEKRGST\TRSDHN\TPSTQHGRSLLPGK ESRAGTPFLGTSK
5754	A	1	191	MOK*ITAWAPAPMKIKIIASPERKYSVWIGGSIWPLST/FQQMWIS KQEYDESGPSIVHRKCF
5755	A	2	1203	LSRRQCQLSHSVLPPLRRRVSLPVAMEEEIAALVIDNGSGMCKAGFAG DDAPRAVFPSPVGRPRHQGVVMGMQKDSYVGDEAQSKRGILTLYP IEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANRE KMTQIMFETFNTPAMYVAIQAVLSLYASGRRTTGIVMDSGDGVTHTV IYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRD IKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCP EALFQPSFLGMESCGIHETTFNSIMKCDVDIRKDLANTVLSGGTTM YPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTP QQMWISKQEYDESGPSI\VHRKCF
5756	A	3	412	SRFPEGLFQPFPG\MKSCGIHETTFHSH/I IKFDVAIR\KDLYANT LLPGGNHGVSGALLTGMQKEIHAPAAQATLRFKIIAPPGSASTRW/V GSVGSILASLSTFQ\QMW\ISKQE\YDESGPLHSSTAKCFLNGLSQI A
5757	A	1	2297	MGRDWSLSLESLEEDRMRESLEHARDLLNCCDQONADHHMDSEVQAEV VSEGDEELIGKWSKAYCHRCEQKDDLKWELIFKREAHEKSLEILQPD HVVEKKNPGGGRNQSTSSSWVGTVAEITTEAVKCKIQVLQQQADDA EERA\ERSQREFREERRARE\QAEAEVASLNRRIQ\LVEEELDRAQE RLATALQKLEEAKE/SLADESERRY*RLFEN\RALKRLKEKIGTSRE IQLK\EAKHIAEE\AD\RYEEV\ARK\LVIIIEGDLERTE\ERA\EL AESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEIEIKILTDLK KEAETRAEFAERSVAKLEKTIDDLDTNSTSGDPVEKKDETPFGVSV AVGLAVFACFLSTLLVLNKCGRRNKFGINRPVAVLAPEDGLAMSLH FMTLGGSSLSPTGKSGSLQGHIIENPOYFSDACVHHIKRRDIVLKW ELGEGAFGKVFLAECHNLLPEQDKMLVAVKALKEASESARQDFQREA ELLTMLQHQHIVRFFGVCTEGRPLLMVFYMRHGDNLNRLRSHGPD KLLAGGEDVAPGPLGLGQLLAVASQVAAGMVYLAGLHFVHRDLATRN CLVGQGLVVKIGDFGMSRDIYSTDYRVGGRTMLPIRWMPPESILYR KFTTESDVWSFGVVLWEIFTYGKQPWYQLSNTAIDCITQGRELERP RACPPEVYAIMRGWCQREPSNATASRMCTPGCKPWPRLHLLSTWMSWA RGPAQGLGVVSRNTGACPQHPP
5758	A	3	636	WAWNQAEAEVASVNGRIQLVEEELDCAQERLATALQKLEEAGKADE SERGMKVIENRALKDEEKMELOEIQLEAKHIAEEADRKYEEVARKL VIIIEGDLERTE\ERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYS QKEDKYEKEIKI\LTNKLREAET\RAEFAERSVAKLEKTIDDLKDL KCTKEEHLCTQRMLDQTLDDLNEM

5759	A	1	239	QCCSGGTHGNPAIGDR\MQKQILPWAPAQM KIRFMAPPERKYSVWIA APILASLSTSSRMWISKQEYDESGPSIVHRKCF
5760	A	3	1458	ADPPPVHTRRQLTMDDDIAALVVDNGSGMCKAGFAGDDAPRAVFP VGRPRHQGMVGMGQKDSYVGDEAQS KRGI LTLKYPIEHGIVTNWDD MEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFN TPAMYVAIQAVLSLYASGRRTTGIVMDSGDGVTHTVPIYEGYALPHAI LRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIK/EEAVLRRP GLRARDGHG\ASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSFL G\MESCGIHETTFNSIMKCDVDIRKDLYANTVLSGGTHQFPPLPCRPG C*KKITALEP\ATMKI\RIIA\PEAQSTPLWNRGAPIL\ASLVHLP AKMWDQKSREYDESGPLPFVHRK\CF
5761	A	171	326	LRLSLFLLQWLLAIVVRHILTGPKQDNSRSTESKRSKVRFPQVSLPS SPSR
5762	A	3	385	KMCDNCKDSAFERKNITEYCRDLIKILKQAEELNEKLTPLKLIDSW MGKGAALKRVAGVVAPTLPREDLEKIIAHFLIQQYLKEDYSFTAYAT ISYLKIGPKANLLNNEAHAITMQVTKSTQNSFR
5763	A	2	314	FFFFISALKALFAFLQILLFQVNVLRITAHIVISFINLLSVTPSKAF LLLAIFICREDYSFTAYATISYLKIGPKANLLNN\EAYVIT\MQVTK STQNSFRVNGY
5764	A	1	176	MRTFALLTAMLLLVA/HAQAEPLQARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA
5765	A	1	2674	GKHKLLSTGPTPEWSIREKLCLASSVMRSGDQNVWSVRAIKPFAEP GRPPDWFSQKHCASQYSELLETTETPKRKRGEKGEVVETVEDVIVRK LTAERVEELKKVIKETQERYRRLKRDAELIQAGHMDSRDLDELCDNI\ KKKLEEEEA EVKRKATDAAYQARQAVKTPPRRLPTVMVRSPIDSASP GGDYPLGDLTPTTMEETSGVTPGTLPTSTPVTSFPGIPDTLPPGSAP LEAPMTPVTDDSPQKMLGQKATPPPSPLLSELLKKGSLPTSPRLV NESEMAVASGHLNSTGVLLLEVGGVLPIMHGGEIQQTPTNTVAASPAAS ESVSQATIVMMPALPAPSSAPAVSTTESVAPVSQPDNCVPMEAVGDP HTVTVSMDSSEISMIINSIKEECFRSGVAEAPVGSKAPSIDGKEELD LAEKMDIAVSYTGEELDFETVGDIIAIIEDKVDDHPEVLDVAAVEAA LSFCEENDDPQSLPGPWEHPPIQQRDKPVPLPAPEMTVKQERLDFEE TENKGIHELVDIREPSAEIKVEPAEPEPVISGAEIVAGVVPATSMEP PELRSQDLDEELGSTAAGEILEADVAIGKDETPLTNVKTASPESM LSPSHGSNPIEDPLEAETQHKFEMSDSLKEESGTFGSQIKDAPGED EEEDGVSEAAASLEEPKEEDQGEGLSEMDNEPPVSESDDGFSIHNAT LQSHTLADSI PSSPASSQFSVCSEDQEA IQAQKIWKKAIMLVWRAAA NHRYANVFLQPVTDIAPGYHSIVQRPMDLSTIKKNIENGLIRSTAE FQRDIMLMFQNAVMYNSSDHDVYHMAVEMQRDVLEQIQFLATQ LIM QTSESGISAKSLRGRDSTRKQDASEKDGGRGRRCAIEADMKMKK
5766	A	1	419	YANVFLQP\VQDDIAP\GSPSIGQR\PMDLST/IKKNI*NG*SEAPA DFQR*HMLMFQNLMLYHSSDHYFYHIAI\EMQ\RDVLEQIQFLATQ LIMQT\SESGI\SAK\SLRGRDSTR\QQDASEMDGGTRGR\RCAIEA DMKMKK
5767	A	2	111	ISAKSA\RGRDSTRKQDASEKDSVPMGSPAFLLSLF
5768	A	3	2884	GKHKLLSTGPTPEWSIREKLCLASSVMRSGDQNVWSVRAIKPFAEP GRPPDWFSQKHCASQYSELLETTETPKRKRGEKGEVVETVEDVIVRK LTAERVEELKKVIKETQERYRRLKRDAELIQAGHMDSRDLDELCDNIA TKKKLEEEEA EVKRKATDAAYQARQAVKTPPRRLPTVMVRSPIDSASP PGDYPLGDLTPTTMEETSGVTPGTLPTSTPVTSFPGIPDTLPPGSA PLEAPMTPVTDDSPQKMLGQKATPPPSPLLSELLKKGSLPTSPRLV VNESEMAVASGHLNSTGVLLLEVGGVLPIMHGGEIQQTPTNTVAASPAA SGAPTLSRLLEAGPTQFTTPLASFTTVASEPPVKLVPPPVESVSHAT IVMMPALPAPSSAPAVSTTESVAPVSQPDNCVPMEAVGDPHTVTVSM DSSEISMIINSIKEECFRSGVAEAPVGSKAPSIDGKEELDLAEKMDI AVSYTGEELDFETVGDIIAIIEDKVDDHPEVLDVAAVEAALSFCEN

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				DDPQSLPGPWEHPIQQRDKPVPLPAPEMTVKQERLDFEETENKGIH ELVDIREPSAEIKVEPAEPEPVISGAEIVAGVVPATSMPEPPELRSQD LDEELGSTAAGEIVEADVAIGKGETPLTNVTEASPEMLSPSHGS NPIEDPLEAETQHKFEMSDSLKEESGTIFGSQIKDAPGEDEEEDGVS EAASLEEPKEEDQEGYLSEMDNEPPVSESDDGFSIHNAATLQSHTLA DSIPSSPASSQFSVCSEDQEAIAQAKIWKKAIMLVWRAAANHRYANV FL\QPVTDIAPGYHSIVQRPMDLSTIKKNIENGLIRSTAEFQORDIM LRFQNAVMYNSSDHDVYHM\AVEMQRDVLEQIQQFL\ATQLLMQTS\ ESGISAKSLRGRDS\TRKQDASEKDSVP\MGSPAF\LLSLFDGGT\R GRPLCPLKPDMDKESSESPSELPL
5769	A	3	627	PRGENRFKAQPEWRKTPCQMMLSQSTFRKT\YIGKIPTTILAL\PYV G\KELNMIIMLPDE\TTDLSTV\EKDSHAKFVEWTSMDMAEEEVK LSIPRFKLEESY\DMESVLRNLGMTDAFEAGARANFSGMS\QTDLSL VQRSTKSI CGRSNEGRPREAASPPKVAI\MMMRCA\RFCPPPPAPD HPFLF\FIQHR\KTNG\ILFCGRFSSP
5770	A	3	626	YNLVTFR/LAVLSFEKDDDHNGHIDFITAA SNLRAKMY SIEPADRFK TKRIAVKIILVKPTTTGT VSGLVCFE\MIKVTGGYPFAAYKNCFLNL SHS/IFVVFTETTEVRKTKIRNGISFTIWRWTVHGKEDFTLLDFIN AVKEYGIEPTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKK YVDLTVSFAPDIDGEDLPGTSK
5771	A	92	265	SFELFADKVPKTA/WLDGKHVVFGKVKEGMNIVEAMERFGSRNGKTS KKITIADCGQLE
5772	A	1	1310	GNSPPSELKWKAKSEDLRHRGLKAQAEIKGSTQQIGFTTDPMARSS PYPTDVARVVNAPIFHVNSDDPEAVMYVCKVAAEWRSTFHKDVVVDL VCYRRNGHNEMDEPMFTQPLMYKQIRKQKPVLOKYAELLVSQGVNQ PEYECVSMHGVNRNKPSSYNSTKSSMDGLILHPATGLVFLVLSKQCEEIH QPVVWTCEQREAEENATAEENRVLLAMVNPTVFFDIAVDGEPLGRVSF EVGRAAACGNGAQKVGGRGRENFPCL*ATGEK\GFWL*GVPCFHRLFP RVLCVQGGELQQRH*WPLVGKPHSMGKKI*KIEELPSLKHTGSPGIL SPWQONAGPQTNGFSPFSICTA\KT\EWLEWPSHVVFVWHK*KEG\MN IVEAHWSRFG\SR\NGKTQQRSPFADCGQLLISLTCVFILTTKIIIS FCRLRRAPLQPHLLAVS
5773	B	47	204	XQHTFCKRCGVQS FYTTPRSNPGGFGIAPHCLDEGTVRSMVTEEFNGS DWEKA*
5774	A	2	402	CGDRGALRPPSCAGRSGPGPPRPPRPLPWHPPAPPAHGAPLARPG ARARRSEKPPSEKPRLRSSPRAQEEGPGEPPPELALLPPPPPPPP TPA\PRRPRRP\PGPGRAAGALGDVPEAAEAYLERVPPSSC
5775	A	2	241	FSCLSLKSWDYRALPPSPAN\LFLVETGFHHVQGASLKLLTSGDPP ASASQTVGITGMSHAWPVSSFYIWSHWAPRNS
5776	A	22	643	VVEFPVLTMAATSGILSALGNFLAQMIIEKKRKKENSRLDVGGPLRY AVYGGFFFTGPL\SHFFYFFMEHWIPPEVPLAR\VRLLLLDRL\FFAP \AFLMLFFLIMNFLEGKAS\TFAAKMRGG\FWPAAEDETCRVWTP\ LQFINI\NYVPFESSGCFPGQPGQLLFWYAYLALLGEVTTWRWENIRC TCGRGSGGLHPPKREQKPIQSGCH
5777	A	23	448	ELESRSVTQAGVQWCDLGS\LQPPPL/SFKQFSFLSLLSSWDYRHVP PCPANVCILVEMGLVGQAGLELLISSDTPISVSQSAGIISVSHGTQP HIGNFLEQLKVVLQCYTSFLCFTKSSTVKHIQLIIKITLRNTKNKA RI
5778	A	25	396	ISGRSTFSLFSRQGLSALSPRLE\CSVAISAHCNLRPLGSSN\GTTG A*HHTRLILYF/LAEMGFHHVGQAGFEVLTSSNPPASASTSARITGM SNRT\GHLNFNHP*MCYKYRCGSLAGRGGSRW
5779	A	80	460	YISLNVTTTHLIFFFFFLRQGL\CSVTQAGV\QWCNLGSLQPLPPRFK \NWDYRCVTPHLANFVFLVEMGF/LPASASQSAGITGVSHCTQLGVF ICICYGSSHGVRQSWHQFCSSKLLVKSGRVGVGLLG
5780	B	1	3811	MVGELRYREFRVPLGPGHLHAYPDELIRQVRVGHGHPYQIRWLILRR GDEGDDGSGQVDCKAEHILLWMSKDEIYANCHKMLGEDGQVIGPSQE

				<p>SAGEVGALDKSVLEEMETDVKSLIQRALRQLEECVGTIPPAPLLHTV HVL SAYASIEPLTGVFKDPRVLDLLMHMLSSPDYQIRWSAGRM IQAL SSHDAGTRTQILLSSSQEAEKHLDFD SRCALLALFAQATLSEHPM SFEGIQLPQVPGRVLFSLVKRYLHVTSLLDQLNDSAAEPGAQNTSAP EELSGERGQLELEFSMAMGTILISELVQAMRWDQASDRPRSSARSPGS IFQPQLADVSPGLPAAQAQPSFRRSRRFRPRSEFASGNTYALLYVRDT LQPGMRVRMLDDYEEISAGDEGEFRQSNNGVPPVQVFWESTGRTYWV HWHMLEILGFEEDEIEMVEADEYQGAVASRVLGRALPAWRWRPMTTEL YAVPYVLPEDEDTECEHLTLAEWWELLFFIKKLDGPDHQEVLQILQ ENLDGEILDDEILAE LAVPIELAQDLLLLTL PQR LND SALRDLINCHV YKKYGPEALAGNQAYPSLLEAQEDVLLDAAQAQAKDSEDAAKVEAKE PPSQSPNTPLQRLVEGYGPAGKILLDLEQALSSEGTQENKVKPLLLQ LQRQPQPFLALMQSLDTPETNRTLHLTVLRILKQLVDFPEALLYPWH EAVDACMACLRSPNTDREHPVHRVHSGTCYCSAPVAFALFHSSPPLC PHPGAPGTDFFLHRLTSVSRDYAVVLNQLGARD AISKALEKHLGKLE LAQELRDMVFKCEKHAHLYRKLITNILGGCIQMVLGQIEDHRRTHQP INIPFFDVFLRYLCQGSSVEVKEDKCWEKVEVSSNPHRASKLTDHNP KTYWESNGSAGSHYITLHMRRGILIRQLTLLVASEDSSYMPARVVVC GGDSTSSLHTELNSVNVMPASRVILLENLTRFWPIIQIRIKRCQQG GIDTRIRGLEILGPKPTFWPVFREQLCRHTRLFYMVRAQAWSQDMAE DRSLLHLSSRLNGALRQEONFADRFLPDDEAAQALGKTCWEALVSP VVQNITSPDEDGISPLGWLLDQYLECQEA VFN PQSRGPAFFSRVRL THLLVHVEPCEAPPV VATPRPKGRNRSHDWSSLATRGLPSSIMRNL TRCWRAVVEKQVNNFLTSSWRDDDFVPRYCEHFNILQNSSSELFGPR AAFLALQNGCAGALLKL PFLKAAHEQQEMAQQERKQQQELHLALKQ EX*</p>
5781	A	1	3135	<p>MLRWTVHLEGGPRRVNHA AVAGHRVYSFGGYCSGEDYETLRQIDVH IFNAGWERA ADEVWLWSLGPRLGTNIWFGKSGQPGGRFPGLSRAVP TVSLRWTKLPPVKS AIRGQAPVVPYMRYGHSTVLIDDTVLLWGGRND TEGACNVLYAFDVNTHKWFTPRVSGTVPGARDGHSACVLGKIMYIFG GYEQQADCFNSNDIHKLDSTMTWTILICTKGSPARWRDFHSATMLGSH MYVFGGRADRFPGPFHSSNEIYCNIRVFDTRTEAWLDCPPTPVLPEG RRSHSAFGYNGELYIFGGYNARLNRHFHDLWKFNPNVSFTWKKIEPKG KGPCPRRRQCCCIVGDKIVLFGGTSPSPEEGLGDEFDLIDHSDLHLIL DFSPSLKTLC KLAVIQYNLDQSC LPHDIRWELNAMTNSNISRPVIVS SHGRGRGCRERKRRHSSSERYCQLMPGANYRAGAGAGARRPRGAR DREEDGGGLEPAAVARDLLRGTSNMSFEELLELSQSVGT KTYKQLVA GNSPKKQASRPPIQNA CVADKHRPLEMSAKIRVPFLRQVVPISKKVS EQFARHIDQQIQGSRIGGAQEMERLAQLQQCLQAVLIFSGLEIATTF EHYYQH YMADRLLGVVSSWLEGAVLEQIGPCFPNRLPQQMLQSLSTS KELQRQFHVYQLQQLDQELLKLEDTEKKIQVGLGASGKEHKSEKEEE AGAAAVVDVAEGEEEEENEDLYYEGAMPEVSVLVLSRHSWPVASIC HTLNPRTCLPSYLRGT LNRYSNFYNKSQSHPALERGSQRRRLQWTWLG WAE LQFGNQTLHVSTVQMWLLLYLNDLKAVSVESLLAFSGLSADMLN QAIGPLTSSRGPLDLHEQKDIPGGVLKIRDGSKEPRSRWDIVRLIPP QTYLQAEGEDGQNLKRRNLLNCLIVRILKAHGDEGLHIDQLVCLVL EAWQKGPCPPRGLVSSLGKSACSSTDVLSCILHLLGKGT LRRHDDR PQVLSYAVPVTVMEPHTESLNP GSSGPNPLTFHTLQIRSRGV PYAS CTATQSFSTFR</p>
5782	A	1	696	<p>GGGLEPAAVARDLLRGTSNMGFEELLELSQSHVGTITYKQLVAGNSPK KQGSRPPIQNA CVADKHRPLEMSAKIRVPFLRQVVPISKKVARDPRF DDLSGEYNPEVFDKTYQFLNDIRAKEKELVKKQLKKHLSGEEHEKLO QLLQRM EQQEMAQQERKAQQE\RHLPLEPKRRAQAQQGHRPYFLKKS EQRQLALAEKFELKRSKKLENFLSRKRRRNAGKDRRHLP LSKE</p>
5783	A	214	348	ILKVVSDF FARSWKNTFHFQILHKGLSLHHGLEDAYDVASRGFSH
5784	A	221	537	PMGASPNGPAHGLKGCKGVVGAVPPMGFRSSGKFGKVTTRDSQEPAW

10432

				FRKGATEFSDRATNRSSNGF*SRRERLYPAS/CEVV*LDDSRIFTFL VIDNRCFRHDSM
5785	A	1	1761	MVLVVVAVVVVVLVAVIVVVVVVAAVVVGAVVVVVVVVVVVVV VVVEEDNQHKGTGAINNNNTAKNPQQSPFHSPTATSTGAEATQMRRNQK TNPHNMTKQVSLTPPKITLAHQQWIQTKKKYLIYLKKHSGVKNKIPRN PTYEGCEGPFQOGELQTTAQONKGGHKQTEDHSMMDRKNQYCENGHT AQAVPNPYTLLSQIPEDAWEFTVLDPKHAVFCIPVHPDSQFLFAFED PSNPMSQLIWTVPQGFNRNSPHLFGQALAQDLSQFSYLDLTVLRMD DLLLATHSETLCHQATQALLNFLATCGYKVS KPQAQLCSQQVKYLGL KLSKGTRTLSEERIQIPILGYPHPKTLKQLTAF LGITGFCQIWI PRYS KIARPLNTRIKETQKANTHLVRWTPEAEVAFQALKKALTHAPVLSLP VGQNFSLYVTEKNRNSRSRSPYTGTSAQLAELIALTRAPELGEGKRVN IYANSIGREREFLLTSKGTLVKHQEAIKRLLAVQKPKEVAVLHCWGH QKGKEREIEENRQADIEARRAARQDPPLEMLTEGFLAFELAMATARA ELSLAIHHCLPPPPQTRCWLPSLRIRQGVCCIPDPAITLTAWPK IPFLGIRKAKNPRSEKTRLATILEAACCHFGSGPPPSWELWEQGPV TVQTHILRS*VGFLGILFTPECFFR*IRYFVLVWICHW*ASVILGGV KETCFVIL
5786	A	1	507	MVSVLVFSDLGFLASRIPRNGIFGHAEPRPALGLTPEHKGNDGDAGR GPLESSSDPFLCGQERRENRTVDSDTLALDAARLTCTRHGLGNQVF CPHNGAQNVDKQYTAAIHSRHTTAHGGYSVLQTPAYSGLNDFSSN KSDFRIGMPLEVLYIICVESPLSWLSI
5787	A	143	358	KHSLKCLSLSSSRWRATLSSVGWHLSSAAMRCTVSAGSSRDEGSIT SCSLKPGPSTHSPACSPSHKQLSK
5788	A	184	290	VCLFKNSMYLLLLPGGPCSQSSQDGRPLPKWQASCSLTWGFLASR IPRNGILGHAVSVIALLEAMGHGREPWN*GQEPFGQRT/WRLATIL EVACHHLGSSGSKDPLVTVD
5789	A	136	351	SSEVPIAAPDQAKGLPLFPHS*VPRFIPKFHEPNRSGAEERHSRGEK RRSI*TWRGVWLGTVGEIGRMAEL
5790	A	253	417	WFSHPQAMGLPKFHEPNRSGAEERHGRGEKRRSI*TWRGVWLGTVGE IGRMAEL
5791	A	415	2879	PCRNNGEPLARLGAAMGALLYQKRSGHPAISGGVEVSDGSATVANSS GGRYVKEAKEATKNGDLEEFKLFNLAKDIFPNEKVLSRIQKIQEAL EELAEQGDDEFTDVCNSGLLLYRELHNQLFEHQKEGIAFLYSLYRDG RKGGILADDMLGKTQVI IAFLSGMFDASLVNHVLLIMPTNLINTWV KEFIKWTPGMRVKTFFHGPKSD/DTDQKQSDSAKEW\VIITTYQMLI NNWQQLSSFRGQEFVWDYVILDEAHKIKTSSTKSAICARAIPASNRL LLTGTPIONNLQELWSLDFACQGSLLGLTKTFKMEYENPITRAREK DATPGEKALGFKISENLMAIKPYFLRRTKEDVQKKKSSNPEARLNE KNPDVDAICEMPSSLRKNDLIIWIRLVPLQEEIYRKFSVSLDHIELL METRSPLAELGLVKKLCDHPRLLSARACCLNLGTFSAQDGNEDGS PDVDHIDQVTDTLMEESGKMIFLMDLLKRLRDEGHQTLVFSQSRQI LNIIERLLKNRHFKTLRIDGTVTHLLEREKRINLFQONKDYSVFLLT TQVGGVGLTLTAATRVVIFDPSWNPATDAQAVDRVYRIGQKENVVVY RLITCGTVEEKIYRRQVFKDSLIRQTTGEKKNPFRYFSKQELRELFT IEDLQNSVTQLQLQSLHAAQRKSDIKLDEHIAYLQSLGIAGISDHD MYTCDLSVKEELDVEESHYIQQRVQKAQFLVEFESQNKFEFLMEQQR TRNEGAWLREPVPSSSTKKKCPKLNKPQPPSPLSTHHTQEEDISS KMASVVIDDLPEKEGKQDLSQYKR
5792	A	16	301	IPASTAPKRSWARLGPPQILVSVATKASFGAPTIPSR\PGPQSVFAN SDLFPAPPQIPSRPVRIPPGIPGVPRRPPAAPSRPTIIRPAEPSLL D
5793	C	78	209	MSVFXXXXXXXXXXXXXXXXXNEETNHPLGVVYRLSDSTQYI*
5794	A	119	231	QTTMCYGKCARCIGHSLVGLALLCISNKRPFELPCVL
5795	A	69	909	EWCLLSPPEGHTFHLIWGITELKTKRRGRKPSRPPMCYGKCARCIGH S\LVGLAILCIAANILL\YFPKGETKNAS\ENHLSRF\WVFFSGIVG

				RL/VLLMLPAQHFLHWGLEQDDC\CG\CCGHEN\CGKRCAMLSSVI GWLSIGI\AGSGLLWSIV/VQPLGLARKDPLCLDS/LSGQWKLQPLP STEGPVTFWITSTWS\ECTEPKHI\VKWNVSLFSILLA\LGGPILIL CLIQVINGS/VLGGICG\FCCSHQQQYGLAKRTNPGTEPQSFLYFHC NLSYLHLYSIC
5796	A	1	200	RGPVLLDTS/TWARCNEPKPI/VEWNDTLFSN/LLASGGIEFILCLI QVINGVLGGICGFCCSHQQQYDC
5797	A	2	424	RLSLTLVAQAAVQWHNLGSLQPPPPGFKRFSCLSLPSSQDHRHTPPC PA/NSFVFLVETRLHHAGQAGLKLPTSG/DTPSSASQSARITGVSHR ARCWDSNSTIFGLSLANSNWRNVFLIVGGERIKGKHTFNTHSMSEF EE
5798	A	46	626	PPPPPLPPPPSPPPPGPFAAARGERGGAAGAAMEPDSVIEDKTIELMN TSVMEDQNEDESPKKNLWQISNGTSSVIVSRKRPSEGNQYQEKDLC IKYFDQWSESDQVEFVEHLISRMCHYQGHINSYLPMLQORDFITAL PEQGLDHIAENILSYLDARSLCAAELVCKEWQQRVISEGMLWKKLIER MVRTD
5799	A	1	1004	MWLILAGLAWAGLWVSDGLKDVLMAGKKSRRGKSAPKHIMSLGPLL MIAFAICHFASVMGFHYLEVNLRLQCCFKYQLIETAFVAVLVQSVLR YSSRIWDKTSLECLKVLTGHTGSGVLCLQYDERVIVTGSSDSTVRVWD VNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDI TLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKNRDKAEVAYTNLW STSTCEFVRTLNHGKRGIAQLQYRDLRVVSGSSDNTIRLWDIECGAC LRVLEGHEELVRCIRFDNKRIVSGAY/DMGFSSLELLATWLPNA*GS SFTAEL
5800	A	1	3084	MAASAWLQWLQKAKGRALRVAGAGGRESAHLILSPCSGPRLLGWPG PVAASCHAGLLPGTGRGWRATVLQRFTYPCSNSTSMEDQNEDESPKK NTLWQISNGTSSVIVSRKRPSEGNQYQEKDLCIKYFDQWSESDQVEF VEHLISRMCHYQGHINSYLPMLQORDFITALPEQGLDHIAENILSY LDARSLCAAELVCKEWQQRVISEGMLWKKLIERMVRTDPLWKLSE GWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRRCGRHNLQR IQCRSENSKGVYCLQYDDEKIIISGLRDNSIKIWDKTSLECLKVLTGH TGSVLCCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHL RFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDD KYIVSASGDRTIKNRDKAEVAYTNLRPGLTSLPRLVFSILRNCQTVF QRRCTILQSCQWYMRVSACSEPPFHNQHWIALLYLAPQITKCVASG FALDSWEAKQLGFCGNLLPQSHQLVWSTSTCEFVRTLNHGKRGIAQL QYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKR IVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLGVFLVNLNYWLRGYQ MPKGVRSQLSYEAGIGSRRWVDAKQPNSSSTQGLCTHCHMFPSSYLHGC FLIIQVSAQFHSKAGLLPHGIQVAASSPKSMSYPLSVSGGAKSLPSS RKSMSYPLSICGGHSGVADTITHRSGPKLRQEALLPIHPSSLLSFD KLCRVHTPVPGAWGGANTNGTIWWTGEEWFFRGKRGSYLKRGLPRS PVAILERGGQILEGHSSGHCPIFSCQFDVSLCQSSSLKGHSHTAKPPN VFPLILLRRTITRIIMKPERVRMRCPLQADHLVSAQFCLFKLFA RTPAQGQSSMAFTGRCSGLLQGP TLKAGAGELVAGIQAAGTSSRR KEREFRFEGVQGGEGLCMKTTAHCPFANGIYRPHFMHENTEA
5801	A	3	267	FAICHFASVMGFHYLEVNLRLQCCFKYQLIETAFVAVLVQSVLR RIWDKTSLECLKVLTGHTGSGVLCLQYDERVIVTGSSDSTV
5802	A	242	401	DLYAATYSHSHT/ILVWSTSTCEFVRTLNHGKRGIAQLQYRDLRVV GSSDNTI
5803	A	2	386	FVFAAARGERGGAAGVMEPDSVIEDKTIELMLPKCMFGILLKKAGY SKRKESWKMLDCCFLSD*SERENPHSFWIGGSEVQNIFQNTSMEDQ NEDESPKKNLWQISNGTSSVIVSRKRPSEGNH
5804	A	1	1248	MAGCRSRAMPREAAKAGEKSSPVVGGTALSTGPPQPLALVLSPL HGAGRACRLLRVARQAHAHLEQLARKCPHSPCSRSLSLHTSLQA EGASSGLGQPRKGLPQCSGGLKGSSSAKVGAAQAEVPRASEASEDC

				QHAVTSHWDYSCSLMLLSFTLKDFLWRFLKGKTVVTSTDSAIGVGIT CYSKSRSPPIGLQTSTSLWTARNRATWQEPGNTNTSVLEDQDEDKSP KKNTPWQISNGTSFV IISRKRPSEGNYQKEKDLYIQYFNQGSSEDQL EFVEHLISRMCHYHHGRINSYLKPMQLQDDFITALPEQGLDHIAENIL LYLVTRSLCAAELDERVITGSSDSTVRVWEVNTGEVLNTLIHNNED VLHLRFSSGLMVTCSKDRSIAVWDMASATDITLRGVLVVH
5805	A	2	1653	RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCL QSMPSVRCLQISNGTSSVIVSRKRPSSEGNYQKEKDLCIKYFDQWSES DQVEFVEHLISRMCHYQHGHINSYLKPMQLQDDFITALPEQGLDHIAE NILSYLDARSLCAAELVCKEQRVISEGMLWKKLIERMVRTDPLWKG LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRCCR HNLQRIQCRSENSKGVYCLQYDDEKISGLRDNSIKIWDKTSLECLK VLTGHTGSVLCLQYDERVITGSSDSTVRVWDVNTGEVLNTLIHNE AVLHLRFNSGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNV VDFDDKYIVSASGDRTIKVVSTSTCEFVRTLNHGKRGIAQLQYRDRL VVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKIRIVSGAYD GKIKVWDLQAALDPRAPASTLCLRTLVEHS\GRVRLQFDEFQIISS SHDDTILIWDFLNVPPSAQNETHSPSG\TYTYISR
5806	A	1	180	NFKRFHKTIAT\ETASYWPK\DRHINQRN\RESPVINPTTYGQLIVD KGAKNTQWGKDNFYFN
5807	A	1	355	RWASGMSTEPGGSRHSLGIQVRGGWGVGTGGEESLTPVADTQWAGS FKVATQERNPQVRQMLRRQKKGNTNKRSEKVRVLQEMQLLQVAAMN YRLRPLEKFGTYFTRMEQLSDKER
5808	A	81	474	LGERRRASLSLSLTPGRRRGFKVATQERNPQRAQMRL\RRQKKGVP FWGDFLTELQ\MGLDSAIPGRPWMATPNKRSEKVRVLQEMQLLQVAA MNYRLRPLEKFVTYFTRMEQLSDKESYKLSQLEPENQ
5809	A	3	383	YGGKEYWDTRRSMVFARHLREVGDDEFRRHLNSTDDADRIPFQEDWM KMKVKLGSALGGPYLGVHLRRKDFIWGHRQDVPSLEGAVRKIRSLMK THRLDKVFVATDAVRKETVPFSSVAFSRLRAV
5810	A	1	148	VLQSYAEGWKEGTWEEKVDERPCIDQLLYSQDKHESSLSSHFPHLL EQ
5811	A	3	1219	PGAMATLSFVFLLLGAVSWPPASASGQEFWPGQSAADILSGAASRRR YLLYDVNPPEGFNLRRDVYIRIASLLKTLKTEEWVLVLPWGRLYH WQSPDIHQVRIPWSEFFDLPSLNKNIPVIEYEQFIAESGGPFIDQVY VLQSYAEGWKEGTWEEKVDERPCIDQLLYSQDKHEYYRGWFWGYEET RGLNVSCLSVQGSASIVAPLLLRNTSARSVMDRAENLLHDHYGGKE YWDTRRSMVFARHLREVGDDEFRRHLNSTDDADRIPFQEDWMKMKVK LGSALGGPYLGVHLRRKDFIWGHRQDVPSLEGAVRKIRSLMKTHRLD KVFVATDAVRKEYEELKLLPEMVRFEPTWEELELYKGGVAIIDQW ICAHASS*SAAGEPETSCAGAGGTGRPLT
5812	A	75	130	IHRE*VPAAQGEELRGAAE
5813	A	1	1940	MATLSFVFLLLGAVSWPPASASGQEFWPGQSAADILSGAASRRR YDVNPPEGFNLRRDVYIRIASLLKTLKTEEWVLVLPWGRLYHWQS PDIHQVRIPWSEFFDLPSLNKNIPVIEYEQFIAQAQSLSHAASVFPK CFSEMDLKWMSFVPPQLEPPLHPKKAATPGCYSDRTRLPVRKAVLRS GRRACGVCFVVSQCSARDKELHLRDAPSFRVPAPEFHLRGAPSRFV PAPELHLRGAPSRFIPAAFEQILIAADLLGVTVPSPWCGSGQSGGPF DQVYVLQSYAEGWKEGTWEEKVDERPCIDQLLYSQDKHEYYRCLLRL LPLPQGWRSQSQVSIAIKGSDTTRPPVEKLSVNSLHVSSARAAGSK AWQGSASIVAPLLLRNTSARFERWDYSLQRVFSVGVDRIIDGVTFFS HPWFCDRPAADVFTRAAAACKAGTCLQETQSLLTWDFVQTRRSVMFARH LREVGDEFRRHLNSTDDADRIPFQEDWMKMKVKLGSAL\GGPYLGV HLRRKDFIWGHRQDVPSLEGAVRKIRSLMKTHRLDKVFVATDAVRKE YEELKLLPEMVRFEPTWEELELYKDG\GVAIIDQWICAHARFFIGT SVSTFSFSDS*GKEKFLGLDPKTDVQQLRRPREGV
5814	A	3	1286	PGAMATLSFVFLLLGAVSWPPASASGQEFWPGQSAADILSGAASRRR

				YLLYDVNPPEGFNLRDVIIRIASLLKTLKTEEWVLVLPWPGRLYH WQSP\DIHQVRIPWSEFFDLPSLNKNIPVIEYEQFIAESGGPFIDQV YVLQSYAEGWKEGTWEEKVDERPCIDQLLYSQDKHEYRGWFWGYEE TRGLNVSCSLVQGSASIVAPLLLNRNTSARSVMDRAENLLHDHYGGK EYWDTRRSMVFARHLREVGEFRSRHLNSTDDADRIPFQEDWMKMKV KLGSALGGPYLGVHLRRKDFIWGHRQDVPSLEGAVRKIRSLMKTHRL DKVVFATDAVRKEYEELKLLPEMVRFEPTWEELELYKDGGAVIDQ WICAHARCLPTSLSAESGSGGFQRFPCPKYSVSEQMVACVHSGHFHT VCLLV
5815	C	164	391	XX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
5816	C	321	341	MAALAS*
5817	A	128	526	FFFFIFKTASHSVVQAGVQWRSLSMQPPPPGLKQFSHLSLLGSWIK GH\LPHPNFCIFSRDGVSPCWLGWSQTPGLRPQSPKCLGLTGCEA TSPWPASLKFLKNCVFHLPGYVYLLHVLGPRSCYKYLQKW
5818	A	3	273	RRPRQRPTDQTQWFSILPDFSLDLQEGPSVESQT\HSDPHIPVDPT THLTFNHLISVCVSLTSLPHLGSPCLWSPALVSQEAASHQDRR
5819	A	1	861	MLDSLALGGLVLLRDSVEWEGRSLLKALVKKSALCGEQVHILGCEV SEEEFREGFDSDDINNRLVYHDFRDPLNWSKTEEAFFGGPLGALRAM CKRTDPVPVTIALDSLSWLLLRPLCTTLQVHLHAVSHQDSCPGDSSS VGKVSVLGGLHEELHGPVPGALSSLAQTEVTLGGMGQASAHILCR RPRQ\RPN\YQTQWFSI\LPDFQPGSPRGALCRVPALIPHIPPKKE REARDSLILPFQFSSEKQOALLRPRPGQATSHIFYEPDAYDDLQED PDDDLDI
5820	A	2	494	LGLLHEELHGPVPGALISLAQTEVTLGGMGQASAHILCRRPRQR TDQTQWFSILPDFSLDLQEGPSVESQPYSDPHIPVSKNAKARTRKC SLVSGHGRENKSCRGWGQGQF*GWGRVAASFVP\QVDPTTHLTFNL HLSKKEREARDSLILPFQFSSEK
5821	A	1	498	VRKVSVLGGLHEELHGPVPGALSSLAQTEATLGGYH/VGQASAHML \CRRPRQRPTDQTQWFSILPDFSLDLKEGPSVESQPYSDPHIPVDP \TTHLTFNLHL\SKKEREARDSLILPFQFSSEKQQA\LLRPRPGQAT SHIFYEPDAYDDLQEDPDDDLNLPQGI
5822	A	3	322	HERQALLKANKDLIPDGMTELTPLLQPLGFEDPVVCEQDVVTAGQD WVTYYDRDYGQVTGEPQERDKALQELRQELNTLANPFLAKYRDFLK S\HELPSHPPSS
5823	A	3	276	MTLPRLVSNWLKQSSHLGLLKHWDYMSEAPHLAKNFLKAYEVVSL FHVEGSGGCRMAVWHRSGEESGKVCSEFHWDSGVLKPKMTN
5824	A	151	204	SGEPFISCGRFWWLQDG/DLMTLPRLVSNWLKQSSHLGLLKHWDYM SEAPHLAKNFLKAYEVVSLSFHVEGSGGCRMA
5825	A	175	457	IHFVLISAHAVGCEGILWGGWSLRGVGVPHSSAKRS*VGIRGPGKGR PGAQLPAGRARASTEVP\SGAPCPLLGAQNDRGLHAPKRTGTGPSNH
5826	A	188	269	IHFVLISAHAVGCEGISPIEEMGVSAISIQEACSPGLQWATSFASA WVSAPLLQMAHICPIILLGSLKGARATNRFRQSLFVQGVSPARFPH LDLLLQ*P*KNDWTDVSHLEQRGTNPG*QOE*SGPLQPWRAFLDGQ C
5827	A	1	542	RHERNISHLDLKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLR GSPLYMAPEMVCQRQYDARVDLWSMGVILYEALFGQPPFASRSFSEL EEKIRSNRVIELPLRPLLSRDCRDLLQRLLEDPSCISFQDFFAHP WVDLEHMPSGESLGRATALVVQAVKKDQEGDSAADLSLY
5828	A	2	889	RGLRIPTWALQELAGRVTRRGPEGGERREPSSASPMRAAFPAGGA GGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPRLDGF ILTERLGSPTYATVYKAYAKOTREVVAKCVAKKSLNKASVENLLT EIEILKGIHHPHIVQLKDFQWSDNIYLIIMEFCAGGDLSRFIHTRRI LPEKVARVFMQQLASALQFLHERNISHLDLKPQN\ILLSSLEKPHLK LADFGF\AQHMSPWD\EKHVLRG\SPLYMAPEMVCQRQ\YDARVDLW SMGVILYGETSFPCFSP

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5829	A	297	331	RLLWGHAGQR
5830	A	3	407	TVYTFRSAIVTARAVWVRPRMDRRADLSSATQSASAEKFGGRVSAGH CALPLPARPVTVASVYGRRLARLRGCLEDSYPSALSQAQVFLDSPAVGCG LETRLFIEAALGPPCRATVTSRGHLLDISITKSPGRPCFL
5831	A	3	410	RVSAGHCALPLPARPVTVASVYGRRLARLRGCLEDSYPSALSQAQVFLDS PAVGCGLETRLFIEAALGPPCRATVTSRGHLLDISITKSPGRPCFLS VCLHGSDQQKRKGAAATAKRKSKGGGVNVEGRCLTWPPEDP
5832	A	1	530	QTIQEDSAATSEILDVMASQKRPSQRHGSKYLATASTMDHARHGFLP RHRDTGILDSIGRFFGGDRGAPKRGSGKDSHHPARTAHYGSPLQKSH GRTQDENPVVHFFKNIVTPRTPPPSQKGAEGRPGFGYGGGRASDYK SAHKGFKGVDQAQGTLSKIFKLGGDRSRSRSGSPMARR
5833	A	198	1175	RANPFRMGNHAGKRELNAEKASTNSEITNRGESEKK\RNLGELSRTTS EDNEVFGEADANQNGTSSQDTAVTDSKRTADPKNAWQDAHPADPGS RPHLIRLFSRDAPGREDNTFKDRPSESEDELQTIQEDSAATSESLDVM ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFGG DRGAPKRGSGKVPWLKPGRSPLPSHARSQPGLCNMYKDSHHPARTAH YGSPLQKSHGRTQDENPVVHFFKNIVTPRTPPPSQKGAEGRPGFG YGGRASDYKSAHKGFKGVDQAQGTLSKIFKLGGDRSRSRSGSPMARR
5834	A	1	651	MGNHAGKRELNAEKASTNSEITNRGESEKKRNLGELSRTTSEDNEVFG EADANQNGTSSQDTAVTDSKRTADPKNAWQDAHPADPGSRPHLIRL FSRDAPGREDNTFKDRPSESEDELQTIQEDSAATSESLDVMASQKRPS QRHGSKYLATA\STMDHARHGFLPRHRDTGILDSIGRFFGGDRGAPK RGSGKRLTPPGKNCSLRVPAPEVTRPDPR
5835	A	3	210	YEMLSDPVKRRAFNSVDPTFDNSVPSKSEAKDNFFEVFTPVFERNR YNFDSWREFSYLDEEEKEKAE
5836	A	71	396	APSARDVSRCAHRARPGAIMLLLPAAADGRGTAITHALTS\ELEDKK ELSESEDEELQLEEFPMKLTLDPKDWKNQDHYAVLGLGHVRYKATQ RQIKAARKYLVLK
5837	A	146	1910	APSARDVSRCAHRARPGAIMLLLPAAADGRGTAITHALTSASTLCQ\ VEPVGRWFEEFVKRRNRNASASFQELDKKELSEESQDEELQLEEF MLKLTLDPRDWKNQDHYAVLGLGHVRYKATQRQIKAAHKAMVLKHHPD KRKAAGEPIKEGDNDYFTCITKAYEMLSDPVKRRAFNSVDPTFDNSV PSKSEAKDNFFEVFTPVFERNRWSNKKNVPKLGDMNSSFEDVDIFY SPWYNFDSWREFSYLDEEEKEKAECRDERRWIEKQNGATRAQRKKEE MNRIRTLVDNAYSCDPRIKKFKEEEKAKKEAEKKAKAEAKRKEQEA EKQRQAELEAARLAKEKEEEEVRQQALLAKKEKDIQKKAIKKERQKL RNSCKIEEINEQIRKEKEEAARMRQASKNTEKSTGGGGNGSKNWE DDLQLLIKAVNLFPARTNSRWEVIANYMNIHSSSGVKRTAKDVIGKA KSLQKLDPHQKDDINKKAFDKFKKEHGVPQADNATPSEFEGPYTD FTPWTTEEQLLEQALKTPVNTPERWEKIAEAVPGRTKKDCMKRYK ELVEMVKAKKAAQEQVLNASRAKK
5838	A	1	1909	DVSRCAHRARPGAIMLLLPAAADGRGTAITHALTSASTLCQVEPVGR WFEAFVKRRNRNASASFQELDKKELSESEDEELQLEEFPMKLTLD PKDWKNQDHYAVLGLGHVRYKATQRQIKAAHKAMVLKHHPDKRKAA\ GEPIKEGDNDYFTCITKAYEMLSDPVKRRAFNSVDPTFDNSVPSKSE AKDNFFEVFTPVFERNRWSNKKNVPKLGDMNSSFEDVDIFYFW\Y NFDWREFSYLDEEEKEKAECRDERRWIEKQNRATRAQRKKEEMNR IRTLVDNAYSCDPRIKKFKEEEKAKKEAEKKAKAEAKRKEQEAKEQ QAELEAARLAKEKEEEEVRQQALLAKKEKDIQKKAIKKERQKLNSC KIWNHFSDNAERVKMMEEVEKLCDRLELASLQCLNETLTSCTKEVG KAALEKQIEEINEQIRKEKEEAARMRQASKNTEKSTGGGGNGSKNW SEDDLQLLIKAVNLFAGTNSRWEVIANYMNIHSSSGVKRTAKDVIG KAKSLQKLDPHQKDDINKKAFDKFKKEHGVPQADNATPSEFEGPY TDFTPWTTEEQLLEQALKTPVNTPERWEKIAEAVPGRTKKDCMKR YKELVEMVKAKKAAQEQVLNASRAKK
5839	A	2	812	RVLELQPVTLTLLGDHGWVEHVDNGIRYKLDVTQCMFSFGNITEKLRV

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				ASLSCAGEVLVDLYAGIGYYTLPFLVHAGAAFVHACEWNPHAVVALR NNLEINA\VADRCQIHFGDNRKLSNIADRVILGLIPSSEEGWPIA CQVLRQDAGG\ILHIHQNVESFPGKNLQALGVSKVEKEHWLYPQOIT TNQWEKWELPGILGEKLLSPATKPQLAKVGRICRNSNRHSSSAGAW TMEDTNSAHTSEILCSPCGSHSPGSGMLPLSFSWL
5840	A	3	231	SFFETESCSVAHPGAQWCDISSLP PPPPG\SSDCPASASRVAGITGT HHHAWPIFV FV FVETGFHCLPQPPIVLGLQA
5841	A	2	300	RRRLALSPAGVHWHGLGSLQPPPPWFERFSCGLLSGWDCCRAPP ASFFVFLVETGFRHVKGDLFLT/S/GDPPALASQGAW\IAGVS\H RTRPQIHFF
5842	A	227	291	NIIFLLEQINFGFWFFFEME
5843	A	1	225	HCNFPPLVQAILGSSNSRASRVAGTTGALQHMQLIFCIVLVEGFH RVAQAGLDLLS\LTIHPPRPPKVLGLQA
5844	A	3	147	LEIFFFFSFTFF/CRWGLTMFIRLVLFNFWPQMILLPLPLPPKVLGL QA
5845	B	47	241	GGKDFNMPLTISRITPGSKAAQSQLSQGDLVVAIDGVNTDTMTHLEA QNKIKSASYNLSLTQK*
5846	A	3	409	CGGIPSOATIFTLSTLISSVTSLNSTSFSTKVHTLSQNLVVFREPLK LTLFLTL*ASAAFIALSN*SRT*RASWGVIC*DCMSSSR\PPEDCFP K*YFCITDMPWLRRKN\FFSTFQSKCRF*GTPICQKDKTSKK
5847	A	1	2209	AAADSTMSYSVTLTGPGPWGFRLOGGKDFNMPLTISRITPGSKAAQ SQLSQGDLVVAIDGVNTDTMTHLEAQNKIKSASYNLSLTQKSKRPI PISTTAPPVQTPPLVIPHQKDPALDTNGSLVAPSPSPTEARASPGTPG TPELRPTFSPAFAFRSAFSSLAESDPGPPRASLRAKTSPEGARDLL GPKALPGSSQPRQYNNPIGLYSAETLREMAQMYQMSLRGKASGVGLP GGSLPIKOLAVDSASPVYQAVIKSQNKPEDEADEWARRSSNLQSRSF RILAQMTGTEFMQDPDEEALRRSSTPIEHAPVCTSQTATPLL PASAQ PPAAASPSAASPPLATAAAHTAIASASTTAPASSPADSPRPQASSYS PAVAASSAPATHTSYSEGPAAPAPKPRVTTASIRPSVYQVPASTY SPSPGANYSPTPYTPSPAPAYTPSPAPAYTPSPVPTYTPSPAPAYTP SPAPNYPAPSVAYSGGPAEPASRPPWVTDDSFQKFAPGKSTTSIS KQTLPRGGPAYTPAGQVPPLARGTVQRAERFPASSRTPLCGHCNNV IRGPFLVAMGRSWHPPEFTCAYCKTSLADVCFVEEQNNVYCERCYEQ FFAPLCAKCN TKIMGEVMHALRQTHWTTFCVCAACKKPFNGSLF\HM EDG\EPYCEKDYNLFSTKCHCCH\FPVEAGDKVIEALGHTWHDTCF I\CAV\CHVNL\EGQPFYSKKDRPLCKKHAHTINL
5848	A	1	537	RTRGGDVKTDLNNIEEFLEETLTPEKYPILAAKHREYNTEDIDIFYK FSAYIKNTKQONNAALERGLTKALKKVDDYLNTPLPQERDAYTCGED KGTRRKFL\DGDEL\TLA\DCNL\LPKLHV\KIVGKKYRNYHIPAD MTGLWRYLKNAYAR\DEFTNTCAADSEIELAYADVAKRLSRS
5849	A	1	654	WEGPTCSMCKVIGIHNACEEAPLHVSFVGQKTELNNCISMLVAANDR VHTIITQLEDSRRVTKENSHVNR\KLSQKFDTLYAILDEKKSELL RISQEQEKKLIFIEALIQYQEQLDKSTKL VETAIQSLDEPGGATFL LTAKQLIKSIVEASKGCQLGKTEQGFENMDFFTLDLEHIADALRAID FGTDEEEEFIEEEDQEEESTEGKEEGHQ
5850	A	141	626	LLWILIAAPPPPPVIRNGARGCSPSPPTTIPNAWGQEP RP RP RP PPSRDA\AGATPSFLPPPLRNGHRDSIHHCSGL/CLDDFESKYSFHP VEDFPAP EYKH FSED\YPSKTNRARG\APPLPPI LQVKPGLVPFL IKRMDLLFFSYGPLHSSSELLHDSS
5851	B	23	160	MQHVCAMRQVDIDAYTTCLYASGTTVPVQLPLLLMALLGLCTLVL*
5852	A	221	1645	APRMRL LAWLI FLAN\WGGA RAEPGKFWHIADLHLDP\DYKVS KDFF Q\VCQSAGSQPRGPTQAPWG DYLC DSP\WAL\INSSIYAMKEIEPEP DFILWTGDDTPHV\P\DEKLGEAAVLEIVERLTKLIREVPD TKVYA ALGNHDFHPKNQFPAGSNNTYNQIAELWKPWLSNESIALFKKGAFYC EKLPGPSGAGRI VVLNTNLYYTSNALTADMADPGQQFQWLEDVLTDA SKAGDMVYIVGHVPPGF FEKTQNKAWFREGFNEKYLKVVRKHHRVIA

10444

				GQFFGHHTDSF\RMLYDYAGVSIAMFITPGVTPWRTTLPGVVNGA NNPAI\RVFEYDRATLSLKDMMVTYFMNLSQANAQGTPT\WELEYQLT EA\HGVPHTAHSMHTVLGRI\VGDKSTLQRY\VYNS\VSYSAGVC DEAC\SMQHVCMRQVDIDATTTCLYASGTTAVPQLPLLLMALLG\L CTTRAVTCQAHSSW
5853	A	3	126	AYGDSMCA\KCVSDRIKHAFFIKEQKIIIVKVLKAQAGSQKAK
5854	C	306	386	MLFLKAIWGGSDSWSREAACPLNCNL*
5855	A	709	1199	AGVGVRGTTGRLVVRKFLTIFGNPLFLVAPPKPHSEWSQRLTY\RR RPSPYNTAL*QK/RRHRSHNQIPPRIVYLLYPRLGKHPN\SACGVC PRQEFEGVRAVRP\KV\LMRLSKTKKHVSRAVGGSNVCLNVFRDRIK RAFLI\EEQKI\VVKVLKAQAGSQKAK
5856	A	1	219	HQGYLLFNLFVEVISSEQSVLAPPVRR*TCIVANLRGVGDPDTSRHC AQGLGFKLLTLYSLLVGSESWGGARA
5857	A	112	314	LCTVCLWALKAGVGPEPERLIYSVPVFV*/HAVCAGIADGGSFSSKV RCLEIIFFYTGISIKMFLYIK
5858	C	133	237	MFMDXXXXXXGGRFKGSLGGPKFTRACKVKFFSL*
5859	C	61	177	MRIHKRLIDLHSPSEIVKQITSISIEPGVEVEVTIADA*
5860	C	100	153	MSPPKSKGPFPRFPGRF*
5861	C	142	195	MSP PQSKGPFKFPGRF*
5862	A	11	90	RPRVRALKAGVGPEPERLIYSVPVFV
5863	A	3	759	TVPLEVVLLRKVGAGGARGVIRLLDWFERPDGFLVLERPEPAQDL FDFITERGALDEPLARRFFAQVLA AVRHCSCGVVHRDIKDNLLAV LRSGELKLIDFGSGALLMDTVYTDGTRVYSPPEWIRYHRHGRSD TVWSLGVLVDMVCGDIPFEQDEEILRGRLFRER\VSPECQQLIRW CLSLRPSERPSLDQIAAHPWMLGADGGAPEQ/DCDLRLCTLDPDVA STTSSETLLRSLHLTGS
5864	A	1	422	IALGAEDAKEKRAHYRELAQAITKTCHESYARSDTKLGPEAFWFNS GREAVATQLSESYIILRPEVVESYMYLWRQTHNPIYREWGWEVVLAL EKYCRTEAGPSGIQDVYSSTPNHDNKQQSFFLAETLKDALPFQDLR
5865	A	2	435	ILAEFGSLHLEFLHLTELSGNQVFAEKVRNIRKVLRIEKPPGLYPN FLSPVSGNWWQHHVSVGGGLGDSFYEYLIKSWLMGKTMEAKNMYE ALET/HKLGPEAFWFNSGREAVATQLSESYIILRPEVVESYMYLWRQ THNTK
5866	A	1	837	MPLVMKAGENQRRQGDRLSGATVIDSLDTLYLMELKEEFQEAkawv GESFHLNVSGEASLFEVNIRYIGGLLSAFYLTGEEENRKMTEGAEKAS VFFRAYAQPSYLA VVSGDGLQEGRGEDTAQGSRGGLGMKLQRETPCW VGQSYREPVPBGVTRITTAHVRIKAIIRLGEKLLPAFNTPTGIPKG VVSFKSGNWGWATAGSSSILAEFGSLHLEFLHLTELSGNQVFAEKAS LLPTLLPAEQORDERAAATGFSEASGSSMLDQQEGSGEPGSPSYH
5867	A	1	415	TKLGPEAFWFNSGREAVATQLSESYIILRPEVVESYMYLWRQTHNPI YR\EWGWEVVLALAEKYCRTEAGPSGIQDVYSSTPNHDNKQQSFFLA ETLKYL LLLFS\EDDLSLEDWVFNTAHPLPVNHS DSSGRAGGRH
5868	A	1	1187	ESFHLNVSGEASLFEVNIRYIGGLLSAFYLTGEEVFRIKAIIRLGEKL LPFNTPTGIPKG VVSFKSGNWGWATAGSSSILAEFGSLHL\EFHL TELSGNQVFAEKVRNIRKVPQVSFEKPPGLYPNFLSPVSGNWWQHHV SPGGLTYIAEWRGGILDHKMGHLACFSGGMIALGAEDAKEKRAHY RELAVQITKTCYESYAR\SDTKLGPEAFWFNSGREAVATQLSEE/YT YILRPEVVESYMYLW\RQTHNP\SYREWGWEVVLALAEKYCRTEAGFS GDSKTCYSRHPQPRTTSRQSFFLAETLNRCLVSACNGPDTGLEARDT AETVISP AVKGSRG EKAMVRETD
5869	A	1	1561	MIFVVIILMVLSPEGGSGLDSSPFLSEANAERIVQTLCTVRGAALK PYPPTGPNFRYSHGVPHLFAYFPPGSTVSDNSFISPQLQHI FERV RQSA DFMPRWQMLRVLEELGRDWQAKVASLEEVFFAAASIGQVHQG LLRDGTEVAVKIQYPGIAQSIQSDVQNL L AVLKMSAALPAGLFAEQS

10445

				LQALQQELAWECDYRREAACAQNFRQLLANDPFFRVPVAVVKELCTTR VLGMELAGGVPLDQCQGLSODLRNQCIFQLLTCLRELFEFRMQTD PNWANFLYDASSHQVTLLDFGASREFGTEFTDHYIEVVKAAADGDRD CVLQKSRDLKFLTGFETKAFSDAHVEAVMILGEPFATQGPYDFGSGE TARRI\QDLIPVLLRHRLVSP\PEGDLWPWHRKL\AGAFLACAHLRD HIACRDHKPGHLPPLGQSPARRSHCRQPPHQRGTGPGWI PHDSLHGG FSPQSRPYPAVVPLIPSPSALGQRSPLGLPSLAWLSSLAPKTQESLG LGNSP
5870	A	1	1532	MPQALERADGSWAWVLLATMVTQGLTLGFPTCIGIFFTELQWEFQA SNSETSWFPSILTAVLHMAGPLCSILVGRFGCRVTVMGGVLAASLGM VASSFSHNLSQLYFTAGFITGLGMCFSFQSSITVLGFIYFVRRRLAN ALASMGVSLGITLWPLLSRYLLENLGWRGTFLVFGGI FLHCCICGAI IRPVATSVAPETKECP PPPPETPALGCLAACGRTIQRHLAFDILRHN TGVCVYILGVMWSVLGFPLPQVFLVPYAMWHSVDEQQAALLISIIGF SNIFLRPLAGLMAGRPAFASHRKYL FSLALLNGLTNLVCAASGDFW VLVGYCLAYSVSMSGIGALIFQVLM DIVPMDQFPRALGLFTVLDGLA FLISPPLAGLLLDATNNF*DVFOQCPSFFP*SKAPLLKGGSFPPPPQ KKEQGKQAVAADA\LERDLFLE\AKDGPQKQSRP\EIMCQS\SRQRP P\AGVNXHLWGCPASSRTSHEWLFWPKA VLQAKQTALGWNSTP
5871	A	946	1279	QTELGVRFPFTLPFLLGSARGCSGFRVLFVDVRVQPGFRKENLIQGD LFFMNRQCSSRQPRP\AGVNXHLWGMSCP/ASRDPAMKWLLWPKAVL QAK\QTALGWNSTPYLECPV
5872	A	3	297	ESCSVTQAGVHW/CNLGSLQSPS\PDSSDSPSSVSRVAGITGMCHHA QLIFVFVETGFHHGEAGLCLRLPKCWDYRCEPPRLHLGLQLNFYK DRCLA
5873	A	276	880	KADSEQHGEAKRRYSSSLAKKEVSKAPEDKKRLEDDKRKKEDKERE KKDEEKVKAEEESKKKEEEKKKHQEEERKKQEEQAKRQKEK\EAAA HMKEKEESIQLHQEAWERHHLKKELCSKNQNAPGSRPKENFFSR LDS SLKKNATFVKKLKTIPQQORDSLSHDFNGLNLSKYIAEAVASIVEAK LKISDVNCAVHLC
5874	A	2	619	LDLDFNAILIVTSLAPFFQDCMSENALHELNIELRNKLYKSYLEA FYKFCCKNHGDVTAEVMCPILEFEADRRAFIITLNSFGTELQGE\DRE TLYPNLGQLLSEGFAL\LAQAEDFDQMKNVADHYGVYKPLFEAVGGI GGKTLEDVFYEREVQMNVLAFNRQPHYGVFYAYVKLKEQEI RNIVWI AECISQRHRTKINSYIPIL
5875	A	1842	2306	GPRRLAAFLTSAGDGVYTRPVVFDCTCATFHREDAYRLPFIPTNHH PTASPE*VPPPHLGLALQLPGDPSHDIHSIGTPNSNADAPKAGGCKW TQTRSVVPNSALGRKGS THLPRIYFTLALPETKLSNCPKAPPIGL EHTSLAWALGTAD
5876	A	301	471	AQSRRRWEMEGRFGCRAERSVQRSPASPFWWAGEYSSGWAGTVCVI AQQAPHLARP
5877	A	269	394	TGAWPSGPHPAWPHGPAAAAGTTCLAQLLCLTGRQQTQCP
5878	A	524	605	VSCPGSNSPLGSSSASGASSLEFHHTA
5879	A	187	401	VSCPGSNSPLGSSSASGASSLNFLPSVPVR*SVSGLNLRVPAMARAV TISGDVTKAWVSGFASLRPVKFL
5880	A	667	890	AHTVHIRRSASRLPAGPASRLVDLSH*DLGHVP/AGFFLIMNVQQEG LADLSTSAHLLGAPLVKGSRPHAWADAW
5881	A	1	163	GLVDES FVDTSPTGPSSADATTSVRAAKKRAPYTLVGSISEPGLG\L ISWWT SN
5882	A	183	428	TNSKNSCGKKSQNTGMVIAHTKALDPSQPVTFTVNTVYAADKGALYV DVIRVNSYYSWYRNYGHLELIQLQLATQFENWCK
5883	A	1	1153	MHNSDGIEMRQKAEIGRVGGLEGIQLGVTEIVNGARMLESYNCK AELGATGLVNYQISVKCSNQFKLEVYLLNAENKVVDNQAGTQGQLKV LGTNLWWPYLMHEHPAYLYSWEGRPDGAQAVGALTGTLAV\EVWLT AQKSLGP/SDFYTLPVGLRTVAVTESQFLISGKPFYFHGVNKHEDAD IQKGFNWPLLVKDFNLLCWL GANTFCTSHYPYTEMLQICYRYGIV

10446

				VIDECPAPSGHT\GPSVPSLLARWQLFNNVSMHHHMWVVEEPVLRDK NHPAMVMWSLAKEPASFLESAGYSFKSLTMEQTARVLDLDTGEAVLQ YRSLPRGAHKTGKKRKRISYNVDLTSCQLAKEKCLKGPSSFLQSRQ ERMNSELRDN
5884	A	401	882	CTNTPPTWTRGRMVIAHTKALDPSQPVTFTVNTVYAADKALYVDVT P\LNSYYSGYRNYGHL\ELI\QLQLAA\QFENWCKTSQSHYSERVWS GNAL*GFHQDPPLMFQ*RGPGKVLEQYHLGLDQKRRKY\VVGELIW NFADFMTNQCVSFLVGNENSANL
5885	A	197	1184	ETSHQVMDRSNPVKPALDYFLNRLVNYQISVKCSNQFKLEVCLLNAE NKVVDNQAGTQCGQLKVLGANLWWPYLMHEHPASLYSWEGRPDGAQAV GALTPGALAV\EVRLTAQKSLGP/SDFYTLTPVGLRTVPVTEsqwaly VDVIRVNSYYSWYRNYGHLELIQLQLPAQFENWCKTSQSHYSERVWS GNAYRVSPGGNLPALPCCSQNLALPTFSPGTVVISLALSILGLWA QETGVLFIVVSQDPPLMFSEBYQKSLLEQYHLGLDQKRRKYVVGELI WNFADFMTNQCKWQFSAWDNVPVLI FSGCLAHS GHFGCKNIGNKGGK LV
5886	A	1	657	MADFGISAGQFVAVVWDKSSPVEALKGLVDELQVKELQREPLTPEEI QSVREHLGHESDLSLLFVQITGKKQNFVEGSSSQLKFSITKKSSPSVK PAVDPAAAKLWTLSSANDMEDDSMDLIDSDELDPEDLKKPDPASLQA ASCGEGKKRACKNCTCGLAKELEKEKSREQMSSQPKSACGNCYLGD AFRCASCPYLGMPAFKPGKALLSNSNLHDA
5887	A	76	615	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALTGNE GRVSVENIKQLLQCL\VPGSTT\LHSA\EILA\EIARILRPGG\CLF LKEPVETAVDNNKSVKTASKL\CSALTLS\GLVEVKELQREPLTPEE VQSVREHLGHESDNLFFVQITGKKPNFEVGSSMQLKLSITKKS
5888	A	102	1292	ACQYCTARIVDFEISAGQFVA*VWDKSSPVEALKGLVDKLQAF/TPG NEGRVSV\ENIK\QLLQ\SAKESSF\DIIL\SGLVPGKAPLWWSA* DFWAGNPPGFLRPGWMMFFFLKEPVETAVR*Q*AKWKTASKLCSALT SGLV/EKLKELQREPLTPEEVQSVREHLGHESDNLFFVQITGKKPNF EVGSSRQLKLSITKKSSPSVKPAVDPAAAKL\WTLSSANDMEDDSMCI FCGCSLTHRWPLEHVRLNMMINQKEDRVDTFFTLDSKFPLEACSHF SFSLAETTTVSLIALNTLQDLIDSDELDPEDLKKPDPASLRAASCG EGKKRACKNCTCGLAELEKEKSREQMSSQPKSACGNCYLGD AFRC ASCPYLGMPAFKPG\EKVLLSDSNLHDA
5889	A	1	747	MGFRYVAQAGLELLSSDPSIPSSKTLQEONDQSYSTLPVFPEVALH TLLWGEDANNSKVKEQLQREPLTPEEIQSVREHLGHESDNLFFVQITG KKPNFEVGSSRQLKLSITKKSSPSVKPAVDPAAAKLWTLSSANDMED DSMDLIDSDELDPEDLKKPDPAS\LRA\ASCGEGKKRACKNCTCG LAEEL\EKEKSREQMSSQPKSA\CGNCYRGAMPSCASCYPYLGMPAF KPGKLVLLSDSNLHDA
5890	A	2	152	YRHMAPHPTNFLKK/FFCRDGGVLMLPRLVFNWSPQGILLPQPPKVL GLQV
5891	A	1	581	EKQSCKSCGETFNSITKRRHHCKLCGAVICGKCSEFKAENSRQSRVC RDCFLTQPVAPESTEKTPTADPQPSLLCGPLRLSKSGETWSEVWAAI PMSYPQVLHLQGGSDGRLPTIPLPSCKLSVPDPEERLDSGHVWKL QWAKQSWYLSASSAELQQWLETLSAAHG\DTAQ\DSPGALQLQVP MGAAAP
5892	A	1	1459	MKENFKHRHVAFISSQEAQEDSREEEDRLSRYFLFLELSYKTT GLNREPTVSLNSKSGTPMDQNEHSHWGPHAKGQCASRSELRIILVGK TGTGKSAAGNSILRKQAFESKLSQTLTKTCSKSQGSWGNREIVID TPDMFSWKDHCEALYK\EVQRCYL VAGP\KPHVLLLVTQLGRYTSQD QAAQVRKEIFGEDAMGHTIVLFTHKEDLNGGSLMDYMHDSDNKALS KLVAACGGRICAFNNRAEGSNHDDQVKELMDCIEDLLMEKNGDHYTN GLYSLIQRSKCGPVGSDERVKEFKQSLIKYMETQRSYALAEANCLK GALIKTQLPKVDKTTKIGKKQSRKTGNSKKQSTSPPPKERSSSPAME QSWTENDFDELREEGFRRSHYSELPEDIQTEGREVENFEKSLEECIT

				RITHTEKCLKELMELKTKARELREECRSLRSQCDQLEERVSAEMDEM NEMKREGKFKEKNKKK
5893	A	2	1126	SYKTTGLNREPTVSLNSKSGTPMDQNEHSHWGPBAGQACASRSELRI ILVGKTGTGKSAAGNSILRKQAFESKLGSQTLTKTCSKSGSWGNGRE IVIIDTPDMFSWKDHCEALYKEVQRCYLLSAPGPHVLLLTQLGRYT SQDQQAQRVKEIFGEDAMGHTIVLFTHKEDLNGGSLMDY\MHDSN KV\LFKLVAAACGGRICAFNNRAEGSNQDDQVKELMDCIEDLLMEKNG DHYTNGLYSLIQRSKCGPVGSDERVKEFKQSLIKYMETQRSYT\ALA EANCLKGALIKTQLCVLFCIQLFLRLIILWLCLHSMCNLFCCLLFS MCNLFCSLLFIIPKKLMIFLRTVIRLE\RKTPrFIVTDPRLFLTSP I
5894	A	1	303	PCGARQCGGPPPR/LCSSRRTSQELLSKPVPPPAPGGPASRVGRGS VSGALSPWNGERQHHRGVVLTHPQSPNHQAGSPNPNTROALATLSV PNKPFIE
5895	A	1	284	ATESCSVAQGVQWCDLSSLQAPPPGFTPFSSLSLQGSWDYRSPPH PANFFVVLVE/MASASQSAGITGVSHRTRPRIAIFNLTTENTNGSVDE D
5896	A	3	338	GIHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYM GHPDQNEQGYLLGSVAMQAEKFPS/EIYPQERHSIRVPESGEHYELH LLHYLQENLGSRIAALKVI
5897	A	1	1200	MKNPAISITENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLT QRQVNITVQKKVSQWVERLTQKEKRPLFLAPDFDRWLDESDAEMELR AKVQLVNNRFGKVYFRLNLTASLGYYVVVIDNRGSCHRGLKFEGAF KYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMAL MQRSDIFRVAIAGAPVTLWIFYDTGYTERYMGHDPDQNEQGYLLGSVA MQAEKFPSEPNRLLLLHGFLENVHFAHTSILLSFLVRAGKPYDLQI AFCDNFAFYICLELANMEEDARSAGVATFVLQEEFDRYSGYWCPKA ETTPSGGKILRILYEENDESEVEIIHVTSPMLETRRADSFYRPKTGT ANPKVTFKMSEIMIDAEGRGNFCK
5898	A	2	594	NRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRV GIHGWSYGGYLSLMALMQRSDIFRVAIAG\APVTLWIFYDTGYTERY MGHPDQNEQGYLLGSVAMQAEKFPSEPNRLLLLHGFLENVHFAHTS ILLSFLVRAGKQ\YDLQIYPQERHSIRVPESG\EHYELHLLHYLQEN LGSRIAALKVI
5899	A	74	250	KTLWMVNRTVLGAGISQQLSAGTAT/DVSKHRLQGFI PCRIPS/ASP QTORKFSLQFHRNC
5900	A	258	552	CMVFHD/VSGACCCNGETTGKISGGGNQLGSSPIGGPNPS/SGSSQT SISGDVVEACCSVLSMVCADPVYKVYVAALLLERELPGVFSGKIFNL LSDCLLW
5901	A	1	1660	MDDRPEERMIREKLKATCMPAWKHEWLERRNRRGPVPPNNKWSPPRI QIKHSRNPPIYPFTLET KDWVSKNQIKQAAQQQTVOQQPLAGSRN QESNFNLTHTYGTQIIPAYKDLAEPWQVATPYLMAINAASSLRTC NNHRPASISYLDVRLCHKRPSKSSVSALITVCSSFAGFMRPPYSL RATVHVSCSPLAALHSIAPSSVKVRVQACGTSASPQIRIMAFRYPGS RAIFPIIPCSAKPVRMSTCSWRATVIAMSLRLTEVLGQQNRYGSNNP YAHGANLCGELPLELYVFPFIRPSFSTRPKTVAVDIASIFKIQQFPH FTTPQLIDLVRFNPSVLLRVGALFHQCSISRSPLRRRSLSDATSSRA RKAVLTRTFGLCYADLKNHLNATFVAVLKTGPLAAMQEYRPEEIES KVQLHWDEKRTFEVTEDESKEKYCLSMPLPYPSGRLHMGHVRNYTIG DVIARYQRMGLGNVLQPIGWDAFGLPAEGA AVKNNTAPAPWTYDNIA YMKNLKMLGFGYDWSRELATCTPEYRWEQNSSPS
5902	A	1	1947	MALRRLSHDVSGALLLANGESTGNSSGGSSPSGGATSGSSQTSIS GDVVEACCSVLSMVCADPVYKVYVAAL\QCMLLVLTEDPSSHFTMR RRLM/AYADEVEIAEAIQLGVEDTLDGQQDSF\CRHLFPPTTIWKPQR TVP/LECTIHLEKTGKGLCATKLSASSEDISERLASISVGPSSSTTT TTTTTEQPKPMVQTKGRPHSQCLNSSPLSHSOLMFALSTPSSSTPS

				VPAGTATDVSKHRLQGFI PCRIPSASPQTQRKFSLOFHRNCPENKDS DKLSPVFTQSRPLPSSNIHRPKSRPTPGNTSKQGDPSKNSMTLDLN SSSKCDDSGCSSNSS/NCCYT\SDETVFTPVEEKCRLDVNTLNSS IEDLLEASMPSSDTTVTFKSEVAVLSPEKAENDDTYKDDVNHQKCK EKMEAEEREAALAIAMAMSASQDALPIVPQLQVENGEDI III IQQDMTF FRHIIPPIQWIYKKESANLLIDSTGQRLRIADFGAAARLASKGTGAG EFQGLLGTTIAFMAPEVLRGQQYGRSCDVWSVGCAI IEMACAKPPWN AEKHSNHLALIFKKLLDFANTACDGDKESEVEDVETDSGNSPEDLRK EIMIGLQYQAEIPPYLGEYDGNKDS PQPKMTGVQNAKEVLST
5903	A	1	4491	PSPEAGGGGALKASSARAAAAGLLREAGSGGRERADWRRRQLRKVR SVELDQLPEQPLFLAASPPASSTSPSPEPADAAAGSGTGFPVAVPPP HGAASRRGAHLTESVAAPDSGASSPAAAEPEGKRAPAAEPSPAAAPA GREMENKETLKGHLKMDRPEERMIREKLKATCMPAWKHEWLERRNR RGPVVVKPI PVKGDGSEMNHLAAESPGEVQASAASPAKGRSPSPG NSPSGRTVKSES PGVRRKRVSVPVFQSGRITPPRRAPSPDGFSPYSP EETNRRVNVKVMRRLYLLQQIGPNSFLIGGSDSPDNKYRVFIGPQNS CAHGTFCHLLFVMLRVFQLEPSDPMWLWRKTLKNFEVESLFQKYHSR RSSRIKAPSRNTIQKFVSRMSNSHTLSSSSTSTSSSENSIKDEEEQM CPICLLGMLDEESLTVCEDGCRNKLHHHCMSIWAEECRNRREPLICP LCRSKWRSHDFYSHELSSPVDS PSSLRAAQQQTVOQQPLAGSRRNQE SNFNLTHYGTQQIPPAYKDLAEPWIQVFGMELVGCLFSRNWNVREMA LRLSHDVS GALLLANGE STGNSGGSSGSSPSGGATSGSSQTSISGD VVEACCSVLSMVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLO RLLPVVDITLVKCADANSRTSQLSISTLLELCKGQAGELAVGREIL KAGSIGGVDYVLNLCILGNQTESNNWQELLGRCLIDRLLEFPFAE FYPHIVSTDVSAEPVEIRYKLLSLLTFALQSIDNSHSMVGKLSRR IYLSSARMVTTVPHVFSKLEMLSVSSVSTHFTMRMRRLMAYADEVE IAEAIQLGVEDTLQRQQHNSFCRHLFPTTIWKPORTVPLECTVHLEK TGKGLCATKLSASSEDISERLARISVGPSSTTTTTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHHSQLMFPALSTPSSSTPSVPAGTATDVSKH RLQGFIPCRIPSASPQTQRKFSLOFHRNCPENKDSDKLSPVFTQSRP LPSSNIHRPKSRPTPGNTSKQGDPSKNSMTLDLNSSSKCDDSGFLS SNSSNCCYTSDETVFTPVEEKCRLDVNTLNSSIEDLLEASMPSSDT TVTFKSEVAVLSPEKAENDDTYKDDVNHQKCKEKMEAEEREAALAI MAMSASQVALPIVPQLQVENGEDI III IQQDTPETLPGHTKAKQPYRE DTEWLKGOQIGLGAFFSCYQAQDVGTGTLMAVKQVTVYRNTSSEQEE VVEALREEIRMMSHLNHPNIIIRMLGATCEKSNYNLFIEWMAGGSVAH LLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDST GQRLRIADFGAAARLASKGTGAGEFQGLLGTTIAFMAPEVLRGQQY RSCDVWSVGCAI IEMACAKPPWNAEKHSNHLALIFKIASATTAPSIP SHLSPGLR\ DVALRCLRTSTFTDRPPSRELLKHPVFRTTW
5904	A	1940	2062	RPLKSQETTETWMKLETIILSKLSQRQKTKHRMFSLIGGN
5905	A	785	892	PKQHGTWMKLETIILSKLSQGQKTKHRMFSLIGGN
5906	A	1	2745	MGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLIDIYRTLHPKST EYTFFSAPHHTYSKIDHIVGSKALLSKCKRTEIITNYLSDHSAIKLE LRIKNLTQSHSTTWKLNLLNDYWVHNEMKSEIKMFFETNENKOTT YQNLWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKEQEQT HSKASRRQEITKIRAELEIETQKTLQKINESRSWFFERINKIDRPL ARLIKKKREKNQIDTIKNDKGDITDPTEIQTIREYYKHYANKLE NLEEMDKFLDTYTLPRLNQEEVESLNRPI TGAEIVAIINSLPTKSP GPDGFTAIFYQRYKEELVPFLKLQFQIEKEGILPNSFYEASIIILIP KPGRDTTKKENFRPISLMNTDAKILNKILANRIQQHIKKLIHHDQVG FIPGMQGWFNIRKSINVIQHINRTKDKNHMIIISIDAFAFDKIQPPF MLKTLNLELEKTTLNF IWNQKRARIKSI LSQKNKAGGITLPDFKL YYKATVTKTAWYQNRDIDQWNRTEPSEITPHTYNCLIFDKPEKNK KWGKDSL FNKWCWENWLAICRKLKLDPLTPYTKINSRWIKDLNVRP

				<p>KTIKLEENLGITIQDIGMGKDFMSKTPKAMATKD KIDKWDLIKLS FCTAKETTIRVNRQPTTWEKIFATYSSDKGLISRIYNELNQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAKHKMKCSSSLAIREMQIKTTMRY HLTPVRMAI IKKSGNNRCWRGCGEIRTLHCWWDCKLVQPLWKS VWR FLRDLELEIPFDPAIPLLLGIYPNDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKMWHIYTMEYYAAIKNDEFMSFVGTWMKLEII ILSKLSQEQT KHRIFSLIGGN</p>
5907	A	1	3297	<p>MGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLIDIYRTLQPKST EYTFFSAPHHTYSKIDHIVGSKALLSKCKRTEIITNYLSDSHSAIKLE LRIKNLTQSRSTTWKLNLLNDYWVHNEMKAEIKMFFETNENKDTT YQNLWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKEKQEQT HSKASRRQEITKIRAELEIETQKTLQKINESRSWFFERINKIDRPL ARLIKKKREKNQIDTIKNDKGDITTDPTIEIQTIREYYKHYANKLE NLDEMDKFLHTYTLPRLNQEEVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLFQSIEKEGILPNSFYEASIIILIP KLGRDITTKENFRPLSLMNIDAKILNKILAKRIQQHIKKLIHHDQVG FIPGMQGWFNIRKSINVIQHINRGKDKNHMII SIDAFAFDKIQQPF MLKTLNKLIGIDGYFKIIRAIYDKPTANIILNGQKLEAFPLKTGTRO GCPLSPLLFNIVLEVLARAIQKEKEIKLISNFSKVSQYKINVKQSQA FLYTNNRQTESQIMSQLPFTIASKRIKYLGIQLTRDVKDLFKENYKP LLKEIKEDTNKWKNI PCSWVGRINIMKMAILPKVIYRFNAIPIKLP TFFTELEKTTFKFIWNQKRACITKSILSQKNKAGGITLPDFKLYYKA TVTKTAWYQYQNRDIDQWNRTEPSEIMLHIYNYLIFDKPEKNKQWGK DSL FNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIK TLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELNQIYKKKTNNPI KKWAKDMNRHFSKEDIYAAKHKMKCSSSLAIREMQIKTTMRYHLTP VRMAI IKKSGNNRCWRGCGEIGTLLHCWWDCKLVQPLWKS VWRFLRD LELEIPFDPAIPLLLGIYPKDYKSCCYKDTCTRMFIAALFTIAKTWNQ PKCPTMIDWIKMWHIYTMEYYAAIKNDEFMSFVGTWMKLEIIILSK LSQEQT KKHGIFSLIGGN</p>
5908	A	1	2202	<p>MKAEIKMLFETNENKDTTYQNLWDTFKAVCRGKFRTLNNAHKRKQERS KIDTLTSQLEKEKQEQTTHSKASRRQEITKIRAELEIETQKTLQKI NESRSWFFERINKIDRPLARLIKKKREKNQIDAIKNDKGDITTDPT IQTIREYYKHYANKLENLEEMDKFLDITYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKSPGPDGFTAKFYQRYKEELRIKYLGIQLTRD VKDLFKENYKPLLEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIY RFNGIPIKLPITFFTELEKTTLKFIWNQKRARVAKSILSQKNKAGGI MLPDFKLYYKATVTKTAWYQYQNRDIDQWNRTEPSEIMPHIYNYLIF DKPEKNKQWGKDSL FNKWCWENWLAICRKLKMDPFLTPYTKINSRWI KDLNVRPKTIKLEENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIGVNRQPTKWEKIFATYSSDKGLIFRIYNELK QIYKKKTNNPIKKWAKDMNRQFSKEDIYAAKHKMKCSTSLAIREMQ IKTTMRYHLTPVRTAI IKKSGNNRCWRGCGEIGTLLHCCWWDCKLVQ LWKS VWRFLRDLELEIPFDPAIPLLLGIYPKDYKSCCYKDTCTRMFTA ALLTIAKTWNQPKCPTMIDWIKMWHIYTMEYYAAIKNDEFMSFVGT WMKLEIIILSKLSQEQTKQRI FSLIDGN</p>
5909	A	1	2868	<p>MKAEIKVFFETNENKDTTYQNLWDTFKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKEKQEQTTHSKASRRQEITKIRAELEIETQKTLQKI NESRSWFFERINKIDRSLARLIKKKREKNQIDTIKNDKGDITTDPT IQTIREYYKHYANKLENLEEMDKFLDITYTLPRLNQEEVESLNRPI TGAEIVAIINSLPTKSPGPDGFTAIFYQSWAETQPKKENFRPISLM NIDAKILNKILAKRIQQHIKKLIHHDQVGFIPGMQGWFNIRKSINVT QHINRAKDKNHMII SIDAFAFDKIQQPFMLKTLNKLIGIDGYFKIIR RAIYDNPTANIILNGQKLEAFPLKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADNMIVYLENPIVSAQNLLKLISN</p>

				FSKVSQYKINQKSQAFLYTNNRQTESQIMSQLPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSGGRKNQYRENGHT AQELEKTTTLKFIWNQKRAHIAKSILNQKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQWNRTEPSEITQHIYSYLIFDKPEKNKQWGD LFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTPKAMATKDKIDKDWLVKLKSFCTAKE TTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKHKMKCSSLAIEMQIKTTMRYHLTPVR MAI IKKSGNNRCWRGCGETGTLHCWWDCKLAQPLWKSVMRFLRDL LEIPFDPALPLGIYPNDYKSCCYKDTCTRMFIAALFTIAKTWNQPK CPTIIDWIKMWHIYTMYYAAIKNDEFVSFVGTMKLEIIILSKLS QEQTTHRIFSLIGGN
5910	A	1	3237	MKAIEIKMFFETNENKDTTYQNLWDAPKAVCRGKFIALNAHKRQKERS KIDTLTSQLEKEKQEQTHSKASRRQEITKIRAELEIETQKTLQKI NESMSWFFERINKIDRLRLARLIKREKNQIDAINDKGDITTNPTE IQTIREYYKHLANKLENLEEMDKFLDTYALPRLNQEEVESLNRPI TGAEIVAIINSLPTKSPGPVGFATAEFYQRYKEELVPFLLKLFQSIE KERILPNSFYEASIIVIPKPGRDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQGWFNICKSVNVIQHINRTKDKNH MIISIDAEKAFDKIQPPMLKTLNKLIGDGYFKIIRAI CDKPTANI ILNGQKLEAFPLKTGTROGCPLSPLFNIVLEVLARAIQKEKEIKGI QLGKEEVKLSLFADDMIVYLENPIISAQNLLKLISNFSKVSQYKIN QKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDMKDLFK ENYKPLLKEIKEDTNKWKNI AFSWVGRINIMKMAILPKVIYRFNAIS IKLPMTFFAELEKTTTLKFIWNQKRARITKSILSQSKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQCNRTEPSEIMPHIYNLYIFDKPEKN KQWGDLSLFNKWCWENWLAICRKLKLDPFLTPYTKIHSRWIKDLNVR PKTIKTL EENLGITIQDIGMGKDFMSKTPKAMATKDKIDKDWLKLK SFCTAKETTIRVNRQPTKWEKIFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAAKHKMKCSSLAIEMQIKTTVR YHLTPVRMAI IKKSGNNRCWRGCGEIGTLHCWWDCKLVQPLWKSVM RFLRDLLEIPFDPALPLGIYPEDYKSCFYKDTCTRMFIAALFTIA KTWNQPKCPTMIDWIKMWHIYTMYYAAIKNDEFMSFVGIMKLEI IILSKLSEEQTKHCIFSLIGKRTFAGKLPVVKPSDLVRLIHYHENS MGETDPIIRLSPPSYALDWTGLLQLKILDGGLPVTSPVDPGSKKNH
5911	A	1	2001	MPHIQVMLMQEMDSHSLGKLCYPYGFABYSPTSSCFHGFVLSVCSSR DKATQVRDALVRQVIVNGGIVLDQFAVHDRVADLIDLVDLSAMM LCGVPTTGDPFVAFALGHPDDFDHLILPKHLVDRYLLEPLLGPVQL LSHSASVHLDLHQFCSDFS YGIQLTRDVKDLFKENYKPLLKEIKEDT NKWKNI PCSWVGRINIMKMAMLPKVIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIKSSLSQKNKAGGITLPDFKLYYKATVTKTAWY YQNRDIDQWNRTEPSEITPHIYNLYIFDKPEKNKQWGDLSLFNKWCW ENWLAICRELKLDPFLTPYTKIHSRWIKDLNVRPKTIKTL EENLGIT IQDIGMGKDFMSETPKAMATKAKIDKDWLMKLKSFCTAKETTIRVNR QPTKWEKIFTTYSSDKGLISRIYKELKQIYKIKTNNPIKKWAKDTNR HFSKEDIYAAKHKMKCSPSRAIEMQIKTAMRYHLTPVRMAIITKS GNNRCWRGCGEIGTLHCWWECKLLQPLWKSVMQFLRDLLEIPFDP AIPLLGIIYPKDYKSCCYKDTCTRMFIVALFTIAKTWNQPKCPTMIDW IKMWHIYTMYYAAIKNDEFMSFVGTRMKLEIIILSKL SQGQKAKH RIFSLIGGN
5912	A	1	2982	MVDIHKPYHPFTWLGVSVSPCGPVLRYSNFFLASSTVQVELLVCGGS SSGSSEQGFVTMRTELNQEEVESLNRPI TGSEIVAIINSLPTKKS PDGLTAEFYQRYKEELVPFLLKLFQSIEKEGILPNSFYEASIIILPK PGRDTTKKENFRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINV IQHINRAKDKNHMIISIDAEKAFDKIQPFM LKTNLKLIGDGYFKIIRAIYDKPTANIILNGQKLEAFPLKTGTROG

				CPLSPLLFNIVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVY LENPIISAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWN IPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKF WNQKRARIKSIKSNKAGGITLPDFKLYYKATVTKTAWYQNRD IDQWNRTEPPEIMPHIYNYLIFDKLEKNKQWGKDSLNFKNWESWLA ICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIKTLEENLGITIQDIG MGKDFMSKTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTW EKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDMNRHFSKE DIYAAKHKMKCSSSLAIREMQIKTTMRYHLTPVRMAIIKSGNNRC WRGCGEIGTLLHCWWDCKLVQPLWKS VWRFLRDLELEIPFPAIPL GIYPNDYKSCCYKDTCTRMFIAALFTIAKTWNQPKCPTMIDWIKMW HIYTMYYAAIKNDEFMSFVGTWMKLETIILSKLSQEOKTKHRIFSL IDRLDQRNLLGSSGAFPLSHDLAERDQASGTGKASPHRQLNPSHPA QPSVDSGLPTANHNTASATFSLPCLWAKAPPAGHLEHGTFRVKSFLG HSPAINQ
5913	A	1169	3269	VHCRFWILALCQMSRLQKSPLFNIVLEVLAKAIKQEKEIKGIQLGK EEVKLSLFADDMIVYLENPTVSAQNLLKLSNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSGLPFTITSKRITYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKF IWNQKRALIAKSSLSQKNKTGGITLPDFKLYY KATVTKTSWYQYQNRDIDQWNRTEPSEIMPHIYNYLIFDKPDKNKQW GKDSLNFKNWESWLAICRKLKLDPFLTPYTKINSRWIKDLHVRPKT IKTLEENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKLSFC TAKETTIRVNRQPTWEKIFATYSSDKGLISRIYNELKQIYKKKTNN PIKKWAKDMNRHFSSEEDIYAAKHKMKCSSSLAIREMQIKTTMRYHL TPVRMVIKSGNNRCWRGCGEIGTLLHCWWDCKLVQPLWKS VWQFL RDLELEIPFPAIPLGIYPEDYKPCCYKDTCTRMFIAALFTIAKTW NQPKCPTMIDGIKMWHIYTMYYAAIKKDEFMSF\AGTWMKLETIIL LRKLSQOQKTKHRMYSLIGGNLTMRFTGHSGSHHTPGPIMRCCAGG GIALGEIPNVNDELMTANQHGTCTIPMQQNCTLTCTTLKLV
5914	A	2821	5794	DAFKAVCRGKFIALNAHKRQERSKIDTLTSQLEKEQEQTTHSKAS RRQETIKIRAELEIETQKTQLKINESRSWFFERINKIDRPLARLIK KKREKNQIDTIKNDKGDITTDPTETIQTIREYYKHLKANLEEM DTFLDITYTLPRLNQEEVESLNRPTGAEIVAIINSLSSTKKSPPGDPGF TAEFYQRYKEELVPFFLKLFSIEKEGILPNSFYEASIIIPKPGRD TTKKENFRPISLMNIDAKILNKILANQIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDKNKMIVSIDAEKAFDKIQPPFMLKTI NKIGIDGMYFKIIRAIYDKTTANIILNGQKLEAFPLKTGTROGCPLS PLLFNIVLEFLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVLENP IVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELP FTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTKKWNIPCS WVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKF IWNQK RARITKSILSQKNKAGGITLPDFKLYYKATVTKTAWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPDKNKKNKQQRGKDSLNFKNWESWLA ICRKLKLDPFLTPYTKINSRWIKDLNVRPKTIKTLEENLGNTIQDIG MGKDFMNTPKAMVTAKIDKWDLTCLKSFCTAKETTIRVNRQPTW EKIFTIYPSDKGLISGIYNELKQIYKKKTNNPIKKWVKDMNRHFSKE DIYAAKHKMKCSSSLAIREMQIKTTMRYHLTPVRMAIIKSGNNRC WRGCGEIGTLLHCWWDCKLVQPLWKS VWRFLRDLELEIPFPAIPL GVYPKDYKSCCYKDTCTRMFIAALFTIAKTWNQPKCPTMIDWIKMW HIYTMYYAAIKKDEFMSFVGTWMKLETIILSKLFQRRKTKHCMFSL IGGN
5915	A	457	651	LVVKTFFHQKKIFGLTSYSGMFVGTWNGNTKVAIKTLKPGTMSPESE LEEAQIMKKLKHDKLVQL
5916	A	3	639	KGDHVHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCRL

				VVPCHKGMPRLTDLVSKTKDVWEIPRESLQLIKRLGNGQFGEVWNGT \WN\GNTKVAIKTLKPGTMSPEFLEEAIQMKKLKHDKLVLQYAVVS E\EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAY IERMNYIHRDLRSANILVGNGLICK
5917	A	1	2523	MHWKRPWQVGGYLTLAATDTVQMLNYMSVRQLSYLNFNTWQFLSWS QMPTQQAYPCVTHTHTPPVLGQMACCISNQRRTAALIGTRPERNVH VNLROGFVVNAHEPWWNEKVARQEPEDAGRGAVNRAWGFSRPLIHWS EGPQAAALGDRDPRWLPYHHAALSGSHAAALSLAPSRSSALAVLIA LLPAAQLHHHVPRSKACDIAYVGGHRRQVWYGQEDGQQILVVPVLLS TTQQKVSALWADRLE\RALLARSLAARLAPPSVHPCWV/VTFPSAVA WINAGSLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRD LRSANILMGNGLICKIADFGLARLIEDNEYTARQDPTRSRGHRSSAM NPYGSRAGRGRVESGLTLQMAATQVTVQWSAHLVSGEAVAWNTFPTA NQDRKELAAALSCSCPSTLCFMLLGLYPTLDHLQVRQSHCLTVSCAWQ GLKPLFLWLAINKAEIICLTLLKYWQADCELLASAYQHAHWTCARTQ SSNLSIADIESLELVVKTFFHQKIFGLTSYSGMFVGTWNGNTKVAI KTLKPGTMSPEFLEEAIQMKKLKHDKLVLQYAVVSEEPYIVTEYM NKGGEDEGTIREEIGQVKAPRRDNIPKPSAAHAAQLVMWHEVRLTRAL CPFWGWLDSWHHFCVELHPTHPLITQKPKGKELTDVVHRSQFSGAQS RVESIWIQRSMTKTPGAKLQKQAYQGVSNPHHHHTGQQLKAVPHPL MEAPDAIDGYRKILVNFTKIYSFAVTNSDYEQPTLVAIGYRCGDP QGTERRTQKPPTEVVTTQLQPQPWLLRGHVGLVLLDHPIFKEKP
5918	A	74	1002	SNESNAVALSTVERTARRDAPQHGTQPRGLPRSSEPHPAQRTAATGK ARQRRKTASAGAREGRRRLAGTTSIPGP/FSAPVPHRRHPQEPRQG PRTPRRAEEKRDQMASHVECRPLGVFECELCTLTAPYSYVGQKPNT QSMVLLEESYVMKDPFTSDKDRFLVLGSCCSLCSRLVCVGPVGV EQHGFHSVPSVLRVTPSEKSLSICHRLTHTKGSCINSQGDDEMGGG RSLRSVAWEYLRLMEELVVQEKLGKEDCKGNSARLGEKESSIKEDPQ PARFSDGPGLSECCSDVTERDDLLQGGSS
5919	A	3	401	RSRGTRAAMASHVECRPLGVFECELCTLTAPYSYVGQKPNTQSMVL LEESYVMKDPFTSDKDRFLVLGSCCSLCSRLVCVGPVGV\CSLFYSKR FCLPCVRENINAFPEIRQDLEKRAKPSKRTPSQPGSRT
5920	A	96	615	NIILRNSIITSRKIKYTTLSTHISIFLFPQISPQMSLIGFFYESEAN KGSHPFPYVVSCLNLAETT/SLFYIICFLKSPDQGGQNAQTMAYNITP LRRAL\VECVQDQFG\FINYEVG\DSKK\LFFHMKEV/SRDGQCSAWN VWPSLLRGPKA\VAAPRP\DR\VSRLKNITL\D\DAADPR
5921	A	1497	2853	EMVLVSSSVWIVMFCSSSTSVKFWMGTSSSHIADEVEFTVVPDMLSAQ RNHAIRIKKLPKGTVSFHSKSDHRFLGTVEKEATFSNPKTTSPNKGK EKEAEDGIIAYDDCGVKLTIAFAQKDVEGSTSPQIGDKVEFSISDKQ RPGQVATCVRLGRNSNSKRLLLGYVATLKDNGFIETANHDKEIFF HYSEFSGDVDSLELGMVEYSLSKKGKGNKVSABKVNKTHSVNGITEE ADPTIYSGKVIRPLRSVDPTQTEYQGMIEIVEEGDMKGEVYPFGIVG MANKGDCLQKGESVKFQLCVLGQNAQTMAYNITP\LRRAT\VECVKD QFGFI\NYEVGDSKKL\FFH\VKKVQDG\IELQA\GDEVEFS\VLIN PAATGKVQAPC\NVWR\VEGPPRLQAP\RPDRVGSIRLKNIT\LD DASAPR\LMV\LRQPKGDQITSMGF\GAERKI\ROAGVID
5922	A	23	206	GVGQRVSGTGRTRAVSPHPWDGFPWPGRLGAVASTANLLDDVEGHA CGEAGGEIEAPTSL
5923	A	1	267	ALFRDKLKHMGKSTRRLKLFELARAFSEKTKMRKSKRKHLKHKQSRIG AAASTANLLDDVEGHACDE\NFRGQASRRAPQGGGRPCREGQ
5924	A	1	267	FFFFFLTIDILLF/CLFLRWSFTVTQAGVQWSDLGSLQPPPPRLKQFS CLSLSSWDHKCLAPRPANFCSFSKDGVS PCWPGWSQTPHLR
5925	A	1	326	MGTSSGSWPRWSVTAMPPTSMRPCSRRSSSCWPCIPRLPASTAP*SM RPHSGPRMTTRSCCLKT/RSYADGYSPPLNVAQRYVVA/W*GTQEKVM PPGRLAIPQRHRAGQQR
5926	A	366	489	QETTPDLETWKWLP*RPWMMSSGFWARWSVTAMPPTSE

10453

5927	A	228	756	KVVQTEERKKANQFDAPISIYEVHLGSWRRHTDNNFWLSYRELADQL VPYAKWMGFTHLELLHINEHPFDGSGWGYQPTGLYAPTRRFGRTRDDFR YFIDAHAAGLNVILDWVPGHFPTDDFALAEFDGNTLYEHSDSRESY HQDWNTLIYNYGRREVSYFLVGNALYWMNRFID
5928	A	1	2709	MGLDDGVARNLGLALSARLADAVAGDVISALLVNAVGIIGLIGLFA TAVAKIVGERWFARRHFFDIAPWMEIEIAIKKRGMKLMRHFTGDRRFA AARYAHQDVNVVIMVSRAQSGAPTIQELKMLRVTVIGNIVQPDNIRS NIHPCCLKCISIRHEYAPAGVQRQYCPSAHAASARSQVAPSPDQCHD RGNRQSPYRQELLTPDADIQTTPRRPPGHHSYRTRHPAADIPAAPGES VQYRKKQTELHTGIFNVVTIRQFLLGFRLVKRVTVTYRHARDGKARK QHRVNRQTCHHQEEQNPVQVGNHPTRTDWHRKGGQQRGKGNHRCQ GKDDAIREFRDPVFFKEHFDHVRNQLERTAPANTVRSVTVLEQTQQA TFAKAHECPAGDNHQQDHHRFEDDPQDARQPAPEHADISSEATCLAA GLGEFTGAGRDMGGLGFYKWNLGWMHDTLDYMKLDPVYRQYHHDKL TFGILYNYTENFVLPPLSHDEVVHGKKSILDRMPGDAWQKFANLRAYY GWMWAFPGKKLLFMGNEFAQSREWNHDASLDWHLLEGGDNWHHGVR LVRDLNLTYRHHKAMHELDFOFYGFELVVDKERSVLI FVRDKEG NEIIVASNFTPVPRHDYRFGINQPGKWEILNTDSMHYHGSNAGNGG TVHSDEIASHVRQHSLSLTLPPLATIWLGVNFTLFSAHAERVELCVF DANGQEHRYDLPGHSGDIWHGYLPDARPGRLRYGYRVHGPWQPAEGHR FNPAKLLIDPCARQIDGFKDNPLHAGHNEPDYRDNAAIAPKCVV VDHYDWEDDAPPRTPWGSTIIEAHVKGLTNLHPEIPVEIRGTYKAL GHPVMINYLIQLGITALELLPVAQFASEPRLQRMGLSNYWGKAGGD VCAASGVCLL
5929	B	76	925	XQCFFLSADSRIAEELLTELHQLSKQTQEERSRSEHNLVNIQKTHERM QTENKISPYRKLRLGLYTAKADAEACNILRKALDMIAEIKSLLE ERRSAAKIAGLYNDSEPPRKTMRRGVLMTLQQSAMTLPLWIGKPGD KPSQPSSPLVLAASKALQVLLGFLLYNLPLCLSHRHHPPQFLSRLRLPL YSGDCISQECNLVFLADVWFGFLPSIYLVFLIILYEGLLGGAAYV NTFHNIALETSDEHREFAMAATCISDTLGISLSGLLALPLHDFLCQL S*
5930	A	3	1066	GSWGYQPTGLYAPTRR\GLNVILDWVQAHFPTDDFALAEFDGNTLYE HSDPREGYHQDWNTLIYNYGRREVSNFLVGNALYWIERFGIDALRVD AVASMIYRDYSRKEGEWIPNEFGGRENLEAIEFLRNTNRILGEQVSG AVTMAEESTDFPGVSRPQDMGGLGFYKWNLGWMHDTLDYMKLDPVY RQYHHDKLTFGILYNYTENFVLPPLSHDEVVHGKKSILDRMPGDAWQK FANLRAYYGWMWAFPGKKLLFMAAKIAGLYNDSEPPRKTMRRGVLM LLQQSAMTLPLWIGKPGDKPPPLCGAIPASGDYVARPGDRLLARLKP LNGERAVDLSLEGGQVTAIATQQGMR
5931	A	53	507	FFVFLVEMGFHHVQAGLELLNSSLDPSSASQSAG/IYRCEPLCPAF FFFSETESRSVAQAVVQWCDLSSLQPPPHFKRFFCLSLSSWDYR HVPPCLANFCIF\VEAGFHHVQAGHKLLISSDPPASVSQSAGITGM SHCIQPHSPVFS
5932	A	1	346	SANATTKTSETNHTSRPRLKNVDRSTAQQLAVTVGNTVVIITDFK\E KTRSSS\TSSSTVTS\SAGS\EQQN\QSSSGVQRAPDKGLPPRSLPT PKGDS\AVNDEIFPEIATWNCEKL
5933	A	1	915	MGKEKTHINIVVNGHIDSGKSTSTGHILIYKCGGINKRSIKKFEKAA EMGKGSFKSFVCDSSWYIPGHRDFITNIFTGTSQADCAVLVVAAGVG EFAAALLQDVYKIGGIGTVPDGQVETVALKPGVVITFAPVNTTTEV KSVKMHHEALSEAFSGDNVGFHVKNVSVKD IHCSNNAGCNCKNDPPME AAGFTAQVI\ILNHPGQ/DCHMAHIACKFAELKEKIDRSSGKKLEDG PKFLKSGDVAIIDMVPGKPMCVESFSDYPPLGCFAACDMRQTVALGV IKAADKKAAGAGKVTKYPPQKAQKAK
5934	A	1	759	VVQTQISKTADELISYWGTSFPPPPFAASLTLYELEYCITIDISLWKF ETSKYYATVIDAPGHRDFIKNMITGTSQADCAVLIFAAGVGFEFAVT FAPVNVTTTEVKSVMHHEVLSEALPGDNVDFDVKNVSVKEVHHGNVA

				GQISAGCAPVLDCHMAHIACKFAKLKKKTGSTSGKKLEDGPTFLKSG DAAIVDMVPGKPMCVESFSVYPPLSRFAVCDMRQTVAVGVIEAMDKK AAGAGKVTKSTQKAQKAK
5935	A	30	707	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYV TIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAVIFKNGQ\T REHALLAYTLGGKQLIVGVNKMDSPEPPYSQKKYEEIVNEVSTYIKK IGYNPDTRAFVP\ISGLNGDHMLEPRANMPWFKGWKSHP
5936	A	1	706	QSEQPCALPSRESTKLGGIGTVSSAPMET\GFSNPGMVVTFAPSPR* QRKVK\SAKMH\HEAL\SEALSQEQLGASNVKNVFCQGMFRPWQTV G*PAKNDPTQWEASWLSLLQVIL\NHPRPK*GAGPMPLYLDC\HTA \HIACK\FAELKEKIDRR\SGKKLEDGPKFLKSGDAAIVDMVPGKP\ MCVESFSYPPPLGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQ KAQKAK
5937	A	364	458	VIEHLVSQDGLDFL/NLVICPPRPPKVLGLQA
5938	A	1	266	EMESRSIA\RMECSGISIAHCKLRLPGSHSPASVSRVAGTTGTCHH ARLIFLYF/LLETGFHCVSHDGLHLL/NLVICPPRPPKVLGLQA
5939	A	1	201	PPTGP/PKLPDPVHLPPFGPPPSAWALPGMSPSPDPDRNKLRIIRI LKNASLSYLQVEVFPYKMP
5940	A	2	142	ESIQDYKHLCDLSFCQ/LPPDPPLTVPQTHNARDQWLQDAFHISL
5941	A	1	432	IHDELSRAARA\PDGPRHAAGANAGPAAGPRRPVNLDSALAALRKE MLSA\VGLRQLDMSLLCQLWGLYESIQDYKHLCDLSFCQDLSSSLH SDSSYPDAGLSDDDEEPPDASLPPDPPLTVPQTHNARDQWLQDAFH ISL
5942	A	3	696	VSMGALGLEGRGRLQGRGSLLLAVAGATSLVTLALLAVPITVLAVLA LVPQDQGG/LGFQKLPEEPEPETDLS PGLPAHLIGAPLKGQGLGWET TKEQAFLTSGTQFSDAEGALPQDGLYYLYCLVGYRGRAPGGGDPQ GRSVTLRSSLYRAGGAYGPGTPELLEGAETVTPVLPARRQVGYGL WYTSVGFGGLVQLRRGERVYVNI SHPDMVDFARGKTFFGAVMVG
5943	A	1	743	MGALGLEGRGRLQGRGSLLLAVAGAT\SLVTLALLAVPITVLAVLAL VPQDQGGVLTETADPGAQAQGLGFQKLPEEPEPETDLIPGLPTAHLI GAPLKGHGL\GWETTKEQ\AFLTSGTQVSDAEGALPQDGLYYIYCL VGITG\RAPPGGGDPQGRSVTLRSSLYRAGGAYGPG\TP\ELLEG\ AETATPVLPARRQGFWPLWYTSVGFGGLVQLRRGERVYV\NIS\HP DMVDF\ARGKTFFGAVMVG
5944	A	1	588	MGLFHVQAGLKLTSCHYQKKRMFSENEENVKRMKTSEQINENICV SLERQTAFLEQVPESFEHLPLPEPPAPLPELVDKTRDTLPPQKPEL KVKRVRFPNGIALTNWITKINPKCAPEEK\YPLFLCHENSNNKLIWK KIGEIKALPLPMAC TLSQFLASNRYFTVQSKDIFGRYGPFCDIKSI PGFSENLT
5945	A	3	497	EDTGTFRIFY\ESAGAVKKARGFLEFVEDFIQVSKNLIGKVIKNGKV IQEIVDKSDMVPVRIEGDSENKLPREDKDDRDSRHQRDSRRCPGGRC RSVSGRRGRGGPRGKSSISSVPKDPDSNPYSVLN/TESDQTADTD ASKSHSTNRHTRSRRRTDEDAVL
5946	A	1	2065	MAELTVEVRGSGNAPYKGF IKDVHEDSLTVVFENNWQPERQVPFNEV RLPPPPDIKKEISEGDEVEVYSRANDQEPGWLLAKVRMMKGEFYVI EYAACDATYNEIVTFERLRPVNQNKTVKKNTFFKCTVDVPEDLREAC ANENAHKDFKAVGACRIFYHPETTQLMILSASEATVKRVNLSMDH LRSIRTKMLMSRNEEATKHLECTQLAAAFHEEFVREDLMGLAIG THGSNIQQARKVPGVTAIELDEDGTGTFRIYGESADAVKKARGFLEFV EDFIQVPRNLVGKVIQKNGKVIQEI VDKSGVVRVRIEGDNENKLPRE DGMVPFVFGTKESIGNVQVLLEYHIAYLKEVEQLRMERLQIDEQLR QIGMGFRPSSTRGPEKEKGYATDESTVSSVQGSRSYSGRGRGRPN YTSGLYGTNSELNPNSETESERKDELSDWSLAGEDDRDSRHQRDSRRR PGGRGRSVSGGRGRGGPR\GGKSSISSVQYRSNIHNCSTLKRIFLAS DMNIVLKDPSNPYSLLDNTESDQTADTDASESHSTNRRRRSRRRR

				TDEDAVLMDGMTESDTASVNENGLDDSEKKPQRRNRSRRRRFRGQAE \DRQPAIDFIYKEVEKVSLWQAKDVIEEHGPSEKAINGPTSASGDD ISKLQRTPGEEKINTLKEENTQEA AVLNGVS
5947	A	1	1876	MADVTVEVRGSNGAFYKGF IKDVHEDSLTVVFENNWPQERQVPFNEV RLPPPD IKKEI SEGDEVEVYSRANDQEP CGWWLAKVRMMKGEFYVI EYAACDATYNEIVTFERLRPVNQNTVKKNFTFFKCTVDVPEDLREAC ANENAHKDFKAVGACRIFYHPETTQLMILSASEATVKRVNLSMDH LRSIRTKLMLMSRNEEATKHLECTKQLAAAFHEEFVREDLMGLAIG THGSNIQQARKVPGVTAIELDEDTGTFRIYGESADAVKKARGFLEFV EDFIQVPRNLVGKVIKNGKVIQEI VDKSGVVRVRIEGDNENKLPRE DGMVPFVFGTKESIGNVQVLLLEYHIAYLKEVEQLRMERLQIDEQLR QIGSRYSYSGRGRRRGPNTYSGYGTNSELSNPSETESERKDELSWS LAGEDDRDSRHQRDSRRRPGGRGRSVSGGRGRGGPR\GGKSSISSVL KDPDSNPYSLLDNT\ESDQTADTDA\SESHSTNRRRR/SIRRRRTD \EDAVLMDGMTSDTASVNENGLVTVA\DYISRAESQSIQRNLP\RE TLAKNKKEMAKDVIEEHGPSEKAINGP\TSASG\DDISKAT/RVLRG EEKINPLKEENTQEA AVLNGVS
5948	A	1	392	TESERKDELSWSLAGEDDRDSRHQRDSWRRPGGRGRSVSGGRGRGG PRGGKSSIS\SVLKQPSNP\YSLDNTESDQTADTDASESH\HSTN RRRRSRRRTDEDAVLMDGMT\ESDTASVNENGLGKRC
5949	A	269	973	PAACPSPANNICFYGECSYYCSTEHALCGKPDQIEG\SLG\AFLPDL SLAKRKTWRNPWRRSYHKRKAWEVD PDYCEEVKQTPPYDSSHRIL DVMDMTIFDFLMGNMDRHHYETFEEKFGNETFI IHLNDRGFGFKYSHD ELSILVPLQCCIRKSTYLRLLAKEEYKLSLLMAESLRGDQEAP VLYQPHLEALDRRLRVVLKAVWDCVERNGLHSVDDDLDEHRAASA R
5950	A	1	106	LVCILNMEGRKALTWKYYAKGFEGKSGFTPLVIP
5951	C	146	280	MVFKDQKMRFCFCNQXXXXLMNLXXXXXVLRKKGGSPPFVFL*
5952	A	2	1929	MAAAAVDSAMEVVPALAEAAPEVAGLSCLVNLPGEVLEYILCCGSL TAADIGRVSSTCRRRLRELCQSSGKVWKEQFRVRWPSLMKHYSPTDYV NWLEEYKVRQKAGLEARKIVASFSCRFFSEHVPCNGFSDIENLEGPE IFFEDELVCILNMEGRKALTWKYYAKKILYYLRQQKILNNLKAFLQQ PDDYESYLEGAVYIDQYCNPLSDISLKDIAQIDSIVELVCKTLRGI NRRHPSLTFFIAGESSMIMEIELQSQVLDAMNYVLYDQLKFKGNRMDY YNALNLYMHQVLIRRTGIPISMSLLYLTIRQLGVPLEPVNFPSSHFL LRWCQGAEGATL\DIFDYIYIDAFGKGKQLTGKECEYLIG\QHVTA LYG\VVNVKKVLQRMVGNLLSLGKREGIDQSYQLRDSLDLYLA\MY PDQVQLLLLQARVYF\HLG\IWPEKSFCLVLKVDILQHIQTL\DPG QHGA\VGYL\VOHTLEHIL\ERKKEEVGVEVKL\RSDEK\HRDVCYS I\GLHYGRHKRYGL/N*LC*FYGWGPHLAWMGHELSRNMNV\HSLP HGHHQPFYNVLVEDGSCRYA\AQEN\LEYNAP\QEISH\PDVGRVY SQRFT\RTHYIPN\AELEIRYPEDLEFV\YETVQ\NIYCKRKENIE
5953	A	3	364	FFSPETESHCIAQAGVQWQMLGSLQSPPPFSCSLSPSSYDYRHAPLH RANFLF\LRDGVSAWCPATAPGLLLIFFGRAPWLPV I PAPRAEA GGSLEARSSRPASLFQVSFFSPFFHMF
5954	A	2	114	FFFFGRDK/SLTMLPRLVSNCAQGILPSWPPEVLRQA
5955	A	3	139	FFFFFETETHVARAGVQWCHLASLQPLPAG\SSHSP\AAASHVAS
5956	A	274	363	LATWMKSNTSCLVTTLKWLPLSRPQRSHA
5957	A	7	1047	ARPGPDMAALYACTKCHQRFPEALSQGGQLCKECRIAPVVKCTYC RTEYQQRLECNGTISAHCNLHLPSSDSPASSSRVAGITGIKTNTI CKKCAQNVQLYGTPKPCQYCNIIAAFIGNKCQRCTNSEKKYGPYSC EQCKQQCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSS SSRAGHQEKEQYSRLSGGHHYNSQKTLSTSSIQNEIPKKKSKFESIT TNGDSFSPDLALDSPGTDHFV IIAQLKEEVATLKKMLHQKQDMILEK EKKITELKADFQYQESQMRKMNQMEKTHKEVTEQLQAKNRELLKQA AALS KSKKSEKSGAITS

5958	A	7	960	ARPGPDMAALYACTKCHQRFPFEEALSQGGQQLCKECRIAHVPVKCTYC RTEYQQRLECNGTISAHCNLHLPSSSDSPASSSRVAGITGIKTNTI CKKCAQNVQLYGTPKPCQYCNI IAAFIGNKCQRCTNSEKKYGPYPSC EQCKQQCAFDKDDRRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSS SSRAGHQEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFV IIAQLKEE VATLKKMLHQKQDMILEKEKKITELKADFQYQESQMRAMNQMEKTH KEVTEQLQAKNRELLKQAAALS KSKKSEKSGAITSP
5959	A	2973	3400	GIIFMCPDMYT\SKTFLKACLFALFFFIYPIYFFLVGIMEEYIKMC NIPQVGIFSFKYLP*SLSV*FFFETESCFVTQAGVLWCYLSSLQPPP PGFKRFSCLSLSSSWDYRHLPCCPANFC/IFSRDGVSPCWPG*SQTP DLR
5960	A	6459	7074	LEARAGSYRDPDLPSSHLLAFFFFFRRSLTLF\SQAGVK\WCDLGS SQPPSPGFKQFSCLSFLSSWDYRHAPPYRG*SFFFFFFFVFLVETGV SPCWARL\VLNARPQVIHPPRASQSA\GTTAVSHHAQPLCLFIYLF I YFY/CIFLRLSFALGPQARVQWHNLSLQPPPPGFKQFSCLSLPSSW DYRWPPPPHPPANFVLLR
5961	A	1	361	VCYPDRDCGESLVAASYRQVPVPHQCGWFHPLKPA/SHPDTVECVFRK TPKIPQKHSGSPR\PPSPSYRGRFLFRFHPPQHGAGQGPSPPPLGRK HRPSHTGSAALRACPPPGAAGLHWSGQL
5962	B	27	288	MRKVHVSTVTPNYAGGEPKRFRTAYTRQQVLELEKEFHYNRYLTRRR RVEIAHALCLSERQIKIWFQNRMRMKWKDHLKLPNTKIRSGX*
5963	A	1	825	MSSFLINSNYVDPKFPPEEYSQSDYLPDHDSPGYAGGQRRSSFO PEAGFGRAACTVQRYAACRDGPPPPPPPPPPPPPPGLSPRAPAP PPAGALLPEPGQRCEAVSSPPPPPPCAQNPLHPSPSHSAKEPVVYP WMRKVHVSTGRYSLSEVGSGWGVVEVEEEKEESNPNYAGGEPKRSR TAYTRQQVLELEKEFHYNRYLTRRRRVEIAHALCLSERQIKIWFQNR RMKWK\DHK\LPNTKIHSGGAAGSAGPPGRPLNGSPRAL
5964	A	656	1165	PPSPLSVGCLSFSSFFFPFFFIQSSLPKSFKRKISVVSTKGVPA DTEGGQPGRRRWGASTATTQKKPSISITTESLKS LIPDIKPLAGQE AVVDLHADDRISEDETERNGDDGTHDKGLKICRTVTQVVPAGQEN GQREEEEEKEPEAEPPVPSQVSVEVAL
5965	A	1	4033	MWRRKHPRTSGGTRGVLSGNRGVEYGSGRGHLGTPEGRWRKLPKMPE AVGTDPTSRKMAELEEVTLTGKPLQALRVTDLKAALQRLGSLAKSGQ KSALVKRLKGALMLLENLQKHSTPHAAFPQNSQIGEMSQNSFIKQYL EKQQLLRQLREAREAAELEESAASEDEMIHPEGVASLLPPDFQ SSLERPELELSRHSRPSKSSSISEEKGDSDDKPRKGERRSSRVQAR AAKLSEGSQPAEEEEEDQETPSRNLVRADRNLKTEEEEEEEEEEEED DEEEGDDEGQKSREAPILKEFKBEGEELPRVKPEEMMDERPKTRSQ EQEVLERGGRFTRSQQEARKSHLARQQQEKEMKTTSPLEEEEREIKS SQGLKEKSKSPSPRLTEDRKASLVALPEQTASEEETPPPLLTKEA SSPPHPQLHSEEEIEPMEGPAPPVLIQLSPNTDADTRELLVSQHT VQLVGGLSPLSSPDTKAESPAEKVPEESVLPLVQKSTLADYSAQKD LEPESDRSAQPLPLKIEELALAKGITEECLKQPSLEQKEGRRASHTL LP SHRLKQADSSSSSRSSSSSSSSSRSRSPDSSGSRSHSPLRSKQ RDVAQARTHANPRGRPKMGRSTSESRSRSRSRSASNSRKSLS GVSRDSSTSYTETKDPSSGQEVATPPVPQLQVCEPKERTSTSSSSVQ ARRLSQPESAEKHVTQRLQPERGSPKKCEAEAEPPAATQPQTSETQ TSHLPESERIHHTVEEKEEVTMDTSENRPENDVPEPPMP IADQVSN DRPEGSVEDEKKESLPSKSFKRKISVVSATKGVPAAGNSDTEGGQPG RKRRWGASTATTQKKPSISITTESLKS LIPDIKPLAGQEAVVDLHA\ DDSRIS\ED\ETER\NGD\DGDP*QRGLKICRTVTQVVPAGQENGQ REEEEEKEPEAEPPVPPQVSVEVALPPPAEHEVKKVTLGDTLTRRS ISQKSGVSITIDDPVRTAQVPSPPRGKISNIVHISNLVRPFTLGQL KELLGRTGTLVEEAFWIDKIKSHCFVTYSTVEEAVATRTALHGKWP QSNPKFLCADYAEQDELHYHRLLDVRPSETKTEEQGIPLPLHPPPP PPVQPPQHPRAEQREQERAVREQWAEREREMERRERTRSEREWD RDK

				VREGPRSRSRSDRRRKERAKSKEKKSEKKEKAQEPPAKLLDDLFR KTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEEBQKER EKEAERERNRQLEREKRRHSRERDRERERERERDRGRDRDRDRDR ERGRERDRRDTKRHSRSRSRSTPVRDRGGR
5966	A	3	5979	KSSSISEEKGDSDDEKPRKGERRSSRVQARAALKEGSSQPAEEEEED QETPSRNLRVRADRNLTKEEEEEEEEEEDDEEEEGDDEGQKSREA PILKEFKEEGEEI PRVKPEEMMDERPKTRSQEQLERGGFRFTRSQE EARKSHLARQQQEKEMKTTSPLEEEEREIKSSOGLKEKSKSPSPRL TEDRKASLVALPEQTASEEETPPPLLTKEASSPPHPQLHSEEBIE PMEGPAPAVLIQLSPNTDADTRELLVSQHTVQLVGGLSPLSSSDT KAESPAEKVPESVPLVQKSTLADYSAQKDLEPESDRSAQPLPLKI EELALAKGITECLKQPSLEQKEGRRASHTLLPSHRLKQSADSSSR SSSSSSSSSSRSRSPDSSGSRSHSPLRSKQRDVAQARTHANPRGRP KMGSRSSTSESRSRSRSRSASSNSRKSLSPGVSRDSSTSYTETKDP SSGQEVATPPVPQLQVCEPKERTSTSSSSVQARRLSQESAETHVTQ RLQPERGSPKKCEAEAEPPAATOPQTSETQTSHPESERIHTTVSH PPPSTPNPQPFSPCWCLQILRISRPLLIKQLIKHSEEKEEVTMDTSE NRPENDVPEPPMPIADQVSNDDRPEGSVEDEEKKELSLRRCQPQLS EEKYSDLAEECLPGPGVFTYPQATFIRGSMIPLAATKGVPAGNSDTE GGQPGRK\RRWG\STA\TTQKKPSISITTESLKSILPIDIKPLAQE AVVDLHADDSEDETERNGDDGTHDKGLKICRTVTQVVPAGQEN GQEEEEEEKEPEAEPPVPPQVSVEVALPPPAEHEVK\KVTLGDTL/ TLRRSISQKSGVSTIDDPVRTAQVFPFPRGKI\SNIVHISNLVRP FTLGQLKELLGRTGTLVEEAFWIDKIKSHCFVTYSTVEEAVATRTAL HGVKWPQSNPKFLCADYAEQDEL DYHRLLDVRPSETKTEEQIPRP LHPPPPPPVQPPQHPRAEQREQERAVREQWAEREREMERRERTSER EWDKDVREGPRSRSRSDRRRKERAKSKEKKSEKKEKAQEPPAKL LDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEE EQKEREKEAERERNRQLEREKRRHSRERDRERERERERDRGRDR DRERDRERGRERDRRDTKRHSRSRSRSTPVRDRDLQSAAPAPIGSG LCPGTRRQARLWFRPRPGPLAVPGSREHPPGALLRTRRSWVWNQFFV IEEYAGPEPVLIGKLHSDVDRGEGRTKYLLTGEGAGTVFVIDEATGN IHVTKSLDREEKAQVLLAQAVDRASNRPLEPPSEFIKQVQINDNP PIFPLGPHYATVPMSNVGTSVIQVTAHDADDPYSGNSAKLVYTVLD GLPFFSVDPQTGVVRTAIPNMDRETQEEFLVVIQAKDMGGMGLSG STTVTVTLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRLRAQDPDL GDNALMAYSILDGEGSEAFSISTDLQGRDGLLTVRKPLDFESQRSYS FRVEATNTLIDPAYLRRGPFKDVASVRVAVQDAPEPPAFTQAAHYLT VPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPERCFISIPEEG TIHTAAPLDREARAWNLTVLATELDSSAQASRVQVAIQTLDENDNA PQLAEPYDTFVCDSAAPGQLIQVIRALDRDEVGNSSHVSFQGPLGPD ANFTVQDNRDGSASLLPSRPAPPRHAPYLVPIELWDWGQPALSSSTA TVTVSVCRCQPDGVSASCWPEAHLAAGLSTGALLAIITCVGALLAL VVLFFVALRRQKQEALMVLEEDVRENIITYDDEGGGEEDTEAFDITA LQNPDGAAPPAPGPPARRDVLPRARVSRQPRPPGADVAQLLALRLR EADEDPGVPPYDSVQVYGYEGRGSSCGSLSSSLGSGSEAGAPGPAEP LDDWGPLFRTLAEELYGAKPPAP
5967	A	16	208	LLPYSTNPPASASRLAVIAGVHHHTQL\IFFLVETGSHCVTQSGCLKL PASSNPPTGLTMLGLQV
5968	A	1	932	MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHG IGRLTAYEFAKLKSKLVLDINKHGLEETAACKCKGLGAKVHTFVDC SNREDIYSSAKVKAEIGDVSILVNNAGVVYTSDFATQDPQIEKTF \EVNVLAFHW\TKAFLPAMTKNNHGHIVTVASAGHVSVPFLAYC SSKFAAVGFHKTLDLALALQITGVIS\LCLCPNFVNTGFIKNPSTS LGPTSSCSRVGPKLVPEEVNRLMHGILTEQKIMIFIPSSIAFLTLE RILPERFLAVLKRKISVK\FEAVIGYKMKPH

5969	A	1	1202	IHTGENPYECHECGKAFSRKYQLISHQORTHAGEKPYECTDCGKAFGL KSQLIHQRTHTGEKPFECSECQKAFNTKSNLIVHQRTHTGEKPYSC NECGKAFTFKSQILVHKGVHTGVKPYGCSQCAKTFSLKSQILVHQRS HTGVKPYGCSECGKAFRSKSYLIHMRTHTEGKPHCECRECGKSFSFN SQLIVHQRIHTGENPYECSECGKAFNRKDQLISHQORTHAGEKPYGCS ECGKAFSSKSYLIHMRTHSGEKPYECNECGKAFIWKSLIVHERTH AGVNPY\KCSQCEKSFSGEITPSLLHQRMHTTEKPYECSECGKAFIR NSQILVHQRTHSGEKPYGCNECGKTFSQKSILSAHQRTHTGEKPKCK TECGKAFCWKSQILMHQORTHVDDKH
5970	A	153	571	LLVFYLPFSLKGGRLRLDMSLLCQLYSLYESIQEYKGACQAASSPN WTYALENGFFDEEEYFPEQNSLHDDRDRGPPRDLSP\APPSPAAT GFWSPSRGSEWEGCDWEALPTGHAVIDCCFCKKAPPLWTVLGHRRG
5971	B	223	347	XNYIRVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL*
5972	A	2	283	LHSRLDGAACILPGHCHGSRVEVITYETHQCGLVGLKLLRGGREQSDR GGSGLT*DGQLGPPAEQRTTQAVIPCCAVIMSLILRLEPTDGQGG
5973	A	3	231	RRQAQIAAGRVLVVALFGGCGGLHSRLDGAAT/CLPGHCHGSRVEVT YETHQCGLVGLKLLRGGREQSDRGGSLGLT
5974	A	2	385	APFMRDPAAVASVGF/PLLGRQAQVAAGRILVVALFGGFGGLHSHLD GAAICLPGHCHGSRVEVITYETHQCGLVGLKLLRGGWEQSDRGGSLGL TEDGQVGASSEDSSIISWPKHAVIVSLILRLEPGDE
5975	A	3	539	RRQAQITAGRVLVVALFGGCGGLHSRLDGAACILPGHCHGSRVEVITY ETHQCGLVGLKLLRGGREQSDRGGSLGLT*DGQLGPPAEHPLITTTI PHLTVIVGLIPGLDPGDGQGGRVPRAGA\ENRSGIPAGRSAS**MTN TGARPFGCWYHCTLLSPIFSPQVILAVFPATDTTEGG
5976	A	1	351	RGGEQSDRGGSLGLTEDGQLGASSEHRTMQAVIPCTTVIISLILRL ESTDGQGG*GARLGARESVDSP*GPLIITIDEEFGGPSWDLVPVYN INSDVGVASRTRDGDLPGGPRR
5977	B	78	448	XQRTVITSGTSSSTIGAGYDVHWYQQLPGTAPKLLIYGNNSRPSGVP DRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGYWVFGGK LTVLGQPKAAPSVTLFPPSSEELQANKATL*
5978	A	1	393	RVLVVALFGGCGGLHSRLDGAACILPGHCHGSRVEVITYETHQCGLVG LKLRLGGREQNDRGGSLGLT*DGQLGPPAEHPSGTTTTSSI*TAIIIS LGLSLEPINCQGGRGGLTGSIEIYNKPLRADYRPHKS
5979	A	3	389	LPGGPGTMAVFGGLPTVQG/RVQALAPVLVACLEGCGGLHSRLDG AAICLPGHCHGSRVEVITYETHQCGLVGLKL/LRGGREQSDRGGSLGL DLGRSAWSLRRIPHDKDHWCLLIDNSQPRLLPGRH
5980	A	1	908	AGHRGRRAFRGKQGQGRSRLGAGFSGWDKRWWVKGVSVAEIEGVT GVPARDNSIQAGGREVGGYALRRRGRNERAEGLVFSDDQTSPIRASFT RRHPGRLCASPSGPLSHWVPGFPHPTLRTQGRPPIMCEIRKEEREQD FSLTMRIFIEKGWMTWDGGRDPSPGNLQLQAPVGGVRVGGGLKAFCRG HCLLHGAPFMRDPAAVASVGLPLLGRQAQVAAGRILVVALFGGFGGL QSHLDRAAICLPSPH\CTGPRVKIHFKNHVGLVGLKLLRGGWEQSDR GGSGLTEDGQLGASSEHSTQ
5981	C	60	392	MGYKKGEGGEGWGENADVLAECKRCWPFXXXXXXXXXXXXXXXXXXXX XX XXRKKKAAVSQDHADAW
5982	C	176	385	MCVSGYXXXXXXXXXXXXXXXXXXXXXXXXXEGSTSFTFCKHICIFTP PFPSFSLFISHFYIDLLFYNTL
5983	A	1876	2540	FLQLGSWLGRGSCQVSRGPGQPRSDNLLVEPKDLKGNLTHFTTLGGF HLLYMMIWIHPPINLCSGSNFFFLFFFFFSFSLRLGLALLPQAGVEW RDLGLLQPLP\PRLEQSC\PSSGSSWDRRFMPWPANFCM/FL*RWG LTVLPRLVSNWAQ/CDPPVSASQSAGITIVSHHVQLEGSTSFTFCK HICIFTPPFPSFSLFISHFYIDLLFYNTLPLPKKKK
5984	A	1	393	AEVAELKAEKENSEAQVENAQRIQVERLKQECRNFQRSAEKAQLEAE KTLEEKQIQWLEEKHKLHERITDREKYNQAEKLRQAAIAQKKRKS LHENKLRLOEKVEVLEAKKEELETENQVLNRQNVFP

5985	A	1	1427	MRERFRNLDEEVEKYRAVYNKLRYEHTFLKSEFEHQKEEYARILDEG KIKYESEIARLEEDKEELRNQVLNVDLT KD SKRVEQLAREKVYLQCK LKGLEAEVAELKAKEENSEAQVENAQRIQVRQLAEMQATVRSLEAEK QSANLRAERLEK/DSLQSSSEQNTFLINKLHKAEREINTLSSKVKE KHSNKLEITDIKLETARAKSELDRENRKIHSELD\YLHLDNEILKAA VEHHKVLVVKDRELIRKVQAAKEEGYQKLVVLQDEKLELENRLADL EKMKEVHDVWRQSEKDQYEEKLRASQMAEEITRKELOSVRLKLOQQI VTIENAEKEKNENSDLKQQISSLQIQVTS LAQSENDLLNSNQMLKEM VERLKQCECRNFRSQAQEAQLEAEKTLEEKQIQWLEEKHKLHERITDR EEKYNQAKEKLQRAAIAQKKRKS LHENKLKRLQEKVEVLEAKKEELE TENQVLK
5986	A	2	1831	NYKTLIIICALFTLVTVLLWNKCSSDKAIQFPRSSSGFRVDGFEKR AAASESNMNMHVAKQOSEEAFPOEQQKAPPVVGGFNSNVGSKVLGL KYEEIDCLINDEHTIKGRREGNEVFLPFTWVEKYFDVYGKVQYDGY DRFEFSHSYSKVYAQRAPYHPDGVFMSFEGYNVEVRDRVKCISGVEG VPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIEVYETAEDRD KNKPNWDVTPKGCFCMANVADKSRFTNVKQFIAPETSEGVSLQLGNTK DFIISFDLKFLTNGSVSVVLETTEKNQLFTIHYVSNAQLIAFKERDI YYGIGPRTSWSTVTRDLVTDLRKGVGLSNTKAVKPTKIMPKKVRLI AKGKGFLDNITISTTAHMAAFFAASDWLVNRNQDEKGGWPIMVTRKLG EGFKSLEPGWYSAMAQQAISTLVRAYLLTKDHIPLNSALRATAPYK FLSEQHGKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKET AGEKLGKEARS LYERGME SLKAML\PLYDTGSRTIYDLRHFMGLGIAP NLARWDYHTTHINQLQLLSTIDESPIFKEFVKRWKSYLKGSRAXHN
5987	A	34	332	LLRQGLALLPRLECSGTISAYCNLCLPGSNHPP\VSVSQVAGTTGVH HHAQLIFVFWVETGFCFHVQYGLGLEFLGSSNPPALTPSPSAGITGVSHC IWAQVF
5988	A	3	396	PAGGPAAGRAAARAGAMAKLLSCVLGPRLYKIYRERDSEAPASVPE TPTAVTAPHSSS/WGYLSLSKVVPFPHYAGTLLLLLAGVACLRSIGR WTNPQYRQFITILEATHRNQSSSENKRQLANYNFDFRSW
5989	A	3	416	GTCPFYLCPPETWVSRPFLLT SNRGNDLLLKLLQHRYPRVMAEEGLR VVRQWLEASSQLEEASIYSRWEVEEDWCLSVLRSYQAEHGPDFFPSV GEDMSADGRRQLALFLARKHLHNFEGTYWNPIPKPKTFKRPWH
5990	A	3	786	LIALRTCTESPGTTHASADAWEAKLLSCVLCPRLYKIYRERDSEGAP ISETETPTADTAPHSSSWDTYYQPRALEKHADSILALASIFWPISYY SCTFAFFYLRYRKGYLSLSKVVPFPHYAGTLLLLLAGVACLRLGIGR\ WTNPQYRQFITILEATHREPSLQKTKRQLANYNFDFRSWPVDFHWEE PSSRKESRGGP\SRRGVALLRPEPLHRTADTLLNRVKKLPCQITSY LVAHTLWRRMLYPGSVYLLQKALMPVL
5991	A	461	660	HTRTVTQSLPCWYFSQTSGRSPRLVKECNGPWIQSIKHLGCLLNQGH SGWGCLPSSSSGSQVQDHV
5992	A	1	1774	MSSSEEVSWISWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYR QALDMILDLEPGIGRWTPNPQYRQFITILEATHRNQSSSENKRQL\YYY FFDFRSWPVDFHWEPPSSRKESRGGPSRRGVALLRPEPLHRTADTL LNRVKKLPCQITSYLVAHTLGRRLYPGSVYLLQKALMPVLVQQA\ RLVEK\CNG\RAKL\LACDGNEIDTMFVDRRGTAEPQGGKLVICCE GNAGFYEVCVSTPLEAGYSVLGWNHHPGFAGSTGVPPQNEANAMDV VDQFAIHRFFHPQDIIYA\LAIGGFTATWAAMSYPDV SAMILDAS FDDLVP LALKVMPDSWRGLVTRTVRQHLN LNNAEQLCRYQGPVLLIR KTQDGNLTPTVP\KDICSNRANCLLVKALQ\HRYPG\VMAEEGLLVA RQWLEASSQLEEASIYSRW\EVEEDWCL\SVLR\SY\QAEHGADFPW \SVGEDMSA\DG\RRQAGPLFPGLGKASCHNFGGPTHCTP\LPSPQN FPRCPWHPLGTQLGLIMEEWGERRHEERPFLFVILLCFMFAVYKFCG KVGGPFLLTTPVPLARFSPFMWLYLTFSNIHPALHEMG
5993	A	3	180	DLKKHEVKHLIDKLEEFRLNRRELIAFEFPVLVALEFALHLPHEV MPHYRRLVQSS

5994	A	1	1015	MIAPLGLGLVARDQYRQAALADWDLKLDGGRQSTGAVSLKEIIGLEG VELGADGKTVSYTQFLLPTNAFGARRNTIDSTSSFSQFRNLSHRSL IGRASGTQGSOLDTGSDLDGDFMDYDPNLLDDPQWPCGKHKRVLIFFPSY MLCTQLPCSQAFKCVHSSDLSLHERNEHPCCKHNCLLQEGHSPLQ APGFRRALVVAPMQVFPLLMALGVTTVIDYVKPS\DLKKDMNKFKE KFPHIKLT\LNKIRTLKRE\MRKLAQEDCALEEPTVPMF\VFYEKLA LKGLNKNQNRKLCAGACVLVSSQYKFGSDLKKHEVKHLIDKL\EEKF RLNRARTGFAF
5995	A	48	327	EELEALRR\QRLAELQAKHGDPGDA\AQQEAKHREAEMRNSILAQVL DQSARAR\VSEQGLIEILKKVSQQTEKTTTVKFNRNRKVMDSDEDDDY
5996	A	52	281	VSKLKHLLKPEKTK\AVENY\LIQMARYGQLSEKVSLSLEELYCYL LYQNMASKGQLHLHWITEFLTLRRCWRE
5997	A	1	280	GNPLFFLELHWNPSLRIQACDRIYRVG\QOK\DVSI PRFVCGGTVEE SILHFQEKKIDLAKQFLSGSGESVTKLTLSDLRVLIGIYPPVDRVSE
5998	A	36	512	LFVLLQVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKMQEAP SATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHC\QYT\WD TQTELLILGITA\ACKLRFDRIFFR\AAEEGHIIPRSLDLLGLEKL DCGRFPSDHWGLLCNL\DIIL
5999	C	205	519	MGKEGVHGGGLINKKCYEMAFPLQAFPVLTSSVSPSPSPLTALHPFXX HTHTNHFIFWAITPYPLLLPKPHGLGARAGWTDTSPPYPSPRVLEN FCFLGFFFE*
6000	A	3	939	FLKLHLQSSVSGLASGGGREGWAGSGVGRGLLHRSRSGPDGSACPEL SASPRPASRGSSSPVRGRQQRPRAAPVAAPWPCWN\AYIDNLMADG T\CVTGAIVRYQDSEPPVWA\AVPGKT\FVNI\TPA*GGLSLVGKD\ RSSFLR*MGLTLWGGQK\CSVIRGLTCLQDGEF/SAMDLRYQEPGG APTFQCSLFTKT\DKDG*VLADGAKEGVHGGT\NKKCYEMASHLSG FPSTDHRLSLPLHRSPTAFAPLSSPYTHHPFLFFGGLPHTPYCCQNH MGLGGQGLMGQTPSPTHIPSRVWYGKLLFFGVFFFE
6001	A	172	407	RKTFFFLKCSLYKQKLWVISVAIHRSLSRKVLSSVFIKKQSDFYQL PPFNKSCFKEVFSISVYSMETNTWNLYSYT
6002	A	1	185	ESSCLSLPSSWDHRHGRPWLADFSVFF/CYRNSLTMLPRLGL\NSWP QAILPPWPPKVLGLQA
6003	A	1	618	MVRTQCLLGLRTFVFAAKLWSFFIYLLRGQIRTVIQYQTVRYDILP LSPVSRNWLAAQVIDKHSVRFFVRKPHVDFLEVVVSQWYELVVFT SMEIYGFAVAGKLDNSRSILKRRYYRQHCTLQSSYIKDLSVHSD SSIVILDNSLGAYRSHPDNAIPIKSWFSDPSDTALLNLLPMLDALRF TADVHSVLSRNLHQHRLW
6004	A	1	478	HPVRFFVHRGPH/VDFSLEVVSQWYELVVFTASMEIYGSAVADKLDN SRSILKRRYYRQHCTLELGSYIKDLSVHSDLSIVILDNSPG\AYR SHPDNAIPIKSWFSDPSDTALLNLLPMLDALRFTADVRSVLSRNLH\ QHRPLTGTGTGTLGEPNQCL
6005	A	2	833	WNSAELGRGGPGAGGAGVIGMMRTQCLLGLRTFVFAAKLWSFFIYL LRRQIRTVIQYQTVRYDILPLSPVSRNRLAQVKRILVLDLDET SHHDGVLRLPTVRPGTPPDFILKVIDKHPVRFVHKRPHVDFFL\EV \VSQWYELVVFTASM\EIYG\SAVGRNLWDNSRSIL*GGRY\YRQPA PLELG\SYIKGPLCWFSDSL\SIVIL\DNSPGAYRSHPGYGG\DN AIPKSWSVTPS\DTALLNLLPMLDALRFTADVRS\VLSRNLHQH RLW
6006	A	2	258	EAESRSVP\RLECSGPILAGCMLHLPGSCHFASASQVAGTTTHARHH TQLIF\AFLVENGLC*PGWSRSPDLVIRLPWPPKVLGLQA
6007	A	60	429	IRGQYMWGPVSSSLFCSMGYLVFGFFSFIFFFCDEVLLLSTRLECNG TISG\HCNLCPLGSSHPVSASRVAGTTGARNKARLIFYFFLVEMG FHHISQDGLDLL/NLVIRPPWPPKVLGLQA
6008	A	1	1047	SCGWTFTSMKLLRHRKHDHRRFTCPVEGCGKSFTRAEHLKGHSI THLCTKPFECFVERCCARVSARSSLYIHSKKHVQDVGAPKSRCPVST CNRLFTSKHSMKAHMVRQHSRRQDLLPQLEAPSSLTSPSELSSPGQR

				ELTNMDLAALFSDTPANASGSAGGSDEALNSGILTIDVTSVSSSLGG NLPANNSSLGPMPLVLVAHSDIPPSI\DSPLVLGTAATVLQOGSFS VDDVQTVSAGALGCLVALPMKNLSDDPLALT\SNSNLAAHITPTSS STPRENASVPELLAPIKVEPDSPSRPGAVGQQEGSHGLPQSTLPSPA EQHGAQDTELSAGTGNFYLV
6009	A	66	423	MEVACRQSTSWQPMDLASSDFRPMQNPTTNRHSQANSCLQGDGSP RRMSASKRYFEKTNACRPSSFTHKSRESSGSPGVSRCTGTGRF*NV TKQPYFTSSKHKRTGKVKVRISVV
6010	A	44	283	FSCLILHDAFPCILHDAFPCSLCSVTGSLVLSRVPLRGTHQKSAIA TSTKIALSNM/KILKHHTDAYFKKQQLFFDVSKK
6011	C	107	118	MAV*
6012	A	197	683	SLEVPLGFLLYLSFILLYSCFPLSNRVLLCHRDFFLSFLDLFLLPAF SPDYVQFLFL*CLPQFSIRH*TL*MLHCKCLDFFFFFFFETRHFHSP \SLRLECSGMISAYCS\PTSWTQVRGTTGTCHHAWLVFIFSVETGFH HVAQPDQLQLP\PRPPKVLRLQV
6013	A	1	415	LWREGPKWN/AARLNESTTFVSRSRPTIACGMVGTIVRFYIKSP\HL FKYAADPRDKHWL\AEQHMRATGG\KMAYLLEEDIPGCGPVMIT EDALDLKLEGIEIPLSLPSWMVEKMRKYMETLRTENEHRAVEAP\PQ T
6014	A	1	1256	VGDNSIDSWKNAGRVFKDSKFDANDPILKDQTEWSGSATFTSDGK IRLFYTDYSGKHYGKQSLTTAQVNVSKSDDTLKINGVEDHKTI FDGD GKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKYLVFEANTGTE NGYQGEESLFNKAYYGGGTNFRKESQKLQOSAKKRDAELANGALGI IELNNDYTLKKVMKPLITSNTVNEGKEEPPRGPAGEVSMGCLASEKGG KSSRSPEDPEKLPIAKPNNAEFYFGQIINALSTRKDKEACAHLLAITA PKDLPFMFLSNKLEGDTFLLLIQSLKNNLIEKDPISLVYQHLLYLSKAE RFKGFRCFRNHHQTGFSPAGANQRGPLAATLSGPGGEGQSAVARLTG EKKNHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAVSATQL
6015	A	2	1594	GRPARGAPQRGQTPEAGADKRATAGLCGGGGGRRRRHRASGRRRAGRGE P\AGLKSQGGRAVPKRAVARGGRO\YSAAIALLEPAGSEIADDLSIL YSNRAACYLKEGNCSCGCIQDCNRAELHPPFSMKPLLRRAMAYETLEQ YGKAYVDYKTVLQIDCGLQLANDSVNRLSRILMELDGPWNREKLSLI PAVPASVPLQAWHPAKEMISKQAGDSSSHRQGITDEKTFKALKEEG NQCVDNKNYKDALSKEYSECLKINNKECAIYTNRALCYLKLQCFEEAK QDCDQALQLADGNVKA FYRRALAHKGLKNYQKSLIDLNVILLDPSI IEAKMELEBVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPPGRP AGEVSTGCLASEKGGKSSR\SPEDPEKLPIAKPNNAEFYFGQIINALS TRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNNLIEK DPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDLSDTPNNH FTLEDIQALKRQYEL
6016	A	1	449	MAEGEITTFALTTEKFNLPNGNYKKPKLLYCSNGGHFLRILPDGTV GTRDRS\DQHIQLQLSAESVGEVYIKSTETGQY\LAMDTDGLLYGSQ TPNEECFLERLEE\NHYNTYISKKHAENWFVGLK\GPRTHYGQKA ILFLPLPVSSD
6017	A	1	153	FNLPNGNYKKPKLLYCSNGGHFLRILPDGTVDGTRMDTDGLLYGSQT PNEE
6018	A	1	528	MAEGEITTFALTTEKFNLPNGNYKKPKLLYCSNGGHFLRILPDGTV GTRDRSDQHSLNYSWTMHQRLQALRTNDHFAGAHAVPSDAQVMGMD AGVYTRKPIPTSTTITLQTTKSTYVHDALFRAGPKMNPYESHVTGAG YETYLQQWECQVKNLEHVQNRAGNYQPLPSKKI
6019	A	223	515	QRGPLPEDPSGWSGWDKGQERPAHRHQMRNVCSWKGWRRTITTTPIY PRSMQRRIGLLASRRMGAANAVLGLTMARKQSC*AMAEGEITTFALT TEKFNLPNGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQH\QT PNEECFLERLEENHYNTYISKKHAENWFVGLKKNNGSCKRGPRTHY GQKAILFLPLPVSYNSRDLFWEG
6020	A	1	812	MAEGEITTFALTTEKFNLPNGNYKKPKLLYCSNGGHFLRILPDGTV

10462

				GTRDRSDQHSGNLNYSWTMHQRLQALRTNDHFAGAHAVPSDAQVMGMD AGVYTSSKTIAAFVIVLLYHSQVHLSVSLIMQKPQVQGPWLALSQQL QEDVGLENWNEVTLESWTSQLHKPLSLVQLQ\LSAESVGEVYIKST ETGQY\LAMDT\DGLLYGSQTPNE\EC\LFLGGLEENHYNTYISK\K HAEKNWFVGLKKNKNGSCKRGPRTHYGOKAILFLPLPVSSD
6021	A	1	1471	MESMFSSPAEALQRETGVPGLLTPLPDLDGVYELERVAGFVRDLGC ERVALQFPDQLLGDAVAVARLEETTGSKMFI LGDTAYGSCCVDLVG AEQAGA QALIHFGPACLSPPARPLPVAFVLSSTFCGLGTLCDLWGP KPRPQSACGAA\GEPACAHAEALATLLRPRYLDLLVSSPAFPQVVG SLSPEPMLERFGRRFPLAPGRRLEEYGA FYVGGSKASPDPLDPLD SRLLLGWAPGQPFSSCCPD TGKTQDEGARAGGLRARRRYLVERARDA RVVGLLAGT LGVAQHREALAHLRNLTQAAGKRSYVLAALGRTPAKLA NFPEVDV FVLLACPLGALAP\QLSGRLFQPI LAPCELEAACNPAWPP PGLAPHLTHYADLLPGSPFHVALPPPESELWETPDVSLITGDLRPPP AWKSSNDHGSALATPRPQLELAESSPAASFLSSRSWQGLEPRLGQTP VTEAVSGRRGIAIAYEDEGSG
6022	A	1	343	PTRPPTRPRTHGQECPLLDPVDFLLFRTRAGDPLRRVSSS\FNKNLI FFSIKPQPPPCLA FHPRDPGGSKRPLFWDPFKGPPILAPILSLTQI FFRWSCFFPKSRIAQGWALS
6023	A	3	919	VCGLIVPQEDMPFCDSGICPDIIMNPHGFPSRMTVGKLIBLLAGKAG VLDGRFHYGTAFGGSKVKDVCEDLVRHGYNYLGKDYVTSGITGEPL AYIYFGPVYYQKLKHMVLDKMHARARGPRAVLTRIITHLSNNLFQRQ PTEGRSRDGGRLGEMERDC LIGYGASMLLLERLMISSDAFEVDVCG QCGLLGYSGWCHYCKSSCHVSSLRIPYACKLLFQELQSMNIIPSTAR TGSVQLYNFIRQGLKANPEFPFEESLETRTKCRTHRIQKRFVKAA LFNNDGRKEGGGLSEHTSLEQPF
6024	A	3	275	GLRLGKIGRD\CLIGYGASMLLLERLMISSDAFEVDVCGQCGLLGYS GWCHYCKSSCHVSSLP\IPYACKLLFQELQSMNIIPRLKLSKYNE
6025	A	455	680	AQEYQKVVGPEGGGSRAHGTRELSVRCCLGHWSGHGSPPALPPYQL LSAASLFQDALQRHCEILCSQTL SMES
6026	A	1	2065	MTASIRRYHTCATDGE PDSSVLVGGDGLTLLVAALGLDLGLPFMLL PPLMEWMRVAITYAEHRRSLTVDSGDIRQAARLLP/GPEHCFSSFR \RLDARAATEKFNQDLGFRMLNCGRTDLINQAI EALGPDGVNTMDDQ GMTPLMYACAAGDEAMVQMLIDAGANLDIQVPSNSPRHPSIHPDSRH WTSLTFAVLHGHISVVQLLLDAGAHVEGSAVNGGEDSYAETPLQAS AAGNYELVSLLSRGADPLLSMLEAHGMGSSLHEDMNCFSHSAAHGH RGIWGLVTLGPLACLEEDHETPSPRVPQSSPSGQEGTGGQLRNVL KLLTQPQAKADVLSLEBILAEGVEESDASSQGSSEGPVRLSRTRT KALQEAMYSAEHGYVDITMELRALGVPWKLHIWIESLRTSFSQSRY SVVQSLLRDFSSIREEEYNEELVTEGLQLMFDILKTSKNDSDVIQQLA TIFTHCYGSSPIPSIPEIRKTLPARLDPHFLNNKEMSDVTFVVEGKL FYAHKVLVLTASNRFKTLMTNKSEQDGDSSKTI EISDMKYHIFQMMM QYLYYGGTESMEIPTTDILELLSAASLFQDALQRHCEILCSQTL SM ESAVNTYKYAKIHNAPELALFCEGFFLKHMKALLEQ\MPSGSSSTAA AAKCAWIHCRTCTRPWQSACTLSTSPPGSAA
6027	A	2	144	LFYEMESCSIAQAGVQWLSLGLLQAPPP\GSCHSPASASC ELMFFKI
6028	A	163	465	RSMRRGRVRILLGQNRDGI VFTDDYFHHQDGYRYNVNQLGDAHDWN QNRQAIDQGRSPVIIDNTNIQAWEMKPYVEVAIGKGYRVEFHEPE TWWKFD P
6029	A	1	1614	MSYGEIEGKFLGPREEVTSEPRCKKLKSTTESYVFHNHNSNADFHRIO EKTGNDWVPVTIIDVRGHSYLQENKIKTTDLHRPLHDEMPGNRPDVI ESIDSQVLQEARPPLVSADDEIYSTSKAFIGPIYKPPEKKRNEGRN EAHVLNGINDRGGQKEKQKFNSEKSEIDNELFQFYKEIEELEKEKDG FENSCKESEPSQEQFVPFYE GHNNGLLKPDEEKKDLSNKAMP SHCDY QQNLGNEPDKYP CNGQVIPTFC DTSFTSFRPEWQSVYFPFIVPYGPPL PSLNYHLNIQRFSGPPNPPSNIFQAQDSDSIQNGYVNNCHVWNWNCM

				TFDQNNNEYTDCSENRSSVHPSGNGCSMQDRYVSNGFCEVRERCWKDH CMDKHNGTDRFVNQQFQEEKLNKLQKLLILLRGLPGSGKTTLSRILL GQNRDGI V FSTDDYFHHQDGYRYNVNQLGDAHDWNQNRATSRLMGMR FWYKMMNTSMSDNDLGAGIKDMTKSSKNKRETDLTITFSTFDLLRGD LTFECMNFVSNPVQTTMPIIR
6030	A	163	1917	SKMSYGEIEGKFLGPREEVTSEPRCKKLKSTTESYVFHNHNSNADFHR IQEKTGNDWVPVTIIDVRGHSYLQENKIKTTDLHRPLHDEMPGNRPD VIESIDSQVLQEARPPLVSADDEIYSTSKAFIGPIYKPEKKRNEG RNEAHVLNGINDRGQKEKQKFNSEKSEIDNELFQFYKEIEELEKEK DGFENSCKESEPSQEQFVPFYEGHNNGLLKPEDEKKDLSNKAMPSHC DYQQNLGNEDPKYPCNGQVIPTFCDTSTSFPEWQSVYPFIVPYGP PLPSLNYHLNIQRFSGPPNPPSNIFQAQDDSQIQNGYVNNCHVWN CMTFDQNNNEYTDCSENRSSVHPSGNGCSMQDRYVSNGFCEVRERCWK DHCMKHNGTDRFVNQQFQEEKLNKLQKLLILLRGLPGSGKTTLSRI LLGQNRDGI V FSTDDYFHHQDGYRYNVNQLGDAHDWNQNRQAIDQ GRSPVIDNTNIQAWEMKPYVEVAIGKGYRVEFHEPETWWKFDPEEL EKRKNKHGVSRRKIAQMLDRYEQMSISIVMNSVEPSHKSTQRP PPPQ GRQRWGGSLGSHNRVCVTNNH
6031	A	133	424	PFLCDFHLVIFISDSLFLMVIDFVNGTFMISFINRILLGQN\RDGI VFSTDDYFHHQDGYRYNVNQLGDAHDWNQNRGLFWAKCPRIEYLARS QKT
6032	A	3	270	FKMESGSVA\KLECRGTISAHCNLRPPGSSDPASASQIAATTGVHH HNRLIPAPLVETGFCVHDQAGLELLT/LVIHPPRPPKVLGLQA
6033	A	407	720	RHNSSNFFFFFFFETESRSIAQACMQWCYLSSLQSLPPGFKRFSCL SLPSSWDDRCPPCLAN\FVFLVETGFCVHGQAGLELLISGDPPASA SQSTGITGMI
6034	A	1	135	KEAPGLKKENN\CFVCAICQINMEGKTLCSKKDRPICKSHAFFHV
6035	C	96	410	MPLKKLPHLFVKGSPNIGKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XX XXXXXXXXXXLV
6036	C	108	422	MPLKKLPHLFVKGTPKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XX XXXXXXXXXXLV
6037	A	2	195	CLPRFMPILPASTSQVAGNTGAHHHARLIFVFLVEVGFFHHVQAGLL /ISLPQMIHPPRPPKVLGL
6038	A	251	377	LGLAQTILDNPLLGGEGLECAPTGPLEPPLAYTVNLILKSKARTEP QKQYFSSHAKNGG*REGVAA*APTGPLEPPLAYTVNLILKSKA
6039	A	175	393	ARPTFRLYLSLPVSQAGQREAER/HPRLVPTGPTHREPSPVRYDNL SRHIVDLSVAPRGEESRRCCQLVHL
6040	A	1	537	MYKYRPGYSSSSTSAAMPHSSSAKVLSTLRARLAQQREAERHPRLVP TGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLGRPTAPYLG RMSYSSQKAQPGVSETEEVALQPLTPKDEVOLKTTYSKSNGQPKS LGSASPGPGQPPLSSPTRGGVKKLLTTEIASSAGAKCD
6041	A	1	1557	MPYSLNLAIRDTFVNASRTLYSSSPRVLSNNSDANLELINTWVAKNT NNKISRLDLSPLSDTRLVLLNAIYLSAKWKTTFDPKKTRMEPFHFN SVIKVPMNNSKKYPVAHFIDQTLKAKLSRGDSLKEPTSIAESSRHPS YRSEPSLEPESFRSPTFGKSFHFDPLSSGSRSSSLKSAQGTGFELGQ LQSIRSEGTTSYKSLANQTRNGSLSYDSLTPSDSPDFESVQAGP EPDPPLGYTSPFLSARLAQQREAERHPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRT SSSSDDSKRSPLG\KTPLGRPAVPRFGKPDGL\RGRGVGFPEPGPTA PYLGRSMSYSSQIAQPGVSETEEVDLRPLLTPKDEVOLKTTYSKSNG QPKSLGSASPGPGQPPLSSPTRGGVKKVSQVGGTTYEISEFDHHCPCW VNNCIGRRNYRYFFLFLSLTAHIMGVFGGLLYVLYHIEELSGVRT AV
6042	A	1	627	TRREAERHPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQS

				PPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSPLGKTPLG RPAVPRF\GKPDGLRGRGVGSPEPGPTAPYLGRSMSYSSQKAQPGVS ETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGSASPGGPPLSS PTRGGVKKVSGVGGTTYEISV
6043	A	3	2267	PTWLERGGGEPAARPQTPOPTAPESRGPSGASALRCRGPTARSLPAA SMLGAPDESSVRVAVRIRPQLAKEKIEGCHICTSVTPGEPQVFLGKD KAFTFDYVFDIDSQQEQIYIQCIIEKLEIEGCFEGYNATVFAYGQT\GA GKTYTMTGTGFDVNIVEEELGIIS\RAVKHLFK\SIEEKKHIAIKNGL PAPDFKVNQAQFLELYNEEVLDLFDTTTRDIDAKSKSNIRIHEDSTGG NLYCGRLPTRTVNTESEMMQCLKLGALESRTTASTQMNVSRRSHAF TIHVCQTRVCPQIDADNATDNKIISESAQMNEFETLTAKFHFVDLAG SERLKRTGATGERAKEGISEINCGLLALGNVISALGDKSKRATHVPYR DSKLTRLLQDSLGGNSQTIMIACVSPSDRDFMETLNTLKYANRARNI KNKVMVNQ\AELVSKSMHFVVKSHDFRWSWSTKPGKRI IDEEGVES INDMFHENAMLQTENNNLRVRIKAMQETVDALRSRITQLVSDQANHV LARAGEGNEEISNMIHSYIKEIEDLRAKLLESEAVNENLRK\NLTRA TARAPYFSGSSTFSPTILSSDKETIEIIDLAKK\DEKLKRKEKRRK KSVAGKEDNTDQEKKEEKGVSERENNELEVEESQEVSDHEDEEEE EEEEEDDIDGGESSDESSESDEKANYQADLANITCEIAIKRKLIDE LENSQKRLQTLKKQYEEKLMLLQHKIRDQTLERDQVLQNLCSVESYS BEKKKK
6044	A	2	323	EDQGLYSIRMEGARGCLAKSLAL*GAGRGFYSGERTWTLSLPSGNCA P\YQRGGWWSHA*AHSNLNGVWHHGGHYRSRYQDGVYWAEFRGGAYS LRKAAMLIRPLKL
6045	A	3	902	PFFCSTISYRLCPEGAAGQKKVLPPLPVVVPVRLVGSTRDTSRMR DPAPEPQRDQTRQQEPMASPMPAGHPADPTKPVGPWQDCAEARQAG HEQSGVYELRVGRHVSVWCEQQLEGGGWTVIQRQDGSVNVT\SW QHYKAGFGRPDGEYWL\GLEPEHH\LTSGDHELLVLKEDWGG\RGA RAHYDGFSLPESDHYRLRLGQYHGDAGDSLWHNDKPFSTVDRDRD SYSG\NCALYQRRGWYHA\CAHSNLNGVWHHGGHYRSRYQDGVYWA EFRGGAYSLRKAAMLIIWPLKL
6046	A	3	218	KAVSLSVTQAGVQW\LISLQSPPPRFNRFSCLSLPSSWDYRQVPPRP ANFCIFSRDRVSPCWPGWSPTPNLK
6047	A	1	297	MVVSIFYPTHDPDSFPVLLCLVLCVLRILRDCNPPRLPFV\IDF\CL GLVNGMPWHSFGGKKREDNVFLHCSHSDLGIVLLAGTASLQDFSFFQ KSPPP
6048	A	1	8157	MTKHYDYIAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVGC VPKVMWHAQAIREAIIHMYGPDYGFDTTINKFNWETLIASRTAYIDR IHTSYENVLGKQNVVDVIKGFARFVDAKTLEVNGETITADHILITGG RPSHPDIPGVEYIDSDGFFALPALPERVAVVGAGYIAVELAGVING LGAKTHLFVRKHAPLRSFDPMISENQSRSGAVRDEIQFYATGARPD AKEMGFIGGKMPTHWGPBGDAGIRKDAAMVADMRVKCAERCDRISL MHAGKVLASGTPQELVEKRGAAASLEEAFAIYLQEAAGQSNEAEAPHR ATAAAKRWNCDAIQYVRTALMGTVILMLIMGYGISMWKTCAKLCW RDFCGSDFRLIKGTPRSSDDSIKILPPILKTSNSGPKGQQSSTKONS SMATDSTQCVKKSRRPKVFDRAALDKAMKLFVQHGYEATSLADLV EATGAKAPTLIAEFTNKEGLFRAVLDRYIDRFAAKHEAQLFCEEKSV ESALADYFAAIANCFTSKDTPAGCFMINNCTTLSPDSGD IANTLKSR HAMQERTLQQFLCQRQARGEIPPHCDVTHLAEFNCIIQGMSISARE GASLEKLIAPERTPPASFRKLRTYPAATLSTGTADEIYVWRGQTP FVMSIAATRQRSSHPTWFNGNTQHAPNFCRFARFAFSVERLGNRRAA FFDFTIRLRFRQNGVPNERFDVNVRSQLSSQALTTTRIPHTIRSASI TKPLSQPSTCRDMSAAHQAIADITPKYMEDLDQRWMDYGVKFLDKM AKSDKPFFLYYGTQFATFAPGCPARSSAWRLTSTISISGMELPMAPA FPIPRQNPWSMAPACLLTGTSGHNGSGAKGEDRGVFGGRPPITEFP FGSTWNFRVCGLRSPVTALCRGEGGQPQGAQVQORPGKITGENFRQG

				NSRGGHQNAAQGHGHPVQRHTGGPRHKKGATEHPGYTSAPANPSAEL KIYDTSSQPLSQILSQVQQDGASIVVGPLLKNNVEELLKLSKALYNI DWHRHAQVKCNGLQINMLMAAAVCAVIASNLGMFVVMAEIMALCAQQ QRGQLWFALGRLGTLALLAIACWLLWQRYGTLDLRLDMMRQQLPLGS DIWLLGVIGFGLLAGIIPHLGWVPOAHANASAPAAALFSTVHVYKRV ILTGHDITDSTSSQDEYNQPOVNI SLDSAGGNIMSNTKDNIGKPM TLFVEYKDSGKKDANGRAVLVKQEEVINIANIQKQNSFRITGTINN PNEARQLSLLLRAGALIAPIQIVEERTIGPTLGMQNIWGWYGRSQPA ELTKLSLFCYIANYLVRKGDVRRNNLRGFLKPMGVILVLAVLLLAQP DLGTVVVLFVTLAMLFLAGAKLWQFIAIIGMGISAVVLLILAEPYR IRRVTAFWNPWEDPFGSGYQLTQSLMAFGRGELWGQGLGNSVQKLEY LPEAHTDFIFAIIGEELGYGVVLLALLMVFFVAFRAMSIGRKALEID HRFSGFLACSIGIWFSPQALVNVRAGAGDVPTKYNSLSCFKETRNAI LGRMLTPAHGHVWLDGEHIQHYASKEVARRIGLLAQNATTPGDI TVQ ELVARGRYPHQPLFTRWRKEDEEAVTKAMQATGITHLADQSVIPFRS RLVKNRKAAWHSGSRDTAATLMLFVLGWLGRRRGLGCCGIWGGFSQQ GLPPAMQKVMYKGLVPEDKTLREIKVTSGAKIMVVGSTINDVLAVNT PKDAAQQDAKAEENKKEPLCRQKLHCCFLTIVASIIVPAAFVLEDDVD FDQMVSLEANRSSYNASFPSSFELSASSHSDDDVIAKEGTSVSIEC LLTASHYEDVWHNSKGQQLDGRSRVIALVPVTPAIQPNARIRRRHV VAERQRIQANFLRGKLTIVIAAVVHIEAALEIIVHSQNRFPVEGQYQ AVQHAVVRIPVGPGRGSGAGSLVAYALKITDLDPLEFDRATVRVLNG DNTRQIVFVRQMQVAHYAKCSFVRHADITNFSRALVLCQCVQRIQQR NRRRRIRPAITEFAEAVGRALRPVHLIKIEVNALSDGIVELCVGVGF AVLFILSGKSAKHRYHRKLGINRVNANCPGFYVNRILAPYINEAIRM LTQGERVEHIDAALVKFGFPVGPPIQLLDEVGIDTGTKIIPVLEAAYG ERFSAPANVVSSILNDDRKGRKNGRGFYLYGQKGRKSKKQVDAIYP LIGTQGGRI SAPQVAERCVMMLNEAVRCVDEQVIRSVRDGDIGAV FGIGFPFPLGGPFRIIDSLGAGEVVAIMQRLATQYGSRTPCERLVE MGAPLDAASDSVRPLTTNGCDESRLMANWLKGQKVEIERVLVSPFLR AEQTL EEVGDCNLNLPSSAEVLPELTPCGDVGLMWIGDKQLLTPLRD QFTRAPLDNDIGVSEATRIDPNAWVERWKAAGHYQAEAAALLQCTADT LADAVLITTAHAWQHOGKTLFISRKTYRIDALAVIMFSFGGLELIGI TAAEARDPEKSIPKAVNQVVYRILLFYIGSLVLLALYPWVEVKSNS SPFVMI PHNLDNSNVVASALNFVILVASLSVYNSGVYNSRMLFGLSV QGNAPKFLTRVSRRGVPINSLMLS GAITSLVVLINYL LPQKAFGLLM ALVVATLLLNWIMICLAHLRFRAAMRRQGRETOFKALLYPFGNYLCI AFLGMIILLMCTMDMRLSAILLPVWIVFLFMAFKTLRRK
6049	A	1126	1355	PQDEAPLVLLSKDVVVQGSAAEQVQVEACGAGSEPHSHRNPGISAQV GLAPSYGAARGRRRPLALQQSPQERRHVG
6050	A	1	1627	MGSRCNLNPPPAHSDTTGKDSFGNIRGAETGQGASACSVTSARVTCG AGSEPHSHRNPGISAQVGLAPSYGAARGRRRPLALQQSPQERRHVGW NSTRGLLPASLPGTASSQSASATASAALPLKVTGPIARNPTPPWTAA AALATRGQRPEKGLFPGPAPFSLGKRKRGRGRTWERRRRVSIETSTC FRPGCERLGAAAGANLSQLASSQRPLRERWVLYTIIMAAAGAPDGM EPGMDTEAETVATEAPARPVNCLAEATAGAGAGTVAEDSGTARGSL QPA\ PAPAQAPGDPVSQASVSNGEDSGGSADSELVDLRI IWNKT KHD VKFPLDSTGSELKQKIHSITGLPPAMQKVMYKGLVPEDKTLREIKVT SGAKIMVVGSTINDVLAVNTPKDAAQQDAKAEENKKEPLCRQKQHRK VLDKGPEDVMPVSVKGAQERLPTVPLSGMYNKSCKVRLTFKLEQDQ LWIGTKERTEKLPMSIK\NVV\SDPI\EGHEDYHNDGRFQLAPTEA \SYWVWVPTQYVDAIK\DTVLGKWQYF
6051	C	47	298	MITSTSQTKGSSSPRISHSCPSSTAYVGRWRGPCGPGAQLPPNIGQP CPYPGPPLPSSYVYNNDQSVWXXXXXXXXXXXXXXXXXX
6052	B	64	362	XCVWHRRKVAVNLAKLKLFRHYVMVICYVYFTRI IAILLQVAVPFQ WQWLYQPTGNNPYLQLPQDEEDVQMEQVMTDSGFREGLSKVNKTAS

				GRELL*
6053	A	1	342	AAGIFWVSILCRNTYSVFKIHWLMAALAFTKSISLLFHSVRALDWGA AGGGLKGPPGSPKSLQTLGLWEGHPPAIHVSTHFTSVASHPSPLST SPAGQLCPPLSLGSAVTVRL
6054	A	1	485	FPVVWSIRHLQDASGTDGKVAVNLAHLKLFHRHYVMVICYVYFTRII AILLQVAVPFQWQWLYQLLVEGSTLAFFVLTGYKFQPTGNNPYLQLP QEDEEDVQMEQVVCGEVEGVHVDQAPSSPGPRFPDKPIWKKSPFLPP NIGQPCPYPGTTPPFQLCVQ
6055	A	696	3195	SGRRTPMASCQRRCPFSSSTWSCPPASWPLASSGCPSSAGTRTASF KIHWMALAFTKSISLLFHSVRALDRGAAGAPITSFESHPPSSLFN FLTTHLMVTVRVNPPPPPSASHPSVRLTVRLSIHPQINYYFINSQG HPIEGLAVMYIAHLLKGALLFITIALIGSGWAFIKYVLSDEKKVF GIVIPMQVLAVYIIIESREEGASDYVLWKEILFLVDLICCAGILF PVVWSIRHLHGCVWHRRRMVAVNLAKLE\LFHRHYVMGARLTHSGF GGITGLLHAHPSPSAAAPSRGPHPGSPARILQSSPMPARAPTVLAPR LLAPLQVICYVYFTRIIAILLQVAVPFQWQWLYQLLVEGSTLAFFVL TGYKFQPTGNNPYLQLPQEDEEDVQMEQVEAHTLKLVDIKSTVSN VFSEMKENMDKELKQIMRIYERRICVADPFVTVMQDFFIDLRLPY SVVRNEQVEIRAVLYNYRQNLKVRVELLHNPACSLATTKRRHQ TVTIPKSSLSVPYVIVPLRPACRKWKSRLSTIISSTVSGKGQVQK EDIPPADLSDQVPDTESETRILLQGTTPVAQMTEDAVDLKHLIVT PSGCGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKGY TQQLAFRQPSAFAAFVKRAPSTWLTAYVVKVFLAVNLIAIDSQVL CGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKDMALTAFV LISLQEAKDICEEQVNIHNRYAATRQLMVAKISGKFSKMDKSKTAGL ADCHSVLDVSNKGVLDRDASTSSGIVDWRGSIQT
6056	A	1	516	LRQPTRPVFGIVIPMQVLAVYIIIESREEGASDYVLWKEILFLVD LICCAGILFPLVWSIRHLKDASGTDGKVPVNLKLFHRHYV\IPA PTPCAPLQVICYVYFTRIIANP\LQVAVPFQWQWLYQLLVEGS\TLA FFVLTGYKFQPTGNNPYLAVAPGGGGGCSRWSK
6057	A	3	528	LSCRVQSVAPPRPRPALPVSAVPGTPTLTALLHP/WLADCDVSD SSCSSLAATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQ LVYVQRAGRVRPGLPREEGGGGGGHWHAHASLLACVQPVQFTGLRR WRTGLQGPGETSTSLRGHLLRLFLLLAALDDRP
6058	A	1	334	EKINDCAEVKQELAASDRERAQSRIQEELEKVASLLHQVSWRQDSRE PDAGRIHAGSKTAKYLAADALELMVPGGWRPGTGSQQLEPPAEGGHP GAAQRQGDLCPCPLH
6059	A	225	843	WTRCWSRLRASGSCEGRRAPPRPRCARYEGGYQRSCGSESACGGR RVLGSSLRQHOGSCRNTRAGMFCGRQYIPHPSAASPRRPLGRSRNTQ MGTPLSRVLLRSCRKKID/SLKQKVTHLRGLQIPHEPELMRKEISRL NKTVGRENK*LSRSEAGAGGLQ\EARDAALERVQMLEQQVSVPRAPD GTDQMSAGRWWPKSWDRLG
6060	A	300	957	GSTKVHAETHALGCSVADSTSRTHQQLHRGAHWGEVGTWRW\HTSVQ SVIEKLQENRLLKQKVTHVEDLNAKWQRYNASRDEYVRGLHAQLRG LQIPHEPELMRKEISRLNRQLEEKINDCAEVKQELAASRTARDALE RVQMLEQQILAYKDDFMSEADRERAQSRIQEELEKVASLLHQVSWR QDSREPDAGRIHAGSKTAKYLAADALELMVPG
6061	A	2	271	FFETESRVA\RLCSGAI SAYCTLCPLGSSDSIASASR\VAGITGE HHHARLILVFLVEMGFHHVGGAGLGLLDLVIHPPRPPKVLGLQA
6062	A	3	376	DYSLGLPVVTTGCWGHMSNAPLRWALNPSYWGKNQLLCPESLALCCG LCCKPRFLEVTSVRSADLYLSSPCLVRRCPFRGKEKPAVGMRMPDN KGWRRALSSSLSPR\VP\APVAASVLTVMN
6063	A	2	70	WSRSPDLMIRLPRPPKVLGLQA
6064	A	3	258	ADPPSPSFCFCFFFETESCVT\RLCSGAILAHCNLC/LPTCHHA WVIFVFLVETEFHHVGEDGLNLL/NFMIYLPKPPKVLGLQA
6065	A	1	408	GFDEWFGSPNCHFGPYDNKARNIPVYRDWEMVGRYYEFPINLKTG

				EANLTQIYLQEALDFIKRQARHHPFFLYWAIDATHAPIYASKPFLGT SQRGRYGDVREIDDFQFRLSFVHKEFPWTLIMREACSFLSL
6066	A	3	25	KKCLWSH
6067	A	3	505	RSEEQPQAGFVPGQDRLRKETRTRTAGLGARASGHRGVACRAAVGRMR LGATRGHSPYSVLEGARLTKNFVKVSVAAQNFRVSPRGVPEVSWVP VSRHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARPNI PVYRDWE MVGRYYEEFPINLKTGEANLTQIYLQ
6068	A	1	1740	MAAVVAATRWQLLLVLISAAGMGASGAPQPPNILLMLDDMGWDLG VYGEPSRETPNLDRAAEGLLFPNFYSANPLCSPSRAALLTGRLP NGFYTTNAHARNAYTPQEI VGGI PDSEQLLPELLKKAGYVSKI V GKW HLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARPNI PVYRDWEMVG RYEEFPINLKTGEANLTQIYLQEALDFIKRQARHHPFFLYWAVDAT HAPVYASKPFLGTSQRGRYGDVREIDDSIGKILELLQDLHVADNTF VFFTSNDGAALISAPEQGGSNPFLCGKQTTFEGBMREPALAWWPGH VTAGQVSHQLGSIMDLFTTSLALAGLTPPSDRAIDGLNLLPTLLQGR LMDRPIFYRGDTL\MAATL\GQKHAHW\TWTNSWENFRQIDFCP GQNVSGVTTHNLEDHTKLPLIFHLGWDPGERFPLSPASAEYQEALSR ITSVVQQHQEALVPAQPQLNVCNWAVMNWAPGCEKLGKCL\TPPES IPKKCLWVPLAPAQTQARPRISSWPCKCLEEGWLWPRSSPNPAPSQT DSTCRRRGTCITISNLPT
6069	A	3	2945	AALKGGTTPPGALAAPREPVAAMP PRAPPAPGPRPPPRAAAATDT AAGAGGAGGAGGAGGPGFRPLAPRPWRWLLLLALPAACSAPP RPVY TNHWAVQVLGGPAEADRVAAAHGYLNLGQIGNLEDYHYFYHSKTFKR STLSSRGPHFTLRMDPQVKWLQQQEVKRRVKRQVRSDPQALYFNDPI WSNMWYLHCGDKNSRCRSEMNVQAAWKRGYTGKNVVVTILDDGIERN HPDLAPNYDSYASYDVNGNDYDPSPRYDASNENKHGTRCAGEVAASA NNSYCVGIAYNAKIGGIRMLDGDVTDVVEAKSLGIRPNYIDYISAS WGPDDDGKTVDGPGRLAKQAFYGIKKGRQGLGSIFVWASGNGGREG DYCSCDGYTNSIYTISSVSSATENGYPWYLEECATLATTYSSGAFY ERKIVTTDLRQRCTDGHGTGTSVSAPMVAGI IALALEANSQLTWRDVQ HLLVKT SRPAHLKASDWKVNAGHKVSHFYGFGLVDAEALVVEAKKW TAVPSQHMCVAASDKRPRSIPLVQVLRTTALTSACAEHSDQRVVYLE HVVVRTSISHPRRGDLQIYLVSPSGTKSQLLAKRLLDLSNEGFTNWE FMTVHCWGEKAEGQWTL EIQDLPSQVRNPEKQGLKEWSLILYGTAE HPYHTFSAHQSRSRMLELSAPELEPPKAALSPSQVEVPDEEEDYTG CHPECGDKGCDGNADQCLNCVHFSLSVKT SRKCVSVCP LGYFGDT AARRCRRCHKGCETCSSRAATQCLSCRRGFYHHQEMNTCVTLCPAGF YADESQKNCLKCHPCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPG TYFDSELI RCGECHHTCGTCVGP GREECIHCAKNFHFHDWKVPACG EGFYPEEMPGLPHKVCRRCDENCLSCAGSSRNCSRCTGTGFTQLGTSC ITNHTCSNADETFCEMVKS NRLCERKLF IQFCCRTCLLAG
6070	A	2	3078	GNAPRPPPPRLPPAAVLAAAVAAAAALPRRGAALKGGTTPPGALAA RAPREPVAAMP PRAPPAPGPRPPPRAAAATDTAAGAGGAGGAGGAGG PGFRPLAPRPWRWLLLLALPAACSAPP RPVYTNHWAVQVLGGPAEA DRVAAAHGYLNLGQIGNLEDYHYFYHSKTFKRSTLSSRGPHFTLRMD PQVKWLQQQEVKRRVKRQVRSDPQALYFNDPIWSNMWYLHCGDKNSR CRSEMNVQAAWKRGYTGKNVVVTILDDGIERNHPDLAPNYDSYASYD VNGNDYDPSPRYDASNENKHGTRCAGEVAASANNNSYCVGIAYNAKI GGIRMLDGDVTDVVEAKSLGIRPNYIDYISASWGPDDDGKTVDGPGR LAKQAFYGIKKGRQGLGSIFVWASGNGGREGDYCSCDGYTNSIYTI SVSSATENGYPWYLEECATLATTYSSGAFYERKIVTTDLRQRCTD GHGTGTSVSAPMVAGI IALALEANSQLTWRDVQHLLVKT SRPAHLKAS DWKVNAGHKVSHFYGFGLVDAEALVVEAKKWTA VPSQHMCVAASDK RPRSIPLVQVLRTTALTSACAEHSDQRVVYLEHVVVRTSISHPRRGD LQIYLVSPSGTKSQLLAKRLLDLSNEGFTNWEFMTVHCWGEKAEGQW TLEIQDLPSQVRNPEKQGLKEWSLILYGTAEHPYHTFSAHQSRSRM

				LELSAPELEPPKAALSPSQVEVPEDEEDYTAQSTPGSANILQTSVCH PECGDKGCDGPNADQCLNCVHFSLSVKTSRKCVSVCPGLGYFGDTAA RRCRRCHKGCETCSSRAATQCLSCRRGFYHHQEMNTCVTLCPAGFYA DESQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY FDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKVPACGEG FYPEEMPGLPHKVCRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCIT NHTCSNADETFCEMVKSRLCERKLFIQFCRTCLLAG
6071	A	3	3204	AGRGRWGGTASREPQKSAGKFFRWGAFRASRTALGPGARSQERGG GGNAPRPPPPRLPPAAVLAAAVAAAAALPRGAALKGGTPPP ARAPREPVAAMP PRAPPAPGPRPPPRAAAATDTAAGAGGAGGAGGAG GPGFRPLAPRPWRWLLLLALPAACSAPPPRPVYTNHWAVQVLGGPAE ADRVAAAHGYLNLGQIGNLEDYHYFYHSTFKRSTLSSRGPHTFLRM DPQVKWLQQQEVKRRVKRQVRSDPQALYFNDPIWSNMWYLHCGDKNS RCRSEMNVQAAWKRGYTGKNVVVTILDDGIERNHPDLAPNYDSYASY DVNGNDYDPSPRYDASNENKHGTRCAGEVAASANNNSYICVGIAYNAK IGGIRMLDGDVTDVVEAKSLGIRPNYIDIYSASWGPDDDGKTVDPG RLAKQAFYEGIKKGRQGLGSIFVWASGNGGREGDYCSDGYTNSIYT ISVSSATENGYKPWYLEECASLTATYSSGAFYERKIVTDLRQRC TDGHTGTSVSAPMVAGIIALALEANSQLTWRDVQHLVKTSRPAHLK ASDWKVNAGAGHKFSHFYGFSGVDAKSLGEEAKKWTAGPSQHMWVAA SDKRPRSIPLVQVLRRTALTSAEHSQDQVVYLEHVAVRTSISHPR RGDLQIYLVSPSGTKSLLAKRLDLSNEGLTNGEFTAHCWGEKAE GQWTLQIQLPSQVRNPEKQGLKEWSLILYGTAEHPYHTFSAHQSR SRMLELSAPELEPPKAALSPSQVEVPEDEEDYTGVCHEPCGDKGCDG PNADQCLNCVHFSLSVKTSRKCVSVCPGLGYFGDTAARRCRRCHKGC ETCSSRAATQCLSCRRGFYHHQEMNTCVTLCPAGFYADESQKNCLKC HPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTYFDSELIRCGE CHHTCGTCVGPGREECIHCAKNFHFHDWKVPACGEGFYPEEMPGLP HKVCRRYGP PGERQATVSSKGVPGGQSLSSSPGAGEGMLHHTVD RSPFTELLRGLRPFVHWMHICWVPAVGRHRAAAG
6072	A	3	3002	AALKGGTPPP GALAAARAPREPVAAMP PRAPPAPGPRPPPRAAAATDT AAGAGGAGGAGGAGGPGFRPLAPRPWRWLLLLALPAACSAPPPRPVY TNHWAVQVLGGPAEADRVAAAHGYLNLGQIGNLEDYHYFYHSTFKR STLSSRGPHTFLRMDPQVKWLQQQEVKRRVKRQVRSDPQALYFNDPI WSNMWYLHCGDKNSRCRSEMNVQAAWKRGYTGKNVVVTILDDGIERN HPDLAPNYDSYASYDVNGNDYDPSPRYDASNENKHGTRCAGEVAASA NNSYICVGIAYNAKIGGIRMLDGDVTDVVEAKSLGIRPNYIDIYSAS WGPDDDGKTVDPGRLAKQAFYEGIKKGRQGLGSIFVWASGNGGREG DYCSDGYTNSIYTI SVSSATENGYKPWYLEECASLTATYSSGAFY ERKIVTDLRQRC TDGHTGTSVSAPMVAGIIALALEANSQLTWRDVQ HLLVKTSRPAHLKASDWKVNAGAGHKVSHFYGFGLVDAEALVVEAKKW TAVPSQHMCVAASDKRPRSIPLVQVLRRTALTSAEHSQDQVVYLE HVVVRTSISHPRRGDLQIYLVSPSGTKSLLAKRLDLSNEGFTNWE FMTVHCWGEKAEGQWTLQIQLPSQVRNPEKQGLKEWSLILYGTAE HPYHTFSAHQSR SRMLELSAPELEPPKAALSPSQVEVPEDEEDYTAQ STPGSANILQTSVCHPECGDKGCDGPNADQCLNCVHFSLSVKTSRK CVSVCPGLGYFGDTAARRCRRCHKGCETCSSRAATQCLSCRRGFYHHQ EMNTCVTLCPAGFYADESQKNCLKCHPSCKKCVDEPEKCTVCKEGFS LARGSCIPDCEPGTYFDSELIRCGECHHTCGTCVGPGREECIHCAKN FHFHDWKVPACGEGFYPEEMPGLPHKVCRRYGP PGERQATVSSKG VPGGQSLSSSPGAGEGMLHHTVD RSPFTELLRGLRPFVHWMHICW VPAVGRHRAAAG
6073	A	1	1181	MEVSRAGLSTVLEAVLCPADLTAASLDAASMPSSSHLPVLGYPVGK SGARPGSTQEVVLTAAAVTQEVVLTAAAVTQEVVLTAAAVTQEVVLT AAAVTQEVVLTAAAVTQEVVLTAAAVTQEVVLTAAAVTQEVVLTAA VTQEVVLTAAAVTQEVVLT TAGAENKPVSAPHSSSTCARTGSPGRPL

				HTQSPPRGHILFGKEKVCYKFKHDILKHLTQLTVDGIVSIPLVQVL RTTALTSACAHSQDQVVYLEHVVRVTSISHPRRGDLQIYLVSPSGT KSQLLAKRLDLSNEGFTNWEFMTVHCWGEKAEGQWTLQIDLPQSV RNPEKQG/DVFCTKCHSHQSFEESQDTSVVAWEGWGCTHGVHCEVP KNLGIRSGKHPLKIKLV
6074	A	3	656	RSAPFELWTQEGGLPSPSGW/VIIQSLKLNLRNRTDSRGRRSSPLISCLA TGAGTSRHLPLDWMSTIGCPGSQASRPESLNHTSGFPGFPAFHPR WWAFSGPQSHINQIPHPKSPLCVGS\LLQRAYTNTLPLFPLQFLRSP TKESTYSQLHPSGSPPGGGPGPRQLGLTSPKASEQPLPGFDWEGQGS DRRAGADGSGRESSGTPGTAVLQRSSCGTSC
6075	A	3	873	AAEGLPPVRIPPFSETTANGTISFTEMVQDMGAGLAVVPLMGLLES I AVAKAFASHNNYRIDANQELLAIGLTNMLGSLVSSYPVTGSFGRTAV NAQSGVCTPAGGLVTGVLVLLSLDYLTSLF\YYIPKSALG\AVIIMG RGPVSTPRSRNALGFLKRLDLLPLCVTFLLCFWEEQDGI LAGALG SLLMLLHSAARPETKSGEGPVLVLQPASGLSFPAMEALREEILSRAL EVSPPRCLVLECTHVCSIDYTVVLGLGELLQDFQKQGVAFEGQLV PRLRVLLSR
6076	A	3	256	HASGMKNDLVYTGVDPETLPNRNGDV/PTGLSPDPQFRTRKIQASL LTLEETMKQLEEELEEFRLKPLLANLCGNSVPHPGCT
6077	A	1	1966	MAEPLLRKTF SRLRGREKLPRKSDAKERGHPAQRPESPPPEPEQA PEGSQAGAEQSPSEASRSPARGAYLQSLPSSRRWVLGGAKPAEDT SLGPGVPGTGEPAGEIWINPIPEEDPRPPAPEPPGPQGSASEGLA PQGAAPASPT/NSLPHQVPGPRQAPLHKDEEAAGTAAPPEPARPPG WQGAREGCPGLRHQPLPPGQQRGGPRAGSRAWGHPEPEGRLPQRRG LTGAPSWAPITHLLPALRGGSRSPTGRTLGPPQAPVRSRGAAAS AGGHPQGPPLPTASGWGQGPNRATARGAGLPAAGPHLPPGAGGRQA PARPGACVGPWREKAPALCPGHRAAAHGLPR\CQAQQLAVRLEPQGL LYAKLTLEQQEAPATAEPRVFGPLPLLLVERERPPGQVPLIIQKCV QGIERRGLRVVGLYRLCGSAAVKKELRDAFERDAAVCLSEDLYPD I NVITAVPSLALEASGALTRGDPVFTGILKDYLRLEPTPLITQPLYKV VLEAMARDPPNRVPPTTEGTRGLLSCLPDVERATLTLLLDHLRLVSS FHAYNRMT PQNLAVCFGPVLLPARQAPT\RPRARSSGPGLASAVDFK HHIEVLHYLLQSWP\IPACPDNLQMSRLTCDPNDSHLCTCRWQTPKW
6078	A	2	82	WCDLGSLOPPPPRFKQFSCSLPRHS
6079	A	1	347	FFFFFFFLETASHSVAQAGGQGHDLSSLQPPPPRFKQFSCSLPSS WDHRHKPPHPP\NFVFLVETGFHHVQGAGLELLTSSDPPASASQMAG ITGVSHCAWPITIFKQSNYGM L
6080	A	1	779	FNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMDKKKBEQNRGKP NWEHLNEDLHVLI TVEDAQNR AEIKLKRAVEEVKLLVPAAEGEDSL KKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAPRIITGPAPVL PPAALRTPTPAGPTIMPLIRQIQTAVMPNGTPHPTAAIVPPGPEAGL IYTPYEYPYTLAPATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR IVTADRSRHRQLTYDLTSELFTQ
6081	A	1	214	HPTAAIVPPGPEAGLIYTPYEYPYTLAPATSILEYPIEPSGVL\ VWL SORKAKNSRTVLTEPSSDLNL TNA
6082	A	3	435	EPFPGDCIPRATLESCRMIALMDTVGSGKLNQEFHHLWNKIKGW Q\KIFK\HYD TDQSGHHQTATKMRNAV/NTDAGFHLNNQL\YDIITM RYADKHMNIDFDSFICCFVRLEGMFRAFHA FDKDGDGIIKLVLEWL QLTMYA
6083	A	2	339	GKPTLREFTHL/WDKIKGWREIFNNITPSQSGTITGYEMRNA/VNDA GFHLNNPLYDII\TSRTADNHMNIDFESF\ICCFVR\LEGMFRAFHA FD\KDGDGIIRLNVLEWLQLTMYA
6084	A	2	775	PSASDQSTWYLDSTLDNIKKTLHKFCGPSPVVFSDVNSMYLSSTE PPAAAEWACLLRPLRGREPEGVWNLLSIVREMFKRDRSNAAPLLEIL TDQCLTYEQITGWVSVRTSASHSSASGHTGRSNGQSEVAHAHACASM CDEMVTWLRLAVLDPALSPQRRRELCTQLRQWQLKVIENVKRGQHKK

				TLERLFPGFRAVEACYFNWEEAYPLPGVTYSGETDRKLALCWARALP SRPGASRSGGLEESRDRPRPLPTEPAVRPKEPGTKRKGLGEGVPSSQ RGPRLSAEGGDKALHKMGPGGKAKALGGAGSGSGSAGGSGSKRRL SSDSSLEPDLAEMSLDDSSLALGAESTFGGFPESPFPPLHGGSR GPSTFLPEPDDTYEEDGGVYFSEGPEPPTASVGPPGLLPGDVCTQDD LPSTDESGNGLPKTKEAAPAVGEEDDDYQAYYLNQDQAGGEEEEKAE GGAGEEHDLFAGLKPLEQESRMEVLFACAEALHAHGYSSEASRLTVE LAQDLLANPPDLKGKKNKVSTSRQTWVATNTLSKAAFLLTVLSEPE HHNLAFRVGMFALELQRPASTKALEVKLAYQESEVAALLKKIPLGP SEMSTMCRABEELREGTLCDYRPVPLMLASFIDVLCAPGSRPPSR NWNSETPGDEELGFEEAVALGMKTTVSEAEHPLLCEGTRREKGDLA LALMITYKDDQAKLKKILDKLLDRESQTHKPQTLSSFYSSSRPTTAS QRSPSKHGGPSAPGALQPLTSGSAGPAQPGSVAGAGPGTEGFTKKN VPSSPHSPCEGLPSEAAALTPRPEGKVP SRLALGSRGGYNGRWGSP GRPKKHTGMA SIDSSAPETTS DSSPTLSRRPLRGGWAPT SWGRGQD SDSISSSSSDSLGSSSSSGSRRASASGGARAKTVEVGRYKGRPPESH APHVNPQSEAAAHFYFELAKTVLIKAGGNSSTSIFTHPSSGCHQ PHRNHLHLCAFEIGLYALGLHNFVSPNWLSTYSSHVSWITQAMBIG SAALTILVECDGHLTPPEVASLADRASRARDNSNMVRAAEALALSCL PHAHALNPNEIQRALVQCKEQDNLMLEKACMAVEEAAKGGGVYPEVL FEVAHQWFWLYEQTA\GGSSAAREGA\TSCSASGIRAGGEAGRMPE GRGGPGTEPVTVA AAAV\TAAATVVPVISVGSSLYPGPGLGHGHPG LHPYTALQPHLP CSPQYLTHPASPLPTPWPMPMPRAVFPV\PSSAYP QGVHPAFL/WGPGGIPGPAPTSPSY
6085	A	193	388	NRNPNFYNSGSSNFLENSIWSHQLSLLWKLNSLSLSLSCFTAKLG DTKELEAFIADLDKTLAK
6086	A	2	353	AAEDLS DALCE\FDAVLADFASPFHERHFHYEEHLERMKRSSASV SDSSGFSDES\ADSL\YRNSFS\FSEKLNSTPDSTPALLSATVTP QKAKLGD TKELEAFIADLDKTLASM
6087	A	315	413	TFERKWGSKNLHSCNGWSWKGVLLLEISQQFSE
6088	A	2	284	ASSLHVS SSKSFRDFLLEEKSVTSHSSGDHVKKVSFKGIENSQAPK IVSPWLSSSVTAPSMVAPVTFASIVEEELQEEAALIRSREKPLALIQ
6089	A	3	189	PSKAPKPVNAWASSLHVS SSKSFRDFLLEEKSVTSHSSGDHVKKVS FKGIENSQAPKIVR
6090	A	1931	3137	KMEISSLKEEINMEPNHSETMFKKAKTKAKKKPRKRS DSSGGYNLS IIQSPSSTGLLKSGKTNSVESLPELLTSDSEGSYAGVGS PRDLQSPD FTTGPHSDKIEAKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPI PSNRIDTTSSASWVAGSFSPVSPVVDLRTIMEIEESRQKCGATPKS HLGKTVSHGVKLSQKQRMIALTTK\DNNSGLNSMQTVICIPSDAP* TVNE*GSSLHVS SSKSFRDFLLEEKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTGPEGNHISDLPLLDSPNPWLSSSVTTPSMVAP VTFASIVGRGTSTKEAALIRSREKPLAL\IQIEEHA IQDLLVFYEAF GNPEEFVIVERTPOGPLAVPMWNKHGC
6091	A	336	410	LLPQFQSLFLVYSEIQLLPGLVFC
6092	A	40	921	TEVPGVHSENDKNQKKKIRKLDPKKKQVDTVQIIQGSKKGSSFLIFF FSPLIILTVELQGVNVVAQELSIQLELFWRTASQSVTEPTAGLCLL NPGEQEMRALRGRRKPLLLIP\SKQDLEWTSSKLOQTCS*GF*\R*K EN*QTERTSTPKPHLVGSSGQGNQAGEGNKGYVPRKRGSQIVPVC R* HDCISRKPCHLNP/YSLS**ATAAKSQDTK/FNVQKSQAFLYTNK QTDSQIMSELPFTIASKRIKYL SNPTYKGCEGPLQKQLQTIQRNKT EPNKWKNI PVMGEEPM
6093	A	1	1960	MPPHSEQHPSPSTRQKRKVP LFVRQCPSFVIQAPKAKMDTFDGRKKQ FTRFLFLFSMDQLGQGRFSMQTLSFALAVYRKDSPLVACQVQALGNL EPSSVEAHVSSHGIAIDRKGWVSLFSIQPGDCFPALESVSPRDRA RRQSSKEEGWCRDRRLKFHSSKGA AIVVSKKYESPFGVCFES LLNPPRLTSRREKTISSSKRCRQCHAEETT VVFWAKESQTGEQTGRG

				AGQRRMGMIICKACSMLEPAERQDLRPTSLVISHGVSVKDRREHCQCP NYYPPLRNMSPLEHSIKICGGKKPQNDSSQRITTTIKVIVNQDFKQPD DTELSQGSRKETSEASLVTLWELVTAGQTPPLVTPRQTGSGVDLQQ TPTDLQLRVLTIRRKTNKQKGHPKPHLYVTIIKDQRTLHPKSTEYT FFSAPHPTYSKIDHIVGSKALLSKCKRTEIITNCLSDHSAIKLELRI KKLTQNRSTTWKLNLLNDYWVYKEMKAEIKMFFETNENKDTTYQN LWDTFKAMYSKGFMALNAHKRKQORSKIDTLISQLETEKQEQTSHK ASRRQETTKIRAELEIETQKTLQKINESRSWFFEKINKIDRTLARL IKKKREKNQIDTIK\KIKVISPPIPQKYKLLFILFGTGTQIN
6094	A	275	1839	CPSVGFSLQAGVVFSGCKLLTAKDF*QQTQGFSSQ/RLSQLHTHGHRAL QKKAISSKNEFTIMGQISEATSALFGEKESKEATLRGEGARNRDDR DSNCRLLQPPGQDGDGQKVPVKYSAGDTQANRVWSGLQQTPTDLQLR VLTVRRTNKNQKGHPHQNPICTSSASSKTKEIQTIREYHKNLYANKL ENLEEMDKFLDITYTLPRLNQEEVESLNRPIITGSKIEAIINSLPTKKS PGPDAFTAIFYQRYKEELRIKYLGIQLTRDVKDLFKENYKPLLNEIK GHKQMEEHSMLMDRKNQYCENGHTAQELEKTALKFIWNQKRAHIAKT ILSQKNKAGGIILPDFKLYYKATVTKTAWYRYQNRDIDQWNRTEPPE IIPHIYNHLIFDKPKNEKWKDPLFNKYWENWLAICRKLKLDLSFL TPYTKINSRWIKDLNGRPKTIKTLEENLGNTIQDIGMGKDFMTKTPK AMATKAKVGKWDLIKLSFCTAKETTIRVNRQPTWEKIFAIYPSDK GLISRI
6095	A	78	1986	EKTKASDWCT*K*RG\DGTKLENTLQDIIQDNFNPNGRQANIQIQE IQIMPQRYSSRRATPRHIIVRFTKVKMKEKILRAAREKEIQTITISEY YKHLIYANKLENLEEMGKLLDITYTLPRQNQEEVESLNRPIAGSEIEAI INSLPTKKSPPGPDGFTAKFYQRHKEELVPFLLKQFQSMEKEVILPNS FYEASIIILIPKGRDTEKENFTPIISLMIIDAKILNKILANRIQQHI KKLIHQDQVGFISGMQGWFEHKSXNVIIHHINRTKDRNHMIIISVDAE KAFNKIQPPFMLKTLNKLGIQLTRDVKDPFKENYKPLLNEIKEDTNK WKNIPYSWIGRINIVEIAILPKVSLERERQHDQTHVQSLEKLDLLE QEYNKLTMMQALAEKMQELEAKLHEEEQERKMQAKAAEHPRCLCY LAAIFSALKNLQDKIRRELERIQAEESVKTLSTRETIEYKKVLDEQI QERENSKNEESKHNEELTSQLLAAENKCNLLEKQLEYMRNMIKHAEM ERTSVLEKQTPLLIPRQGRSVLDLQQTPTDLQLRVLTVRRTNKNQKG HPHQNPICMSPSSKTKEERSSSPPTERSWTENDFDELREEGFRRSNY SELKEELQTHGKEVKNLEKKIRMAN
6096	A	870	1860	TRKSRRNG*IPGHIHPPKTK\QEEAESLNRPIITGSEIEAIINSLPTK KSPGTDGFTAKFYQRYKEELVPFLLKLFQSIKEEILPNSFYEASII LIPKPRDRTTKKENFRPISPMNIDAKTLNKTLANRIQQHIKKLIHHD QVGFI/HCNARLVQHMQINKRNPAK*NRQKPHDYLNRCRKG*QN STALHAKTSQ*ISVGSSGQGNQAGEGNKGYSIRKRGSQ\MSLFAEDV IVYLENPIVSDQNLKLI SNFSKVSQYKINVLNSQAFLYTNNRQTES QIMSEVPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTTF HANG
6097	A	453	545	VGEVLLDNILWSLMMVYRWGFAVDVLSVC
6098	A	1	235	REVLITTNVCARGIDVKQVTIVVNFDPVKQGEEDYETYLHSIGRT GRFGKKGLAFNMIEVDELPSLMKIQDHFRRS
6099	A	3	706	SAGDTQQTGSGVDLQQTPTDLQLRVLSVRRKTNKQKGHPHQNPICT PPSKTKGVNAMLKRVAVAAASKPHVEIRQDGDQFYIKTSTTVRTEI NFKVGEFEEETVDGRKCRFFDMLRDLLKNVDLKGFEPPDVRILLTKY SNSNGSQSPWMEEQIRDAWGSMLVKNVRETDEVGKVPQAKGNVVI TSLMTNRGFFEEGEATFAPSFLMNIKGNKTSVVKNSILEQQQLTVN
6100	A	368	798	LSYIYMHPIQ/RAPRFIKQALRDSQRDLDSHTIIMGDFNTPLSTLDR PTRQVKNKDIQELNSVLHQVDLIDYRTFHPKSTEYTFSSAPHRTYS KIDHIVGSKALLSKCKRGEIITKIKLELRIKKQTQNRSTTWKLNLL LNDY
6101	A	1	666	MPVTLGTSMRSDSLGEPQTEVEPPLVIPRKTGSGVDLQQTPTDLQLR

				VLTVRRKTNKQKGHPHQNPICTSPPSSKTKAQNLLKLISNFSKVSQYK INVQKSQAFLYNNNRQTESQIMSELPFTIASKRVKYLGIQLTRDVKD LFKENCKPLLKEIKEDTNKWKNI PYSWIGRINIVKMAIQPKVIYRFN AIPIKLPITFFTELEKTTLKF IWNQKEPAFPRQS
6102	A	412	681	GDIIPKCSQPLNIHFHYVFKMR*GSSRPGRGPEIRCFSPAARLLLT HQQWPQLWAIQQVALLPHAGGADHVILFSPVSKATEKIVG
6103	A	489	587	EVPNFPTFPCLLLSPNCLNLCLLTSKAVAST
6104	A	1	1474	MDMLDKGMIQVPVESLECEHFVQEPVLPSELSEKQEPWNQPSLDL EPSFATYMACSMLPAERQDLRPTSLVISHGVSVKDRREHCQCPNYYP PLRNMSPLEHSIKICGGKKPQNDSSQRITTTIKVIVNQDFKQPDDEL SQGSRKETSEASLVTLWELVTAGQTFQDDRMGTAPVYSSQRERRR RVISACPTPEPLVTPRQTGSGVDLQQTPTDLQLRVLTIRRKTNKQKG HPPKPHLYVTIIKDQRTLHPKSTEYTFFSAPHPTYSKIDHIVGSKAL LSKCKRTEIITNCLSDHSAIKLELRICKLTQNRSTTWKLNLLNDY WVYKEMKAEIKMFFETNENKDTTYQNLWDTFKAMYSKGFMALNAHKK KQQRSKIDTLISQLTELEKQEQTHSKASRRQETTKIRAEKKEIETQK TLQKINESRSWFFKINKIDRTLARLIKKKREKNQIDTIK\KIKVIS PPIQKYKLLFILFGTGTQIN
6105	A	1	903	MNGIYSRDTRELFPLCAMGALKEKSVACNVERPSPENHDGQGVDEP LSETGFKQAAAAGIFLNNVKFTHAFSSDLMRKTQPPLLIPRQTGSGV DLQQTPTDLQRLITVRRKTNKQKGHPYQNPICTSPPSSKTKLEKQEQ QTHSKASRRQEI TKIRAEKKEIETQKTLQKINDSRSWFSEKIDKIHR LRARLIKKKRGKNQIDA IKDDKGDITTDPTETIQTIREYYKHYANK LENLEEMDKFLDTYTLPRLNQEEVESLNRPITGSEIEAI INSLPTKK GPGPDRFTAIFYQRYKEEL
6106	A	803	1184	YSLMVVCISLVFDDGDVHMGFCGCPFCLLVLLTVRTLSCRSVGV WRSTPDPVCLGISSGGRASAKVGAPPAASLPPCSLISDSCAGSEQGS VGVGPSRPGAGYNLLVCRLRLPLGKRSIRVRVT
6107	A	1458	1568	TQTNLQEKNTTQSKSGQRV*TDTSRKKTTFMQPTDT
6108	B	24	2456	MGVSSGDLKGLLHPRVRVGNFYVTKGQSVEQVVFVAVGALAKATYDR LFRWLVSRIQTLDTKLPRQFFIGVLDIAGFEIFEFNSEFQLCINF NEKLQQFFNQHMVLEQEEYKREGIDWVFI DFGDLQPCIDLIEKEE RLKPSRKKITKKHTKKRTASLILHAMICCSLNSSKTKNTKCLNSIN QRLKIWSLQKDLKMCGTAGRCKTLHGTSQNLNTTAIHVVLAAGSPKDA DDTSIYMFYQKHILYCIVDSECKSRDVLQSYFDLLGELMKFNVDFAK RFNKYINTDAKVLKQINSSLVDSNMLVRCVTLSDRFEQVDMKAA LLSIPGFVERLCKLATRKVSESTGTASFLQEELEWYTWLDNALVDA LMRVANESEHNQVFWFEQHGVLVSGAEKAPGTTIDQAPRIYRWSLT RTQAQWQSAMTWSMAFTETFLTERDKQSKWSGIPQLLLKLHTTSHL HSDFVEQNILKPLLVI PRQTGSGVDLQQTLDLQLRVLTVRRKTNK QKGHPHQNPICMSPSSKTKKAKNLDKRLDEWLTRINSIEKTLNDLME LNTMARKLRDACTSFSSQFDQVEERVSVIEDQMNMKREKFKREKRI KRKQSLQEIWDCVKRPNLRLIGVPESDGENGTKLENTLQDIIQENF PNLARQVNIQIQEIQRTPQRYSSRRGTPRHIIVRFTKVEIKEKILRA AREKGRVTHKGKPIRLTAVLLAETLQARREWGPIFNILKEKNFQPRV SYPAKLSFISEGEVKSFTDKQMLRDFVTTTRPALQELLKEALNMERN RYQLLQKHAKL*
6109	A	82	1210	LVEGKLTNRKNIHTKTPSVHHHQRPKCGREMWGQSPHTESLLGHHL VELWEEGHCPLDPRMVDPPACTMYLEKPQTLNASL/WKAARSQVPQ GGGKGTCKSETEIQATIREYYNKHYANKLENLEETEFKLDYTLPR LNQEEVESLNRRITGSKIEAI INSLPTKKSPGRDGTAEFYQGYKEE LVPFLLKLQFQIEKEGILPNSFYEASIIILIAKPGRDATTTKNFRTI SLMNIDAKILNKILENQIQHIKKLIHNNQVGFIPGMQGWFNHKS NVIHHIKRTKNKNHMIISIDAGKAFDKIQPFMLKTLNKLGDIDMYL KIIRAIYDKPTANIILNGQKLEAFPLKTGTROGCHSYSTLTTPIQHS V

6110	A	1261	2396	LNALYFLLLPDCPGQN**TASKTNKEEKREESNRCNKK**S\NITTN PTEIQTITREYYKHLIYANKLENLEEMDNFLDITYTLPRLNQEEVESLN RPITGSEMEAIINSLPTKKSPPGPDGFTADFYQSVGSSGQGNQAGEGN KGHSIRKRGSIQIVPVCRA*HDCISRKPRLSPKSP
6111	A	1	819	MCHSAIFTVLQPPPLVVIIPROTGSQVDLQQTPTDLQLRVLTVRRKTKK QKGHPHQNPICMSPSSKTKATFEDSVWHFAERIIIPDPNVIKLRKEEL TLNNIRQYYVLCHEHRKDKYQALCNIYGSITIGQAIIFCQTRRNAKWL TVEMIQDGHQVSLLSGEL\TVEQRAFFI\QRFDRGKETVLIT\TNVC ARGIDVKQVTIVVNFDPVVKQGEEDYETYLQRIQRTGRFGKKRLAF NMIEVDELPSLMKIQD\HFNSSIKQLH\AEDMDEIEKIDY
6112	A	1	1068	MASWEGKDLTPVPQDTRKGSVLRRISSLVPPYEKHPQISLWGNKCDL SLSGGESSSQNTNVLSLEDLKPFIILLNDMEHLWSLLSNCKKTKREKA SATRVYIVLDNSGFELVTDLILADFLLSSELATEVHFYGTIPWFVS DTTIHDFNWLIEQEGVEAEKKAISLLSKLRNELQTDKPFIPLVEKFV DTDIWNQYLEYQQSLLNESDGKSRWFYSPWLLVECYMYRRIHEAIIQ RHRINLSSDFLITPDFYWDRENLEGLYDKTCQFLSIGRRVKLNAQRE FGFLCDCTVAIGDVYFKAHKSVLASFNSYFKMLFVHQTRFISLPLTA ATTGLRLTHSQVPFGKTGFNKSHRKAS
6113	A	3	655	LLSNDQRCISISFNKTRKASATRVYIVLDNSGFELVTDLILADFLLS SELATEVHFYGTIPWFVSDTTIHDFNWLIEQVKHSNHKWMKSCGAD WEEYIKMGKWVYHNHIFWPVPHEYCAMPQVA\HDLAELQKAHLILF KGDLYNRKLTGDRKWEFSVPFHQALNGFHPAPLCTIRTTLKAEIQVGL QPGQGEQLLASEPSWWTGKYGIFQYDGPL
6114	A	3	225	GACGRPPFPFPRPLPRGAPP/PAMAAPFSPPPASAPGAAPTFFPPSLGP AWHPALFLTGINLTCFSKEREKEAQSWY
6115	A	2	624	NRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRV IHGWSYGGYLSLMALMQRSDIFRVAIAGAPVTLWIFYDTGYTERYMG HPDQNEQGYLGSVAMQAEKFPSEPNRLLLHGFLENVHFAHTSIL LSFLVRAGKPYDLQIYPQERHSIRVPESGEHYELHLLHYLQENLGS IAHWLFNQMRFRNQQTQN
6116	A	2	594	NRGSCHRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRV GIHWSYGGYLSLMALMQRSDIFRVAIAG\SPVTLWIFYDTGYTERY MGHPDQNEQGYLGSVAMQAEKFPSEPNRLLLHGFLENVHFAHTS ILLSFLVRAGKQ\YDLQSYQERHSIRVPESG\EHYELHLLHYLQEN LGSRIAALKVI
6117	A	4	310	PVLCGILEWSQTLMTVNEFISIIYIVNEPRDVGCLAQHQLFDQIPELK QDISIPDYCSLGDGEEEEITINAWFGPQGTISPLHQDPQQNFLVQVG AAAGIVAF
6118	A	1	601	LQKWSLEYIQEIAQCRTVPVEVGSRYTDEEWSQTLMTVNEFISKYIV NEPRDVGILAQHQLFDQIPELKQDISIPDYCSLGDGEEEEITINAWF GPQGTISPLHQDPQQNFLVQVMGRKYIRLYSPQESGALYPHDTHLLH NTSQVDVENPDLEKFPKFAKAPFLSCILSPGEILFIPVKYWHYVRAL DLSFSV\SFWS
6119	A	3	306	EIIAFS/DRAED/FRKLGCEVLGVSVDSQFTHLAWINTPRKEGGLGP LNIPLADVTRRLSEDYGVLTDEGIAY\VCAPAGWKPGSDTIKPNVD DSKEYFSKHN
6120	A	1	774	PTRTKGFAGQGSGLGAENAGPRVIVRASRGLPTQLSVMASGNARIGK PAPDFKATAVVD\GAFKEVKLSYKGYVVLFFYPLELHFCGAPTEI IAFSNPCRGTSRKLGL*SAGASRWDS\HFTHL\AW\INTPRKRGEAL GPL\NIPPALLNGEPERLV*GIYGRK*KTG*GAFAYKASLFIKLGK GCPFAKITLLIDL\PVGTLPDEGFCGLVQGLSQVHKTSHGKGFVPA \GWKALPVATD*APTWMARKYFSKHN
6121	A	3	306	KNWPPPRFF/YKGPSSSSSSSSSSSSSSSSSPLTPFFPSSSPGVCPL KGSSSSSPPKKP\GRPPSSSQKGGKPPFFKPPNFFPKNSPTPGGAP LKPFWKNF
6122	A	1	200	PPHNVPRRWSANLYLTP\SNMVLLTAIALIGVCVFILAIIGILHWQE

				KKADDREKRQEAHRFHFDAM
6123	A	2	298	NREEQNLVAYPHDGKIFFCTSDIPPENELLFYYSRDYAQQIGQKNY RCTLCDKSFTQKAHLESHMVIHTGEKNLKCDCYCDKLFMRRLQDLKQHV LIHT
6124	A	1	211	VSPHVLIRQSSRHLSLYLQAPFV*MAGCLETGSHV*TYKDLHVT ITRHLPLKWKTRSTLNFQVARSS
6125	A	1386	2151	DYLCEKHQYRQLCGYLQPCQGSPCVWTPRAGSGRAALRTGMAVLARA AGQRLRARLPPQAQRARAAAGALRERGLCAPPRPPAPGAGRQSPQOS GELRVPSTTSSTCRSCWSARPWGSRRGRAVPQRRRNATATGSPRPLR RLRPAASPRGAASERPNWPDPPRP\RTARSRALNLRSSSKVNATLV PCHKETEAQRGVWTGETIPVRTCFGPLIGQQSHSMEVAEWTDKAVNH IWKAPRNTALKMTQTYNDPAD
6126	A	1	1337	MRNKAVGQARAPPAQLAGWAAPFPKLLDGRPQVFPMPQPVAGCTAT GPREKLGGPGRPRGRVAASVQRLMNEMNLSVPGMEQLTSSSVSNALP VSGSHLGLAASPTHTSAIPAGILSYLADRPPPYIHPNSINVDGNTA LSITNNPSALDPYQSNNGVLEPGIVSIDRSVNTH\GAQSLHPSDG HEVALDTAITMENVSRVTSPISTDGMAEELTMDGVAGEHSQIPNGSR SHEPLSVDSVSNLAADAVGHGGVIPMHGNGL\ELPVVMTDHIASR VNGMSDSALS\DSI\HTVAMSTNSGPRESSAVAPVASHFSVHVFLPS FIWVSPADAETLGESLLGLTVYGSNDQDPYVTLKDTEQYEREDFLIK PSDNLIVCGRAEQDQCNELVHGNIAVGNMTPVIEVWDLDIVDSLEP VFTLGSKLSKKKKKKGKKVKKLINI
6127	A	1	2412	MKMNLSPVGMAQLTSSSVSNALPVSGSHLGLAASPTHTSAIPAGLPV AIPNLGPSLSSLPALSMLPMGIGDRGVMCGLPERNYTLPPPPYPH LESSYFRITLPGILSYLADRPPPYIHPNSINVDGNTALSITNNPSA LDPYQSNNGVLEPGIVSIDRSVNTHGAQSLHPSDGHEVALDTAIT MENVSRVTSPISTDGMAEELTMDGVAGEHSQIPNGSRSHPELSVDSV SNLAADAVGHGGVIPMHGNGLELPVVMTDHIASRVNGMSDSALS SIHTVAMSTNSVSVALSTSHNLASLESVSLHEVGLSLEPVAVSSITQ EVAMGTGHVDVSSDSLSFVSPSLQMEDSNSNKENMATLFTIWCTLCD RAYSPDCPEHGPVTFVPDTPIESRARLSLPKQLVLRQSI VGEVGVW TGETIPVRTCFGPLIGQQSHSMEVAEWTDKAVNHIWKIYHNGVLEFC IITDENECNMMFVRKARNREEQNLVAYPHDGKIFFCTSDIPPEN ELLFYYSRDYAQQIGVPEHPDVHLCNCGKECNSYTEFKAHLTSHIHN HLPTQGHSGSIGPSHSHKWKCSMCPQAFISPSKLHVYFMGHMGMK PHKCDFCSKAFSDPSNLRTHLKIHTGQKNYR\CTLCDKSFTQKAHLG V\HMTIHTGE\KNLK\CDY/CVDKLFYGGSRDLQGRHVLH\TQER\ QIKCPKCDKL\FLRTNH\LKKHLNSHEGKR\DYVCEKCTKAYLTKYH LTRHLKT\CKGPTSSFVQAPEEEEEDDSEEDLADSVGTEDCRIN\S AVYSADESLSAHK
6128	A	1	1767	MQALIPLESFGMTQTSGVSTETGDVVKDMGVNNQSKEGRCPWKDHE AAPWIEKPKKRGNEGKSKKFKNNYSTQPARMERKEEILNPPFEGKD GDTGSI PHKSKEIGFTFPKMDSSFSHTPDTPTEAVDRKGGNFQVN FVELGTLGENKISTVKASTVTEPPAKVTDVSCQEIQGAGFVPSVVS EENKTDAAANRYTAVADKPSERSNDGKSSGSAACEKLPTPTQVVKEG DSFPDTLAKNGQEIAPAQISKSLMVDNYTKDGVPGQERPKGPSAVVP STSTGGVALPITTAIETVNIHGDHSLKNKAELADSMKNEAGIDEGHV IGESSEVHSGASKHSVEKVTELAKGHLLPG/CASRRPEPTRRGQSPR R/T/HADRGNFPAHPVNEEKETKEGSVAVQIPDLLEDKAQKLSFCED QNAQDRNSKGSDSLNNKKVDLTLLSPKSENDKLKEISLACKITELESV SLPTPEIQSDFLHSKVEAPPSEVADTLVIMTASKGVRLPEPKDKILE TPQKMTESKESKTPGEGKKEDKSRMAEPMKGYMRPTKSRGLTPLLK STIQEQERHKQLKSAGMNLPGWNVACGPF
6129	A	893	3822	GKGNHATVNLLSFLQRPQVGSVHPPVVG/HGNQRKSIHVDSLEPQR DLGREAWDIESTPIMMKKKKKPKQKRYSQPRAGGPSDDDNADKPKG HPFAADTQKSGVLPSPQPTTMGTEYGLVSGENLKRECLVNSSAARLVA

				ENFVSESLRIPLYPSEEAPKTAISSQSKLRVEEESKSNKSVLQNDK KLLKQHEYKPPQAPHLKTPVDKSQSVGPLNLKGPLAEVSAYNVETPL DIRLKEGCSFFLDQEVMGVVSKEPTAAKEIPNLVPTLIASNPCECNLK EGNNEKMTKLQNVKLKEFPPEGAEEDKELKKEAFPNERQEISIFTSE QLQGQVLVQVPGVENEPFKRMAGDGKSRKGRSSGKMRDTSKVKAK SELPFLDSQKDGRAVLIPSEPVSKTEGTTQDKSEELGLNSSKQPG TKADLTEAVVMGEPKEMTQPKVAGTMQALIPLESSESGMTQTSGVSTE TGDVVKDMGVNNSKEGRCPWKDHEAAPWISEKPKKRGNEGSKKFK NNYSTQPARMERKEEILNPPFEGKOGDTGSI PHKSKEIGTFFPKMHD SSFSHTPDTPTEAVDRKGGNFQVNFVELGTLGENKISTVKASTVTE PPAKVTDVSCQEQIQGAGFVPSVSEENKTDAAANRYTAVADKPSKRS NDGKSKKVNSSPEKHILENKIDATKIHPMETTGDQIGEG\WPIWT KIEIL/RFTCPRTPELINKSSPLEVLESAACEKLPTPTQVVKEGD SFPDTLAKNGQEIAPAQISKSLMVDNYTKDGVPGQERPKGPSAVVPS TSTGGVALPITTAIETVNIHGDHSLKNKAELADSMKNEAGIDEGHVI GESESVHSGASKHSVEKVTTELAKGHLPG/CASRRPEPTRRGQSPRR /T/HADREPKDKILETPQKMTESKSTPGEGKKEDEKSRMAEPMKGY MRPTKSRGLTPLLPKSTIQEQERHKQLKSAPLYGGCEINLIQF
6130	A	1	1965	MQALIPLESSESGMTQTSGVSTETGDVVKDMGVNNSKEGRCPWKDHE AAPWISEKPKKRGNEGSKKFKNNYSTQPARMERKEEILNPPFEGK GDTGSI PHKSKEIGTFFPKMHDSSFSHTPDTPTEAVDRKGGNFQV FVELGTLGENKISTVKASTVTEPPAKVTDVSCQEQIQGAGFVPSVVS EENKTDAAANRYTAVADKPSKRSNDGKSKKVNSSPEKHILENKIDAT KIHPMETTGDQIGEG\WPIWTKIEIL/RFTCPRTPELINKSSPLE VLESAACEKLPTPTQVVKEGDSFPDTLAKNGQEIAPAQISKSLMVD NYTKDGVPGQERPKGPSAVVPSTSTGGVALPITTAIETVNIHGDHSL KNKAELADSMKNEAGIDEGHVI GESESVHSGASKHSVEKVTTELAKG LLPG/CASRRPEPTRRGQSPRR/T/HADRGNFPAHPVNEEKETKEGS VAVQIPDLLEDKAQKLSFCEDQNAQDRNSKGSDSLNNKVDLTLLSPK SENDKLKEISLACKITELESVSLPTPEIQSDFLHKSVEAPPSEVADT LVIMTASKGVRLPEPKDKILETPQKMTESKSTPGEGKKEDEKSRMA EPMKGYMRPTKSRGLTPLLPKSTIQEQERHKQLKSAGMNLFPWGNVCA CGF
6131	A	1632	2783	VILLSKSLIQENFFFFF*QSFALVAQAGVQWSNPCS\LQPPPPGFN GFSCILIPSSWDYRRVPPCPA\NFVFLVETGFHHVQAGLELLTSGD PPTSAQSAGITGVSHHAQPAEDIANNVTLLFFPLHLFL
6132	A	240	564	NGWEFKHGSPWPGGFFFFFETESRVA/TRLECSGVI PAHRNLCL PGSSDSPASASQLTGTGTAHHARLI FVFLVETGLRHLQSAGLELL/ NLIHQPNPQELGLQA
6133	A	1	1898	MAASGRGLCKAVAASPPFAWRDNTTEARGGLKPEYDAVVIGAGHNG VAAAYLQRLGVNTAVFERRHVIGAAVTEEIIPGFKFSRASYSLL RPQIYTDLELKKHGLRLHLRNPYSFTPMLEEGAGSKVPRCLLLGTD AENQKQIAQFSQKDAQVFPKYEEFMHRLALAIPLDAAAPVDMAAFQ HGSLLQMRSLSTLKPILLKAGRILGAQLPRYEVLTAPITKVLQDWF ESEPLKATLATDAVIGAMTSPHTPGSGYVLLHHVMGGLEGMQGAWGY VQGGMGALSDAIASSATTHGASIFTEKTVAKVQVNSEGCVQGVVLED GTEVRSKMVLSNTSPQITFLKLTPEEWLPEEFLEISQLDTRSPVTK INVAVDRLPSFLAAPNAPRGQPLPHHQS IHLNCEDTLLHQA FEDA MDGLPSHSDLGSAKIHTPKDRKCIPGEKSEDEGRPVIELCIPSSLD TLAPPGCHVVSFLTQYMPYTLAGGKAWDEQERDAYADRVFDCIEVYA PGFKDSVVGRDILTTPDLERIFGLPGGNI FHCAMSLDQLYFARVPL HSGY\AGPLQGLYLCGSGAHPAPYSEILTSITKRVPIQHVPHPQLRL WAVDLAPPQTFGAGSLEGARIY
6134	A	163	513	CLLFFLTSPHSFVFGTFVFDENRVYAPGFKDSVVGRDILTTP\DLER IFGLPGGNI FHCAMSLDQLYFARVPLHSGYRCPLQGLYLCGSGAHP GGGVMRAAGRNAAHVAFRDLKSM

6135	B	1	720	MGCKHWMTCGRARKEGKDDSYMQTOWLHRAFAAPPETCFPLRDHIQ TGRDLYILGTFEKCVFWGGAEREVWRERHQREPGLRAAFAGQLEFPA GVGLAGPALGAAGQPCWPRGNEGLSTRASCGGCTGSSSSASPPVLC SISHQALAAFLRGRSRDLQRAMPEPPTPSMGSCAAGASPTSTTPCSK EPSPIDHPRAEECECTARDWQAAPPAALVRDPLGEASWAPESGGDME SLYI*
6136	A	133	311	QLHADKVS RFATHA/GVPWCDHGLFQFPQPPLKRSSCLSLWSSWDYR HAPHPAIIICLLL
6137	A	1	1098	MGFHHVQGAGLELLISSDPPALASQGAGITGSWKWILAPVILYICER ILRFYRSQQKVITKVNMHFPPLAVIRVIFYRTTELNFYVVTLKEEL GNWAQWVVMHPSKVLELQMNKRGSMEVGQYIFVNCPSISLLEWHP FTLTSAPEEDFFSIHIRAAGDWTENLIRAFEQQYSPIPRIEVDGPF TASEDVQYEVAVLVGAGIGVTPFASILKSIWYKFCADHNLKTKKI YFYWICRETGAFSWFNNLLTSLEQEMEELGKVGFLNYRLFLTGWDSN IVGHAAFNFDKATDIVTGLKQKTSFGRPMWDNEFSTIATSHPKSVVG VFLCGPRTLAKSLRKCHRYSSLDPRKVQFYFNKENF
6138	A	2	241	PPRFKRFSCLGLSSSWDYRCTPPRSANFCI\LVEMGFHHVQGAGLEL LTSDDPPTLASQSAGITGVSHHAGPHRFLINIY
6139	A	3	335	YFISSHFII SFHYVISFHLITFHLISFH/HHFISSFHFIISSFHLFIS FH/HHHLINSFHLISSFHHFIISSFHLISYLSISFQF/HFHYFMSSHLI SSFHLITSHHFINFIISSFH
6140	A	3	137	GVSPCWPGWSRAPDLK*SAHLGLPKCWHYRRPIHDCGQAPHLHC
6141	A	967	1386	KKKKIFIGHQLRWL*RIFFFFFETGSHSVFPQAGVQWCDHGSLOPQS PWAQRSSNLSLPSSWDYRHLPPCLANF\FIFFVEM\GLTMWPRVLN S\G\PSDLPASVSQ/SAGITGVSHRNWPMKIFFFQATASHVAQAG VQWCNLSLQALPPAFMPFSCLLPQPP\SSWDYRSLPPCLANF/CFG FLVETGVSPCWPGWSRTPDLR
6142	A	278	643	GRQERGERERSSRPLGGRKCQ/HWLAVNAQQKLLALQVEKAKVEGV APALGILVVAGCSFAIRRYQKKSDSLKQPQNPVLEAAGVVPVEMSLP HASSSLTLVPCLRRSLDPFLCFPLSLAKV
6143	A	18	479	QRTFCCKGWKGAAKILIDLNNLFLCKLEQKGTDL\LVIAMENYGS LG SKKGVDLPG\AVDLLAMSEKDIQDLKFGVEWDVDMVFASFIHVASNV HEIRKAIANWSKVPTCPPELGSYLPRGTETHSYFYISYSSDQIQIC KPLHYSYGRNYDTL
6144	A	3	282	RSPPA\GSPPPSAPAPRLPPPPAPPPALPFPASRPTFPFPLPVSLPV LPSSRSLSLPPAFLFSFFCIGVLGLLHTRALSIAAYIKAGAIMQLYC
6145	B	26	2671	MAAPGAPAEYGYIRTVLGQQILGQLDSSSLALPSEAKLKLAGSSGRG GQTVKSLRIQEQQVQOTLARKGRSSVGNLHRTSSVPEYVYNLHLVE NDFVGGRSVPVKTYDMLKAGTTATYEGRWGRGTAQYSSQKSVEERSL RHPLRRLEISPDSSPERAHYTHSDYQYSQRSQAGHTLHHQESRAAL LVPPRYARSEIVGVSRAGTTSRQRHFDITYHRQYQHGSVSDTVFDSIP ANPALLTYPRPGTSRSMGNLLEKENYLTAGLTVGQVRPLVPLQPVTO NRASRSSWHQSSSFHSTRTLREAGPSVAVDSSGRRRAHLTVGQAAAGGS GNLLTERSTFTDSQLGNADMEMTLERA VSMLEADHMPPSRISAAATF IQHECFQKSEARKRVNQLRGILKLLQLLKVNEDVQRAVCGALRNLV FEDNDNKLEVAELNGVPRLLQVLKQTRDLETKKQITDHTVNLRSRNG WPGAVAHACNPSTLGGQGGRI TRSGVRDQPDQHGLLWNLSSNDKLKN LMITEALLTLTENIIIPFSGWPEGDYPKANGLLDFDIFYNVTGCLRN MSSAGADGRKAMRRCDGLIDSLVHYVRGTIADYQPD DKATENCVCIL HNLSYQLEAELPEKYSQNIYIQNRNIQTDNNKSIGCFGSRSRKVKEQ YQDVMPPEEKSNPKGV EWLWHSIVIRMYLSLIAKSVRNYTQEASLGA LQNLTAGSGPMPTSVAQTVVQKESGLQHTRKMLHVGDP SVKKT AISL LRNLSRNLSLQNEIAKETLPDLVSIIPDTPVSTDLLIETTASACYTL NNIIQNSYQNARDLLNTGGI QKIMAI SAGDAYASNKASKAASVLLYS LWAHTELHHAYKKAQFKKTD FVNSRTAKAYHSLKD*
6146	A	2	355	FYFLRWSFTLIAQAGVQWRDLGSPQPLPPRFKQFSCLSLNSWDYRH

				APPRPANFLCF/LVETRFLHAGQAGLELLTSGDPPTLASQSAGITGA SHRNRPVQSILRLEGLLETIVQPPT
6147	A	3	277	FFLETEFRSTQSPRLECSGAISAHCNLQLPGPSHSPASASRAAETTG LCHHARLIFVFLVEMRPHHVQSGLEL\ROAICLPRPPKVLGPQA
6148	A	20	364	LHHFPKPICPAHFSACIHWPHQPHPTCACTQAHMCKPKH/THTHACTH /ICVLSGTHPWVHTGVCARSSSSS/PSSSSSLRYTRQVHALLHTAQ PQRLKASEPTPAQLQPGRQEGLTG
6149	A	3	301	STATWAGVQWCNLSLQPLPSGFKPFSCLSLPGSWDHRHLPPCPANF LYCFFLVEMGFHYVGQAGLKLLT/S/GDLCASAPQSAGSTGVNHRVR LGLLIYIP
6150	A	15	352	DSIFTLVCAEHINFLRAGQHWGCVIDCLHYNKQAVTGDHSSSYAERS STPENGREGTREQGERRGCTWGRGGG/QERPSIPDRQKNQGRGGGG NPLSGRGKVKAITIILLII
6151	A	20	416	LVEDFVWYQAAPTLLRALLPSLIGFAGCPSLLHSPLIGHSTAALRGAG SAPVGCGLWWGCGVADPAGSARTMGTRDDEYDYLKVVILIGDSGVGKS NLLSRTRNEFNLESKSTIGVEFATRSIQVDGKTIKAQ
6152	A	24	156	SSFVMELCPELVGWSH*LQE*SRGPLR*RTHSSRYMVKRQE
6153	A	128	880	HYLDVAPFLFPDRALLPSLIGFAGCPSLLHSPLIGHSTAALRGAGSA PVGCLWWGCGVADPAGSARTMGTRDDEYDYLKFAQCLQALGSRHLST PPHRWQPRWCSTQGTGGKVVGAVVGGVWGFTEPRLPAQWCSSGTQAW ARATCCRASPATSSWRARAPSAWSSPPAASRWTPSRRRSGTPLA RSATAPSPQLSLLPSSLWLATSSPTITIALAMAAGNLCPLPSSCR RRRRWCQASQQRGCL
6154	A	310	719	LRTYPTIRGPVREEKWGYVQTESRSVAWAGVQWHC\FTELRGFLVSL TSRMKPRTLAVSPALKVARLEFVSSDVQRWGFHHVGPAGLELLTSS DLPVSASQMAGITGRHRAWPEHVYMDFVHFLKQTEGNLLDL
6155	A	1	169	FFETGSCSVAQAGMQCSDHGSLOPCPPG\SWDPPALASQSAGITSMS HHNHPKLFI
6156	A	525	972	NHLGGFKQILMPRLHPMPKMSFLQVSARQLYFFFFFFFETESHISIVQ AGVQWRDLGSLQPLPPGFKQF\SCLSLPSSWNYRHTLPRPANFLYFL VETGFHCVAQAGLKLLSSGNLPALASQSARITGMSHHARLAVVFFKA LLSSSRTRI
6157	A	300	500	DGLCSKQT*NGVPSITNPIKTANQHOGKKQHPIQGNRTAPSSSVSYM KRCELLPKGTGLEVVRESG
6158	A	1	1889	MGLLQGLLRVRKLLLVVCVPLLLLPLPVLHPSSEASCAYVLIVTAVY WVSEAVPLGAAALVPAFLYPFFGVLSNEVAAYFKNTTLLLVGVIC VAAAVEKWNHLKRIALRMVLMAGAKPGMLLLCFMCCTTLLSMWLSNT STTAMVMPIVEAVLQELVSAEDEQLVAGNSNTEEAEPISLDVKNSQP SLELIFVNEDRSNADLTLMHNENLNGVPSITNPIKTANQHOGKKQH PSQEKPVLTSPRQKQKLNRYRSHHDQMICKCLSISISYSATIGGL TTIIGTSTSLIFLEHFNQYPAAEVVNFQW\FLFSFPISLI\MLVV SWFWMHWLFLGCNFKETCSLSKKKKTKREQLSEKRIQEEYEKLGDIS YPEMVTGFFFILMTVLWFTREPGEVPGWDSFFEKKGYRTDATVSVFL GFLFLIPAKKPCFGKKNNDGENQEHS LGTEPIITWKDFQKTMPEIV ILVGGGYALASGSKSSGLSTWIGNQMLSLSLPPWAVTLLACILVSI VTEFVSNPATITIFLPILCSLSETHINPLYTLIPVTMCISFAVMLP VGNPPNAIVFSYGHQCIKDMVKAGLVNVIGLV\IVMVA\INT\WGV S\LFHLDTPAWARVSNITDQA
6159	A	41	570	SLHDSTADSIRTTCQGVISTLKAHYLRRTFQHILEAADGEDPSYIK\ EFWRNYSIMDAVDMIAWEELKPALMNSMWKKIWPECVQAQRFSDAD NIAQLQKNIVTLARNVAPEEVAEAAVDQLLQSHEEDLSNEELMRLEQ ELAVGEEEREDGPWALWQLTTGRLSAALSHFEAGL
6160	A	3	367	HASAHAFQGLSCVSKLMRDVCGQPCFSPRGMV/LYLQWGKRKYSR\G NSSWQIKEKVVRFSTAFCSVNEWKFADILSMADHLKKCSYNVVEKRE EAIPLPCMCVTRELTKGRSLRSVLKPVL
6161	A	74	295	AEDKSQMLLDLRWSYIRTSSSADRSHASGPRIAHKWSTVDRNRPRY

				DSNNELAEKEQLS*ICSI CSRVFFKA
6162	A	32	342	LMKKIWSLYLGDRAGICLKRKKIGRVVWHVPVPAARGAGVGGSL GSLRLQRAVIALHSSLGDRVTVSKKKKKIKHTSVFHF SFNHNHALK NTLEHMEQI
6163	A	184	556	QTVARRCTALTFIASEEKVLVADKSGDVYSFVSLEPHGCGRLELGH SMLLDVAVSPDDRFILTADRDEKIRVSWAAAPH SIESFCLGHTEFVS RISVVPQTQPGLLSSSGDRHPEALGVQERP
6164	A	251	1133	PND SKRLILFRTKWPQCLSVRTVARRCTALTFIASEEKVLVADKSGD VYSFVSLEPHGCGRLELGHLCMLLDVAVSPDDRFILTAARDEKMRVS WAAAPH SIESFC\LGHTEFVSRISVVPHSARA\LLSSSGDGTLLRWE YRSGRQPALLSPWPVCRSSVDPQAPQKFAASRIAFWCQENCVALLCD GTPCGLHLPAGRPQTAVGVQAAAGVPAPSVGRGFRGDPGAVGAPGLA RKPPWCSYRHRVGDQWQSVPESTVLKKVSGVLRGNWPMLERLCRRRQ LSAVSYKAHVPTT
6165	A	1	392	APMAGCLS FYYLIQQGDDKGFSLYTRDGAGLYKEIWKADRP GNAAWN LAEGEFNAPYPMEVIFEDAFNGPKGGYVALDDISFSPVHCQNQTELL FSAVEASCNYEQDLCNFYQDKKRP GWT\RVKGKPNML
6166	A	3	1459	KLPPPPGECTFEQDECTFT/AGEKKPEQLAQEEG\ETPTS YTGPKGD HTTG VVVSSHLASECPFGLNSDALLPKKICSLVLLLT SFLAASADSG TMLLRWGCLKSKIKMSVGLVPSEISLLGLQMAAFLHMAFPLCQCTP DMYLLLT VGNRNHGRQKQIKGALLYWTF TCRHCARNLNILSTTCKD KVGEFAKLSKIELLEATEKSIGPPEMHKYHCELKNLREKKBQLEDLL ATKIASKVAKLGILLGMP TLEIGGKEGGWGTGYWLR AEKEDGYLC IEGSEGLNTEKIVPVMQERN SININKKDVHSETPAKGHQLQRPKVDK SMKMG RNQHKAENSKTQITSSPPKDPKSSPAREQTCMENEFDKLTE VGFRRWAITNSPELKEDVLTQCKEAKNLEKRLDKLLTRIT SLEKSMN DLMELKNTGRELCEAYTSINSRIDQVEERISEIEDQLNEIKQDDKIR EKRVKRNKQSPKKYGTL
6167	A	1	393	MYGGGTGLLSVYLKKEEDSEESLLWRRRGEQSISWLRLALIEYSCERQ HQLLRVKYTAMQGQDFGGCCSSPGKRSDGLGYAAEII FEAIRGV SIR SDIAID DVKFQAGPCGEMEDTTQQSSGYSED LNEIEY
6168	A	1	1137	MKRKHVPIDDKMLQOKALRLHEDFSKSGSPETS DTKPFTASPEQLQSS EISAQKGGDEV TWQFPSSSTSSMSGSLKPPPLDQGHYMYVDSVYVKHF QEVAQLISPLTTAPMAGCLS FYYQIQQGN DNVFSLYTRDVAGLYEEI WKADRP GNAAWNLA EVEFSAPYPMEPFPLGDKLLGFPVDFGEFRYQ VLMG PLLRLLTHTRGMHTWVVFPAQVKAVLTSDSPMVTGRRWLTEL TVKVAGREESKTGVI FEVAFNGPKGGYVALDDISFSPVHCQNQTEL LFSAVEASCNFEQDLCNFYQDKEGPGWTRVKVKPNMYRAGDHTTGLG KSEICLCGDILGSRELYWPFLHTCKDIDLKKKGSCEEAKTISSLVF DHF
6169	A	1	1793	MAETAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIR KSDGTLQEH DGEICEIHVAKYAEIFGLTSAEASKDIRQALKS FAGKEV VFYRPEEDAGDEKGYESFPWF I KRCATAVGRQORTHADKERGAREKGG EKKAKAKTSGTRKRGGGRERKKKGEQEGKDQRNAQT KGEKRQPHK ANTPPKTLQQRKEKKTGDSHRRKKLKFKESEKVL SQEWEHDFVIETM ATGARPQLLFSAVEASCNFEQDLCNFYQDKEGPGWTRVKVKPNMYRA GD\HTTGLGYLLANTKFTSQPGYIGRLYGPSLPGNLQYCLRFHYAI YGFLKMSDTLAVYIFEENHV VQEKIWSVLES PRGVWMAEITFKKPM PTKVVFMSLCKSFWD CGLVALDDITIQLGSCSSSEKLPPPPGECTFB QDECTFT/AGEKKPEQLAQEEG\ETPTS YTGPKGDHTTG VGYMYIE ASHMVYGQKARLLSRPLRGVSGKHCLTFYHYHGGGTGLLSVYLKKE EDSEESLLWRRRGEQSISWLRLALIEYSCERQHQI FEAIRGV SIRSD IAID DVKFQARP\CGEMEDTPQQSSGYSED LNEIEY
6170	A	2	392	RNKKQGYPAHFVSTFFYPK*KSGGYQAVKRWTKGVNLFQEIEILVP IHRKVHWSLV\QYLQDESKTKRNSDLNLEWTHHSMKPHEIPQQLNG SDCGMFTCKYADYISRDKPITFTQVSEDPLHPFTCY

6171	A	2	386	MNLLVERNKKQGYPALHVFSTFFYPKLKSGGYQAVKR\WTKGVNLF QEIIIVPIHRKVHWSLVVIDLRKKCLKYLDMSGQKGRICEM\VLGY LQDESKTKRNSDLNLEWTHSMKPHEIPQQLNGE
6172	A	3	162	GGGVLTLLVEVSNIFLTIRMMMKISNAQDHLRYVKNKGPWAPSCWVS CSCWT
6173	A	3	407	TRRADPLRTWRWHNLLVSFAHSIVSGIWALLCVWQTPDMLVEIETAW SLSGYLLVCFASAGYFIHDTVIVASGQSASLL\EYLVHVMAMGAFF SGIFWSSFVGGGVLTLLVEVSNIFLTIRMMMKISNAQDHL
6174	A	13	367	KYLFFFLKDHTKVGKRRMSIRLHQNLGRGRTKSLCKLVAGANCRDQ DDPSPRNQPPRSATFRPSPNRCH*IPQ*PYSACPHPGSGGQFRSLR GLIVEYRSSERHISYRRYAGLCEY
6175	A	3	413	AAIEELCGRQAARAEAVRGLRGPRGLR/WPLPWHPPAPAHGAPLARP GARARRSEKPPSEKPRLRSSPRAQEEGPEPPPELALLPPPPPP PTPATPTSSASNLDLGEQRERWETFQKRQKLTSGKCRQAPARHL
6176	A	2	445	RPLPWHPPAPAHGAPLARPAGARR/CEKPPSEKPRLRSSPRAQEE GPGEPPPELALLPPPPPPPTPATPTSSASNLDLGEQRERWETFQK RQKLTSEGAACKLLDTEFYQGLVKHTGGCHCGAVRFEVWASADLHIF DCKYRNYI
6177	A	2	265	FLMESRSVTRLECSSTITAHCNLCPLVSSDSAVSASQVAGTTGMRHH ALVIFVFLVETGFHHVGDGLHLL/NIVIHLPRPPKVLGLQA
6178	A	1	394	WLVGFGFGEFIESRPVAQAGVQWRNLGSLQSPSKFRFSFLNLP SLDYRHTPPSLANFLYLVQMGFHHVGDGLELLTS\DPPTLASQSAE ITGVSHRTQPSAILLQSQSLLPLRTFISSVPVTE
6179	A	3	1306	HEISLGAICAVLLVIMGLFATRCNREKKDTRSYNCRVAESTYQHHPK RPSRQIHKGDITLVPTINGTLPISRSHRSPSSSPTLERGQMGRSQS HNSHQSLNSLVTISSNHVPENFSLELTHATPAVEQVSQLLSMLHQGQ YQPRPSFRGNKYSRSYRQALQMDKFSKDSGRGDSEAGDSYDLGR DSPIDRLLEGFSDFLTDGRIPAAMRLCTEBCRVLGHSDQCWMPPL PSPSSDYRSNMFIPEGEEFPTQPQQHHPQSLEDDAQPADSGEKKKS STFGKDSP\KMRTLGDSTSTSSLLSEMSSVFQRLPPSLDITYSECSEV DRNSLERRKGPLPAKTVGYPPQGVAAWAASTHFQNPPTNCGPPLGTH SSVQPSSKWLPAEEIIPENYEEDDFDNVLNHLNDGKHELMASELVA EINKLLQDVRS
6180	A	21	376	GVSTVIGIGRSRLELWAPPEKYTPPGRPSHPLWLWEGEGGSIRREID TTSSPHQVPVQSWFDDMGNTLNLIPIFEELNGAKDVYTSL/GAAA GPLDCPAFKRRPFHYGTFFHCAFTI
6181	A	3	471	HASAHASAHQVYVVKRPYVDEFLRGMGELFECVLTASLAKYADPVT DLLDRRGVFRARLFRESCVFHQGCYVKDLSRLGRDLRKTILDNSPA SYIFHPENAEVPVQSWFDDMAYTELLNLIPIFEELSGA*DVYTSL/GA AAGPLACPASKRRPSQ
6182	A	1	1953	MNKLRSFRKKDVYVPEASRPHQWQTDEEGVRTGKCSFPVKYLGHV EVDESGRMHICEDAVKRLKAERKFFKGFFGKTGKKAVKAVLWVSADG LRVVDEKTKDLIVDQTIEKVSFCAPDRNFDRAFSYICRDGTTTRWIC HCFMAVKDTGERLSHAVGCAFAACLERKQKREKECGVTATFDASRTT FTREGSFRVTTATEQAEREIIMQMQUAKAETDKIVGSSVAPGNT APSPSSPTSPTS DATTSLEMNNPHAI PRRHAPIELARQGSFRGFPA LSQKMSPFKRLSLRINELPSTMQRKTDFFIKNVPEVEGEAESISS LCSQITNAFSTPEDPFSSAPMTKPVTVVAPQSPTFQANGTDSAFHVL AKPAHTALAPVAMPVRETNPWAHAPDAANKEIAATCSGT EWGQSSGA ASPGLFQAGHRRTPSEADRWLEEVSKSVRAQQPQASAAPLQPVLP PPTAISQPASPFQGNFLTSQVPVGVVVPALQPAFVPAQSYPVANGM PYAPNPVVGITPSQMVANVFGTAGHPQAAHPQSPSLVRQQTFFH YEASSATTSPPFFKPPAQHLNGSAAFNGVDDGRLASADRHTVEPTGTC PVDPFQAWAALENKSKQRTNPSPTNPFSSDLQKTFEIEL
6183	A	3	240	PPTAISQPASPFQGNFLTSQVPVGVVVPALQPAFVPAQSYPVANGM PYAPNPVVGIVCSNCHFIFTLDMGTWVW

6184	A	1	462	MNNPHAI PRRHAPIEQRLARQGSFRGFPALSOQMSPFKRQLSLRINEL PSTMQRKTDFFPIKNADSGLVHKYSLPFRTVSQAFVWPLYSYASLYRS ILVIKSVAKVLDLIDLIVDQTIKVSFCAPDRNFDRAFSYICRDGTTT RWICHCFMAVKDT
6185	B	1	546	MVKPLSLQMVPLHSSLGNRGSLSSENKNTGVWESAASCCMAGCGGPAD GICSEPLGHDQDGRAQSLLLWAKLTRKDRFSSQPRSIPSFDFLKAKA LAKQRETIWEKVFSFPQAGVLSPPGSATLLSTLEQGAVGQKPPSVPC LMGLFVEHLTTWQLTSSVQASKSKREDSPETVIAKQKAQSF*
6186	A	1	1846	MWSVPCLEKVDVLAWTVLCLAVKIKMNKLRSFRKKDQVYVPEASRP HQWQTDEEGVRTGKCSFPVKWQRLFIQSLLAMRSLASASCCHQPAVY SSHGTQAVHAKGCLQAHARACCPSCSTSPAAAAI FAAATPDGPPLPS RPLVNLIEKSQALVRETLTSQASAPNSGRAGQVTVCLS/GANAARW PALEAPVDGTGLWPETQAVSQCLG*E\HSACLERKQKREKECGVTATF DASRTTFTREGSFRVTTATEQAEREEIMQMMDAKKA\QTSVN*TAF PRGRTSTTSTGRLWLMGRPASLARGMSVWMAAGLSAVITSWTRPSR RTSVCGVGTARPATPSQAPLTLMTSAEL*RMFVGNNTSMGTGPSRR PGPCQQPAPSCITSGVLRGT/SAPER/PPCPGPTSEPLVI/VAPASA GATAHGVTAAARSVAEVTSPAWCSAPSTMRTPTTCASASHGQLTGVP AIFTLARRPSAGLLGWWRTWLCMGPQGCS/SPIGPCTRGLQS\PPRM AGRQGHGHPAQPPVEEAPSPAPCTASRLTGPAARRPWRRLSVPGCLG SPLPFRPVTCSAVQPGARSPGESVLSVVALASGSGALLAGVKGVLC IPQAPWKTGHL
6187	A	1	1542	MVILLPGEILIYNEESPRNFSKHIISTFLNTNEPSKVQKTGKKAVKA VLWVSADGLRVVDEKTKDLIVDQTIKVSFCAPDRNFDRAFSYICRD GTTTRRWICHCFMAVKDTGERLSHAVGCAFAACLERKQKREKECGVTA TFDASRTTFTREGSFRVTTATEQAEREEIMQMMDAKKVPVEVEGEAE SISSLCSQITNAFSTPEDPFSSAPMTKPVTVVAPQSPTFQANGTDSA FHVLAHPAHTALAPVAMPVRETNPAHAPDAANKBIAATCSGTEWQ SSGAASPGLFQAGHRRTPSEADRWLEEVSKSVRAQQPQASAAPLQPV LQPPPTAISQPASPFQGNALFTSQPVVPGVVPALQPAFVPAQSYV ANGMPYPAPNPVVGITPSQMVANVFGTAGHPQAAHPHQSPSLVRQQ TFPHYEASSATTSPFFKPPAQHLNGSAAFNGVDDGRLASADRHTV TGTCVPDPFEAQWAALENKSKQRTNPSPTNPFSSDLQKTFEIEL
6188	C	539	1039	MPYPAPNPVVGITPSQMVANVFGTAGHPQAAHPHQSPSLVRQQTFP HYEASSATTSPFFKPPAQHLNGSAAFNGVDDGRLASADRHTVPTGT CPVDPFEAQWAALENKSKQRTNPSPTNAFLHVTYRRRLKLNFKQSLW LCILSIPDREQGVAVKGAQTLCPD*
6189	A	303	2235	VKIKMNKLRSFRKKDQVYVPEASRPHQWQTDEEGVRTGKCSFPVKY LGHVEVDES RGMHICEDAVKRLKATGKKAVKAVLWVSADGLRVVDEK TKDLIVDQTIKVSFCAPDRNFDRAFSYICRDGTTTRRWICHCFMAVK DTGERLSHAVGCAFAACLERKQKREKECGVTATFDASRTTFTREGSF RVTTATEQAEREEIMQMMDAKKAETDKIVVGSSVAPGNTAPSPSSP TSPTSDATTSLMNNPHAI PRRHAPIEQRLARQGSFRGFPALSOQMS FKRQLSLRINELPSTMQRKTDFFPIKNAVPEVEGEAEISSLCSQITN AFSTPEDPFSSAPMTKPVTVVAPQSPTFQANGTDSAFHVLAHPAHTA LAPVAMPVRETNPAHAPDAANKBIAATCSGTEWQSSGAASPGLFQ AGHRRTPSEADRWLEEVSKSVRAQQPQASAAPLQPVLPPTAISQ PASPFQGNALFTSQPVVPGVVPALQPAFVPAQSYV\ANGMPYPAPN VPVVGITPSQMVANVFGTAGHPQAAHPHQSPSLVRQQTFPHYEASSA TTSPPFFKPPAQHLNGSAAFNGVDDGRLASADRHTVPTGTGTCVPDPFE AQWAALENKSKQRTNPSPTNPFSSDLQKTFEIEL
6190	A	795	2728	GLSNFFRGRVPVQPLLQFKILYIHRLEYWASNPQTPHLGQAVKIK MNKLRSFRKKDQVYVPEASRPHQWQTDEECARTGKCSFPANDLGHA EFFESRGMHICEDAVKRLKATGKKAVKAVLWVSADGLRVVDEKTKDL IVDQTIKVSFCAPDRNFDRAFSYICRDGTTTASHGFCR\CFMAVK /DTQGERVEHMQ*ICA\FAALFRRARQKREKECGVTATFDASRTTFT

				REGSFRVTTATEQAEREEIMKQMQDAKKAETDKIVVGSSVAPGNTAP SPSSPTSPTS DATTSLEMNNPHAI PRRHAPIEQ LARQGSFRGFPALS QKMSPFKRQLSLRINELPSTMQRKTD FPIKNAVPEVEGEAESISSLC SQITNAFSTPEDPFSSAPMTKPVT VVAPQSPTFQGT EWGQSSGAASP GLFQAGHRRTPSEADRWLEEVSKSVRAQQPQASAAPLQPVLPQPPPT AISQPASPFQGNALTSQPVVPVGVVPALQPAFVPAQSYFVANGMPYP APNPVVGITPSQMVANVFGTAGHPQAAHPHQSPSLVRQQTFFHYEA SSATTSPFFKPPAQHLNGSAAFNGVDDGRLASADRHTEVPTGTCTCPVD PFEAQWAALENKSKQRTNPSPTNPFSSDLQKTFEIEL
6191	A	1	1825	MNKLRSFRKKDVVPEASRPHQWQTDEESVRTGKCSFPVKYLGHV EVDES RGMHICEDAVKRLKAQRKFFKGFFGKTGKKAVKAVLWVSADG LRVDEKTKDLIVDQTIKVSFCAPDRNFDRASFIYICRDGTTTRRWIC HCFMAVKDTGERLSHAVGCAFAACLERKQKREKECGVTATFDASRTT FTRERSFRVTTATEQAEREEIMKQMQDAKKAETDKIVVGSSVAPGNT APSPSSPTSPTS DATTSLEMNNPHAI PRRHAPIEQ LARQGSFRGFP LSQKMSPFKRQLS\LRINELP/SPTMQRKTD FPIKNAVPEVEGEAES ISSLC SQITNALSP\PEDPF\SSAPMTKPVT\VLAPQSPTFQGTNE\W GHSSG\AASPGLFQAGHRRTPSEADRWL\EEVSKSVRAQQPQAPAAP LQPVLPQPPPTAISQPASPIQGNALTSQPVVPVGVPAHMQPAFVP\ AQSYFVANGMPYPAPNPVVGITPSQMVANVFGTAGHPQAAHPHQSP SLVRQQTFFHYEASSATTSPFFKPPAQHLNGSAAFNGVDDGRLASAD RHTEVPTGTCTCPVV\PFEAQWAALENKSKQRTNPSPTNPFSSDLQKTF EIEL
6192	A	164	282	LMKYIYSKKNHLMKMLITIKISILKALSPFVIRTLPN
6193	A	193	274	HCSGIQRFIHC LLIVKMHRLWKHSLG
6194	A	3	247	FFFFFNRGFIAALFKITKIWKQPRCPSVSEWDKLWY/YTIEHNSALK RNLGSCPQKMRKLSILLSKRRQSEKATYYITATM
6195	A	70	1130	ASRCVAPGRGA/PASPHDVLCLVSPCFEHRKAVPMAPAPASPGSS NDSSARSQERAGGLGAEETPPTS VSSESLPTLSDDSDP/DCP/SAPGAA DSEDTEGFGVPRHDPLPDPLKVPPPLDPSSICMVDPEMLPPKTAR QTE NVSRTRKPLARPNSRAAPKATPVAAAKTKGLAGGDRASRPLSA RSE PSEKGRAPLSRKSSTPKTATRGPSGSASSRPGVSATPPKVP\V YLDLAY\LHSGSSAHLVDEEFFQVRVRLCYVISGQDQRKEEGMRAGP DAATGQOSSIWDRDLQVRVTPGPLVVTLP TFDVSAMHTWYAETHAR HQALGITVLGSNSMVMQDDAFPAKVEF
6196	A	57	361	GLTMDTQKDVQPPK\QQPMI\YICGECH/TPENEIKSR\DPI\RCRE CGY\RIMYKKRTKRLGRFLMARWNAGEFQREWPSPYTLGFGSLPHFW IVCYSFSIFALQ
6197	A	2432	3682	NSLILLFFFFRQSLTLECSGVISAHNLHLPSSSNS/P/ASAS*V AGITGMHRHAWPICIFLVETGFRHVGQAGLELLTSGDPPAPTSQSM* ATTSGLILLLSKILFPFHSTKVFK*SCPS*KILKEENCSVINWFNS ESSYTSKEKNNLVPNAC*EI\TM*VATNCDF/T/SLL*RSNYPKLPH NNETTSQKIHLKIKISRPATSGQW\ILFSLVWWRARKG*GILMIHNG ILY*TIC*IKLHRLP*GMDYPNQPD/MKSGWDKMSHTL*F*GKEIV FDFQNQQNKLSTLYLSVQE**HEEFFRDLKYNKPGSTIKSLVSF/H SLTLFFFFFFFEARSHSASQAGVQWGNIGSLQPAPPGLKRSSYLSLS SWDYRRVPPHPANFCIFCR/GWGFGVSPCCPGSSGTPVLKWAHL SLPNC
6198	A	1	632	KYRQDLTVPPGYCTGEQGAGGRPGETEPWLRPPALLPS\DFLLCASS SGAVLPVRTQDPFLPYPPRAC PQQAASSATTSRPCPEVKEAGWGSP GHLARHALSHVPPPARVVLRLRERWHFCGDGRVLLGSRALRERHLGL MGYQLL/PGEWPWPGPWRI LTPSLRVTCRPLLSQPLPFEELESQRG/ LCPQLKSYLRQKLQALGLRWGPEGG
6199	A	2	313	EVRYDLTQYEHCPDDVLVLGTDGLWDVTTDCEVAATVDRVLSAYEP NDHSRYTALAQALVLGARGTP\RDRGWRLPNNKLGSGDDISVFNPP GRARQLLLRG

6200	A	401	532	KALISPFSLPLSVVPSSPTMASSTSLPSNCSSSSGIFSPSPAN
6201	A	1	864	MAGVPVGSTQPPPCQPKILKERLSSPKTEGALNEPTIDYGFQRLQK VIPRHPGDPERLPKLGEPPWSISSSSNPTRVLAALVGRATCQNWPC GEIHPSGHYTEPLDRARAGRSPPQEALSVTQSRVAVLLALNVKVERE FKGRHHSPTFHGALVLEDANECYQKEVGVSHSVIFGKDWMTYIKPL LCQAHIVILQTGDSLFTPMGKTWSFLYPGFLPWCSSGRIGSRVGLEN ECKVSLSGSSSQPMGEPEGRWSSPEVGPLASPGSPLIAWAKLRFVPP VDDLPLV
6202	A	9	811	YIVTTLRQLGTRGTGPRFIYTALNEPTIDYGFQRLQKVIPRHPGDPE RLPKREVILKRAADLVEALYGMPHNNQEIILKRAADIAEALYSVPRNH NQLPALANTSVHAGMMGVNSFSGQLAVNVSEASQAT\DOGFTRNSSS VSPHGYVPSTTPQQTNYNSVTTSNMNGYGSAAAMSNLGGSPFTLNGSAA NSPYAIVPSSPTMASSTSLPSNCSSSSGIFSPANMVS AVKQKSAF APVVRPQTSPPTCTSTNGNSLQAISGMIVPPM
6203	A	299	826	LEGHCHNLSSLQISASLGFKRFS\CLTSPSSW\DSRNTPPCPANFC/ EFLVENG FHHVQGAGLKLTTSSHPPSMASQSAGITGMSHQAWPTFPV LINFNSLKMCRMCPMATHLGQCPSREYKIHSCSCAELEGQAHHEPDV GVTISIRKCPVPNALWWKELVPGAQGHGPHLEPEGLG
6204	A	1161	2627	RSDATNWGLSHLCFWFWFLRLSLFSLPRLEC NVTISAHCNLFCL LGSSNSPVASL VAGITGRHHAQLI/LLYFFFFLVKTRFHHVDQAD LELLTSGDPPTSASQSAGITGVSHCAR/LSHLCFLPPCLLFY/CYFI YVMLLCY*WSLFLVAQGVQWHDLSLQPLPPGFK*FSCLSLLSSWE YRRSPHPANFFFFFLRR/RSRFVAQGVQWCNLDLSLQPPPPSFKH FSASACRVAGITVACHHAWLIF/IFLYF**RQGFTILARLVLS*PR DPPPSASQSAEITGVSHHAWPILFIYLRQSL/DSVAQAGVQWYNLGS LQPPPPGFKQFSCLSFLSSWDYRRVPPCPANFLCF**RQDFTMLARL VSIS*PHDLPASASQSAEITGVSHRAWPIFCIFF/CFEMESRSVAQ AGVQWRDLGSLQAPPPGFTPFSCLSLPSWDYRCPPPRPANF\CIFS RDGVSPWSLSPDLVICLPRPPKVLGLQA
6205	A	24	617	DPVSTKNTQISHMWWCTPVVPATQEAAREFLENFLSPSTGFECSL FFFFFFFFLSQGSHTVQAGVQWCDHGS LQPQPP\GRKPSSPLCLLS SWDNH/RPANFFYKTTVKSP EE/FLQLAVVGCFACARVYSAFQTEKP QHSSSVGLHRSSFEISAFSHFPI*VFVPWSPPLQYEEPTLSFPSS SIPHCPTSTPPND
6206	A	239	1789	ATAPGQIFFFFFFLRWSLTLSRLECSDAIMAHCNLKLGSRNPPTS AS*V\AKDYSTHQAWLISYF\FFIETGFRHVAKAGLKLTTSSDPPA PASQSAGIKRVRHHVWPSFSYVKNHLFSRGLRALS YKLK*QMQLFFN FLSILSHDFVAVPSCHD\HLRSPETCH**CSVTHLEGLQVHF*L*DV IPVLIQGVSLNSSSSSFLEESQ*DNLILSREWGSHSNLSY\SKVIM* HLTATSSCDTELASASV*VLS*PL*LRLSR*SF*TFLWLLFRDRIQ IIFCLFLKRWSL/DSVTQAGVQW/RNHGSLQPQT PGLGSDTESFFF* ARVSLCHPGLEVQWCNHGSLQASNS*AQVILPP*LPN*LRLQACTIM PG*FCF*ILVEM\GLAMPSLVSNS*AQ/CNHPVLASQSSGITGMRH CARLGRES*FDPLH*TVCPICNFFFFLRRSFALVAQAGVQWRDLSSL QPLPLGFR*FSCLSLLSSWDYGHPSLRSANF/CVFLVEMGVSPCWTG WS*TPDLR
6207	A	2	208	LEHALRPSSKMLLKCSQGGTPQEPPNPRIKRASSLNFLNKSVEDPTQ HGG\QVFLSAALSAPAPWTSPH
6208	A	1	419	SAFSVAVTKKLPTGAACPIKF\TKILMNEGGHYNASSGKFR\CGVLG IYYFHL\HITLGNK\DLAIGLGAQRPSTASGPLMPNTGNHDVSGST ILALKQGDEVWLQIFYSEQNGLFYDPYWTDSLFTGFLIYADQDDPNE V
6209	A	756	966	VGRRILLRKNFGQAQWLMPIIPTLWEAEVGGELLEQSSSLGKFFKKLA GHGRPQNKTLSLKKLKEKNLSK
6210	A	24	365	PTEY/ENL/FPCIKEAF/VVEEWKETLAVL/WPAKQYPFVTPIEER ILMEEGKAFPPSRSTAKQKLDGNPVSPTPV\IGLSPTPNKEEKQDPD

				WPLEPTGHLDGARDTAGPSWLHHRF
6211	A	32	188	KIFFFFLPPQFKILFKRPTGLRVPGKRRALGSGPKAKKAWPTR RLPSFNGYLEGSSNGASTESPGNFVPGKTLQPPGVELGRGRWTAQGO PSRPVALGA*KL
6212	A	122	339	EKGFWFCAQGGKNLPGGNSLEPSASGLKEIFGLNLLNNWE*RGGPKT PGNFWIWKGGV*PLWPGWG*NPGL
6213	C	56	118	MKALPSSQSCGPTSVNSPFH*
6214	C	345	410	MKACHLGTPTQFTGVSCGVQKAF
6215	C	7	438	MQVETGRGLGVGRREGRRQGLAKPRQLPESLLHSARHPSKLGRPKVAS LHEGTAQLTILWANFSQLSFPLDLFLIKRPLXXXXXXXXXXXXXXXXXX XXXSSKLXRD DHA
6216	A	2	80	FLHFYFQTYSKQNNHLNCQKNSNFTQ
6217	A	3743	4059	GCAVFFFFFFFLRWSLLPRLE/CSGTVSAHCNHLHLGSSSSRAAASQ VAGTTGMHHHARLIFVFLVEMGFHHVSNS*PQAIHPPQRPKVLGIIG RDNRHLGLMEWSF
6218	A	3	402	DTMVHLTPVEKGAVTALWGKVNVDVGEALGRLLVGYPWTQRFES FGDLSTPDVAMGNPKVKAHGKVLGAFSDGLAHLNLTGTFATLSEL HWDKLHVPD*NFRLLG\NGLD*MLAHKFGKKISPNOGKLG
6219	C	295	618	MARKCSVAFSGGPGCTWDNLKGTFAHTEVSLHCDKAAPWIPEELSGS WGNVAWSCVLGPFTFGKRISTPPVAGLPNQENWLAWCWLNALGPTSN HLSLAFLAGPISN*
6220	A	2	338	IKKAL*HE*LREKKKSPIRTSQSSKAP*NLPRSSSSSESSNNYQLL* AHKLQKVKEMGKLLLETPNLPLLSQKVAEPLNQPIITSSKIETLIKPY HPEKSYGHDEVTAKFSRA
6221	A	1	2349	AAAMDEQAGPGVFFSNHHPGAGGAKGLGPLAEAAAAGDGAAGAAR AQYSLPGILHFLQHEWARFEVERAQWEVERAELQAQIAFLQGERKGQ ENLKKDLVRRIKMLEYALKQERAKYHKLKYGTENLQGDMMKPPSYSDS EGNETEVQPQNSQLMWKQGRQLLRQYLQEVGYTDTILDVSKRVRA LLGFSIDVTDREDDKNQDSVVGTEAEVKETAMIASELTDASVLD NFKFLESAAADFSDDEDDDDVDGREKSVIDTSTIVRKKALPDSGEDR DTKEALKEFDLVTSEEGDNESRSAGDGTDEKEDQCLMPEAWNVDQ GVITKLKEQYKKERKGGKGVKRPNRSLQDMLANLRDVEDELPSLQPS VGSPSRPSSSRLPEHEINRADEVEALTFPPSSGKSFIMGAEALESE LGPGLAGLTVANEADSLTYDIANNKDALRKTWNPKFTLRSHFDGIR ALAFHPIEPVLITASEDHTLKMWNLQKTAPAKKSTSLDVEPIYTFRA HKGVPVLCVVMSSNGEQCYSGGTDGLIQGWNTTNPNDPYDSYDPSV RGPLLGHDTAVWGLAYSAAHQRLLLSCSADGTLRLWNTTEVAPALS NDIKELGIPASVDLVSSDP SHMVASFSGYTSIFNMETQQRILTLES NVDTTANSSCQINRVISHPTLSISITAHEDRHIFKFDNNTGKLIHSM VAHLEAVTSLAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEFTAHRK KFEESIHDVAFHPSKCYIASAGADALAKVFV
6222	A	2	1802	YLQEVGYTDTILDVSKRVRLALGFSSDVTREDDKNQDSVVGTEA EVKETAMIASELTDASVLDNFKFLESAAADFSDDEDDDDVDGREK SVIDTSTIVRKKALPDSGEDRDTKEALKEFDLVTSEEGDNESRSAG DGTDEKEDQCLMPEAWNVDQGVITKLKEQYKKERKGGKGVKRPNR KLQDMLANLRDVEDELPSLQPSVGSPSRPSSSRLPEHEINRADEVEAL TFPPSSGKSFIMGAEALESELGLGELAGLTVANEADSLTYDIANNK DALRKTWNPKFTLRSHFDGIRALAFHPIEPVLITASEDHTLKMWNLQ KTAPAKKGPVLCVVMSSNGEQCYSGGTDGLIQGWNTTNPNDPYDSY DPSVLRGPLLGHDTAVWGLAYSAAHQRLLLSCSADGTLRLWNTTEVAP ALSVFNDTKELGIPASVDLVSSDP SHMVASFSGYTSIFNMETQQRIL LTLESNVDTTANSSCQINRVISHPTLPISITAHEDRHIFKFDNNTGK LIHSMVAHLEAVTSLAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEF TAHRKKFEESIHDVAFHPSKCYIASAGADALAKVFV
6223	A	5175	5804	IANNKDALRKTWNPKFTLRSHFDGIRALAFHPIEPVLITASEDHTLK

				MWNLOKTAPAKK*EYSTLTLEFYFK*HLSILLYSI
6224	A	3	115	HETDYHKQPWQGEISGIVSTESQ*WGLGGGEVKVKE
6225	A	2	28	TIADRELRYSEDEGRRRGE*REEEGEAARRKRVAKQVGKRANEERK TEERWGDREGRRRSEEMEVSQKERGHATSGREEKENTG*GPRAEI
6226	A	1	236	RTRGRTRGSTHAFVRQLMQRNLDTGPIAGHDNLQKQKENSTPDSSL PETSNEKHISPENMSLKTLRNSNP*DLYDEI
6227	A	3	178	LFGYLPK*VDNMSTKKPCTWIFTLALCITARTWKQPRCPLVGKWIRC SAEALGNRSI
6228	B	1	1050	MVSIWPRDLPASASQSAGITGLIGALVLSVGIYAEVERQKYKTLES AFLAPAIILILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLI MELIGGVVALTFRNQQLLRQQLVLSHTLGCADLSDGPGSGPVKMFMG VPVIPAQPPELLASRLSRGYGLVLSWLEPRYKEMISGMYLGEIVRN ILIDFTKKGFLFRGQISETLKTRGIFETKFLSQIESDRALLQVRAI LQQLGLNSTCDDSLVKTVCVVSRRAAQLCGAGMAAVVDKIRENRG LDRLNVTGVDGTLYKLHPHFSRIMHQTVELSPKCNVSFLLSEDSG GKGAALITAVGVRLRTEASS*
6229	A	3	250	SLCQPGWSAVADSRLTASSISQFTPFSCLSFPSSWDYRRLPPRAIF LYF**RRGFTVLGWSRSPDLVIRLSRPPKVLGLQV
6230	A	135	466	GIDTILTLNQ*SLKTRQ*FTLIIF/IFFFLLRWL/DSVAQAGVQW RDLGSLQAPPRGFTPFSCLSLPSSWDYRRLPRPANFFYF**RRGFT MLARMVSI*PRDLPAEFL
6231	A	593	1030	KCNSSSLNMNEFKPNPFCMKPNSSLIPLGLSAIKVSNKNTNT*NMITI *ILWIIFFFFFLIWSL/DSVAQAGAQCWHLGSLQAPPPEFTPFSCLS LPRSSWDYRHPRPA/NFFVFLVERGFTVLARMVSI*PRDLPALAS QSLWIL
6232	C	17	145	MHRDLFFNIQFISSVYTSLYLLEKICLCKFSIKTLGLIHTMW*
6233	A	82	377	IPGLKRSLLHLSLLNSQSCATLPSYFFFFFFFFFFYFLERRDLAMLPR FSSSPGLK*SLHLGFPEHWDYSHEPPSWLLFFFFIFNNRRVFLNPKF YHNV
6234	A	281	1102	RMNIFPWGWPGLHGSQOATLTGPPGVCSPPNPRQNKGRPSLTWKS CGMFSICFFCSVTKTFLKLQPHQRLKSSKTTYAT*DILKRKVKLCEC RPSFLPFFTAWKPLRICWGAEEGLSSLKEGMLVDSLQPRKPRRCPL PHNRLSTAPTFFDPESIPTDPTLHPLCPKEQRPDPPELPSLGEAPWR *SLPFLHSTPCSLKECETMKPHMCRSPCRGVLTSPATCAQWPDQGWG PVIPGAPFSDEVTVCNSQLLLPEAPACSGNQCLSWFKK
6235	A	2	260	LSLTQAGVQWCDHSSLQ*RLSNWDHMHAPSCLAIFYF*ETTSYYI AQSYLKHGLGSSNPPTSASQGTATGISHWARLDTSQFGH
6236	A	3	224	KSCPPTPGNGAGASLEDLWWSRAGRWGTSKPCPLSAGCPLAFGPP ARLTGASMPPLSALNG*ERRKRQPL
6237	A	3	307	EAWRMSWGPP*ER*PLPSP*GVCSSC/APPLPSVSAGLGEPRPPDVE DMSSSDSDSDWDGGSR/PFTISTPRPRLGCLLHAVLFLARW/PSLP SV*PRTPHCEH
6238	A	265	315	MNEWTRPSCPYPSPHCEP
6239	A	359	785	GNPSWSFPKAMDSPSLRELQQLLEGTEC/GDPCPEAW/PMSWGPP *ER*PLPSP*GVCSSC/APPLPSVSAGLGEPRPPDVEDMSSSDSDSD WDGGSRLSPFLPHDHLGLAVFMSLCCFWPVGIAAFCLAQKVSCLVGL GGDWA
6240	A	3	277	YWAHGKIHSLOAGSGQSCPGTTPGNGAGASLEDLWWSRAGRWGTSK PCPLSAGCPLAFGPPARLTGASMPPLCECPTCRGYFPRNRWPP
6241	A	8	370	RLGEEKAAATGVVHGLDCFFSPRAPTRPGSRLSQDPPGCEI*NPSWS FPKAMDSPSLRELQQLLEGTECEDPCPEAWAGIELGSPFKRDSLCL VPEGFCSSCSPPLPSVSAGLGGTKAP
6242	A	1	351	KTGSHSVAEAGVQWHHPSSL*PQPPGFKQSPHLRFPKCDHRRTPPC PGNFFDLR*RWGSHHVAQAGLELLNSRDPASTSQSARI TAMSHRAR PVSTFLSTSTSCPVLSTFHRSLI

6243	A	2	1036	SHTLSYLKLEVRMDLKAKMPDDHARKILLSRINNYTIPPEEIGSF LFHAINKPNAPIWLILNEAGLYWRAVGNSTFAIACLQALNLAFLQY QDVPLVNLANLLIHYGLHLDATKLLQALAINSEPLDLF*AGEMAY LALKNISGALEAFRQALKLTTCPECENSLKLIRCMQIYPFLYNITS SVCSGNCREKTLDNSHDQKQYFDNSQSLDAAEEEPSESGTDEDPAFS VENSGRSDALRLESTVVDESHGSDEMENSDETKMSEEILALVDEFQ QAWPLEGFGGALEMKGRRSRLTRNTGAEERSPGWKWPETLAMETAEV KMMKQONGLHSRSNV
6244	A	31	372	KRVRLGWVAHTYNPSTLGGQRRIT*TQEALTSLDNIVRTHLYKKFY KLAQVWACGQTCLEGGKEGYVNMSNVHTGGQGDPCGLLGSLSLGRIF GCTWDSYRHAAIAMIFGKLG
6245	A	816	931	DRVLLYCPGWNAV*TWLTVASASSAQAILLPQPPCLA
6246	A	3	119	RRGLAVLPRLVLNSWPQVIFLPHAPKVLGL*AQL
6247	A	2	285	RSVLCECRNSVVSQIWGNRLYLVEYPIMKVEKWAGCCGSCL*SQHF GRLRGVDRLRSGVQGPQGHDETPSLLKMQKWAGVWWLVPVVPACSL
6248	A	3	437	RPRRLFLLRWSFALVAQAGVQWHDLGSPQPPPPGFK*FLCLSLPSS* DYRNVPPHPANFVFLVETGFCHVGQAGF*LPTSGDLSAWASQSAGIT GVSHLARQAASDFNSRDRRSQIPSNQDANQNMEMLNKLKDFPIVT CNT
6249	A	3	459	VLITANLIPAKQCFDCNFLSTFSSVTTEAFVFLCLLVTCVTCMNLFI IIFVHFFSRRVVFLLPILGAPCKMGILFMIQTFLPSLNIQFQGSKCI QQYRILNFYAM*SVTLFLWPIVYKYSFSTISRPTLYNRSTLLPRKDR WKGARQQTPO
6250	A	2	342	FKRQSLTLTPRPEYSGTIIAHYNLKLCCSNPPSSASQEAGTTGTYH DT*LIF*FFVETGSPYVAHAGLELPVSSNPPTSASQSGRIIDMSHHI RKTALLSGKEWTRPPTHLL
6251	A	2	207	ARGDPESTVAEFTPTIPHCSMATLIGLPIKVKLRLSLPQSFKVSW *APGVRPGIEGLLLRMTGRA
6252	A	1	90	RWLIPISPAL*EAEAGRLLLETRSLRPAWST
6253	A	3	290	RQGFPLCNHKGTVTADLOPLPGLK*ISHLSLLSSWNYRCTPPHPAD F*FFVERRSHYVA*ACLELLCSSDLPALISQVRGITGMSTTPGPICL L
6254	A	2	378	AGFTAHVIIILNHPGQ*SAGYAPVLDCHTAHIACKHAELNEQIDRRSA KKLEHGPNFLNSGDAAIDDMDTVKPMCVESFSHYSPFGRFADRMRH TVAAASVIMALDKKAAVAGKGSNSGQKAHKAK
6255	A	3	735	NASGTTLLEALDCILPPTRPDKALRLPLQDVYKIGGIGTVPVGRVE TGVLPKPM\VV\T\FAPDNVTEV*SV*LS\HEALS\EALPGDN/VGA FNVKNVSVKDVRRGNVAGDSKNDPP\QEAAGFTAHIILNHPGQINA GYAPVLDCHTAHIACKYAELEKEIDR\RSKK\LEDGPKFLKSGDAA IVDMVPGKPMCVESFSDYPLGRFAVRDMRQTAVAGVIKAVDKK\AA GAGKVTKSAQKAHKAK
6256	A	328	621	PVFLFCFVLFETESRSVAQAGVQWRDLGSLQALPPGSTPFCSLSLPG GWDYRCPPPCSANFFCIFSRRDRVSPC*PGWSQFPDLMIRRARPLFLK NRKL
6257	A	1	1245	MKAARFVLRSAGSLNAGLVPREVEHFSRYSPLSMKQLLDGSEN ACERTSFAFLRQELPVRLANILKEIDILPTQLVNTSSVQLVKSUYIQ SLMDLVEFHEKSPDDQKALSDFVDTLIKVRNRHNVVPTMAQGIIEY KDACTVDPVTNQNLYFLDRFYMNRISTRMLMNQHILIFSDSQTGNP SHIGSIDPNCDDVAVVQKFPDQPIHIVYVPSHLHMLFELFKAGPT PNSAVQVQNSCRWYGSIQSPECSTNAMRATVEHQENQPSLTPIEV IVVLGKEDLTIKISDRGGVPLRIIDRLFSYTYSTAPTVMDSNRNA PLAGFGYGLPISRLYAKYFQGLNLYSLSGYGTDAIIYLKALSSSEI EKLPVFVNKSAFKHYQMSSEADDWCIPSREPKNLAKEVAM
6258	A	1	248	FPDQPIHIVYVPSHLHMLFELFKV*YFTIIEILPFFKGLTSYIFIS FIIRHKTEASISFPKNASSPPKRKKLYSQCLTKYM
6259	A	1	1456	RLELESRTTASPTLPRLFTPRHPQTPAQAGAHKPASAPAVLARTTRA

				PSEPGSAPSSLRPSSQPQSPPGRVGVKMKAAARFVLSAGSLNGAGLV PREVEHFSRYSPLSMKQLLDFGSENACERTSFAFLRQELPVRLAN ILKEIDILPTQLVNTSSVQLVKSUYIQSLMDLVEFHEKSPDDQKALS DFVDTLIKVRNRHNVPTMAQGIIEYKDACTVDPVTNQNQLQYFLDR FYMNRISTRMLMNQHILIFSDSQTGNPSHIGSIDPNCDDVAVVQDAF ECSRMLCDQYYLSSPELKLTVNGKFPDQPIHIVYVPSHLHMLFEL FKNAMRATVEHQENQPSLTPIEVIVVLGKEDLTIKISDRGGGVPLRI IDRLFSYTYSTAPTVMDSNRNAPLAGFGYGLPISRLYAKYFQGDNL LYSLSGYGTDAIYKALSSSEIEKLPVFNKSAFKHYQMSSEADDWC IPSPREPKNLAKEVAM
6260	C	63	302	MIYKEKRESVSKEDLARATLVTITNIGSVARMCAVNEKINRVVFG NFLRVNTLSMKLLGICTGLLVKRSTKSIVSXT*
6261	A	1	2063	MGYGVTAFFIWAFFSRVLSSCPASKKNELMTAMDICALSLRCATEDP GVAMGRRPACCYRYCKNKPYPKSRFCRGVPAKIRIFDLGRKKAKVD EFPLCGHMSDEYEQLSSEALEAARICANKYMKSCGKDGFIHVRRL HSFHVIRINKMLSCAFRAHASKCFQNFNGMIYKEKRESVSKEDLARA TLVTITNIGSVARMCAVNEKINRVVFGNFLRVNTLSMKLLAYALD YWSKGQKALFLEHEVCVETVNDGQFHSVELVTNLQTLNLVVDKGP KSLGKLQKQPAAGINSPLYLGAFPFWFGMDIGGTLVKLSYFEPIDITA EEEQEBVESLSIRKYLTENVAYGSTGIRDVHLEKDLTLFGRGNL HFIRFPTQDLPTFIQMRDKNFSTLQTVLCATGGGAYKFEKDFRTIG NLHLHLDELDCLVKGLLYIDSVSFNGQAECYFANASEPERCQKMP FNLDDPYPLLVNIGSGVSI LAVHSDNYKRVGTGSLTGCESEFEEA LEMASKGDSTQADKLVRDIYGGDYERFGLPGWAVASSFGNMIYKEKR ESVSKEDLARATLVTITNIGSVARMCAVNEKINRVVFGNFLRVNT LSMKLLAYALDYWSKGQKALFLEHEFGYNIGVIS/SS*DSHTGLSQ LHFEREVRRLSL*GFAHVPLALVCGHLPQW
6262	A	2	527	ILAVHSDNYKRVGTGSLGGGTFLGLCSLLTGCESEFEEALEMASKGD STQADKLVRDIYGGDYERFGLPGWAVASSFGNMIYKEKRESVSKEDL ARATLVTITNIGSVARMCAVNE*INRVVFGNFLRVNTLSMKLLAY ALDYWSKGQKALFLEHEGYFGAVGALLGLPNFS
6263	A	2	186	RNGLRYRQPI*CLIAENFPGLARDIDIWKLETQGVNRFNLKRSSQR QMIVKLSKVKNREF
6264	A	3	180	EMGKGIDSLFNEIIAENFPGLARDIDIWKLETQGVNRFNLKRSSQR QMIVRLS*VKI
6265	A	3	474	GTDVGVKAAHALSHKKLCLKMTQVTTQWLEILQRLCLHDQLSVQHR GLVIAYNLLAADAELAKKLVESELLEILTVVGKQEPDEKKAUVHTA RECLIKCMDYGFIPVS*TATLRDAGSGPVLCRVLGWLGSPGESGHL GIIAVTMKSQYKGT
6266	A	2	651	HSEGRQRKRVRQKTDTVREKGRERERQTGRERE*DRRQTQ*DRQRG RERDKDRDRDREKERDRQTEKETQRERQRTERNRQREGPSPVAIQ LFFHFLFLFFSFFLSCISVCMVCMYVCMYVCMYVCMYVCMYVCMYV TGSHSVAQACSAVVRSLGHCSLRLPGSSSHSSPPASRVAGVTGACPTA PDSISYFQVRDGGFTTLARAGLELLTSG
6267	A	56	901	EEIAVSILLPSALPAPATVGPVALVDGLGGWLCQQAQREQPAE*QP GVLVPPGGRERQGGCSFRGQSLALLSSADFTGPGYKPHSLSKENLV KIIQLDKKPQEGVFPTLGVSMRIKGRDCLSSIRSPRVLSPADRFSM CFPTVKDSVQRTSASAPSSLMIAAEEKCHSSE*PTASGSPQHQTH PGATGPAPLQVETQYTRLSSGLAGPRTLSNESECSKPTLEPKAFWVN KAKFCLCYLVVSPQLIPRHGSDMGSGHTFEIPLARKGCPRQAVW
6268	A	132	378	YHSQRCRRGVIIVLSKSKARSRRSRMKQYKNETVKDKGKYHKNVSMI SLK*LEKPVRLPLEYYYYYYYYYYYYYVQVLS
6269	A	3	399	QRDLTRHISLKSCTGVHLPEPNLNSARRIRNISGHRKSETEKESGL* PALRQILNASWRKVIWEQVIQLVS*TTRELRR*LSVGIDDVGEVT VLVVVFLCSSTIVALLCFSYVSCCLPCWCLLSLCSSF
6270	A	2	250	KKARRSGVILAHCSLELPGSSGSSLSFPASSWDYRSAPPPPSNIFLL

				LF*GRVLTMLPRLASNSWAQAILLRWPPKVLGLQV
6271	A	118	184	QKEKL*KMGAVLKSLCNASIILIRNANKCNRRKSYQPFSSFMNIDAK VLNKI
6272	A	798	1096	KIMLEHLYSFFEAESRSVIQAGVQWRDLCSLQAPPPGFTPFSCSLQ SSWDYRHLPPHPTNFFCIFSREVSPEC*PGWSRSPDVVICLPWPPKV LGLQA
6273	A	3	163	HASAHASGHASGGAEGKQAEVANQDSTEDLPAENGEAKTDDSPASDE AGENDA*SDEAGENDA
6274	A	3	330	INIRFYLSIKASARSTQG*VSSCTKLQIFFFFFFFEMESCSVTQAGV QWRNLSSLQPLPPGFKQFSCSLSPSS*DYRCPPPRPANFCIFS RDGV SPC*PGWSQTPDLR
6275	A	167	363	SPYKSNLLEPSASRFKQFFCLGPLNNWDYRLFPPFPNGFVFKQNR VFFFWPSLV*TPDSRGIP
6276	A	2	354	GWKDMFNVNVLALSICTREAYQSMKERNVDDGHIININSMSGHRVLP LSVTHFYSATKYAVTALTEGLRQELREAQTHIRATCLKPEDVAEAVI YVLSTPAHIQIGDIQMRPTEQVT
6277	A	196	321	EQTKAKCPGAHEQVKN*NN*GHLLSPAHSFHLQKQFDKMI
6278	A	1	923	MERWRDRALVTGASGGIGAARALVQQGLKVGCARTVGNIEELA ABCKSAGYPGTLPYRCDLSNEEDILSMFSAIRSQHSABVDICINNAG LARPDTLSSGSTSGWKDMFNVNVLALSICTREAYQVHEGSGMWTGDH IN*HQ*ACLATRVLPVSVTHFYSATKYAVTALTEGLRQELREAQTHI RATWQLRREEAAAGYQAAITVKLGFCGLHPLPSTSPRPGKAQPLRRP SLLAQCSIPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAV IYVLSTPAHIQIGDIQMRPTEQVTY
6279	A	28	311	AGVQWCRLLSSMQPPRRKLKSLFHLSPSSWDYGCTPPIARLIFVETG FHHVA*AGLKLSSLNLPT*ASQSAGITGMNHQALQFVISIFKSSSFG
6280	A	1	304	QFQGLITLGIHTHTPTQTSFLSSVDLHTHCSYQMMLPESVAIVCSPK FQETGFFKLTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRA VTITDLR
6281	A	62	299	LFFSPQTHPTQTAFLLSSVDLHTHCSYQMMLPESVAIVCSPKFQE*V* RAWFWVFQGGSSREESLRGKGLYSCGLVLCKIP
6282	A	110	276	QSETLSQKKKKKKKNW/YKCGGTHL/LIQATREAEAEELLQTG\GRGC SEPRLLHSTPAW
6283	A	380	507	SMNPGSPVCVMLITRIP/FCIAHAHLRCCMVL*LHHFHFRLSIC
6284	A	14	235	DRVSLCHPGGGCSELRSCHCNLAWVTEQNFVSKQKEKKR*LLYT*L VLPMSDGLHVAQDSFECSSTQICKLS
6285	A	494	789	DHRFAPSHLADFYFFCRDGVVQ*NDLDSWA*PPGLKDHLPS*DHR FAPSHLADFYFFCRDGVVQAGLKLSSSNVPALASQAGIIGVNHCT QPTLCLFKMMYLFNFCHHWVLHLPakeIPEPVFKLPRVFTYFPNCLS K
6286	A	3	107	HIQLCR*LIHTHTHTHTHTHTQFYLFK*HSAC
6287	A	2	214	VDFFFFFFKLDRVSQCCPSWKFSG*WLFTRTDHRTLPQTPIKQSS CLSFPSRWYKCVQHVSSLSPS
6288	A	3	213	LLKQNKH*SRILYPTKLSFMNEREIKSFSKDHMLREFVTTTRPDLQEM QKGVNLNLKTKGWHAP*NLKA
6289	A	1120	1668	SGDALFPLFFLFNFRVTCLRSSLWMHLGKQLPEPPNSRPTVETQKGS S*DT/PPR*SP*ACFHNSLFPRFG*PTLI*QEHLTTCLL/PGDFFFF FF*DRVLPYCPGWEYSAKTMAHGSPNLE*SSHLSLSPSSWDHRRMPL CLAN*KKKKKFQRHGLMLPKLVLSWAQVIVLLWPPKVLGLQG
6290	A	186	297	PNLG*LNPPPPRLKHFSCGLPSSWNKKAIACHGAK
6291	A	59	132	KAVDKKAAGAGKVTKSAQIAQKAK
6292	A	1	335	QISAGYAPVLDCHTAHIAKFAELKEKIDRRSGKKLEDGPKFLKSGD AAIVDMVPGKPMCVESFSDYPPPLGRFAVRDMRQTVAVGVIAVDKKA AGAGKVTKSAQIAQKAK
6293	A	1	457	FETRAGSIAQAGVQWCHLGLLQPPPPGLKRSSCPQP*VTWDYRRTPS

				SPG*FLYFL*KTGCHHVAPGCLKLVSSSDLPLFLASQSAGITDRHQPP CLGPKLWTLRKLGDIFLWFHDNLGYTLGRNTHFSTSRAVIITVFR SFKHSTPDFSG
6294	A	76	343	YTFSSFLYFFTFPLDNSKPKIFFFFFFFFFFFFFKETWIVLIGLNA YM*TPPQK*EALLGNTITHVTRLAKHSVLLT**IE*VHDSTF
6295	A	362	561	LEHNIFLSFETDSRSVAQAGLQWCNLSLQLLPPGFKRFSCISLVS *KAFCGPPQLLNFTPIVQY
6296	A	3	349	FFLETEPSCSVAQVGVQWPDLSLQPHLPRFK*FSCSLSSWDYRH APPHSANLYIFSRDGVSPHWPGRSQTPDLRRPTLLSLPKRLDYSVSH RAQPWPYFRNKEEARPNPFFS
6297	A	42	266	KLILLKIQYFNLLMKCCFRIKGLKEEQRPVVKPFMTGAAEQIKHIL ANFKNYQVNTLSIWIKGLYNFNCKSKN
6298	A	106	860	RRRRLPSVAIMIYRDLSHDEMFSDIYKIREIADG\LCWEV\EGKM VSRTEGNIDDSLIGNASA\EGP\EGEGTEQHS*SLVVDHCHRTYHL AVKASFT\KEAYK\KYIK\DYMTINQQGNLKQORPERSKTFY*QGA V EQIKHILA*FQKTTQSFME\NMNPDGMVALLDYRED\GVVTPYMI F FKDGLRNGKNVKNCGQLFWDLSPVIINWASAWSSTQHQLKTKWGLM VIFELLHFILDWGFLEVEAIVF
6299	A	10	281	SRSFFLSFFLFVEMECHSVAKSGMQWRNIGSLQPPPPGFGNQSFLSL PNSWDYRCLPLHLANFCIISRDKVSPCWSAWFSRST*PTPDLK
6300	A	3	111	FIKIHLPLMLPRLV*NSWPQAILLPWPVKVLGLQA
6301	A	2530	4923	TVPHH/AFILFFF/CFFERESYSAAQTGVQWHNLGSLQPLPPGFK*F SCLSLPSCWDCGHHGVSL
6302	A	2	300	GSFALVAQAGVQWDLGSSQPPPPGPKQFSCSLSSWDYRRALPWL ANFVFLVETGLHHVGQAGL*LLTSSDPPALASQSAGITGVGLASTY FIEVI
6303	A	1	453	RRDYVFIEFCVEDGKDVNVNFEKSKLTFSCLGSDNFKHLNEIDL FH CIDPNDKSKHRTDRSILCCLRKGESGQSWPRLTKERAKLNWLSVDFN NWKDWEDESDMSNFDRFSEMMNMGGDEDDVDLPEVDGADDVSLKI LFSGYFHTIK
6304	A	305	432	FLHFK*MMNMGGDEDDVDLPEVDGADDVSLKILFSVYFHTIK
6305	A	3	306	HEKVTKEPTRRSARLSAKPAPPKPEPKPRKTSKKEPKAKISRGAK GKKEEKQEAGKEGTAPSENGETKAEIHSRSTVNVTSTRGTPPSTL HRKLN
6306	A	1	122	TRPEFPGRTPPSQKG*GKKEEKPET*KERTGPSEKGETKA
6307	A	2	392	CSCSAEAASSGGAAPVRCFTFCFTDIVIMPKGKSPENTEGKDG S\K VTKQEPTRRSARLSAKPAPPKPEPKPRKTSK\KEPKAKISRGAKG K KEEKQEAGKEGTA\PS\EHGETKA\EEA\QKTESVDNEGE
6308	A	3	426	AGNSSIQHGGWTLRHSILSFLSLLPFSRGPQCMGAVQPLVLKQPRD ASLRGCLLGYDSTATGLY*ILCNLRRHPGVMPSCGARVLRDHN PEDI EWLCSCLLEVLSGSLSSSTPGLTLADQAGHSGGIMPLEGSLRSDCC
6309	A	3	374	HAGLGAHPLHHPVIQQEGFLPAPRGFGYRSEVD*IRIPAESTGQNSQ CQLRK*KDDSYFHCYFCGCVCTCRGLQSSTSHQCAAL*LLLPVC LTMLRCISSLIYT*NLKTVHSVRLNFIYN
6310	A	1	230	SGRPFLFFFQGKERVYFIPVVVLFYTVVVQ*LRKNVVRWQKTM EPPR SWLMQLGHTEEGPGYPLLGETETKLRTA
6311	A	2	100	RRPFFFFFFFASCI*NLISPNVQLSNFTCILRN
6312	A	2	192	PDDFFIQRCKVVAQRLWVIAFLRLMTSITSLVQLLQTNADFS LPLA FPLLAIGPIPSISHFP
6313	A	1	451	NTFMVLQVIKFTKDLPVFRSLPIEDQISLLKGAABEICHIVLNT TFC LQTQNFLCGPLRYTIEDGARAPYLTDPRPGVTORDEIDQLQEEMAL TL QSYIKGQRRPRDRFLYAKLLGLLAEELRSINEAYGYQIQHIQGLS AM MPLLQEICS
6314	A	231	1335	EKQESVTATPTRDVMASREDELRCNVVCGDQATGYHFNA LTCEGCKG FFRRTVSKSIGPTCFAGSCEVSKTQRRHCPACRLQKCLDAGMRKDM

				ILSAEALARRAKQAORRAQOTPVQLSKEQEELIRTLGAHTRHMG MFEQFVQFRPPAHLFIHHQPLPTLAPVLPVTHFADINTFMVLQVIK FTKDLVPFRSLPIEDQISLLKGAAVEICHIVLNTTFCLQTQNFLCGP LRYTIEDGARVGSQVELLELLFHFHDTLRKLQLOPEYVLLAAMALF SPAPYLTDPRPGVTQRDEIDQLQEEMALTLSYIKQQRRPRDRFLYA KLLGLLAELRSINEAYGYQIQHIQGLSAMMPLLQEICS
6315	A	636	852	FRGSGPRDKTPNCLISLLFSWQPHYFLQRFYAKLLGLLAELRSINE AYGYIQHIQGLSAMMPLL*EICS
6316	A	1	690	MCPSEMKLPEERSGSNICCSAIFAVLQPLLVI PRQTWSGVDLQQTPT DLQLRVLFVRRKTNKQKQHPHQNPICMSQSSKTKARQASIQIQEIQR MPQRYSSSRATPRHIIVRFTKVRMKEKMLRAAREKGRVTHKGKPIRL TVDLAETLQARREWGPIFNILKEKNFQPRISYPAKLSFISEGEIKS FTNKQMLRDFVTTRPALQELLKEALNMERNNQYQPLQKHAKL
6317	A	3	302	GFRGCKPQALAASTWC*LCSCTEVKN*GLGTSTWISEDVRKHLVDQA EVCCCKGALVDNLCQGSGTEGKCGVRAPTQSPQWGTAWWSYQKRATIL QIPEW
6318	A	1919	2245	PMQRSP*RT*WS*KPWQENYVMRAQDSVADSINWKKG*QRLKIK*MK *SKKRSLEKKE*KEMNKASKKYGT*KDQIYVGLVYLKVTGRMEPSW KTLCRILSRRTSPT
6319	C	395	1096	MAPDDTSGLLEFVGVPQLTFAWVSPAEEAEQRILNLSKCCCLIGPL EASSQRGTRPCLLLKKFTFHKAIDIDSESCDAGQSK*FTIWKGFT ILDAIKNICDSREEVRILTGTGVGKKFILILMNEFEGFNTSVEGVTA HVVEIARELELQGHSEDTVTELLQSHDKTWMNEELLLLDKQPKWFLEM ESTLGEDAVNTVEMTTKNSDYINLVDKAVAGFEKISSSFERSSTV
6320	A	304	475	PRQTGSGVDLRQTPTDLQLRV*LLEGKITNRKQHLHQNPICTSPSS KTKGKDQIYV
6321	A	224	1767	HCLSNVSAGLHPFTSYCLLHEKKFKA AVLSLGEGGCDGADGADGDDG SGMAKSGPLAAGLLEFAGGFLQTLFAWVSAEEAEQPIILLNSKCCCL IVPLEASSWRGTRPCEVIVSEAGASIYSVSPEANKEMPGLDPNLSA VSIARRVQDPLAELVKIEPKHIGVGMQYQHDVSTLLKATLDSVVEEC VSFVGVDINICSEVLLRHIAGLNANRAKNIIEWREKNGPFINREQLK KVKGLGPKSFQCCWAFIRNQPGLYPNVLSANLKLQAKFQGVAVTS SADVEVTNEKQGGKSKTAVNVLLKPNPLDQTCIHPESYDIAMRFLS SIGGTYLEVGPMPQKINSFLEKEGMEKIAERLQTTVHTLQVHHRW VFSQPEGDFRDTDF**TWIFKEEGIVCLEDLQIGTVLTGKVENATLF GIFVDIGVGKSLPIRNVTEAKLSKTKKRRSLGLGPGERVEVQVLN IDIPRSRITLDLIQGVMSIPRRPADDFIFSFPQIDKDKSVVCKL
6322	A	2	64	AFRFSVVRIHERSHTGEKPYECKQCGKAFISSSHFRLHERTHMGEK V*EYKQHSEAFGCSSSF*IHKRVTGQKLCEYKHCSKALD*SSFF*A RKNSHW*ETL
6323	A	168	501	VCSSAQ*QTCFSLVSPM*NLIKEFLNNIKFPQQDGTSGALVSGEN VDYRKIVGVSGVGSYLGSKI FRLGAVAHTCNPSTLGRRGGQITRSGD GDHPGQQGETPSLLKI
6324	A	165	548	SPSQHSLVPSTPLPGSVLWGIGGCLPCAEGSRSSQQGDGWLRRSSVD LAVGDGEGKEVPRPLALGCDLARDGSRTLSPLGPCPKPLGQRWES*E LRKVPGLAPDLSVESAPRSWEAPECCQMLQLSP
6325	A	18	225	TLGLK*SSHLSSLSSWDYRCMPPHLAN*NFCLFVF*RWGLAVLPRLL LNSWPSAILPPWPLKVLELQV
6326	A	724	900	MTSFSDKFQSFQNRGSTIVTIAHFWSRKYLSKDECS*NACVVFIHSI *KWANTKTIFIPD
6327	A	15	185	VPFENPWVDPVRVPRVRFSTGTFRCCA*IS*LLQSGSSQASLCRY NEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR*PRQACVIMRR VKNMQP
6328	A	199	544	PARLGLLEEGRYLITGRGWVWLTPIPAFWAEVARSQGGQKIETILA NMVKPHLY*KYKKLAGGGGYL*S*LLGRLRQENGVNLLGGGACSEP RSCHCTPAWATEQDSVSKNKK

6329	A	837	1096	VQVQGLSILAHLQRVDPVLPNPFLWVGTHLAVLSGDKDDCWVGALAT GVEILLDVGTGQWAGNVGKAAGCGVRGIWGGRCQERRGQ
6330	A	454	526	AEIVPLHSSLGDRARLCLKKKKKK
6331	A	258	488	NTVSTRKYKKLARRSGGCL*SQLLGRLRQENDVNPGGGACSEPRSRH CTPAWATERDSVSKKKKKKCFQSSILLK
6332	A	3001	3080	YEIIKFHKSEYLLIKVIRKCKQIGL
6333	A	6181	6292	LSICRTSFMNPGPSMLLSPEHENDRREEAGCGGSRL
6334	A	3	222	ASVTACRLNCQGCSPQPFPCPHLAAPL*VPNPQLETFFP*ARTQR IPLPSG*PGTPSPKPTNHIPLTDPL
6335	A	2	227	FFETESRSLTQAGMQWPNLGSLOPPRPGFKQFSCSLSPSRWDHRHMP SGLANFCIFSRDGVSPY*SGWS*TPDLR
6336	A	2	218	TWRLAVAQAGVQWRNLSSLQPLPPGFK*SSCLSLPSSWEYRLLPPRP ANFYIFSRDRVSPCWPGWSQTPDLR
6337	A	31	165	GSHTVTQAGMQ*SNHGSLLQLYLP SLRFRSYLNLPSWDQORSNKEG
6338	A	122	376	KMGPLSSSSSLPEAECPPDRAATLGMNKM LSHHWSSIAFPVDPGMG*K AASGPDFETGQAEARLSPPPSLQESSVWPGDFPHQIC
6339	A	3	268	GRVAVRKEKGSFWLVFNWLSDLNWPLPPLPGELA*TFLKSSLRRPA PAPRPPPPQTPSPTPRSLAVSSEGWRLLSMTLESDDLDPDL
6340	A	2	218	IYTHIH*IDPMFSL*GHMEGEVWGLATHPYLPICATVSDDKTLRIWD LSPSHCM LAVRKLKKGKRLSHLNVD
6341	A	1	5748	MPLKLQNCALALHPERVLVATGQVGKEPYICIWDSYTVQTI SVLKDVH THGIACLAFDLGQCSVKAVIDNARRNECGYIPVKLYLQKHSFSLIC LPFYSFLDFLDINQRLVSVGLDSKNAVCVWDWKRGKMLSMAPGHTDR FWSLCGNALTPKRGVFGKTGDLQTLCLACARDELTYSGALNGDIYV WKGINLIRTIQGAHAAGIFSMNACEEGFATGGRDGCIRLWDLTFKPI TVIDLRETDQGYKGLSVRSVCWRGDHILVGTQDSEIFEIVQERNKP FLIMQGHCEGELWALAVHPTKPLAVTGSDDRSVRIWSLVDHALIARC NMEEPIRCAAVNADGIHLALGMKDGSTVLRVRDMTEVVHIKDRKEA IHELKYS PDGTYLAVGCNDSSVDIYGVAQRYKKVGECLGSLSFITHL DWSSDSRYLQTN DNGNKRLFYRMPGGKEVTSTEEIKGVHWASWTCVS GLEVNGIWPKYSDINDINSVDGNYIGQVLVTADDYGI IKLFRYPCLR KESLADSHSDESDSDLS DVPELDSEIEQETQLTYRRQCSAGCTSRAP ASAQLLVKPQEAFTHGRRQRGSSYRGYDCRSNLFYTTQIGEIVYHAA VGVIYNRQNTQRFYLGHDDDLCLTIHPLKDYVATGQVGRDPSIHI WDTETIKPLSILKGHHQYGVSAVDF SADGKRLA\QLA*MIAILLC SG TGRKERNFQ*QEEVKIRFLL*R*TPMCLIN*LQLELNT*NFGVKQGE D*LEEKAT*AHWGKMTQ*CVQCMDGLKRW/HFSGTSTG DVC IWRDIF LVKTVKAHDGPVFSMHALEKGFVTGGKDGIVALWDDSFERCLKTYAI KRAALAPGSKGLLEDNPSIRAI SLGHGHILVGTKNGEILEVDKSGP ITLLVQGHMEGEVWGLATHPYLPICATVSDDKTLRIWDLSPSHCM LA VRKLKVKQGNVGLLEPPYRVPTGAPPSGVMRRGQPSFRPQNGRTTDS LHHVPGKATGTECQPVKAARKGAILCKTTGAELPKTMGTHLLHQGL DLRFAGGPLQTFFAWVPPTPRGITSGGCKTVKRVTELIPVETPLYKV SSNPCWGGLTQSGGTGSRTHLMKHS DYPLAEGVHYTGGNPTCPDCPD SSELGAQSSEAA DSQSDSRPFPQELGSLRQS VAKWPLRICAAALCLG LKELVAAHAGGDL L IHLHRSMEKVVFPQDSTITHCLSWLGVGAPL VLCSSQKAATLV LRESEQVKGDSDLFGNGVAATRTFSELVAKKLARG CSPQWNSESHLVKEKLARGSRPELNGGRCCCFSPDGKALAVGLNDG SFLMANADTLEDLVSFHHRKDMISDIRFSPGIWVPVIGEVDVTASCL TSDKMVLATGDDLG FVKLF RYPTKGKFGKFKRYVAHSTHTVNRW TY DDSM LVTLGGTDMSLMVWTNEMEGYREKRPCDSESDIDSEEDGGYD SDVTRENEISY TIRALSTNIRPMLGIKPHLQQKEPSIDERPPVSRAP PQPEKLQTNVVGKKRP IEDLVLELIFGYRGRDCRNNVHYLNDGDDI IYHTASVGI LHN VATGSQS FYQEHND DILCLTVNQHPKFINIVATGQ VATAPSIHIWDAMNKQTL SILRCYHSGVCSVSFSATGKLLLSVGLD PEHTIT IWRWQEGAKIASRAGHNQRI FVAEFRPDSDTQFVSVGVKHY

				KFWTLA GRALLS XKGLLSTLEDARMQTM LAIAFGANNLTFTGTISGD VCVWKDHILCRIVARA HNGPVFAMYTTLRDGLIVTGGKERPSKEGGA VKLWDQELRR CRAFTLETGQATDCVRSVCRGKGKILVGT RNAEIEV GEKNAACN ILVNGHVDGPIWGLATHPSRDFFLSAAEDGT VRLWDIAD KKMLNKVNLGHAARTVCYSPEGDMVAIGMKNGEFIILL
6342	A	2	252	PPE*LGPN GCGPPTPLPKFW*ILSKNGGSPPIIGPGPILKPP*PL RWIPPCPLPSPKCLRLPGHKPSAPQ PEN
6343	A	289	395	SRICPHRDTRKEYNSY TIAFLINLLKFAELDCIVYFRLNDN*M*IFR CSTIFYNPALAFLHILRKPPTSFF*GRFLLSEMP C*MLLLII*IPNY LIQIIKRSI
6344	A	262	389	PQVTF SIASRYATILL*FF*PCLVFYSLPNQFYVQGLANA
6345	A	1	103	QSFTYCFESF*NLSVFLYCLIYRITN*VYYLYVE
6346	A	7	156	LFSFHVSGTMAHTCN PSTLTG*GRIT*GLEFKTSLGNTVRSHRYRKK KIA
6347	A	94	469	NCTYVIKVYNLIRHMYTPITAIKIISTRFKIYWYSLIFS*ICHI FE TRSLTPIAQAGVWCHDHSS LQPLPPGLR*SSYLSLSSSWDYRHTPPC SANLCVCVCRDRRVSPCYPGWLLNINVCII
6348	A	1	226	FFEMESH SVTQAGVQWPD LGS LQPLPPGFK*FFCLSFPSWDYRHTP PHPAYFCIFSRNGVSPCWPGWPRTDPDR
6349	A	3	308	KDEKGEEDGKEDKNGNEKGEDAKENDDGKEKGDKKEGKDVKVEDEK EREDGKEDEGGNEEEAGKEKEDLKEEEEGKEEDEIKEDDGKKEEPQS IV*NCPM
6350	A	1	239	MDGGTEKPFACPV L*CTKRYKNVNGIKYHAKNGHRTQIRVRKPPFKCR CGKSYKTAQGLRHHTINFHPPVSAEIIIRKMQQ
6351	A	219	690	RRMHAYVSLDPLERPPFFFFFLFFFFFLLRRSFALVAQAGVHWRD LGSPQPPPPRFK*FSCLSLPSSWNYRHAPPRANFVFLVETGLQLPT SGDLPASASQSVGITGVSHCAWPGNWLLKETRCGSSVGRQITGPITP DAWVDPGIPDRYLQA
6352	A	3251	3700	KWPYWLKEESSKLLHHQETS*HSNLGN*ASGLRTL PYRAEQGKE*GM QTSGR*TR*KEALFSITTDQRRPAVGSSSLPAGHL CSSQRRRAFTDL RGEDVLADWSMGGYGWPRRGPRIPTLVGRGAHSMATTTTDPHRVLPA YHQCSPCI
6353	A	3	347	DAWEQTQDTEL VETRPA GDGTFQKWA AVVVP SGEEQRYTCHVQHEGL PQPLILRWEQSPQPTIPIVGIVAGLVVLGAVVTGAVVAAMWRKKSS DRNRGSYSQA AV*DSFLVWD
6354	A	3	174	VVVP SGEEQRYTCHVQHEGLPKPLTLRWDRKGGSYSQAASSDSAQGS DVSLTACKV
6355	B	10	720	MAPRTLVL LLSGALALTQTWAGSQSMRYFSTS VSRPGRGEP RFI AVG YVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETR KVKAHSQT DRENLR IALRYYNQSEAGSHTLQMMFGCDVGS DGRFLRGYHQYAYDG KDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQRAYLEGTCVDG LRRYLENGKETLQRTDPPKTHMTHHPISDHEATLR CWALGFYPCGDH T*
6356	A	3	223	GEKPHKCGDCGKAFNSPSHLIRHQRIHTGQKSYKCHQCGKVFSLRSL LAEHQKIPFGDNCFKCN EYSKPSSIN
6357	A	1	179	RSQVIRHQRIPTGQKSYKCHKC/GQGFSLRSL LAEHQKIHF*DN*CT GNEYSKPSSINCH
6358	A	38	294	LHLMQNRRLHTGDKLHKYDDC\GKAFTSHSHLIRHQRIHTGQKSYKC HQCGKVFSLRSL LAEYQKIYF*DNSSECNEYSKPSSIN
6359	A	2	244	DTSKGIADVPEWFKGSRLNYAENLLRHKENDRVALYIAREGKEEIVK VTFEELRQEVALFAAAMRKMGMYNSVQRMNLYL
6360	A	339	1079	ILSLPLPLLAGGTDIISCFMGHNSFLPVYKGEIQARNLGMAVEAWNE E*KAGWGESGELACTKPIPCQPTHFWNDENG NKYRKAYFSKFP SIWA HGDY*RINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFQVEVE DSL CVPQYNKYREERVILFLKMASGHAFQPD LVKRIRDAIRMGLSAR

				HVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFSNPETLD LYRDIPELQGF
6361	A	1	1047	MVSISWPRDLPASASQSAGITGLIGALVLSVGIYAEVER/HEI*NP* KCLPGSSHHPPHPPGRRHVHGLLHWCAGVPP*QPPELLASRLSRGYG LVLSWLEPRYKISMISMYLGEIVRNILIDFTKKGFLFRGQISETLKT RGIFETKFLSQIESDRALALLQVRAILQQGLNSTCDDSIKVTVCGV VSRRAAQLCGAGMAAVVDKIRENRGLDRLNVTVGVDGTLYKLHPHFS RIMHQTVKELSPKCNVSFLLSEDGSGKGAALITAVGVRLRTEASS
6362	A	2	55	FFLRRSFTLVAQAGVQWRDLGSLQPPPLRFR*FSCSLSPSSWDYRCL PPLLANFLHFQRRSFTILARLLVSNS*PRDLPASASQSAGITGMSH HACPMI*FFFETEFHSCCPGWSAVA
6363	A	167	293	VVKLLGILLNQMKTKMNFQDFTVMTQKMSEKDTKEEILKSSQFHH HORA*KLFDDDETGGKISGFL
6364	A	3	226	FLR*SLAVNQAGVQGRHLRSLQPLPPRFKLFSLLYLPSSWDYSHAPL FPANFCIFSRNDVSPCWPGRSQTPDLK
6365	A	1	648	MVDVGKWIPTLLSPQEIASIRKACVFGTSASEALYVTNDNEVFVFG LNYSNCLGTGDNQSTLVPKKLEGLCGKKIKSLSYGSGPHVLLSTEGK EYKADARWVYFDPTIVSVEILTVALDGSALFLIYAIVKEKYRQV RSWKCESLALLYQVNSLGIKRQSWREQQVCGLSPPSGGLTGSAALG GGPFCGHPVTPKSLAKHLYPVTRQFDS
6366	A	26	612	VGAGGRGWRFAAAVRRRAAGGGLRPGPAPGPRAGGGGPRGAHLALLRR AGALRAGKEYGKADARWVYFDPTIVSVEILAVALDVSLALFLIYAIV KEKYRHFLOITLVCCELYGCWMTFLPEWAHPEAPNLQQPATGWLYW LGFTLFFF*RCVGFLIPRNWLLWAVHGPRTSRKWHQKGNQFQWKEVF SGTFQNP
6367	A	3	292	TPWLRDFHDPIVEVEVSVPGEPLLFSAAPGLPEPRAGHSVPSSGLSVV AFPSFSSDNVPGSLEHLLVLHFPGGDVSLLRPLCLPI*ETFMIPLSR LRPCPSRVSPSFSQHQAQCLSLGLVILSPVASVWLLFHRFLLTMSQVP WSIFLFSISPATCPCSCALCAFLSRSEELRSHLCHR
6368	A	237	1202	LSPRVQVGPAAASAACAGETMWLPWALLLLWVPGCFALSKCRTVA GPVGGSLSVQCPYEKEHRTLKNKYWCRPPQIFLCDKIVETKGSAGKRN GRVSIIRDSPANLSFTVTLENLTEDAGTYWCGVDTPLWRDFHDVVE VEVSVPASTSMTIASITAAKTSTITTAFFPVSTTLFVAGTHASAS IQEETEEVNSQLPLLLSLALLLLLLLVGASLLAWRMFQKWKAGDH SELSQNPQAATQSELHYANLELLMWPLQEKPAAPPREVEVEYSTVAS PREELHYASVVFDSNTNRIAAQRPREEPDSDYSVIRKT
6369	A	2	58	PRVRCFIYTGKAPNLDKMAADDLLAAADKVR*EGSKPRQNG
6370	A	1	1136	MSSGPVAESWCYTQVHFLFNCFLFFYQQIKVVKFSYMWTINNFSFC REEMGEVIXSSTFSSGANDKLKWLVRNPKGLDEESKDYLSLYLLLV SCPKSEVRKFKFSILNAKGEETKAMESQ\AYRFVQGDWGFKKFI RRDFLLDEANGLLPDDKLTLCFCEVSVVQDSVNISGQNTMNMVKVPEC RLADELGGLSENSRFTDCCLCVAGQEFQAHKAILAARSPVFSAMFEH EMEESKKNRVEINDVEPEVFKEMMCFIYTGKAPNLDKMA\NDLLAA DKYAL\ERLKVMCEDALCSNLSVENAAEILILADLHSAQDKTQAVD FINYHASDVLETSGWKSMMVVSHPHLVDEAYRSLASAQCPFLGPPKR LKQS
6371	A	21	358	GCRHSASCAAPRALGPAPAPQR*PKAGRVFPERTS*T*G*PAPGRRH PGPRIGRRRRSGCSRVRSSVRDC/PSSRSKASNPPLSLSSST\GC DGARPPCSV*RWSRFPGARR
6372	A	1	1458	SLPRNLPTVITISQDFGDASPRTNQGEADDSSTSEESPEDSKYFLPYH PPQRRMNLKGIQLQRAKSPISLKRTSDFQAKGHEEGTDASPPSCGS LPITNSFTKMPRSRSSIMSITAEPGNDISIVRRYKEDAPHRSTVEE DNDSGGFDALDDELAAGETVAQSPPGVPCQPPLFQGSPLCQLRLP TDETKDEWSSLMGKHQRYQVLKRDDSHERYSFQPSIIHSSSSSHQSE GLDAYDLEQVNLMFRRKFSLERCNRNRPQRKGLAKAMQHGRGKVGPR YPAPVIHDTVEPDPSGLRSLWGTGCAQGPCSTRR*MATASPPSSP

				CWGATREGASCTRSSLALWPRKPASVRATSCCC*KAASEARGVSRW THAPKRKPTGPSRGAAAPSRCT\KGQPRSPAENPWACRI*CGQHLQS PELRSSSTALQVWNSRERKFI PAGVPEAGEGHGGRPDHIGGLVLHPAE PEHLQAPAGRLHHVPEV
6373	A	103	226	CCFEILKLMKILISEMHLMLFFL*QLRKSA*IPYVPELFLS
6374	A	112	303	SGVMVSFNVRVLLIILEWNPFLTYSPPRLGLEIFFLFYFNVFFFRKTP LLLCITIKYFISLNCIDF
6375	A	3	109	AWKFFFYFILLFFFLKHHFYVQ*NISLA*KKKK
6376	A	22	175	THDHVSVYFFFLGLKSTEIQCDIKMQIFLFI*VENHLPVSIYILKYF LWIL
6377	A	1596	1878	TMSDTTFKALR*QLPVTRTKIDWNKILSYKIGKEMQNA
6378	A	394	626	SDSVNPQLRVFKILN*SLGILKTHIQIKLFFFFFFFSALTFALGTL LVC VSIYLYGLPRQDTSIQOGETASKERVIGV
6379	A	2	101	KTLVPLILPIITLANPCKKD*YPYVVKISIAAC
6380	A	1	297	SRFKRFFCLSLPSSWDYRHAPTHALANFVFLIETGFLHVGOAGLKL T*GDLPALASQSAGITGGNHCTRQVQCFFRCWGYTRESGQKLDPA RV MFENK
6381	A	1	394	TGTHHFYLLLVLLFLEMGPQSITQADVQGHNHSSLPQPTPGLKQSS RLSL*NSWDYRHTPPHPANFFRIL*RQGSYVAQG*SQTPLKQFSR LGFPKRWGYRHESPHMARDRYSYCPHPDEETGDPER
6382	A	3	160	QL*WSHLKMLQRYSSCNV**KRRGLIRTYGLDMCSQSLCQYAKDIG FIKLD
6383	A	1	1240	MRRRKRAPAGILFLRPRRRGWPRGSGYRALPLGDFDRFQOSSFGFLG SQKGCLSPERGGVGTGADVPSWPSCLCHGLISFLGFLLLLVTFPIS GWFALKPEEAERVKAQVQALGLAEAQPMVAVQSVGAHPVPVYAFSI KGPSYGEDVSNTTTAQKRKCSQTQCPRKVIKMESEEGKEARLARSS EQPRPSTSKAVSPPHLDGPPSPRSPVIGSEVFLPNSNHVASGAGEAE ERVVVISSESDAENSPAQAATPDAEPHSEPPDHQERPAVHRGIR YLLYRAQRAIRLRHALRLHPQLHRAPIRTWSPHVQASTPAITGPLN HPANAQEHQAQLQRGISPPHRIRGAVRSRSLRGSSHLQWLNNFF ALPFSSMASQLDMSSVGGPHAPQLIPDTHLPTLIEGR
6384	A	3	3129	KLGSMEPAPARSPPRQDDPARPQOEPTMPPPETPSEGRQPSPPSPTE RAPASEEEFQLRCQQCAEAKCPKLLPCLHTLCSGCLEASGMQCPI CQAPWPLGADTPALDNVFFESLQRRLSVYRQIVDAQAVCTRCKESAD FWCFECEQLLCAKCFEAHQWFLKHEARPLAELRNQSVREFLDGTRKT NNIFCSNPNHRTPTLTISIYCRGCSKPLCCSCALLDSSHSELKCDISA EIQORQEELDAMTQALQEQDSAFGAVHAQMHAAVGQLGRARAETEEL IRERVRQVVAHVRAQERELLEAVDARYQRDYEEASRLGRLDAVLQR IRTGSALVQRMKCYASDQEVLDMHGFLRQALCRLRQEEPQSLQAAVR TDGDEFKVRQLDLSSCITQKDAAVSKKASPEAASTPRDPIDVDLA EEAERVKAQVQALGLAEAQPMVAVQSVGAHPVPVYAFSIKGPSYGE DVSNTTTTAQKRKCSQTQCPRKVIKMESEEGKEARLARSSPEQPRPST SKAVSPPHLDGPPSPRSPVIGSEVFLPNSNHVASGAGEAEERVVVIS SSESDAENS/CEWPRSSAQDSCLPFPQVPGGTATAGDSQTCLAPGE FSSEALSPKLC*GQSPNDSCMPGPPQPSHYTRARSSSEMLIACVQST VSFLECPRLPSGASLCIFCPLSPQ*GGLDKNPFLGLLQPVGASEGVS GHRAAI*GPNK*GLTPSM*KDI*IHSTVKQVASWVVTLLSLEVYY*R LDYHLSRGKGLNRVKGWTGWPLRSLPALSLRFCIGKCMETAEAP QSSPAHSSPAHSSPVQSLRLRAQGASSLPCTYHPPAWPPHQPAAEQAA TPDAEPHSEPPDHQERPAVHRGIRYLLYRAQRAIRLRHALRLHPQLH RAPIRTWSPHVQASTPAITGPLNHPANAQEHQAQLQRGISPPHRIR GAVRSRSLRGSSHLQWLNNFFALPFSSMASQLDMSSVVGAGEGR AQTLGAVVPPGDSVRGSMESQVQVPLEASPI TFPFPCAPERPPISP VPGARQAGL
6385	A	2	416	ACCLLYRGDMVPKDVNAAIVTIKTKRRIQFVD*CPTGFMDGINYQPS TVVPVENLDKVQRAVCMLSNNTTAAEAWARLDHKFDLMYAKRAVHW

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				YMGEAMEEGEFSDAREDMAALDKDYEEVDADSVQR*GDEGQY
6386	B	95	412	TNRSIQFGDWCPTGFKVGINYQPPTAVPAGDLANVQRAVCMLSNTTA IAEAWARLDHKFDLMYAKRAVHVWYVGEEMEEGDFSKAREDMAALEK DYEEVCVDSVE*
6387	A	2	614	GALNVDLTFEQTNLVPYPRIHFPPLATYAPVISAEEKAYHEQLSVAEIT NACFEPANQMVKCDPRHGKYMACECLLYRGDVVPKDVNAIAAIKTKR SIQFVDWCPTGFKVGINYQPPTVPGDLAKVQRAVCMLSNTTAIAE AWARLDHKFDLMYAKRAVHVWYVGEEMEEGEFSEAREDMAALKKDY EVGADSADGEDEGEY
6388	A	151	1605	RGKTLRGLWRFGKIPTHSENMRRECISIHVGQAGVQIGNACWELYCL EHGIQPDGQMPDKTIGGGDDSFNTFFSETGAGKHVPRAVFDLEPT VIDEVRTGTyrQLFHPEQLITGKEDAAANNYARGHYTIGKEIIDLVLD RIRKLADQCTRLQGFLVFHSGGGTSGSFTSLMERLSVDYGGKSKL EFSIYPAPQVSTAVVEPYNISILTHTTLEHSDCAFMVDNEAIYDICK RNLDIRPTYTNLNRLIGQIVSSITASLRFDGALNVDLTFEQTNLVP YPRIHFPPLATYAP\VISAEK\AYHDQLSVAEITNACFEPANQMVKCD PRHGKK\MACECLLYRGDVVPKECHMLAILPPS\KTKRTYPCFVDWVR PSGFHRCGISTIQP\PTLLVPG\GDTGARYQRSCVHC*ANTTAI\AE AWARLDHKFDLMYAKRAV\HWY\VGEEMEEGEFSEAREDMAALEK YEEVGVD\SVEGEDEGEY
6389	A	1	251	CLKEISFLNGSLTPGA AVKSWLTATSACSPKGFSCLSLSSSWNYRCA PRPTNFCIFSKDRVSLFLLFSLFLPLLARLVLY*PQVIHLPWTP KVLGL*AAVKS WTATSACSPKGFSCLSLSSSWNYRCA PRPTNFCI FSKDRVSLFLLFSLFLPLLARLVLY
6390	A	3	446	RLFFFFFVFLVEMGFCHVGQAGLKLVTSCDPPTSASQSAGIAGVSHR A*PNTSLK*KLTDSPGICFFVCFEIES
6391	A	2	176	CKFAHGNAELHEWEERRDALGMKLNKARKDHLIGPNDNDFGKYRFLF KDLN*YAGFYV
6392	A	186	374	GWQPYWGLWVLRAAGRMPAHQALPTYARSFSLSVSGAFVKTWLPFIL LLGIILTVSLVFNLR
6393	A	872	1122	LRPWKPLCSSVERLWLP AVELLP PPPAGVLPQPSAQYGERRTFGLTC QGGPGTRAGPSMGCTGYT*RVSIQVASGPFHHWPL
6394	A	3	415	ERLWLPSEVELLP PPPAGVLPQPSAQYGERRTFGLTCQGGPGTRAGPS MGCTGYT*RVSIQVASGSPPLASRMVQRGWLGPFVRLLPAAALGDM CAHLASSSPCSPLLTVPASQVPPKELDPISPCSLRPRKVS GP
6395	A	3	349	VSVVEFLCSKRFAQWHLAQHQLLHTGEKPFPCLECGRCFRQRWSLA VHKCSPKAPNCSPRS AIGGSSQRGNH*KGKDLRSFHFMEGPRKKG EEPQVIQGRVRTKPGSPAAQS
6396	A	2	352	EGAAPSSGGPLRDFWGFPRNTNKPCSGTG*SLQRICWMA SLAPPGPA PRGQAPHTHRPLGRPSRGAQVQPAQAQATSKQSPGPGFWSQLPQD LTTASVSPSVNGASKACLECKS
6397	A	2	361	GGEDPPALCRKPTAQQTGKKHSGTAAVRSRERHKEVRAGHSLSALD SPPSLLPGILSPVHQCDVTRVDPIPSLLTALLWLPSAPK*RSEPHKP GVGDPVWSAPPTSGEDLILLATSAH
6398	A	11	967	GSWSGLGARPPGGWNYTGSKKLSPGGEAL*MKRSKELITKNHSQEET SILRCWKCRKCIASSGCFMEYLENQVIKDKDDSVDAQNICHVWHMNV EALPEWISCLIQKAQWTVGKLNCPFCGARLGGFNFVSTPKCSCGQLA AVHLSKSR TDYQPTQAGRLMRPSVKYLSHPIVQSGCDKEALLTGGS ENRNHRLNMMARNNDPGRLTEALCLEVRPTYFEMKNEKLLSKASEP KYQLFVPQLVTGRCATRAFHRSKSHSLDLNISEKLTLLPTLYEIH SKT TAYSRLNETQPIDLSGLPLQSSKNSYSFQNPSSFGS
6399	A	105	465	SRAYCSLTLD FPGKQSSHLSPQVAGPTGACYHAWPIF*ILAQMRSH YVARAGLELLSSRDPPASASQSAGVTGISHHAWPVLLLYLAGTQSPE HFIYDGLDNVSSCLHANFSSLSYST
6400	A	1	463	HKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYDILELPYHGD TLSMF IAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETE

				VDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQVKKIEVNE SGTVA\SSSTAVI
6401	A	3	569	NQASLSFLHLRPPYSGHLIRGTPGRGWGKVGAASQRGPRLEQPLAAIC RFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHGPQAL*K VKIEVNESGTVASSSTGESGSGEAPRVSPSPFRITGPQTRKGPRSP LGTEQLCLCSAITHSPVVSQPGKRAWDHGTLPRLMAPKFPDCEKAS
6402	A	3	194	FFFFTCTQMFITALFITAPNWKQPRCPSIGQ*TNLFNEAVLSREESI KTKTRDRCYHMDRISK
6403	A	2	223	EMESCSITQAGVQW*DLSSLQPPPPGFQRVSCLSFPSSWDYRYLPFR LANFCIFSRDGVSPC*PGWSRTPDLR
6404	A	2	247	RLFFFF/CFEMESHSVTQAVVQWRDLGSLRPPPPGFKQFSCLSLS SWDYRHTPPHPANFCIFSRDGVSPCWPG*SRTPDLR
6405	C	65	211	MSPNWRWGPPCLATPQGVTPSDTQPCQALGLGPHPRNVQPPIISGT G*
6406	A	1	112	GGRGCNQS*SRHCTPAWVTKQGPISDIDILIRPPLTI
6407	A	259	380	GCVQQGVNVQHCAGQQHL*ENGPGSSDCGWHRGHPLCRL
6408	C	5	160	MGFEGGPKILNWKFKKVXQXSCLXKGQXESIFLNTXKVIRAGDTXK SVLG*
6409	A	117	207	KKTMFRQKLFYKRKQLQKQPRP*GAGFKV
6410	C	155	394	MLKWIYRIFVNLFLVFRVFNCSFLCAECISLPGQECGGAEVSSFSR TFPQHLLSLYLMXXXXXXXFLQALGLCYPIQ*
6411	A	68	547	LDNRCERCLTEGGWLTSHHTAPRGKGTWGQKKEPASWGPWGCQW*RG *WPTGCKQGRGSPSPQPLGSGGRHEPGQAKATKASPSQEGDKGRP RQQGSPWSKSSPRPISDPPTPGDGKGPSSTSLRL*TRLEPDLVSL GISAGPTRWTLTSAVQLQ
6412	A	11	321	KNFYLF*DGVSILVAQAVQWRDLGSPQPPPPGLKLLSCLSLPSSWDY GHVPTMG*FCTFSRDGVSPCWSSWSRNSRISDASACLGLPKCWEFT RRDNSAPRS
6413	A	17	237	YVAQAGLNLASSQSSCLSLPKHWDYECEPLCLAFFFFLL*RQGLAM LPRIPLPIKISIRWRNGQKMHQVL
6414	A	806	1681	AMGIHCLTTRTTERSMPTTSAAVLPGPMRQWQLQLPCCIITQSRPCP SCHKSRIQWPVTSPPPLSIPTIDTCCRPQELLPQLLLQQQPLLLLL QLPLHITGGIGAPCVLQPSPLLERATVTGMRVSCPKLQQPRGILC TTWPGMSGSSMPIGRVTATNAKARCRHAADTALPAASASCVGTTTAA CWAANAASATTPSCACCFMPPASCSTSLCCWALHCRPCCEPTRPST WLPSSCFPGSC/CRDHHCRLLGRCVGFNGYRPFCLL/SSCRR/PSC STSLCCWALHCRPCCEPTRPSTWLPSSCFPGSCCSQPHCPTTLWSTL TPLSHGRLWLQSQTLSSPWALWKSRSVSGSLH
6415	B	61	516	MTTLKKNLADDDAVSCLVLGTENKELLVLDPEAFTILAKMSLSPVPV FLEVSGQFDVEFRLAAACRNGNIYILRRDSKHPKYCIELSAQPVGLI RVHKVLVVGSTQDSLHGFTHKGKKLWTVQMPAAITMNLLEQHSRGL QAVMAGLANGE*
6416	A	360	861	RCGSFLQLLLPMPKPADTALPAASASCVGTTTAAACWAANAASATTP SCACCFMPPASCSTSLCCWALHCRPCCEPTRPSTWLPSSCFPGSCCS QAECLWHSPLWPS*RTRAWRVCCAGLGCSSMGCCCCGARPHGSLG ASTPMTWVPATTCRQPWAPARRLGP
6417	A	2	263	NPRDGPTAACWAANAASATTPSCACCFMPPASCSTSLCCWALHCR PCCEPTRPSTWLPSSCFPGSCCSQP*SPLSSCKPLKPPVF
6418	A	18	211	NEPRASTLTSSKAGQRQAPWTLFPNSYPL*EYPPANPFQGGPHDCRA QTKDMGAQAPRVPEAGP
6419	A	2	549	NGFRGAHSQCFFACVLPQAMSTGGRQLPHPCMNPPSPGDSMDAVIK GAAVDLGCTWKGAKPLGLWHCGG*PIENRAGAGET*SLHI*TPVRSP GFLGTSPMGSPGPAKNGHSCARPLLSPLPYPPKERPLPPPHWLQSE DLPPPRGPEALMPQELGLERC*YPLPQVPRFRGTGAGLVQA
6420	A	368	623	LVCVFFFF*ERESCSVTQAGVQWCDLGSLOPPPPRSKQFSCVLVPS

				SWDYRHTPPCLANLCLIFKSRNPKYFIFIPFPNCYEW
6421	A	42	179	CYAFNFCIYELVHLKIKDTYCHIFKLNLYRGKPPVKEKQYFSDKN
6422	C	28	219	MQILLKSKPKGSTKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXFRCHD*
6423	A	2	161	KNLH*MESYSVAQAGVQWHDLGSVQPLPPGFKRFSCFSLSSWDSRL YFRCHD
6424	A	363	750	REQDPACAWSSS/APNSSWSLHGEAVSHRECLSSPVLPGPDSSKALS SAAAALSMSSGRGGGSLVPFSGPVSGVARWIASCVAGESCLA*AGTR TRCTAPSEAT*SSTRGLSRGAASLAASVHHGSRMSL
6425	A	890	1879	LWGLVTSSCLSFSRRNFTTEIFQEDLMLSPLNLLSLVMWLCTLWTS LAALSMSSGRGGGSLVPFSGPVSGVARWIASCVAGESCLA*AGTRTR CTAPSEAT*SSTRGLSRGAASLAASVHPGSRMSL*VAGKPKPGPTE AAPSCRSSSITTCPLP'TLSHSSSTADRALKASPGLSLRGPGSSGGE LCARLSPSSSGMDTFPCLRSPTSSWRRFNNSLLALARPRAASAKPTA LSTRW*ITCRSCSEL*TAKPCPVTVMGVLGSGFPWPPEVLPPLVSL QAQQQHLASLPFPFSMRMVRGAQAPSCRVRPRARGETPPRLPSGSR
6426	A	8	363	AEVQWRNLSSLQPPPPGFK*FLCLSLPRS*DYRLAPPCSANFCMVKT EFHHVGVQVLELLASSDPPPALASASQSAGITGVSHHAWPRASLLSL VIALKQASFFCSHAKPQVSQHFTN
6427	C	87	287	MIFFSFVCNTWCHSPFCATVTEYHSLIXXXXXXXXXXXXXXXXXXX XXXWEGLFCCIITQRKVEG*
6428	C	11	328	MHMYGXXXXXXXXXXXXXXXXXXXXRISEHILCIFRSNYRMIFSFVC NTWCHSPFCATVTEYPRLIXXXXXXXXXXXXXXXXXXXXXWEGLF CCIITQRKVEG*
6429	C	76	276	MIFFSFVCNTWCHSPFCATVTEYHRLIXXXXXXXXXXXXXXXXXXX XXXWEGLFCCIITQRKVEG*
6430	C	7	324	MHMYGXXXXXXXXXXXXXXXXXXXXRISEHILCIFRSNYRMIFSFVC NTWCHSPFCAPVTEYHRLIXXXXXXXXXXXXXXXXXXXXXXWEGLF CCIITQRKVEG*
6431	A	1	336	FFFFFFRQSLVAQAGVQWCDLCSL*SPPPTLSTPLASASQVAGTTG AHH*TGIIFVFVETVFCVHAQAGLELLGSSDPPASASQSAGITATV PSLL*LFIKQKQKQNRTY
6432	A	3	1105	DKDCSRAFLLYGSYSRAPALGGTARTLLGLLNEAKLEFHSVVLLEPG NKHAVTELSKIKKELIEKGHWDDVFLDSTQRPNGGKPIDNPPHPGSS NPLRKVIIETGNLIQTIDVPDSTTAAAPENNPINLADVIAATGTT KKNSSQDDLFPSTSDTPRAKVLKIEEVSDTSSLOKEKPLLIPIILQRL SELKRFDMAVMFMSETTEKNRYGSEQEFVDDLKNMWFGLYSRGNEEG DSSGFEHVFSGEVKKGVTFGHNWIRFYLEEKEGLVDYYSHIYDGPW DSYPDVLAQMFWNDGYYKEVGSAPIGSSPEFEFALYSLCFIARPGKV CQLSLGGYPLAVRTYTWDKSTYGNKKYIATAYIVSST
6433	B	52	936	MAYLKIQKYEEAEKDCTQAILLDGSYSKAFARRGTARTFLGKLNEAK QDFETVLLLEPGNKQAVTELSKIKKELIEKGHWDDVFLDSTQRQNVV KPIDNPPHPGSTKPLKKVIIETGNLIQTNDVPDSTTAAAPENNPIN LANVIAATGTTSKKNSSQDDLFPSTSDTPRAKVLKIEEVSDTSSLOPQ ASLKQDVCQSYSEKMPIEIEQKPAQFATTVLPPIPANSFQLESDFRQ LKSSPDMLYQYLKWLSSHQDNTRAQRLEKAGWQLAFLRYYYHLLDV QKITVCMWQKAF*
6434	A	1	309	LPPIPADSFQLESDFRQLKRSPDMLYHD*KQIEPSLYPKLFQKNLDP DVFNQIVKILHDFYH*GKKSPLLIIFEILQRLSELKRFDMAVMFMSET EKKIARGII
6435	A	1	936	MAALYACTKCHQRFPEALSQGGQLCKECRIAPVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPSSSDSPASSSRVAGITGIKTNTICKKCAQ NVQLYGTPKPCQYCNIIAFIGNKCQRCTNSEKKYGPYSCEQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSSRAGH QEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFVIIAQLKEEVATLKK MLHQKDQMLEKEKKITELKADFQYQESQMRAMNQMEKTHKEVTEQ

				LQAKNRELLKQAAALS KSKKSEKSGAITSP
6436	A	1	1023	MAALYACTKCHQRFPF EALSQGOQLCKECRIAHVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPSSSDSPASSSRVAGITGIKTNTICKKCAQ NVQLYGTPKPCQYCNI IAAFIGNKCQRCNTSEKKYGGPYSCQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSSRAGH QEKEQYSRLSGGGHYNSQKTLSTSSIQNEIPKKKSKFESITTINGDSF SPDLALDSPGTDHFVIIAQLKEEVATLKKMLHQKQDMILEKEKKITE LKADFQYQESQMRAMNQMEKTHKEVTEQLQAKNRELLKQAAALS KSK KKSEKSGAITSP
6437	A	602	745	TPASLKIPVE**NTLLAKMVIS*PRDLPASASQSAGITGVSHRARC
6438	A	1447	1931	RKVFKWLSAPLDVSNCPSLCKD*W*RV*RFPETFFPAR*GAENPTLP CCHYSIN/HFTVFSFLF/IFFFW*SLTLVPQAGVQWRDLGSLQPLP PGFKRFSCLSLPSSWDYRCLPPCLANFLYF**RQGFTVLARMVIS* PHDLPASASQSAVFSYLIFFLPY
6439	A	1	74	FWRPVRQSEYKQVNKGQDSTFPI*CLQNTNDYRFRVCA*RRCLDTS QELSGAFSPSAGFVLQRSEVMLTGDMSGSLHDSKMNSMPTDEQIAAI IALGFATLAILFGFI*QSEYKQVNKGQDSTFPI
6440	A	2	174	FFFIFFFLLENLF*PSNFGSYKPVHCCVFFCCCCFFFLAVFFFVCFC FFFSFSFLFF
6441	A	1	271	PPRFFPEFFYSGPPKPPFFKTPVFLGVKPGVSSSPPYQKKPTNFGPK MGAL*RIPLFETPIWVFPKGFHKKKPPVLN*PPTRKPPDPKI
6442	A	3	128	FFNKKPPPFGRGWPFLLPATLRF*G*KIFPPPPPPPEVRFP
6443	A	1	154	LVWS*EASKIPGGAEAAHPPTF
6444	A	2	230	FFFESGSRSVTQAGVQ*HSLGSLQPLPPRFK*FSCLSLPSSWDYTHV PTRPANFCIFSGDGVSSCWPGWSRTPNLR
6445	A	70	550	NQVIWESFQAGRHGHPFAPSLAPSASSFLSSFCPSGKAEETLESI* SSGKPGVGEATSLFPSIS*MFWEGPENGTOEPAGMPIPHTPPSCSN PAIHSFGTGAPGRREEALHCPP*HIPSHPPSRPPLAPLSLRFPT PMAVNDQDRSHVCFPLGLI
6446	A	77	485	NLVYVSSICFTWTFHFERKKFYVSHIVLYKVASPIKCLYCHSGHTQ VVQYLNGEAARLGQGLL*NVIIIFICLLSLSLSSFFSGPMLKM*N FVFK*CFYNFIRKPKFVFFVTLDENSLYIGTSNVITVLNKFH
6447	A	3	349	KVEDPSPVWRNSIFWKVITFKVYFFCLFVLETESLSVVQAGVQWH SLGSLQPLPPGFKQFSCLSLLSS*DYRCTPPRPADFCIFGRDGVSPY WSG*S*TPDMLCPAWLPKVL
6448	A	1	189	FFF*IGPHSVAQAGVRWCDLGSCSLNLPSSDPPASASQVAGTTGVH YYTQLIFKFFIEMRAP
6449	A	2	304	LDTPLGAAPAAFFLPSLNQCLIYNPMPVRPLKAWRLKTGILTEPRVK GEALGAGMMPTGVSTASSPSYPLAPLGPRLPLQDCMHQALS*APLSD ALCIAL
6450	A	21	359	SLQPSPAFFSPAFCGLL*PSVVQPSPAFSSLL*PSPAFSSLL*PSL LWPSFSGLL*PSLTFSNLL*SSLLPSTEETPAGQRQELQLFPVGGAA DAYFPFKCFKILSSECLK
6451	A	2	170	LSLLSS*DYR*APSQLANFSIFL*RWGLAVLPRLVSDSWPQMILLPP VPDVLELKA
6452	A	3	112	EKKMADFHKKEEMDDQDKAKGRKETLILERENKSM
6453	A	4041	4215	GRVVMWVVQGFLLGFFFFFVFLTLSCCLKHSSDVWGETSLLKWV LVLAFWGGGP
6454	A	3	309	PPPPK*IL*RAPNPPLSSSSFSNPPTWGPQPPPPSKFSKFARFPFL PPPPFPKKEPPSSSLFFPTKEGTVI*KNPPFSGFQSPDSIK*GRVEP PGGTKRG
6455	A	2	439	RTSAREKRDNLRLKKLGDSSKNSDC*SVSSNTDADATQEKNNATSNR KSSVGVKKNSKSRTLTRQMSRIPASSNSTSSKLTHINNSRVPKLLK KPAKPLLSKI KLRNHCKRLEHKNASRKLEMGNLVLKEPKVVLNKL HKKR

6456	A	1	146	LGEWVGLCKIDREGKPRKVVGCSVVVKDYGKESQAKDVIEEYFKCK K
6457	A	59	431	PTAMAEEGIAAGGVMDVNTALQEV\KLTALIHDLARGIREAAKALDK YVYQSQYCGFLQPEQNCHPREEGMEFMVLAQKF*MASVLPET*EK\R QAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDNKKLGEWVGLL *ILWVLATGTKLPPKRRHGVHGVSAKVLNGIRPTGNLKGAKPIFV CLHPTVMSLCMSSWWRPFVLNTKST
6458	A	242	431	LHFHCNLFRRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVRL LRIVLGLMFSDACIWG
6459	A	65	473	PTAMVEEGIAAGGVMDVNTALQEV\KLTALIHDLARGIREAAKALD KRQAHLCVLAFNCDEPMYVKLVEALCAEHQINLIKVDNKKLGEWVG LCKIDREGKPRKVVGCSVVVKDYGKESQAKDVIEEYFKCKK
6460	A	32	485	HLVLASLLACLASIFLPSVGLGQCDLVGSQKTIPRNEGLPRKQTFLS DLLPSCWFPYSPRLAIKTTIPLHQKPAKPKNITLTFLLSV*N WAIGKLFGLPSGL*GQEGPPFQRESCAI*GRKECCAKRPKRILTDRP RWVPHSVYQH
6461	A	3	336	FFFFDIGSCFFA*AGVQWHDHGSQPPGLK*HDIPTTAS*VAGTT GAHHHA*LIF*LSVKMGSSPLVAPGWSMKSWTQANPSLLQPPQSAWD YRCEPPCLVRNTFEYV
6462	A	2	280	VLGIWVRVPGSGKMEKRESEKQILPRPIGCIWERGKSPGEAPSALPM PWSNPPPGTCTPSCPTYRCTPLPR*TDAPSRHTHLAPRNGETIFA
6463	A	1	171	MWGWEKIKINTFVYCWWEFKLVQNFSTTWQHILKF*MSFDALLGI YPKYILTNTV
6464	A	21	404	LSTGTSSAMVSRTEGNIDDSLIGNASAEGPEGEGTESTVITGVDIV MNHHLQETSFTKEAYKKYIKDYMKSIGKLEEQRPERVKPFMTGAEE QIKHILANFKNYOFFIGENMNPDMVALLDYRE
6465	A	42	266	KLILKIQYFNLLMKCCFRIKGLLEEQRPERVKPFMTGAEEQIKHIL ANFKNYQVNTLSIWKGLYNFNCKSKN
6466	A	60	656	RRRRLPSVAIMIIYRDLSHDEMFSDIYKIREIADGLCLEVEGKMVS RTEGNIDDSLIGNASAEGPEGEGTESTVITGVDIVMN\HDLQETCF TKEAYKKYIKDYMKSIGKLEEQRPERVKPF\MTGAEEQIKHILANF KNYOFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEMEKCVSTR KWVKINNVKKT
6467	A	176	552	MRSSKQMKPNFPRCSSITVLSVRGMVFLTLACPRFKMSSRTDFRFG NPQVT*GSTICIFRLPSILSMRTTK/DQGMFIWQFQGMRFHF*SS THLVTFLLPGIM*E*FQSLKPEPFSFLLSCYCH
6468	A	98	509	RATEKWKGRKNHLSWKCFPLKIFFRRSLAMVLCTSKLRPSVLSMRT TKARECLSGSSNA*GFTSSRLRHSLSRFC\ARNHVGMIPIVA*T*ALF LSSAPSLPKMPALPGWLCGLDKPSSFSGDFLEPKGFFALAPP
6469	A	204	401	WHEFTGAENHCKTLPKENF*WCLCKSHPSEPKNAAYNRTLCDLGISK SEVSLGTSFEMWTSQQQE
6470	A	249	906	RIHFPRVSGPSQSNPKFAVASRGFFSLSLSSAQPDPLPPPLGEALAL SLHPVPRRSTETVAGDSSELQGLRSPQQLAGLAFRLFLFPFP *RCKSKPN*NDRRRSSVDSQIHLVGRESAHLPLGLRVCSLPLARC FGQVLQGVPLWIPSPGGS/AGVSGRRREERHMGVVVMRVRVEARVS S*ESKI/SRALR*STHLGLPKCWDYRREPPCPAH
6471	A	401	659	LIDLRFIYLFYLR*GLRLVP*AGVHWCNLSLQSLPPGFKRFSCLS LSSSWDYRHAPPHPAHFCIFSRDAVSPCWG*SQTPDLR
6472	A	1271	1538	ARGCKRPCRQIASMLQLCILHACWALVPQLHAAPGLAIQRLCICPY LGSWPSTLGRVPPLSPSTSPRPSAFGASLNPPRHSSGPLR
6473	A	1	369	ACSSCFHAGLEHVRVRGSGHSGVAAARRSEAPDLFC*PPSLPVPSTP FSPSPAPAMNQATSDPTHCTPTRLPTCPNAAP*AGPTADTPS*GIPD LPAPVVLKTPQHLDLPVCSLGGPPLGPTET
6474	A	3	340	ETRSYSVTQAGAEWHDHRS*P*PPGLR*SSHFSLSNWDYRCVPPH SANFLVIFVEIVFHHVAQAGLELLGSSDLPT*ASQSTGITGVNHCPA

				EKEVLPREKAMQRGGSQA
6475	A	21	273	GMNERGNITKEIKKIWEYYE*LGTSQLDITLD*TNSQKDTNYQNQLT KYRKYGLEPITSYDIISNFKRLPKKSPGLDGTGEFI
6476	A	2	3204	FGEPTSEQTGTAAGKTIAQTTAPVSWKPQDSSEQPQEKLCNPCAMF AAGEIKTPTGEGLLDPSKTMSIKERLALLKKSGEEDWRNRLSRRQE GGKAPASSLHTQEAGRSIIKKRVTESRESQMTIEERKQLITVREEAW KTRGRGAANDSTQFTVAGRMVKKGLASPTAITPVASAIICGKTRGTTT VSKPLEDIEARPDMQLESCLKDRLETFLRRLNNKVGGMHETVLTVT GKSVKEVMKPDDDETFAKFYRSVDYNMPSRSPVEMDEDFDVI FDFPYAP KLTSSVAEHKRAVRPKRRVQASKNPLKMLAAREDLLQEYTEQRLNVA FMESKRMKVEKMSSNSNFSEVTLAGLASKENFSNVSLRSVNLTEQNS NNSAVPYKRLMLLQIKGRRHVQTRLVEPRASALNSGDCFLLLSPHCC FLWVGEFANVIEKAKASELATLIQTKRELGCRTYIQTIEEGINHTHT HAAKDFWKLGGQTSYQSAGDPKEDELYEAAI IETNCIYRLMDDKL PDDDYWGKIPKCSLLQPKEVLVDFGSEVYVWHGKEVTLAQRKIAFQ LAKHLWNGTFDYENC DINPLDPGECNPLIPRKGQGRPDWAI FGRLE HNETILFKEKFLDWTELKRSNEKNPGELAQHKEDPRTDVKAYDVTM VSMPTTAGTILDGVNVGRGYGLVEGHDRRQFEITSVSVDVWHILEF DYSRLPKQSIGQFHEGDAYVVKWFMVS\RLYCVRGEVPVEGNLLEV ACHCSSLRSTSMVVLNVNKAIIYLWHGCKAQAHTEKVGRTAANKIK EQCPLEAGLHSSSKVTIHECDEGSEPLGFWDALGRRDRKAYDCMLQD PGSFNFAPRLFVLSSSSGDFAAATEFVYPARAPSVVSSMPFLQEDLYS APQFALFLVDNHHEVYLWQGWPIENKITGSARIRWASDRKSAMETV LQYCKGNLKKPAPKSYLIHAGLEPLTFTNMFPSEWHEHREDAEITEM DTEVSNQITLVEDVLAKLCKTIYPLADLLARPLPEGVDPLKLEIYLT DEDFEFALDMTRDEYNALPAWKQVNLKKAAGLF
6477	A	250	5816	DFNKKNLSFLGFPRQRKVSSSQKEFSLEDKEQLANHERGIDAQLLVA LPKVAELRQIFEPKKKEFLEMKRKERIARRLEGIENDTQPIILLQSCT GLVTHRLLEEDTPRYMRASDPASPHIGRSNEEEETS DSSSLEKQTRSK YCTETSGVHGDSPYGSGTMDTHSLESKAERIARYKAERRRQLAEKYG LTLDPADSEYLSRYTKSRKEPDAVEKRGKSDKQEESRDASSLYP GTETMGLRTCAGESKDYALHAGDGSSDPEVLLNIENQRRGQELSATR QAHDLSPPAAESSSTFSFSGRDSSFTVPRSPKHAHSSSLQQAASRSP SFGDPQLSPEARPRCTSHSETPTVDDEEKVDERAKLSVAARLLFRE MEKSFDEQNVPKRRSRNTAVEQRLRLQDRSLTQPIITTEEVVIAATL QASAHQKALAKDQTNNEGKELAEQGEPPDSSTLSLAEKALFNKLSQPV SKAISTRNRIDTRQRRMNARYQTQPVTLGEVEQVQSGKLI PFSPAVN TSVSTVASTVAPMYAGDLRTKPLDHNASATDYKFSSSIENS DSPVR SILKSQAWQPLVEGSENKGMRLREYGETESKRALTGRDSGMEKYGSFE EAEASYPILNRAREGD SHKESKYAVPRRGS LERANPPITHLGDEPKE FSMAKMNAQGNLDRDLRPFEEKVEVENVMKRKFSLRAAEFGEPTSE QTGTAAGKTIAQTTAPVSWKPQDSSEQPQEKLCNPCAMFAAGEIKT PTGEGLLDPSKTMSIKERLALLKKSGEEDWRNRLSRRQEGGKAPAS SLHTQEAGRSIIKKRVTESRESQMTIEERKQLITVREEAWKTRGRGA ANDSTQFTVAGRMVKKGLASPTAITPVASAIICGKTRGTTTPVSKPLED IEARPDMQLESCLKDRLETFLRRLNNKVGGMHETVLTVTGKSVKEV MKPDDDETFAKFYRSVDYNMPSRSPVEMDEDFDVI FDFPYAPKLTSSVA EHKRAVRPKRRVQASKNPLKMLAAREDLLQEYTEQRLNVA FMESKRM KVEKMSSNSNFSEVTLAGLASKENFSNVSLRSVNLTEQNSNNSAVPY KRLMLLQIKGRRHVQTRLVEPRASALNSGDCFLLLSPHCCFLWVGEF ANVIEKAKASELATLIQTKRELGCRTYIQTIEEGINHTHTHAAKDFW KLLGGQTSYQSAGDPKEDELYEAAI IETNCIYRLMDDKLVPDDDYWG KIPKCSLLQPKEVLVDFGSEVYVWHGKEVTLAQRKIAFQLAKHLWN GTFDYENC DINPLDPGECNPLIPRKGQGRPDWAI FGRLEHNETILF KEKFLDWTELKRSNEKNPGELAQHKEDPRTDVKAYDVTMVSMPQTT AGTILDGVNVGRGYGLVEGHDRRQFEITSVSVDVWHILEFDYSRLPK

				<p>QSIGQFHEGDAYVVKWKFVSTAVGSRQKGEHSVRAAGKEKCVYFFW QGRHSTVSEKGTSAALMTVELDEERGAQVQVLQKQEPCCFLQCFQGGM VVHSGRREEEENVQSEWRLYCVRGEVPVEGNLLEVACHCSSLRST SMVVLNVNKALIYLVHGCQAQHTKEVGRTAANKIKEQCPLAAGLHS SSKVTIHECDEGSEPLGFWDALGRRDRKAYDCMLQDPGSFNFAPRLF ILSSSSGDFAAATEFVYPARAPSVVSSMPFLQEDLYSAPQPALFLVDN HHEVYLWQGWPIENKITGSARIRWASDRKSAMETVLQYCKGKNLKK PAPKSYLIHAGLEPLTFTNMFPSEHREDIAEITEMDTEVSNQITLV EDVLAKLCKTIYPLADLLARPLPEGVDPLKLEIYLTDEDDEFALDMT RDEYNALPAWKQVNLKKAAGLF</p>
6478	A	553	7399	<p>NFNKKNLSFLGFPRQRKVSSFQKEFSLEDKEQLANHERGIDAQLLVA LPKVAELRQIFEPKKKEFLEMKRKERIARRLEGIENDTQPIILLQSC GLVTHRLLEEDTPRYMRASDPASPHIGRSNEEEETSDSSLEKQTRSK YCTETSGVHGSDPYGSGTMDTHSLESKAERIARYKAERRRQLAEKYG LTLDPEADSEYLSRYTKSRKEPDAVEKRGGSKDKQEESRDASSLYP GTETMGLRTCAGESKDYALHAGDGSSDPEVLLNIENQRRGQELSATR QAHDLSPAEESSTFSFSGRDSSTFTEVPRSPKHAHSSSLQQAASRSP SFGDPQLSPEARPSTGKPKHEWFLQKDSEGDTPSLINWPSRVKVRK LVKEESARNSPELASESVTQRRHQAPVHYVSFQSEHSADFVRVPSKA AGSTRQPIRGVYQPADTGHTAKLVTPETPENASECSWVASATQNVPK PPSLTVLEGDRDSPVLHICESKAEEEEEGEGEGEEKEEDVCFTALE QSKKTLLEAGDGLVRSPEDPSRNEFDGKPAVSTVTLEHQKELENVA QPPQAPHQPTERTGRSEMVLYIQSEPVSDAKPTGHNREASKKRKVR TRSLSDFTGPPQLQALKYKDPASRRELELPSSKTEGYPGEISMLDTK VSAQLRSAPLASANACRRPELKSRSVERSAEGPGLTGVERERGRSRK PRRYFSPGESRKTSEFRTPITSAERKESDRCTSHSETPTVDDEEK VDERAKLSVAARLLFREMEKSFDEQNVPKRRSRNTAVEQRLRLRLQD RSLTQPIITTEEVVIAATEPIPASCSSGTHPVMARLPSPPTVARSAVQP ARLQASAHQKALAKDQTNKGKELAEQGEPSSTLSLAEKALFNKLS QPVSKAISTRNRIDTRQRRMNARYQTQPVTLGEVEQVQSGKLIPFSP AVNTSVSTVASTVAPMYAGDLRTKPPLDHNASATYKFSSSIENS PVRSLKSQAWQPLVEGSENKMLREYGETESKRALTGRDSGMEKYG SFEEAEASYPILNRAREGDHSHKESKYAVPRRGSRLERANPPITHLGE PKEFSMAKMNAAQGNLDRDLRFEEKVEVENVMKRKFSRAAEFGEP TSEQTGTAAGKTIAQTAPVSWKPQDSSEQPQEKLCNPKAMFAAGE IKTPTGEGLLDPSKTMSEKERLALLKKSGEEDWRNRLSRRQEGGKA PASSLHTQEAGRSLIKRVTESRESQMTIEERKQLITVREEAWKTRG RGAANDSTQFTVAGRMVKKGLASPTAITPVASACGKTRGTTVPVSKP LEDIEARPDMQLESCLKDRLETFLRRLNKNVGMHETVLTVTGKSV KEVMKPDDDETFAKFYRSVDYNMPSRSPVEMDEDFDVFDPYAPKLTS SVAEHKRAVRPKRRVQASKNPLKMLAAREDLQEYTEQRLNVAFMES KRMKVEKMSSNSNFSEVTLAAGLASKENFSNVSLRSVNLTQNSNNSA VPYKRLMLLQIKGRRHVQTRLVEPRASALNSGDCFLLLSPHCCFLWV GEFANVIEKAKASELATLIQTKRELGCRTYIQTIEEGINTHTHAAK DFWKLLGGQTSYQSAGDPKEDELYEAAIETNCIYRLMDDKLVPDDD YWGKIPKCSLLQPKVLFVDFGSEVYVWHGKEVTLAQRKIAFQLAKH LWNGTFDYENCNDINPLDPGECNPLIPRKGQGRPDWAFGRLTEHNET ILFKEKFLDWTELKRSNEKNPGELAQHKEDPRTDVKAYDVTRMVSM QTTAGTILDGVNVGRGYGLVEGHDRRQFEITSVSDVWHILEFDYSR LPKQSIGQFHEGDAYVVKWKFVSTAVGSRQKGEHSVRAAGKEKCVY FFWQGRHSTVSEKGTSAALMTVELDEERGAQVQVLQKQEPCCFLQCFQ GGMVVHSGRREEEENVQSEWRLYCVRGEVPVEGNLLEVACHCSSLR SRTSMVVLNVNKALIYLVHGCQAQHTKEVGRTAANKIKEQCPLAAG LHSSSKVTIHECDEGSEPLGFWDALGRRDRKAYDCMLQDPGSFNFAP RLFILSSSSGDFAAATEFVYPARAPSVVSSMPFLQEDLYSAPQPALFL VDNHHEVYLWQGWPIENKITGSARIRWASDRKSAMETVLQYCKGKN LKPPAPKSYLIHAGLEPLTFTNMFPSEHREDIAEITEMDTEVSNQ\</p>

				ITLVEDVLAKLCKTIYPLADLLARPLPEGVDPLKLEIYLTDEDFEFA LDMTRDEYNALPAWKQVNLKKAKGLF
6479	A	380	999	AGAKGGPGGRGMKKTNSLTPLLSAYRLLPVLSKGGWILGFSVCPF APGLMAKGVSPCDTAVKRDNIH*VGGGVS*KCP*RSS*WSGPVPALT ALFLVDNHHEVYLWQGWPIENKITGSARIRWASDRKSAMETVLQYC KGEAPSNMPAARNRWGSPSGMRSQETPPFFCACQPASIHKAQVVD NPIFSPLKPFEDVIKFLD
6480	A	78	200	KKGSPFFPKVGGQGNLGLLEPLPPKLKFFCFKPPKRGDYSSSSSS SPDSSSSKKKGVSFPWPGGV*TPKEGGL
6481	A	179	384	FNSYYMYVYVYVHICVFLYVCICIYRYIYLCIAVITCLMNEW**FKC KGNDARGYEKKLPSKYBIEKE
6482	A	76	205	RKKPEPEKTCFDNITGNTYPCNSTYEHDSD*YYVNRT*LCAER
6483	A	2	774	HSYSHSHGHCGSPAGDTEQGYKVPWPVCSLFPDGSHPGV*QPIHEPA /QGRGGLPPWGAA*TPRAWLA*RPRG*AALPWA*TSPGRPASAPLA HTGSGCPSRPTRAPGSP/IPIQNIKRYPYGEAFVPSRAG\PTVGVT RSFHLAPSLPPFPSS*LSPSLPPRTTTSCTRAILTPSS*QKLLYPPS RP\VLLVRRARPPAAAPTSEEPPERSPWETPHAAPSQHELHETHS VAQSDLLPAPEAM*PGSVSSRFLLY
6484	A	2	732	GRRRPGPKPPRAPGRDRDRCNF*PCCPPGAKSSAACCCSDIRRAARA IPLGNPCSPLSAP*AP*NPLCRTVMGRSPMTLSLGSRTPTSLPAPF PWSRPFGE*PTHPRARSLGTLWPMPTTP*IQAAATPWRR*PPATQAS TPHSLRGSSSSSQPRLAPLRPTSSRACMAGPTTAAAGALGPVTLGVL TPQAWASLRTPGRLLTSLSPRQPLQQRQWQQQQLQPPRPLWQP CRRHRTI
6485	A	2	338	CTTAIPTPEEMTRLRSMNRQLQINVDALTEVDLLQSRGNFDPKAMN NFYDNI*PGPDVPPKPSKKGPTDSEPKTSSGPCSNIGCLLSCKFFHA CSRQNPPICIHQSTLAA
6486	A	84	300	RVGARGKMTALASGQLGPLMCQFGLPA*AVEAANKGDVEAFAMQN ISKPEQI*GDTKDKTD*KEDLSLD
6487	A	91	668	SRAQVVLHCVLREWAGRRSPAPPSPWPVLHVPDPQSWQLSSVALGC SPGWSSALAWLFLQALGMFSAALASGQLGPLMCQFGLPAEAVEAANK GGKVAAPGTPRPEPGAGSIPVPLDLQKWG*GGKGHSPSALDPIALIP SFGARVRHHLVSLTCS\DVEAFAMQNNAKPEQKEGDTKDKKDEED DMSLD
6488	A	1	414	LQPGPAGAQQVDLA/SVV*PPEIMAPI\LANADVQERLLPYLPSE\ SLPQTADDEI\QNTLTAPSSQQALGMF\SAA\LASQVGAPFMCQFG LPAEA\VEA\ANKGDVEAFAMQNNAK\PEQKEGDTKDKKDEEDM SLD
6489	A	205	553	LSRPRHHKASTTGAQMQRTRSMRQEPEKAILTLRGSREPTPRAPQL VPSVPSSWLFLSLHSIAQTPLPHTHSTHTPRSQPALPSQAPVVPQH PPPHE*ALSPDNLFMILKSP
6490	A	3	347	SFFFVLRRSLAVAQAEVQ*RNLSLQPPPPPEFKRFSCFSLPSGWDYR RPPPRPANFLYF**RGVSTMWGQWSRTPDLRGDLAHLGSPKVLGMT GREPPCLGPLNGLTFLPEIS
6491	A	280	406	FFVFLGETGFHRVSQDGLNLLTL*SARLSLPRCWDYRREPPH
6492	A	1665	1789	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6493	A	1431	1555	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6494	A	1740	1864	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6495	A	1173	1297	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6496	A	1027	1149	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6497	A	631	744	VIEHLVSQDGLDFLT*SARLGLPKCWDYRREPPRPVH
6498	A	166	352	IFFVFLVETGFHVSQDGLDLLTS*STRGLPKCWDYRREPPRPAPS SPIFHTVAPIQYTHP
6499	A	2250	2374	FFVLLVETGFHRVSQDGLDLLTS*SAHLGLPKCWDYRHEPP
6500	A	150	370	EKELAFFPQGGGNGLG*LKPPPLR*RDFSCLALPRGGNGRGAPPS

				PTNFGFLGGNGVYPSGPGGFETPDLK
6501	B	174	350	MDEKTKKAEEMALSITRAVAGGDEQVAMKCAIWLAEQRVPLSVQLKP EVSPTQDIRFLM*
6502	A	1	498	EFRAPGPLGPRTRRPARRVAGSGGPG*G\TIFPAPPPSPAPLPGPPL SLSLPPKPLPLRRTGASREERGLCLETRDARGAPASGGPPGLGTPRL GGVRASFPRFFPRLVPFPFPAPSADLSRRPLPSHRPTQDPGLVIGQC DASRLPRGQRGTHRAWAAPEATRPG
6503	A	919	1761	RAFSFNREEPTADEQGLPTS VAGRP AVIAAVPSWHARGTERRAPGRT D*HHPHLLGAQPSAALLPGLP*HCGHISAGGRREAGNIPGRKIIYPP PQGFYGSNNQHQAYIKLSDA/ RSLTR*IQSSMTSCRVL R*GPSLPS AGSSPGLGMSCLTSGTSCGYMTSSWP\ PPTDADLLCSRDCVSVRAGS PGL*L*HGLGPPPV/SPRSLRTPCMRH*SAEQETFLFSFPHPNLLGR PLPNSKLRGRQPLLSKTL SWHQPSRGLIWCCSGSGFGDFCGLKIEQKM S
6504	A	131	575	VFALKPGTPGALPQVGVLRDLERPGWVVSGRFPFPASSHLGLVPFPPPA PKCGTLSRRPLPSHRPTQDPGLVTGQL*CFPTAAGTATAHTGLGPRR KPHRPWLSCSWSPRLFPDPEVSI FPRKARSPPGEWGTATPDGREDQ ESRGNGP
6505	A	2	291	HEPQLNSNNVALHGA VIPGPPFLFGACINLMNFMVALFIPEYKIARG VQKHTYKHNGSLTNT*RGSDIEDIEPLLRDSTIWELFSFEPPGNQCP EL
6506	A	1	267	PRFKLFPCLSLSS*DYR*VPAITPG*FLYFF*VKTGFHHVGTGLE LLTSGDPPTSASQSAGITGMSHCTWPI SFLYLWHTGGKKKEC
6507	A	1	216	HEWMGTRVGEWMDWEKGGWKMDGKVDK*MNGWMEGCLYQWLNTILC QELIPYTCCLCFSGWIYIFKQSILD
6508	A	74	357	WFPWDQPGSQGEGRDQREPSGCRLOAPLSLSLCSFQASCSSRSSGAA STERSDGAACRETLTAVSGWTNRGSHSPRGKSCARPRPPPEDAATQ
6509	A	2	375	RHEVKPQWTPG*DTDHLPNLSVALGPTRQPGRRQRPEGTQVPSIPAS SIPASQSQQPQSPNPSLLHPRTPTPSLP IPASLIPASPKTQTL*I PASEVGTVSNPTPWTRKLGPEANRLSLMV
6510	A	3	148	HERRETVIRRGKHLRLVPTRWAGKGLLG*SICFWSFSLGHHWSV C
6511	A	50	255	LSMVSTVLVTTIMKLC SY*K*QIQSWLPCLTHTKTHTHTHTHTHTK VLHTLTCKQYAIIGNVLSFY
6512	A	268	355	EFFILTFKNNIFIYRYNRISREWTQKYAM
6513	A	2	206	RKGSICLDILRSQWSPALTM SKVLLSICSLLDWPNPDDPLVPEIARI YKSDRDKYNRICREWTQKYAM
6514	A	1	317	FFFFFFPLFRQCLTSPRLEYSGTISAHCSLSQPGSSDPPTSALRVA ETTGTTRHAWLIFVF*VETGLHHVVLAGLELMGSRNQPTSASQSAGI TGVNHRWLW
6515	A	2	210	KEKIFSPGFKHPPPPFF*KTPLKGKRIFFSPPRKNWPPQRIFFKAP PSSSSSSSSSSSAQI*SFNSP
6516	A	674	985	WFFFWLCHPGWSAVAWHDLSSLQPPPPRLM*FSCLSLSNWDYRRA PPFLASFVFLVDTAFRHLGQAGLELLTSSDPPTLASQSAGITGVSHR TQLRSSFDS
6517	A	2	337	HVLISSALILIIISCLLLALELVCCCLSRSSRNTFSRCTYSGLSKTP PHWAARARLDDVFSRLTFSSHSLNMELVQDLTASAPMYSSTSRDPPA SASQSAGITSVSHRARP
6518	A	3	260	CLGLLVIFVCNFQSIRDYRRPPLH*LIFFVFLVEMGFYYVG*AGLEL LTS*SARLLASLRAGITGVSHRARPRSFVFGFGWQDHG
6519	C	38	478	MSEIKKRN SFNPQARKVD TNLYXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXIFKEWT MMQMICEHFDEKVIRRIQHKFNCKHAYLGRVGGRVGXRGFAMTLNR ASFXGA
6520	C	33	317	MLTNHLHHWPFFKNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

				XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTRCPRITTFFLRG *
6521	A	1	253	RRLLLLRWFSFALVAQAREQWCNLG*LQPPSPGFKQFFCFSSLNSW DYRRAPSCPANFVFLVEMGLYIFKEWDNDGRMICEAF
6522	A	2	411	GVLRLSSACPOACPSSTSTGP*AALAGFTTTGSGLCWAWTPPSSSFV SGSSREAPSGTATTSWTRNVTATSATTANRMAMCTSTRARLLAPT TNCSPRSKLTLPIDPCSGGCRLTCKDNTPLRGTGQGRROGTF
6523	A	2	222	THIGLPKC*DYKCEPPVHRQFL*F*VETRFHHISQAGFKLTSTGDPF ALASQSGRITGVTTTRTQPLNGFYKVM
6524	A	2	261	VVVVSQYAAERPSVVAHACNPSTLGGRGRWLT*GQQVETSLASGYLP TLASPKCWDYRREPLRLACFNFFVETRNLTLVLPISVQQ
6525	C	203	355	MVALSTRGQVHLSGAVVPSSFLIFLIAPSGEQEVDIAMVAGYAVTSV VLL*
6526	A	2	671	GVGGVGRGMLPPAPPAPAPGFPSTILWPSPL*LPPLGLGTGFLP FGHGCPPLSQSPWILFPWGGAQAQPL*P*PRHPCPPHPRQSYGRQL PTFWLAPPSFCLSLVFSSLSLILSLSSVSRVLLP*HPPPHISFHPL GFLS*ASPISGVGGIKAFPLPLRFQPPF*PLIPTPLSLPKMGALWGR L*HSTPAQAMGSRAPFSGLAQASTYLLQPPGVVGS
6527	A	3	477	AGKFPLRSGHFPCLTVEVSCGPFKPSVIPLSPCGASAPSPRFLLS PSGLVRAVLHCTLLVAS*APPPASPPGVAVFSPVSIWHPSRLPGS YGLCGQHLRDPKPRSRTHFRAGVPPLVSCSLPSNPLMTSGVQRP PKGLENSLLQLADLNK
6528	A	1	381	VKAAWGKVGAGAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVK GHGKKVADALTNAEAHVDDMPNALTALSDLHAHKLVRDPVNFKLLSH CLLVILADHLPAEFTPAEHASMDKFMAVSSTGA
6529	A	1	2654	MSFFSTLKTALSLKEKLAATGVLVLICALVGAGFAWERHQLKQAIK IGSLDQAVKERDKSIMDLNQTETMNAEQHFHSQEVKNESEQAKYA DRQMERKAEVQKQLVAAGNVRQRI PADTQRLRESISEFNADADKGI FMSDKVTVKQTINKATSIYKIEQITVGKPGSEQYRRAPELADQLGLK HPDCIEHVFPPTYADEQCTHVLTEEDFFSTEEREGVDRICIGVICSSVS DELFPPNVPEYGGIGYQFLYEGDELKCYEHDIESKAKELTVNSNNTVQ PVALMRLGVFVPKPSKSGESKEIDATKAFSQLEIAKAEGYDDIKIT GPRLDMDTDFKTIWIGVIYAFSKYGLSSNTIQLSFQEFKACGFPSKR LDAKLRITIHESLGRRLNKGIAFKRGKDAKGGYQTGLLKSWRADSKL WELFQLDYRVLLQHHLRALPKKEAAQAIYTFIESLPQNLPLPSFAR IRERLALQSAVGEQNRIKKAIEQLKTIGYLDCSIIEKKGRESFVIHT YLIPAI PPQHIIQCDPFLSHILDFYSPSSTHRSCRASRSHQIESEA WLPTEAGNHQNDSGYNLNVEEIRVLYAWRMPKHVVTHLAKDQLHKVA QRANRMLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVD YANIIDIYEHGRVGPKYRDYRSEGVSKTVSTVSLAHAMRAHPHLLME DLRILVIDLDPQSSATMFLSHKHSIGIVNATSAQAMLQNVSRREELLE EFIVPSVVPGVDMVPASIDDAFIASDWRELCNEHLPQONIHAVLKEN VIDKLKSDYDFILVDSGPHLDAFLKNALASANILFTPLPPATVDFHS SLKYVARLPELV/KLISDEGCECQLATNIEKQTNWNP
6530	A	1	945	MPASIDDAFIASDWRELCNEHLPQONIHAVLKENVIDKLKSDYDFIL VDSATVDFHSSLKYVARLPELVKLISDEGCECQLATNIGFMSKLSNK ADHKYCHSLAKEVFGDMLDVFLPRLDGFERCGESFDTVISANPATY VGSADALKNARIAAEDFAKAVFDLEQVFKLSTGRQATFIEEVIPPNQ VESDTFVDQHNNGRDQASLTPKSLKIRSTIKHQQFYPAIGVRRATG KIEILDGSRRRASAIENVGRLVLTQDEISVQEAQNLAQDVQTALQ HSIREIGRLRMKNMGMSQKDIAAKEGLSQAK
6531	A	146	4368	LGFLRLRLSEMPRKQGDYRT/SDMEIRGRVEQRVGYTIEQINHMRDVF GTRLRRAEDVFPFVIGVAAHKGGVYKTSVSVHQAQDLALKGLRVLLV EGNDPQGTASMYHGWVDDLHIHAEDTLLPFYLGEKDDVTYAIKPTCW PGLDIIPSCALHRIETELMGKFDEGKLPTDPLMLRLAIETVAHDY DVIVIDSAPNLIGITINVVCAADVLIPTPAELFDYTSALQFFDMLR

				<p> DLLKNVDLKGFEPPDLAILFHVTAVHMFSLGIEINLPFELQRNFQLM RDLDQRTGVRKTRKNNENFGCSPASSFSHLRERRDPGFSHDPGDQR QEAQNLAQAVQTALQHSIREIGLRLMRSKNDGMSQKDIAAKEGLSQA KVTRALQAASAPEELVALFPVQSELTFSQKTLCAVGDENGNKLEF DQLIQNISPEINDILSIEEMAEDEVKNKILRLITKEASLLTDKGSKD KSVVTELWKFPEDKDRFARKRVKGRAFSYEFNRLSKEKSKLSNLREYQ NRIAGIAKRSKAVLGWASTAQFGTDNQFIKDDAARAASILEAARKDP VFAGISDNATAQIATAWASALADYAAAHKSMRPEILASCHQTLENC LIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLG AATADACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDMQSVGVY SQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTIYVNRK SVVDNGSGSLLHSFTNAAGEQITVTCSLNINIGQIALSFSKAPDKGT EIAIETEINIEAAPELIPLINHEMKYTLFPSQFVIAAEHTFRTLKE YLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVWATIIRGKFQT VYRDIIERVKSSGAMGMFAGADAASFFQQLPKISSSQPKTISRHLHL FLPNFLKLTDTFLETIEENGVLGIHDTAHKGSLLAWLAFLLACFLGE GSSFAKTARYETVGKGLLLLLLVLTAGEVRIVSEHTFSAAATSSHLMCL FNLQVVSQGNVLPFPQIEALVRAPNPQEHQEEAKETDADSLCKL DLGIARTRVRIIRPHTSPALSPQHPTPAVHAHLVDEPHASAVQTSV STSVGEPTRWVPGAPSGVAGTAGWRRAGRLKAVATELLPMNGSLWST QARISPAFLKVNQTLMDYRTGRVQPAIPQSLPEALRLAADLAEQKQ RLEQKMLMDAPKVEFAERVATASGVLIGNYAKVLGLGQNYLFTWLRL NGILIAITGERRNVPKQDSISHAGHILSQCANLAATTSEYFIHKPHRL IAAETGYSQSTVVRAFREAVNKGILSVEIVGDHRRERANLYRFTPS FLAFAQQAKNALIESKLKISSAATKSKVTAWEARARGHYHKGDSR </p>
6532	A	820	2011	<p> TTTLVRLPCRSPKRRIKALRSQRLGLPMMRVPSFRLRVTSPTFMKSL TWQVHLLVLMMLVMPWTCNPSVCTASYVAAMCWWQAPMAPAKPQPSR WKTSKARMYQSQKVAKTSTLTVLSLLLITVPAAYFTRLLMMLLPLMR VPSFRLRVTSPTSMKSLTWQVHLLVLMMLVMPWTCNPSVCTASYVAA MCWWQAPMAPAKPQPSRWKTSKARMYQSEKVAITSTLTVLSLLLITV PAAYFTRLLMMLLPLMRVPSFRLRVTSPTSMKSLTWQVHLLVLMMLV MFWTCNPSVCTASYVAAMCWWQAPMAPAKPQPSRWKTSKARMYQSEK VALTSTLTVLSLLLITVPAAYFTRLLMMLLVSKSL/CTCSLNINIGQI ALSFSKAPDKGTEIAIERGANGDVLDMQSVGVYSQLRRRYVLVASSD GTSKTATFKMEDFEGQNVPIRKGRNTIYVNRKSVVDNGSGSLLHSF TNAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIERATDDACTF IPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVL VASSDGTSTKATFKMEDFEGQNVPIPKGRKNIYVNRKSVVDNGSGS LLHSFTNAATADACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVL DMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRN NIYVNRKSVVDNGSGSLLHSFTNAATADACTFIPVTRDQSDIYEV FNVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATF KMEDFEGQNVPIRKGRNTIYVNRKSVVDNGSGSLLHSFTNAAGEQI TVTCSLNINIGQIALSFSKAPDKGTEIAIERGSST </p>
6533	A	1	3039	<p> MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMSIGNIIDIEHGRVPHYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSRLEELLEEIVPSVVPVGVDMVP ASIADDAFIASDWK/ELCNEHLP\LVKLISDEGCECQLATNIGFMSK LSNKADHKYCHSLAKEVFGDMLDVFLPRLDGFERCGESFDTVISAN PATYVGSADALKNARIAAEDFAKAVFDRISYAKIIKKFRSTIKHQF YPAIGVRRATGKIEILDGSRRRASAILENVGLRVLVTDQBISVQEAQ NLAQDVQTALQHSIREIGLRLMRMKNKGMSQKDIAAKEGLSQAQVTR ALQAASAPEELVALFPVQSELTFSQKTLCAVGDENGNKLEFQDLI QNISPEINDILSIEEMAEDEVKNKILRLITKEASLLTDKGSKDQSVV TELWKFPEDKDRFARKRVKGRAFSYEFNRLSKEKSKLSNLREYQNRIA </p>

				<p> DI AKRSKAVLGWASTAQFGTDNQFIKDDAARAASILEAARKDPVFAG ISDNATAQIATAWASALADYAAAHKSMRPEILASCHQTLNCLIES TRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATA DACTFIPVTRDQSDIYEVFNVAGSSFSGSYAAGDVLDMQSVGVYSQLR RRYVLVASSDGTSTATFKMEDFEGQNVPIRKGRTNIYVNRKSVVD NGSGSLLSFTNAAGEQITVTCSLNYNIGQIALSFSKAPDKGTEIAI ETEINIEAAPELIPLINHEMKKYTLFPSQFVIAAEHTVQAAYEAQRE FGLDLGSLQFRTLKEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQ SFDVWATIIRGKFQTVYRDIIRVKSSGAMGMFAGADAASFFKQLPK DFFQPAEDYIQTYPVHYIGTPFRTTHST </p>
6534	A	1	2607	<p> MSFFSTLKTALSLEKLAATGVLVLICALVGAGFAWERHQLKQAI EK IGSLDQAVKERDKSIMDLNQTIETMNKAEQHFHSQEVKNESEQAKYA DRQMERKAEVQKQLVAAGNVQRIPADTQRLRESISEFNADADKGT VKQTINKVISIYKIEQVTVGKPGSEQCRRAFELADQLGLKHPDCIEH VFPTYAQEQCAHVLTEEDCFSNAERDGGDRICIGVICSWEFAKACGFA SKRLDVKLRLAIHESLGRRLRSGIAFKRGKDAKGGYQPGLLKVERFD AALAHIFDTSDPSTAHNSMRLHQLIESEAWLP IEAGNHQNDSGYNLN NVSREELLEEFIVPSVVPVDVMPASIDDAFIASDWREL CNEHLPQG NIHAVLKENVIDKLKSDYDFILVDSGPHLDAFLKNALASANILFTPL PPATVDFHSSSLKYVARLPELAASAPEELVALFPVQSELTFSDYKTL C AVGDEMGYKNLEFDQLIQNISPEINDILSIEE MAEDEVKNKILRLIT KEASLLTDKGSKD KSVVTELWKFEDKDRFARKRVKGRAFSYEFNRLS KEKSKLSNLREYQNRIADIAKRSKAVLGWASTAQFGTDNQFIKDDAA RAASILEAARKDPVFAGISDNATAQIATAWASALADYAAAHKSMRPR EILASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRL PLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGSSFSGSYA AGDVLDMQSVGVYSQLRRRYVLVASSDGTSTATFKMEDFEGQNVPI RKGRTNIYVNRKSVVDNGSGSLLSFTNAAGEQITVTCSLNYNIGK IALWFSKEPKDKGTEIPFEGENQF </p>
6535	A	1	4557	<p> MSFFSTLKTALSLEKLAATGVLVLICALVGAGFAWERHQLKQAI EK IGSLDQAVKERDKSIMDLNQTIETMNKAEQHFHSQEVKNESEQAKYA DRQMERKAEVQKQLVAAGNVQRIPADTQRLRESISEFNADADKGI FMSDKVTVKQTINKATSIYKIEQITVGKPGSEQYRRAFELADQLGLK HPDCIEHVFPTYADEQCTHVLTEEDFFSTEEREGVDRCIGVICSSVS DELFPNVPEYGGIGYQFLYEGDELKCYEHDIESKAKELTVNSNNTVQ PVALMRLGVFVPPKPSKSGESKEIDATKAFSQLEIAKAEGYDDIKIT GPRLDMDTDFKTWIGVIYAFSKYGLSSNTIQLSFQEFKACGFPSKR LDAKLRLTIHESLGRRLRNKGIAFKRGKDAKGGYQTLGLLVGRFDADL DLIELEADSKLWELFQLDYRVLLQHHLRALPKKEAAQAIYTFIESL PQNPLPLSFARIRERLALQSAVGEQNRI I KKAIEQLKTIGYLD CSIE KKGRESFVIHTSKVPDKRSSQLIESEAWLP IEAGNHQNDSGYSLNVE EIRVLYAWRMPPKHVVTHLAKDQLHKVAQRANRMLNVLTEQVQLQKDE LHANEFYQVYAKAALAKLPLLTRANVDYAVSEMEEGYVFDKRPAGS SMKYAMSIQNI IDIYEHRGVPKYRDYSEAYVIFISNLKGVGELISD EGCEQLATNIGFMSKLSNKADHKYCHSLAKEVFGDMLDVFLPRLD GFERCGESFDTVISANPATYVGSADALKNARIAEDFAKAVFDPSPGD RVEQVFKLSTGRQATFIEEVIPPNQVESDTFVDQHNNGRDQASLTPK SLKSIRSTIKHQFYPAIGVRRATGKIEILDGSRRRASAILENVGLR VLVTDQEISVQEAQNLAQDVQ TALQHSIREIGLRLMRMKNJGMSQKD IAAKEGLSQAKVTRALQAASAPEELVALFPVQSELTFSDYKTLCAVG DEMGKNLEFDQLIQNISPEINDILSIEE MAEDEVKNKILRLITKEA SLTLDKGSKD KSVVTELWKFEGKDRFARKRNRIADIAKRSKAVLGWA STAQFGTDNQFIKDDAARAASILEAARKDPVFVHIFDNATVQSATAW ASALADYAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNKAML ESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQS DIYEVFNVAGSSFSGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTST </p>

				KTATFKMEDFEGQNVPIRKGRTNIYVNRKSVVDNGSGSLLHSFTNA AGEQITVTCSLNYNIGQIALSFSKAPDKGTEIAIETEINIEAAPELI PLINHEMKKYTLFPSQFVIAAEHTVQAAEYAQREFGLDLGSLQFRTL KEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVDWATIIRGKF QTVYRDI IERVKSSGAMGMFAGADAASFFKQLPKDFFQPAEDYIQT PVHYIGTPFRTTHST
6536	A	3	2847	ELHAYAMSIQNI IDIYEHRGVPKYRDR\LAHAMRAHPHLLMEDLRIL VIDLDPQSSATMFLSHKHSIGIVNATSAQAMLQNVSRLEELEEFIVP SVVPGVDVMPASIDDAFIASDWRELCNEHLPQGNIHAVLKENVIDKL KSDYDFILVDSGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYV ARLHELVLKLSNEGCECQLATTIGFMSKLSNKAADHKYCHSLAKEVFG GDMLDVFLPRLDGFERCGESFDTVISANPATYVGSADALKNARIAAE DFAKAVFDQNVGLRVLVTDQEISVQEAQNLAQVQALQHSIREIGL RLMRMKNMGMSQKDIAAKEGLSQAKVTRALQAASAPEELVALFPVQS ELTFSDYKTLCAVGDEMKGYNLEFDQLIQNISPEINDILSIEEMAE EVKNKILRLITKEASLLTDKGSKDKSVVTELWKFEDKDRFARKGVKG RAFSYEFNRLSKKSKLSNLREYQNR IADI AKRSKAVLGWASTAQFG TDNQFIKDDAARAASILEAARKDPVFAGISDNATAQIATAWASALAD YAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAAE MMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPDTRDQSDIYEVF NVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTATFK MEDFEGQNVPIRKGRTNIYVNRKSVVDNGSGSLLHSFTNAAGEQIT VTCSLNYNIGQIALSFSKAPDKGTEIAIETEINIEAAPELIPLINHE MKKYTLFPSQFVIAAEHTVQAAEYAQREFGLDLGSLQFRTLKEYLSH EQDMLRLRIMIWRTLATDTFDIALPVNQSFVDWATIIRGKFQTVYRD I IERVKSSGAMGMFAGADAASFFKQLPKDFFQPAEDYIQT PVHYIGTPFRTTHST
6537	A	1	4236	MSFFSTLKTALSLKEKLAATGVLVLICALVGAGFAWERHQLKQAIK IGSLDQAVKERDKSIMDLNQT IETMNAEQHFHSQEVKNESEQAKYA DRQMERKAEVQKQLVAAGNVQRIPADTQRLRESISEFNADADKGI FMSDKVTVKQTINKATSIYKIEQITVGKPGSEQYRRFELADQGLK HPDCIEHVFPPTYADEQCTHVLTEEDFFSTEEREGVDRICIGVICSSVS DELFPNVPEYGGIGYQFLYEGDELKCYEHDIESKAKELTVNSNNTVQ PVALMRLGVFPKPSKSGESKEIDATKAFSQLEIAKAEGYDDIKIT GPRLDMDTDFKTWIGVIYAFSKYGLSSNTIQLSFQEFKACGFPSCR LDAKLRLTIHESLGRRLNKGIAFKRGKDAKGGYQTGLLKEAAQAIY TFIESLPQNPLPLSFARIRERLALQSAVGEQNR I I KKAIEQLKTIGY LDCSIEKKGRETHIFDTS DPSTAHNSMRLHQLIESEAWLPIEAGNHQ NDSGYNLNNVSREELEEFIVPSVPGVDVMPASIDDAFIASDWREL CNEHLPQGNIHAVLKENVIDKLKSDYDFILVDSGPHLDAFLKNALAS ANILFTPLPPATVDFHSSLKYVARLPELKNRPTIGRTLNP SILSGFD SSSASGDRVEQVFKLSTGRQATFIEEVI PPNQVESDTFVDQHNNGRD QASLTPKSLKSIRSTIKHQQFYPAIGVRRATGKIEILDGSRRRASAI LENVGLRVLVTDQEISVQEAQNLAQVQALQHSIREIGLRLMRMKN DGMSQKDIAAKEGLSQAKVTRALQAASAPEELVALFPVQSELTFSY KTLCAVGDEMKGYNLEFDQLIQNISPEINDILSIEEMAEDEVKNKIL RLITKEASLLTDKGSKDKSVVTELWKFEDKDRFARKRVKGRAFSYEF NRLSKEKSKLSNLREYQNR IADI AKRSKAVLGWASTAQFGTDNQFIK DDAARAASILEAARKDPVFAGISDNATAQIATAWASALADYAAAHKS MPRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVSDG VMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGSSF GSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTATFKMEDFEGQ NVPIRKGRTNIYVNRKSVVDNGSGSLLHSFTNAAGEQITVTCSLNY NIGQIALSFSKAPDKGTEIAIETEINIEAAPELIPLINHEMKKYTLF PSQFVIAAEHTVQAAEYAQREFGLDLGSLQFRTLKEYLSHEQDMLRL RIMIWRTLATDTFDIALPVNQSFVDWATIIRGKFQTVYRDI IERVKS

				SGAMGMFAGADAASFFKQLPKDFFQPAEDYIQTPYVHYIGTPFRTHST
6538	A	65	316	SSAGWKKSFGNCLKKDAASAPANIPIAPEDLTRSIMSRYTVWNLPRM MVAHTSKDWLTGRAMSKVSVARVRQIMMRRRSISCS
6539	A	54	265	KKDAASAPANIPIAPEDLTRSIMSRYTVWNLPRMMVAHTSKDWLTGR AMSKVSVARVRQIMMRRRSISCS
6540	A	2034	2175	EMPGHARCYADQQRYPFLPGSEVLP/ASINVAWRPVDNLNTCSTRSP E
6541	A	33	285	SSAGWKKSFGNCLKKDAASAPANIPIAPEDLTRSIMSRYTVWNLPRM MVAHTSKDWLTGRAMSKVSVARVRQIMMRRRSISCS
6542	A	1	2448	MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMSIQNIIDIYEHARGVPKYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSRREELLEEIVPSVVPVGVDMVP ASIDDAFIASDWRELCNEHLPQGNIHAVLKENVIDKLKSDYDFILVD SGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPELVKLI SDEGCECQLATNIGFMSKLSNKAADHKYCHSLAKEVFGGMDLVFLPR LDGFERCGESFDTVISANPATKSKLSNLREYQNRADIARSKAVLG WASTAQFGTDNQFIKDDAARAASILEAARKDPVFAGISDNATAQIAT AWASALADYAAAHKSMRPEILASCHQTLNCLIESNRNSMDPNKA MLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRD QSDIYEVPNVAGSSFGSYAAGDVLDQMOSVGVYSQLRRRYVLVASSDG TSKTATFKMEDFEGQNVPIRKGRNTIYVNRKSVVDNGSGSLLHSFT NAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIETEINIEAAPE LIPLINHEMKKYTLFPSQFVIAAEHTVQAAEYEAQREFGLDLGSLQFR TLKEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVWATIIRG KFQTVYRDIIERVKSSGAMGMFAGADAASFFKQLPKDFFQPAEDYIQ TPYVHYIGTPFRTHST
6543	A	1	2979	MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMSIQNIIDIYEHARGVPKYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSRREELLEEIVPSVVPVGVDMVP ASIDDAFIASDWRELCNEHLPQGNIHAVLKENVIDKLKSDYDFILVD SGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPELVKLI TIGRTLNPISILSGFDSSASGDRVEQVFKLSTGRQATFIEEIVPPNQ VESDTFVDQHNNGRDQASLTPKSLKSIRSTIKHQQFYPAIGVRRATG KIEILDGSRRRASAILENVGLRVLVTQDEISVQEAQNLAKDVQALQ HSIREIGLRLMRMKNMGMSQKDIAAKEGLSQAKVTRALQAASAPEEL VALFPVQSELTFSDYKTLCAVGDEMKGYNLEFDQLIQNISPEINDIL SIEEMAEDVKNKILRLITKEASLLTDKGSKOKSVVTELWKFEDKOR FARKRVKGRAFSYEFNRLSKEKSKLSNLREYQNRADIARSKAVLG WASTAQFGTDNQFIKDDAARAASILEAARKDPVFAGISDNATAQIAT AWASALADYAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNKA MLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRD QSDIYEVPNVAGSSFGSYAAGDVLDQMOSVGVYSQLRRRYVLVASSDG TSKTATFKMEDFEGQNVPIRKGRNTIYVNRKSVVDNGSGSLLHSFT NAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIETEINIEAAPE LIPLINHEMKKYTLFPSQFVIAAEHTVQAAEYEAQREFGLDLGSLQFR TLKEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVWATIIRG KFQTIY
6544	A	1	3276	MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMSIQNIIDIYEHARGVPKYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSRREELLEEIVPSVVPVGVDMVP ASIDDAFIASDWRELCNEHLPQGNIHAVLKENVIDKLKSDYDFILVD SGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPE

				LVKLISDEGCECQLATNIGFMSKLSNKADHKYCHSLAKEVFGGDMLD VFLPRLDGFERCGESFDTVISANPATYVGSADALKNARIAEDFAKA VFDPSGDRVEQVFKLSTGRQATFIEEVIPPNQVESDTFVDQHNNGRD QASLTPKSLKSIRSTIKHQQFYPAIGVRRATGKIEILDGSRRRASAI LENVGLRVLVTDQEISVQEAQNLAKDVQTALQHSIREIGLRLMRMKN DGMSQKDIAAKEGLSQAKVTRALQAASAPEELVALFPVQSELTFSDY KTLCAVGDEMGNKNLEFDQLIQNISPEINDILSIEEMADEVKNKIL RLITKEASLLTDKGSKDKSVVTELWKFFEDKDRFARKRVKGRAFSYEF NRLSKEKSKLSNLREYQNRDIADIAKRSKAVLGWASTAQFGTDNQFIK DDAARAASILEAARKDPVFAGISDNATAQIATAWASALADYAAAHKS MPRPEILASCHQTLLENCLIESTRNSMDATNKAMLESVAAEALMMSVS DGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGS SFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFE GQNVPIRKGRTNIIYVNRKSVVDNGSGSLLHSFTNPAGEQITVTCSL NYNIGQIALSFSKAPDKGTEIAIETEINIEAAPELIPLINHEMKKYT LFPRKLWGLCIMIWRTLATDTFDIALPVNQSFVDWATIIRGKFQTVY RDI IERVKSSGAMGMFAGADAASFFKQLPKDFFQPAEDYIQTPYVHY IGTPTFRTTHST
6545	A	1	67	MTKCSHLNLYLFSWLRDNGILITGERRNVKQYIISRGYFTLKET VIDTSNGSRISFTTRITGKGQQLMKRLLDADVVRTTSIVMLAKVTF LSCITMSDFTFSGYELACFVTHSGLSRASAGHILSQCANLAATTSEYF IHKPHRLITAETGYSQSTVVRAFREAVNKGILSVEIVIGDHRERRAN LYRFTPSFLAFAQQAKNALIESKLIKISSAATKVAVLAKTLALFNFL STPPCQNDTPSPCQDDVAIKNKKSQVKKTKRSVSGGAGTTSCLKLTS WIAKAKAKADNRLSKKRTQKHEFKQKVEAAARKYAYLKNKRSPIG GISNFDNLPHCMTVNEALNAVLAKNKDNEQWGAAGAYIADITDGED RARHFGLMSACFGVSGVYMQTRYRGKLVSQGFVVQMILTPRADGT FITSTDSETVHYHYGPKDLVTILFYIFITIIILHAVVQEYILDKISKR LHLKSVKHSKFNESGQLVVFHFTSVIWCIFYVVVTPQALTRVLNCLL ALGSNAAVMGECGFAQLQQTWASALADYAAAHKSMRPEILASCHQT LENCLIESTRNSMDATNK/ADAGICRSRDDRER*RCYASAFIPRDDP ACSVGGSYR*CVITEF
6546	A	1	3435	MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMSIQNIIDIYEHRGVPKYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNALQNVSRREELLEEFIVPSVPG VDVMPASIDDAFIASDWRELCEHLPGQNIHAVLKENVIDKLKSDYD FILVDSGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPE LVKLISDEGCECQLATNIGFMSKLSNKADHKYCHSLAKEVFGGDMLD VFLPRLDGFERCGESFDTVISANPATYVGSADALKNARIAEDFAKA VFDPDILVLQPLAIESRRYSSYQLVARPHLLKRVIPPNQVESDTFVD QHNNGRVQASLTPKSLKSIRSTIKHQQFYPAIGVRRATGKIEILDGS RRRASAILENVGLRVLVTDQEISVQEAQNLAKDVQTALQHSIREIGL RLMRMKNDGMSQKDIAAKEGLSQAKVTRALQAASAPEELVALFPVQS ELTFSDYKTLCAVGDEMGNKNLEFDQLIQNISPEINDILSIEEMAED EVKNKILRLITKEASLLTDKGSKDKSVVTELWKFFEDKDRFARKRVK RAFSYEFNRLSKEKSKLSNLREYQNRDIADIAKRSKAVLGWASTAQFG TDNQFIKDDAARAASILEAARKDPVFAGISDNATAQIATAWASALAD YAAAHKSMRPEILASCHQTLLENCLIESTRNSMDATNKAMLESVAAE MMSVSDAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRD QSDIYEVFNVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDG TSKTATFKMEDFEGQNVPIRKGRTNIIYVNRKSVVDNGSGSLLHSFT NAAGEQITVTCSLNYNIGQIALSFSKAPDKGTEIAIETEINIEAAPE LIPLINHEMKKYTLFPSQFVIAAEHTVQAAEYAREFGLDLGSLQFR TLKEYLSHEQDMLRLRIMIWRTLATDTFDIALPVNQSFVDWATIIRG KFQTVYRDI IERVKSSGAMGMFAGADAASFFKQLPKDFFQPAEDYIQ

6547	B	9377	49839	TPYVHYIGTPFRTTHST MLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYAVSE MEEKGYVFDKRPAGSSMKYAMS IQNI IDIYEHRGVPKYRDRYSEAYV IFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSR EELLEEFIVPSVVPQVDMVP ASIDDAFIASDWREL CNEHLPQONIHAVLKENVIDKLKSDYDFILVD SGPHLDAFLKNALASANILFTPLPPATVDFHSSSLKYVARLPVELVKLI SDEGCECQLATNIGFMSKLSNKADHKYCHSLAKEVFGGDMLDVFLPR LDGFERCGESFDTVISANPATGFDSSSASGDRVEQVFKLSTGRQATF IEEVIPPNOVL DGLPGMKILDVPRRRASPILENVGIRVLVTTQEIS VQEAQNLAQDVQTALQHSIREIGLRLMRMKN DGMQKIDIAAKEGLSQ AKVTRALQAASAPEELVALFPVQSELTFSYKTLCAVGDEMGNKNLE FDQLIQNISPEINDILSIEE MAEDEVKNKILRLITKEASLLTDKGSK DKS VVTELWK FEDKDRFARKRVKGRAFSYEFNRLSKEKSKLSNLREY QNRIADI AKRSKAVLGWASTAQFGTDNQFIKDDAARAASILEAARKD PVFAGISDNATAQIATAWASALADYAAAHKSMRPEILASCHQTLEN CLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQL GAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGV YSQLRRRYVLVASSDGT SKTATFKMEDFEGQNVPIRKGR TNIIYVNR I KSVVDNGSGSLH SFTNAAESPRNSMDAPNKAMLESVAAEMMSVSDG VMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSF GSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKTATFKMEDFEGQ NVPIPKGSTNIYVIRIKSVVDNGSGSLH SFTNAAGWANAMADYAQA HKSMPCREILASCPQTL ENCLIESTRNSMDATNKAMLESVAAEMMSV SDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAG SSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKTATFKMEDF EGQNVPTRKREASTLT VLSLLITVPAAYITRLMLLTLENCLIEP PPN SMDPFNKAMLESVPPPEMMSVSDGVMRPPLEFLEMILPVQLGAATA DACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLR RRYVLVASSDGT SKTATFKMEDFEGQNVPIRKGSTNIYVNR IKSVD NGSGSLH SFTNAAE MIVSDGVMRLPLFLAMILPVQLGAATADAC TFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVAVASALADYA AAHKSMRPEILASCHQTLENCLIESTRNSMDATNKAMLESVAAEMM SVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN AGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKPATFKME DFEGQNVPIPKGSTNIYVNR IKSVDNGSGSLH SFTNAAGEQITVT CSLNYNIGQIARRFQSANKALVAMKLGAA TVDACPFIPVTRDQSDIY EVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKTA TFKMEDFEGQNVPIRQGREN IYVNR IKSVDNGSGSLH SFTNAAES TRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATA DACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLR RRYVLVASSDGT SKTATFKMEDFEGQNVPIRKAHKSIPRPEILASCH QTLENCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMI LPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD QSVGVYSQLRRRYVLVASSDGT SKTATFKMEDFEGQNVPIRQGR TN I YVNR IKSVDNGSGSLH SFTNAAGEQITVTC SLNYNIGQIALSDGT SKTATFKMEDFEGQNVPIRQSDGIYVNR IKSVDNGSGSLKHSFTN AAATANACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGS EDIYVNR IKSVDNGSGS IHSFTNAAGEQITVTRSLNYN IAMILHV QLRAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSV VTKILRPGSREISGLVDHTGGRQIALIGFPPTGGMAIPLKKT KLGNL FQSSGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQ SVGVYSQLRRRYVLHEIMSVSDVVRRLPLFFAMILLVQLGPATADAC TFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRY VLVASSDGT STPATFKMEDFEGQNVPPPQAWKPINKAKVGICSHQKI MSVFDGVMRLPLFLAMILPVQLGPATVNACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKTATFKM
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			<p>EDFEGQNVPIRKGRTNIVSRIKSVVDNGSGSLLHSFTNAAGEQITV TCSLNYNIGQIALSFYKAPEKGTETAIERGAAGKIPPLAHESMMSAP NQILYTLGQVKLSVIRLQHIKSKDASDKFWPASLTPWKTCVIESTRD SMYATNKAMLKSVAAEMMSVSDGVMRLPLFLAMILPVQLGAATDDAC TFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRY VLVASSDGTSTKATATFKMEDFEGQNVPIRKAYFTRLLMLLHIILCRVG KFWLPAPQTLKNCLESTGNMMDATNKAMLESVAAQIMSVSHGVMRL PLFLAMIMPVQLRAATADACTFIPVTRDQSDIYEVFNVAGSSFGSYA AGDVLMQSVGVYSQRLRRRYVLVASSDGTSTKATATFKMEDFEGQNVPI RKGRNNIYVSRIKSVVDNGSGSLLHSFTNAESPRNSMDATNKMTMLE SVAAEMMSVSDGVMRLPLFLAMILPVQLGAATDDACTFIPVTRDQSD IYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLVASSDGTSTK TATFKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGSLLHSFTNAA ESTRNSMNALNKAMLESVAAEIMSVSDGVMRLPLFLAMILPVQLGAA TADACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQ LRRRYVLVASSDGTSTKATATFKMEDFEGQNVPIRKGRTNIVNRIKSV VDNGSGSLLHSFTNAAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLV ASSDGTSTKATATFKMEDFEGQNVPIPKGRNNIYVNRKSVVDNGSGSL LHSFTNAAAWASALADYAAAHKSMRPEILASCPQTLNCLIESTRN SMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADAC TFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRY VLVASSDGTSTKATATFKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGS GSLLSFTNAAAWASALADYAPAHNLMRPEILASCHQTLNCLIES TRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATA DACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRL RRRYVLVASSDGTSTKATATFKMEDFEGQNVPIRKGRNNIYVNRKSVVD NGSGSLLHSFTNAAGSSFGSNAAGDVLDQMOSVGVSQRLRRRYVLV SDGTSTKATATFKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGSLLH SFTNAAAWASARVDYPEAHKFMPRPKILASGHQTLTKCLIESTRNSM DATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTF IPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVL VASSDGTSTKATATFKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGS LLHSFTNAAAWASARAEPAAHKSMRPEILASATQTLNCLIESTR NSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADA CTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRR YVLVASSDGTSTKATATFKMEDFEGQNVPIRKGRNNIYVNRKSVVDNG SGSLLHSFTNAAESTRNSMDATNKAMLKSVAAKMSVSDGVMRLPLF LAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGD VLDQMOSVGVSQRLRRRYVLVASSDGTSTKATATFKMEDFEGQNVPIRK RTNIYVNRKSVVDNGSGSLLHSFTNAAESTRNSMDATNKAMLESVA AEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYE VFNAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLVASSDGTSTKAT FKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGSLLHSFTNAAAWA SALADYAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNKAMLE SVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSD IYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLVASSDGTSTK TATFKMEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGSLLHSFTNAA AWASALADYAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNK AMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRD QSDIYEVFNVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLVASSD GTSTKATATFKMEDFEGQNVPIRKGRNNIYVNRKSVVDNGSGSLLHSFT NAAAHKSMRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAPE MMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVF NVAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYVLVASSDGTSTKATATFK MEDFEGQNVPIRKGRTNIVNRIKSVVDNGSGSLLHSFTNAAAGSSFG SYAAGNVLDQMOSVGVSQRLRRRYVLVASSDGTSTKATATFKMEDFEGQ VPIRKGRNNIYVNRKSVVDNGSGSLLHSFTNAAVAGASYPLMRVPSF</p>
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				RLRVTSPTSINQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIPKG RKNIIYVNRKISVVDNGSGSLLHSFTNAAGSSFGSYAAGDVLDMSVG VYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIPKGRKNIYVNR IKSVDNGSGSLLHSFTNAATDDACTFIPVTRDQSDIYEVFNVAGS SFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKMEDFE GQNVPIRKGRKNIYVNRKISVVDNGSGSLLHSFTNAAEEMMSVSDGV MRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGSSFG SYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKMEDFEGQNV VPIRKGRNNIYVNRKISVVDNGSGSLLHSFTNAAAWASALADYAAAH KSMRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVS DGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVAGS SFGSYAAGDVLDMSVGVSQRLRLRYVLVASSDGTSTKATFKMEDFE GQNVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTNAAAWASALADYA PAHKSMRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAAEMM SVSDGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNV AGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKME DFEGQNVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTNAATADACT FIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYV LVASSDGTSTKATFKMEDFEGQNVPIPKGRNNIYVNRKISVVDNGSG SLLHSFTNAAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGT SKTATFKMEDFEGQNVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTN AAAKMMSVSDGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDI YEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTK ATFKMEDFEGQNVPIPKAWASALADYAAAHKFMPEILASCHQTLN NCLIESTRNSMDATNKAMLESVAAEMMSVSDGMRLPLFLAMILPVQ LGAATADACTFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDMSVG VYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVNR IKSVDNGSGSLLHSFTNAAGEQITVTCSLNYNIGQIALSVSKAPDK GTEIAIERGDSTXLGTATADACTFIPVTRDQSDIYEVFNVAGSSFGS YAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKMEDFEGQNV PIPKAEMMSVSDGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSD DIYEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTST KTATFKMEDFEGQNVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTNA AGSSFGSYAVGNVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKME DFEGQNVPIPKGRKNIYVNRKISVVDNGSGSLLHSFTNAAAWASALA DYAAAHKSIPRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAA EMMSVSDGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEV FNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATF KMEDFEGQNVPIPKGRNTNINVRKISVVDNGSGSLLHSFTNAAGSSF GSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKMEDFEGQ NVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTNAAESTRKSMDATNK PMLESVAAKMMSVSDGMRLPLFLAMILPVQLGAATADACTFIPVTR DQSDIYEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSD GTSTKATFKMEDFEGQNVPIPKGRKNIYVNRKISVVDNGSGSLLHSF TNAAEEMMSVSDGMRPPLFLAMILLVQLGAATDDACTFIPVTRDQSD DIYEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTST KTATFKMEDFEGQNVPIPKAHKSMRPREILASCHQTLNCLIESTRN SMDATNKAMLESVAAEMMSVSDGMRLPLFLAMILPVQLGAATADAC TFIPVTRDQSDIYEVFNVAGSSFGSYAAGDVLDMSVGVSQRLRRRY VLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVTRI KSVVDNGS GSLLHSFTNAAMIPHVQLGAATADACTFIPVTRDQSDIYEVFNVAG SSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKMEDF EGQNVPIRKGRNNIYVSRI KSVVDNGSGSLLHSFTNAAGPSALADY APAHKFMPGRKILGSLPPDAENCLIESTRNSMDATNKAMLESVAAEM MSVSDGMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLDMSVGVSQRLRRRYVLVASSDGTSTKATFKM EDFEGQNVPIRKGRNTNIYVNRKISVVDNGSGSLLHSFTNAAGEQITV
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				<p> TCSLNYNIGQIALQLCRRYVLVASSDGTSTKATFKMEDFEGQNVPI QGSKNMYVNRIKSVVDNGSGSLLHSFTNAAAKDYERFLTVMRLPLS LAMFLPFLGAATADACPFIRVTRDQSDIYEVFNAGSSFGSYAAGD VLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIQQA KMLSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEV FNVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATF KMEDFEGQNVPIRKAPVDACTFIPVPRDQSDIYEVFNAGSSFGSYA AAWASALADYAAAHKSMRRRKILASCHQTLNENCLIESTRNSMDATNK AMLESVAAEMMSVSDGVMRPLFLAMILPVQLGAATADACTFIPVTR DQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSD GTSTKATFKMEDFEGQNVPIRKGRNTNIYVSRIKSVVDNGSGSLLHSF TNAAGSSFGSYAAGDVLDMQSVGVYTQLRRRYVLVASSDGTSTKATF KMEDFEGQNVPIQGRKNINLGAATADACTFIPVTRDQSDIYEVFN AGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKME DFEGQNVPIRQGRNNINVNRIKSVVDNGSGSLLHSFTNAAEQITVT CSLNYNIGQIALSSPKRRRIKALLGAATADACTFIPVTRDQSDMYEVF NVAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFK MEDFEGQNVPIRKGRKNINVNRIKSVVDNGSGSLLHSFTNAAATAYA CTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLNMQSVGVYSQLRRR YVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNNINVNRIKSVVDNG SGSLLHSFTNAAAHKSMRRPEILASCHQTLNENCLIESTRNSMDATNK RMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTR DQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSD GTSTKATFKMEDFEGQNVPIRKGRNTNIYVNRIKSVVDNGSGSLLHSF TNAESTRNSMDATNKAMLLSVASEMMSVSHGVMRLPLFLAMIMPVQ LGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVG VYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNNIYVTR IKSVVDNGSGSLLHSFTNAAAWATEMMSVSDGVMRLPLFLAMILPVQ LGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVG VYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVN IKSVVDNGSGSLLHSFTNAAEMMSVSDGVMRLPLFLTMILPVQLGA ATDDACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVY QLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIPKGRNNINVTRIKS VVDNGSGSLLHSFTNAAEQITVTRSLNYNIGQIALSVSKAPLGAAT ADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQL RRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRKNIYVNRIKSVV DNGSGSLLHSFTNAAVARKDPVFGGISEKPTVQIATAWASALPDYAP AHKSMRRPKILASCHQTLNENCLIESTRNSMDATNKAMLESVAAEMMS VSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNVA GSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMED FEGQNVPIRKGRNTNIYVNRIKSVVDNGSGSLLHSFTNAAAASKSPGF SGIPDHAHQIRYRVGKWHWLLTPQHINLCRVGKFWLPATQTLNENCL IESPRNSMDPTNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGA ATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVY QLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVNRIKS VVDNGSGSLLHSFTNAAESTRNSMDATNKAMLESVAAEMMSVSDGVM RLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGS YAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNV PIRKGRNTNIYVNRIKSVVDNGSGSLLHSFTNAAATADACTFIPVTRD QSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDG TSKATFKMEDFEGQNVPIRKGRNNIYVNRIKSVVDNGSGSLLHSFT NAAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSD IYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSK TATFKMEDFEGQNVPIRKGRKNINVNRIKSVVDNGSGSLLHSFTNAA AWASALADYAAAHKSMRPENWASCHQTLNENCLIESTRNSMDATNKA MLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRD QSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDG </p>
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				<p> TSKTATFKMEDFEGQNVPIRKGRNTNIYVNRKSVVDNGSGSLLHSFT NAAESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQL GAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGV YSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVNR KSVVDNGSGSLLHSFTNAAWASALADYAPAHKSMRPEILASCHQT LKNCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILP VQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQS VGVSQSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYV NRKSVVDNGSGSLLHSFTNAAEMMSVSDGVMRLPLFLAMILPVQL GAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGV YSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVNR KSVVDNGSGSLLHSFTNAAEQITVTCSLNYNIGQIALSFSKAPDKG TEIAIERTLENCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLP LFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAA GDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIR KGRNTNIYVNRKSVVDNGSGSLLHSFTNAAEMMSVSDGVMRLPLFL AMILPVQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDV LDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGR NNIYVNRKSVVDNGSGSLLHSFTNAAEMMSVSDGVMRLPLFLAMI LPVQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLD QSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNI YVNRKSVVDNGSGSLLHSFTNAAEMMSVSDGVMRLHLFLAMILPV QLGAATADACTFIPVTCQSDIYEVFNAGSSFGSYAAGDVLDMQSV GVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVS RIKSVVDNGSGSLLHSFTNAAWASALADYAAAHKSMRPEILASCH QMLENCLIESTRNSMYATNKAMLESVAAEMMSVSDGVMRLPLFLAMI LPVQLGAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLD QSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNI YVNRKSVVDNGSGSLLHSFTNAAADMMMSVSDGVMRLPLFLAMIMHV QLGAAPADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGNVLYMQSV GVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIPKGRNNIYVI RIKSVVDNGSGSLLHSFTNAAATDDGCTFIRVTRNQSTFYEVFNAG SSFGSYAAGDVLDHIQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDF EGQNVPIRKGRNTNINTRI KSVVDNGSGSLLHSFTNAAVPHSIKSLT VASSSIGSYAAGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKM EDFEGQNVPIRKGRNTNIYVNRKSVVDNGSGSLLHSFTNAAAGSSYGS YADGDVLDMQSVGVYSQLRRRYVLVASSDGTSTKATFKMEDFEGQNV PIRKDGALNMQSVGVYSQLRQPLCAGGKLRWHQQIRNLQDLGAATG DACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLR RRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVXPSYVACY ELVASSDGTSTKATFKMEVFEGQNVPIPKGRKNIYVNRKSVVDNGS GSLHSFTNAAATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGD VLHMQSVGVYSQLRRRYVLVASSDGTSTKATFKILLHSFTNAAEQI TVTCSLNYNIGQIALSFSKAPNKGTEIAIEREISQKVTGGLGAATD DACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYSQLR RRYVLVASSDGTSTKATFKMEDFEGQNVPIPKGRKNTNINTRI KSVVD NGSGSLLHSFTNAAVWANALANYAQAHNLIIPRKILASCHQKLKTCL IKSTRNSMDATNKAMLESVSAEMMSVSDGVMRLPLFLAMILPVQLGA ATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDMQSVGVYS QLRRRYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRNNIYVNRKSV VDNGSGSLLHSFTNAAEMMSVSDGVMRLPLFLAMIQHVLGPATG NACTFIPVTRDQSDIYEVFNVTGSSFGSYADGNVMMMQSVGVYSQLR RCYVLVASSDGTSTKATFKMEDFEGQNVPIRKGRKNIYVNRKSVVD NGSGSLLHSFTNAAAHKFMPRPEILASCHQTLDCNVIESTRNSMDAT NKAMLESVAAEMMSVSDGVMRLPLFLEMILPVQLGAATADACTFIPV TRDQSDIYEVFNAGSSFGSYAAGDVLDNMQSVGVYSQLRRRYVLV SDGTSTKATFKMEDFEGQNVPIRKGRNTNIYVNRKSVVDNGSGSLLH </p>
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				<p> SFTNAAEMMSVSDGVMRVLFLAMILPVQLRAATD NACTFIPVTRDQ SDIYEVFN VAGSSYGSYVAGDVMDMQSVAWASALVDTFPAHKSMPRP KIRASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRL PLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYA AGDVLD MQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQNVPI RKGR TN IYVNR IKS VVDNGSGSLLHSFTNAAESTRNSMDATNKAMLE SVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSD IYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGTSK TATFKMEDFEGQNVPIRKGR TN IYVNR IKS VVDNAYFTRLLMLLREQ ITVTCSLNYNIGQIALSFSKAPDKGTEIAIERAWASALAEYAAAHKS MPRPEILASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVSDG VMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSF GSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQ NVPIRKGR TN IYVNR IKS VVDNGSGSLLHSFTNAAEMMSVSDGVMR LPLFLAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSY AAGDVLD MQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQNV IRKGR TN IYVNR IKS VVDNGSGSLLHSFTNAAEQITVTCSLNYNIG QIALSFSKAPDKGTEIAIERGSSTCFRRLLEWFPEENLWLAWASALA EYAAAHKFMPRPKILASCHQTLTGLIESTRNSMDATNKAMLESVAA EMMSVSDGVMRLPLFLAMILPVQLGAATADECTFIPVTRDQSDIYEV FN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGTSKTATF KMEDFEGQNVPIRKGRNNIYVNR IKS VVDNGSGSLLHSFTNAAATAD ACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRR RYVLVASSDGTSKTATFKMEDFEGQNVPIPKGRNNINVNR IKS VVDN SGSLLHSFTNAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACT FIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYV LVASSDGTSKTATFKMEDFEGQNVPIRKGR TN IYVNR IKS VVDNGSG SLLHSFTNAAAGMPLNKPAGILSQQKMMRVSAGVMRLPLFLAMILPV QLGAAPVD ACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSV GVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQNVPIPKGRNNIYVNR IKSVVDNGSGSLLHSFTNAAEQITVTCSLNYNIGQIALSFSKAPD KGTEIAIERAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPV TRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASS DGTSKTATFKMEDFEGQNVPIRKGR TN IYVNR IKS VVDNGSGSLLH SFTNAAAHKFIRPEIRASCHQTLKNCLKESTRNSMDPTNKAMLESV AAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTFIPVTRDQSDIY EVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGTSKTA TFKMEDFEGQNVPIPKGRNNIYVNR IKS VVDNGSGSLLHSFTNAAEQ ITVTCSLNYNIGQIALSFSKAPEKGTEIAIERESTRNSMNATNKAM LESVAPEIMSVSDGVRRLPLIFLAMILLVQLGTATADACTFIPVTRDQ SDIYKVFNVAGSSFVSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGT SKTATFKMEDFEGQNVPIRKGRNNIYVNR IKS VVDNGSGSLLHSFTN AADLKNGLIEPTANSMNALNKAMLESVAAEIMSVSDGVMRLPLFLAM ILPVQLGAATDDACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVYSQLRRRYVLVASSDGTSKPTATFKMEDFEGQNVPIPKGRKN INVNR IKS VVDNGSGSLLHSFTNAAAWASALAEYAAAHKFMPRPEIL ASCHQTLNCLIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLF LAMILPVQLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGD VLD MQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQNVPIRK RTNIYVNR IKS VVDNGSGSLLHSFTNAAEQITVTCSLNYNIGQIAL SFSKAPNKGTEIAIERGVLT KVGAEHINLCGVRKILASCHQTLNCL IESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGA ATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVLD MQSVGVY QLRRRYVLVASSDGTSKTATFKMEDFEGQNVPIRKGRNNIYVNR IKS VVDNGSGSLLHSFTNAAEQITVTCSLNYNIGQIALSFSKAPDKGTE IAIERGLGAATADACTFIPVTRDQSDIYEVFN VAGSSFGSYAAGDVL DMQSVGVYSQLRRRYVLVASSDGTSKTATFKMEDFEGQNVPIRKGRN </p>
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				NIYVNRIKSVVDNGSGSLLHSFTNAAAHKFIRREFLASCHQTLKNC LIESTRNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLG AATADACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDQMOSVG SQLRRRYVLVASSDGTSTATFKMEDFEGQNVPIRKGRNNIYVNRIK SVVDNGSGSLLHSFTNAAAHNFMRVPEILPSCHQTWKTALIKSTPNS MNATNKAMLESVAPEMMSVSDGVMRLPLFLPMIWPVQLGAATADACP FIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYV LVASSDGTSTATFKMEDFEGQNVPIRKGRNTIYVTRIKSVVDNGSG SLLHSFTNAAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIERDA SLNFAQRGQVHWLTTPPAHKSMRPEILASCHQTLNENCLIESTRNSM DATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATADACTF IPVTRDQSDIYEVFNAGSSFGSYAAGDVLDQMOSVGVSQRLRRRYV VASSDGTSTATFKMEDFEGQNVPIRKGRNTIYVNRIKSVVDNGSGS LLHSFTNAAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIEREST RNSMDATNKAMLESVAAEMMSVSDGVMRLPLFLAMILPVQLGAATAD ACTFIPVTRDQSDIYEVFNAGSSFGSYAAGDVLDQMOSVGVSQRLR RYVLVASSDGTSTATFKMEDFEGQNVPIRKGRNTIYVNRIKSVVDN SGSLLHSFTNAAAGEQITVTCSLNINIGQIALSFSKAPDKGTEIAIE RGSSTX*
6548	A	3	127	LFHPCQDSQQHH*CVCCRLTGHGAA*VHGPCQAVQTYRASH
6549	A	2	323	GVGAGGCLREAAAGHVTGRAPHGRRPSSARPERPARPRPWGAATAAR NEDSDQDRRGAEAVCLDPSQPPPTKALNGAEPNYHSLPSARTDEQAL LFFHPCQDSQQHH
6550	A	2	94	WRDLGSPQPPPPGFKRFFCLILPTRCRSPR
6551	A	171	632	YVKVREMGLASKKWNLISMFGNSDLMSGKLVHISRNYFIFSRQSFT LVGQAGVQWRDLGSPQPLPGFKRFSLSLPSSWDYRHTPPHPANFV FLVETGFLHVGQAGLELPTSGDLPASASQSPGITGVSHCTWPIPSHL LKKKIKKINIHL
6552	A	3	325	TFNVPMYVAIQAVLSLYASGRTTGIVLDSDGDVTTMYPGIADRMQK BITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWITHKQY DEAGPSIVHRKCF
6553	A	2	171	LAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWITHKQYDESG PSIVHRKCF
6554	B	104	1164	MCDEDETTALVCDNGSGLVKAGFAGDDAPRAVFPSIVGRPRHQGMV GMGQKDSYVGDEAQSKRGILTLPYIEHGIITNWDDEKIIWHHTFYN ELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAIQAV LSLYASGRTTGIVLDSDGDVTHNVPIYEGYALPHAIMRLDLGRDLT DYLKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENEMATGRHP SILPWKRATSCQTGQVITIGNERFRCPETFFQPSFIGMEVGGHFTRP PYSIMKCDIDIQEGPCMPNTVMFGGHPRLYPWEFADPHARKRFTGA GTPGTHEESKDKDSFAPRRSGKILG*
6555	A	1	308	LRPWC/GHLRT*QYHTLRAARLDPNFAIA*MEAKATDGPFPFE/VR GFPTIYF\SPANRLHPRTSEGGRLSDFLSYLHVEATNPPVIQEV* PKKK\KKAQEDL
6556	A	2	589	AIRTAKGEKFVMQEEFSRDGKALERFLQDYFDGNLKRYLKSEPIPE NDGPVKVVVAENFDEIVNNENKDVLEFYAPWCGHCKNLEPKYKELG EKLS\KDPNIVIA\KMDATAN\NVHSPYEVGRF\PSHILLSKPNKKL NPK\KYEGRREL*FLLAIQREATKPPPVIVQ*FIPKYRRRRHQED LLKPVAQTPTL
6557	A	1	129	YDKPHVLVDILVDDSGKESLIGYRPTEDYDLRNCILVGINQME
6558	A	23	116	SVLSKPKVKMPHILFTLSCTVSHSIWLIPIM
6559	A	1	1582	GRGWRAVLGWSRRRSGLEPATVGGSMALLFLPLVMHGVSRAMGTA DLGPSSVPTPTNTVIESYNMNPVYWEYQIMPQVPVFTVEVKNYGVK NSEWIDACINISHHCNISDHVGDPSNSLWVRVKARVGQKESAYAKS EEFAVCRDGKIGPPKLDIRKEEKQIMIDI FHPSVFNVDGEQVDDYD ETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCLAI PVSSLN

				SQYCVSAEGLVHVGVVTEKSKEVCITIFNSSIKGSLWIPVVAALLL FLVLSLVFICFYIKKINPLKEKSIILPKSLISVVRSATLETKPESKY VSLITSYQPFSLKEVVCEEPLSPATVPGMHTEDNPGKVEHTEELSS ITEVVTTEENIPDVVPGS\HLTPIERESSPLSSNQSEPGSIALNSY HSRNCSESDHSRNGFDTDSSCLESHTSSLDSEFPNNKGEIKTEGQE LITVIKSPPPSFC\YDKP\HVLVDLLV\DDSGKESL\IGYRPT\EDS QRNFHEISLSCTQL
6560	A	69	523	PLGCASSQSIASRNTLCTTASSCCPQVLAHS\KAAEYMTRWKVQOM PHSQDRALQSVFCAPFHS**LVALPTGHR*MTPAQFSECFQATSGGS D*DPFLAPSFL\VPGLPVAPGLLLPLGPVHSRATMEEGQATHEELTV FIGLRPGVGRS
6561	A	101	1469	RTHPTFPHPGTGPTSAPPSGALEGTAGTITSNEWSPTSPEGSTASG GSQALDKPIDNDGEGVWSPDIEQSFQEAALAIYPPCGRRKIILSDEGK MYGRNELIARYIKLRTGKTRTRKQVSSHQVLARRKAREIQAKLKDQ AAKDKALQSMAMSSAQIISATAFHSSMRLARGPGRPAVSGFWQAGAL PGQAETSHDVKPFSSQOTYAVQPPLPLPGFESFAGPAPSPSAPPAPPW QGR\SVASSKLWMLEFSAFLEQQQDPDTYNKHLFVHIGQSSPSYLRP YLEAVDIRQIYDKFPEKKGGLKDLFERGPSNAFFLVKFWADLNTNIE DEGSSFYGVSSQYESPENMIITCSTKVCSEFGKVVEKVEYARYEN GHYSYRIHRSPLCEYMINFIHKLKHLPEKYMMSVLENFTILQVVTN RDTQETLLCIAVFEVSASEHGAQHIIYRLVKE
6562	A	1	1290	MPAAACRQDKKSGRFYSFTEAEGTVAVTQGAEGRAAPWSLPSVKKA QEKVWGEERRPPALGRNELIARYIKLRTGKTRTRKQVGLKRRVGVPG VVPQHQSAPKVSSHQVLARRKAREIQAKLKDQAAKDKALQSMAMSS SAQIISATAFHSSMALARGPGRPAVSGFWQAGALPGQAGTSHDVKPFSS QOTYAVQPPLPLPGFESFAGPAPSPSAPPAPPWQGRSVASSKLWMLE FSAFLEQQQDPDTYNKHLFVHIGQSSPSYSDPYLEAVDIRQIYDKFP EKKGGLKDLFERGPSNAFFLVKFWVRGREGTSQRQKAGPGLEAKTQA YQLIPPQKPPPAEPERTLAVGHPTCRFVGEENGLKKPIDLPKFPQQL QSRKASWRRKYLSPREKDCSRSEGAHIMRDWVSELVTRRPGKTA EVQVLLL
6563	A	604	1047	SNRTDNPTSVAYLSKETDVVAKGWPCHLWVVVAVAILVLEAIKIIQ GKDFTVWTSHDVNGILGAKGNSWLSKRLRLRYQALLLEGPVLIHTC VALNPAIFLPEDGEPIKHDIYQIQAQTYVT*EDLLEVPLANPDNLNLY TNGSSFV
6564	A	1	1410	METPGKAFRQIDRKTSAAWSFSPRTSVTGLRGGDGMKGALGDPSA PPVPANLRLANSTVNSDGSVTVTIVWGLPEEPDILVHHYNVFWSWTI SSKSLVPTKKKQKRTTDGDWQAAPPATGCRHWWKPAVLLSLVGTWR TFMSSQGIVNTPVSTLHLAQVRPRTHQFWTDFGDHEGTITNRQASSG TKYQAPVGQLKATSMAAGLKTQVSCFLGKGSMLTPGLFGVGTGGQA RVQVFKNVSVSAAKSDLPWSSIWSGRKTSVSAASLLGGGEGFPTRI HIPFSLDLKQIKAGLGRFSDDPDRDQEEQAQKEKRDQRKAAALVMA LRQTNLGGSERTENGAGQSPERAGIALGDLIQTGRKTPQPVAYLSKE IDAVAKVWPHCLKLVAAVAVFVSEAIKIIQGKDLTVWTTHEEPVGSS AQSQHQPDQPRYTCKLLEDLHLLFRKEISQTKKAPILFDPVIKREK
6565	A	510	755	LDTECPHKGSPSPHQSRGPTLGGRRDGGKMAAETGYWRCLPESRTCA EEAVHLWPAVLRDPRWGNPGDGAWPCYMRGPRLE
6566	A	59	413	SWPSDKQTLVVQRGQKMEQANHPDPTDHMSQLMWT/VLPQGFSDSPH LFGQALAQDLGHFSSPGTLVLQYVDDLLLATSSSEASCQQATLALLNF LANQGYK/LSRKAQLCLQVVKYLCL
6567	A	1	565	KKTSKEISKGPQKPPGYRLRPLQAVGGGEFGPTQVHVHFSLSDLKQI KVDLGKISDDPDRIYIDVLQGLQTLDSLWRDVMLLLDQTLAFNEKNA ALAAAEFGDTWYLSEVNDRMATAERDKFPTEDGEPKCDQCCIIVQ TYAAQDDILEVPLANPDNLNLYTDGSSFVENGIRRAGYAIIVSDVTILE
6568	A	126	492	CNNSMTSLQVRLKVCPRPCRTSM/LPIRII*KLPQVCLDLL*IREGE WDMYPCWAKFPCPYSLKGT*PIAWGILWSFGDFFAY/IPLMQQKH*

				FSSQNTRRNEEGQI*WPLLMHSQKPAPLPVV
6569	A	1	342	FLFAFEDLTDHTSQLTWTILPQGFDRDSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSSEASCQATLDFLSFLANQGYEASRSKAQLCLQ QDRGYQATDDLTNGTPNELN
6570	A	55	219	LGNKHLGSLDPRGSWVTGEYIFLRPPIAA*GRQ*DPLPPELWWTSL LNNSWAFS
6571	A	339	1371	ASHPLRGLLCGPSLPNEPCPLLHGTQSHRPLKG*GVRAHSTGLAGSS TCRPLRDPLGEASWAPESAQGL*IHQSALCI*LKLKPAGQRAKLGDRL LDIPDRKSSTILGRAGDLQPAPEPPTLSVGSCAAQASPMNPAPCS TAPSPIDHSRAEECGRIARDWQAAPPAGPCGIHWVKPAGLLSLLRDC KYTNRHSVSSSRFANTNQHPASSSGFVNAPIDTLYLANLVGTWRTFV ASSGIVNAPISTLSKQTTWLYQSAGCGKESTQASGAQTGGTSFKSLE TTGSISEASSAKHCTELFSRFTTFNPDSVPSDGVVGDAGTVWPGVL KGEPCHLGTCTYRCVLDPHPTPSESDTIQGIHVQVCYMSLTHDADVCD TNDPVTHNTKKYIYSTEIFTSNPELRSEDETVFRALEKWKTSBQTI GEMDFYICNDPDPDSALYQNGLSKMQDTVSLSVFSPSVA
6572	A	749	1003	QLKKGTSNLLVSKPSPVWIPTGTLTQIMGTGVANIC*PVF*KD*GEL GKMNYAMMSTITQKKEENPAFLKWLWEALRKYTPLSP
6573	A	1	1632	MVCPEFVPSDVRMCPEFLPSVGVVSLTSGVKLQTFDLDTKVLHVPF SLSDLKQIKADLGKFSDDPDYKDVQLGGLQTFDLAWRDVMLLLDQI LAFIEKNAALAAAREFGDTWYLSQVNDRMATAKERDKFLTQQQAIPTM DPHWDFDSHDGDSHKLHLLTCVLEGLKGIRKKPMNYSMMSTITQGQE EKPSAFLERLREALRKYTPLSPESLEGQLILKDKFITQSAADIRRLQ QKQALGPEQNLQELLNLATLVFYNRDQEEQAQKEKRDQRKAAALVRA LRQTNLGGSERTEYGAGQSPRRDILAKAGAIIMNMGKLPICPLL EEGINPEVWALERQFGRKNARPVQIRLKDPTTFYQRYPLRLEAH KALQDIVKHLKPQGLVRKCSSPCNTPVLGQKPNQGWRLVQDLRLIN EAVIPVYLVVANPYTLLSQIPEEAWEFVMDLKDFAFFCIPLHSGSQF LFAFEDPTDHMSQLMWMVLPQGFDRDSPHLFGEALAQDLGHFSSPGTL VLQYMDLLLATSWEASCQATLELSS
6574	A	307	543	DENIHLNPLSKQDTPAVGNWMTAVATSCWIGVKKGPCSCSILQR GALGREFVPPFFSCHSIIYLTKIPGISKLLGCS
6575	A	1	1149	MDGTGDHYVKKRKPDPTRQTSLLTSLWDLKIKTIELVEIESRRMAT KAWEGPAMEHTCHLASSYQTSVETALGHPIEEAAEAEPKQNSGINV VLAVISELLRLPPVSI IQSNEARVAGPHDQNHHSFCRGLHWPLYSG GNWGLLFGLELKSIPWEKLSHVYMSRGLSQGPMGDERYMREKRQGC SKGSEEMGASYSGGFENLCVGTLYLANLVGTWRTFASSGIVNAPI SILSKRTNQLSVKWTNQLSVKWTNQDSTLPLRAATLTAKVCSFTPE ARETTNPPGGMNSRRALRVVTLTVKVCFSFIEPVVRPGTHQKEETL NTSEHQKEQTLDTPPLRTVTLTPRVHGFIEVSETKNPPIPDTPALW EAEAGGS
6576	A	119	409	GDICHHLGLTPVGSHSLSCSR*QVA*VGA VTAATIGTGILLQQLAF LVCNWLLLSGSSSENFPRSALICFKSEREKGTCIQVGPNSPPPTACKG HN
6577	A	1	2433	MPQVDHLVFVHVGIGPVCDLRFRSIECGLRRIRKKPMNYSMMSTIT QRKEENPSVFLEWLWEALRKYTPLSPDSLEGQLILKDKFITQSATDI SRKLQNRALVPEQNLVLLNLATLVFYTRDQEEQAKKEKRDQRKAAA LVMALKQTNLGGSERTENGAGQSPGMAFYQCGLQGHRLKDCPTRNKL PPRCPCLCRGNHWKATAPEDKEDGEPIKHDCQQIIVQSYAPQEDRLE VPLANPDNLNLYTDGSSFVENGIRRAGYAIIVSDVTILEMRKCAGQERD RFPVSGVVPGRTRRRVSDGGPQPWPRENLTVA AAAAPPLPHRALTYFSP PRPRSSASMCPSQSPRPPLLRPPCSYRELSRVLDIHSYPGIPQIFA EYPLLVRQVLGNANKLNSGPLLGYSSLSPTRRLGYEDSTDVGEED SFLGQTSIHTSAPQTFSYFSQVSSSDPFGNIGQSPLTTAATSVGQS GFPKPLTALPFTTGSQDVSNFSPSISKAQPGAPPSSLMGINSYLP QPSSLPPSYFGNQPGIPQPGYNPYRHTPGSSRANPYIAPPQLOQQC

				TPGPPAHPPSPGPPVQMYQMPPGSLPPVPSSVQSPAQQQVPARPGAP SVQVPSPFLLQNQYEPVQPHWFYCKEVEYKQLWMPFSVFDLSNLEEI YNSVQPDPESVVLGTDGGRYDVYLYDRIRKAAAYWEEPAEVRRTWTF YKGD TDSRFIPYTEEFSEKLEVP SLNEVPLHYLKPNSFVKFRMIQD MFDPEFYMGVYETVNQNTKAHPQOQELDLSNPRNTTLERQTFYCVVP GESTWVKEISFI
6578	B	97	1065	MHAVHTSLVERTILTITTKERGSTLQYPLRPGAHKGLQDIVKRFKAQ ALIRKCSSPCNTPIILGVQKPNGQWRLVQDLRLINEAVIPLYPVVNP YNLLSQIPEEAWEFTVLDLKD AFFCIP LHSQS QFLFAFEDPTDHTSQ LTWTVLPPGFRDSPPLFGQALAQDLGHFSSPGTLVLQYVDDLLATS SEASCOQATLDLLNFLANQGYKTHSRSDAPVGFTDRHLVATEKIPR GREPLSSLA VYTRGRPTRTGARRTIVSRIRDRFRFFRYRLAQREPPL YQO SLLIHLQLDSQPALS VVIGKVPNVVELTPNFGTAAQV*
6579	A	1	2403	MSMGFLVEESEFPVVWRGLMVMSAIEKLLRQVSGYLLAQGVSRNVVHE PGVGSSQVSPCPTVAKLNSGAKYRAPVGQLKATSAATRLKTRVSG FLGRGSLTSPDSLEL GALVCL EPASTFPVLLGRAKGRQKPFSSGV RTTRGPISLPPYPSLP IAPRPINDNPPLISPAQKEICEEISKGQKQK LGYRLCPLQAVGGGEFGPTWVHVPFSLSDLKQIKADLGNFSDDPDRY INV LQGLGQIFYL IWRDVMLLLDQTLAFNEKNAALAAAEFGDTWYL SQVND RMTAEERGKIPNGQQA VPSMDPHWDLSDHGDSCSKHLLTCV LEGLRRIRKKDQEEQAQKEKQDQRKTAALVMALRQTNFGGSERTENG AGQSPERDTLAKAGAI IYMNMGKLPICCP LPEEGINPEVWALEGQF GKAKNAHPVQIRLKDPTTFPYQRQYPLRPEAHKGLKDIVKYLKAQAL VKKCSSPCNSPILGVQKPN SQWRLVQDLRLINEAVIPLYPVVNPYI LLSQIPEEAWEFTVLDLKD AFFCIP PHSDS QFLFAFEDPTDHMSQLM WTVLPQGFKDSPHLFGQALAQDLGYFSSPGTLVLQYVDDLLATSSE ASCQOATLDLLNFLANQGYKRLLTMDPRTQRDSQAPLYSNQGENQRD KKSKEVQREEETDKEGVRKRERERQRRSQRERKRDGTSVSTLAVLE EPFSLPMRYGGPYLGLAKTRADSLCLWGGVEGEARVAGAGASCSTRP VRVPGEHRLGRPCTGHGQ PAPAGLDRGMCSFWAARVPGLGGA KSHGD CH
6580	A	1	2838	MSGTLKGMLPKRDLPIYPIYPDLCP LGPNACETNFLSPLFSEKEISK EISKGPQKPLGYRLCPLQAIGAGEFGPTRVHVPFSLSDLKQIKADLG KFSDDPDRHIDVLQGLGQTFDLAWRDVMLLLDQTLAFYEKNVALAAA REFGDTWYLSQVCLTIEGQEI DFLDSGTAFSVLISCPGQLSSRSVT IRGILGQPVTRPEAHKGLQNTVKHLKAQGLVRKCSSPGNTPIILGVQK PNRQCRLVQDLRLINEAVIPLYPVVNPYTL LLSQIPEEAWEFMVLDL KDAFFCIP LHSQS QFLFAFEDPTDHTSQLMWMVLPQGRDSPHLFGQ ALARDLGHFSSLGTLVLQYVDDLLATSSEALCQOATLDLLNFLANQ GYKVSRSKAQLCLQDGEPIEHDCQQII VQTYATRDDLLDVPLTIPD LNLYTDGSSVVENGIQRTGYTIVSDVTILESPVAAI LLLAFGACIF NLLVKFVSSRIEAFELQMVLMQEPQMSSTNNFYRGPMDRPAGTSPGL ESSPLKDTTTAGAVTLTTEVCSFTPEPARPRTHQKEETPNTSEHQKE QTPDTLPLRTVTLTASVHGFILEVSFDQEPTNSRHILVTTKGPLIIA KWRKTINVSAAVLVSSTILSRVQGLLQVLGQGCFC CIGERNYSNQ GPGTIAGSWAGVSTAASNATLAAAPKFGDTWYLSQVND RMTAEERD KFPTGQQAIP SMDLHWDLNSDHGDWSRKHLLSCVLEGLRRIRKKAMN YSMLSTVTQKEKNPSAFLEQLWGALRKYTPLSPKSLEGQLILKDKF ITQSAADIRRLKQKQALGPEQNLEALLNLATS VFYNRDQEEQAQKEK RDQRKAAALVMALRQTNLGGSERTENGAGQSPERAGIALGDLIQTRG KTPQPVA YLSKEIDAVAKVWPHCLKLVA AVFVSEAIKIIQ GKDLT VWTHE
6581	A	1908	4698	SNDRTEDDCGKHPFMSSPP\TEPWVCLIEGQEI DFLDTGTTF SVL IPCLGR LSSRSVTIQGILGQPVTRYFSHLLSCNWETLLF SHAFLVMP ESPTPLGRDILAKAGAI ISMKTGNKLPICCP LLEGINPEVWALEGQ FGRAKNAHP LQIRLKDPI SFYQRQYPLRPEAHKGLQDIVKHLKAQD

				SVRKCSSPCNTPILGVQKLSQWRLVQDLRLINEAVIPLYPVVRNPY TLLSQVPEEAWEFTVLDLKDFAFFCIPLHSDSQFLFAFEDPTDHTSQL MWMVLPQFRDPSPHLFGQAQADLGHFSSPGTLVLQYSEIAKTLTYTL IKEMERANTHLVEWEPEAETAFTLQALVQAPALSLPTQONFALYV IERAGIALGVLTQTHRTTPQPVAYLSKEIDVVAKGWPCHLRTVVAVA VLVSEAIKIIQKDFTVWTTTHDVNGILGAKGGLWPSDNCLLRYQALL LEEPVLQIHMCIAINPATFLPEDGEPIKHDCQQIIVQTYATQDDLLE VPLANPDFNLVNSGSSFVENGIQIRAGYAIIVSDVTVLGSKPLSPGTST QLAELVALTRALELGKGRINVTDSKYAYLILHAHAAIWKEREFLT SGGTPIKYHKEIMELLHTVQKPKEVAVLHCQSHQKGSARRIFCLTRI PGTRVCKNPHVSLSGISEWPLRDHTPLCFRPKALLAWVHEEICSMSGC KDPGWNLSKVSEEDRKMQESLETSRDLLNGFDQNVNDNMDSKVQAEQ ASDGDEELIGKWRKGLSMLWKILSIENMMNVWKGDTIKDAIIVIEKA VKAIPETINSCQRNLCPDVVHDFTRFTTEPIKDIKEIGDLAIKLG FESSNSTQFLNQFVPDDRSLSPHNKLLKPYKPEFYSSYPLVSLDHYV DQVGARISMSFCVTTVTEASGSGSWTCGVSQKLKLSYAD
6582	A	1529	2945	TWQPQCSIIGTKRNRPKKEKRDQKATALVTALRQTNLGGSERTENR AGQSPERDTLAKAGAIYMMNGNKLPICCPLPEEGINPEVWALEGQF GKAKNAHPVQIRLKDPTTFPYQROYPLRPEAHKGLKDIVKYLKAQAL VKKCSSPCNSPILGVQKPNLSQWRLVQDLRLINEAVIPLYPVVRNPYI LLSQIPEEAWEFTVLDLKDFAFFCIPPHSDSQFLFAFEDPTDHMSQLM WTVLPQGFKDSPHLFGQALAQDLGYFSSPGTLVLQYVDDLLLATSE ASCQATLDDLNLFLANQGYKRLLTMDPRTQDQSQAPLYSNQGENQRD KKSKEVQREEETDKEGVKREKREKRRSQREKRDGTSVSTLAVLE EPFSLPMRYGGPYLGLAKTRADSLCLWGGVEGEARVAGASCSTRRP VRVPGEHRLGRPCTGHGQPAPAGLDRGMCSEFAARVPGLGGAKSHGD CH
6583	A	3	154	KSEGNEKSEDAEVLDPSPGIMKTDNTEVLLSADFTGAIKVFVNKRK NVS
6584	A	3	425	GDSCAVCIELYKPNDLVRILTCHNHFHKTCDVPWLEHRTCPMCKCD ILKALGIEVDVEDGSVSLQVPVSNEISNSASSHEEDNRSETASSGYA SVQGTDEPPLEEHVQSTNESLQVLNHEGKFCGQWDVIPSCLTNPTL
6585	A	3	223	RLSQSVTQAGVQWHDLSLQPLPSKSKRFSCLSHPNSWDYRHTPQHP ANFCIFFFCRDGVSPCWPCWSCPGLK
6586	A	3	330	MWEEVTCPICLDPFVEPVSIIECGHSFCQECISQVGKGGGSVCPVCRQ RFLKLNLRPNRQLANMVMNLKEISQEAAREGTQGERCAVHGERLHQTH LDQPKTCFCILLYGT
6587	A	50	1740	RSPHCCLTAHLTMASARLTMMWEEVTCPICLDPFVEPVSIIECGHSF CQECISQVGKGGGSVCAVCRQRFLLKNLRPNRQLANMVMNLKEISQE AREGTQGERCAVHGERLHLFCEKDGKALCWCAQSRKHRDHAMVPLE EAAQEQVRPKRHLEKLQVALGELRRKQELAELKEVEIAIKRADWKK TVETQKSRIHAEFVQQKNFLVEEEQRQLQELEKDEREQLRILGEKEA KLAQQSQALQELISELDRCHSSALELLQEVIVLERSESWNLKDL ITSPELRSVCHVPLKMLRTPCAVHITLDPDTANPWLILSEDRRQVR LGDTQQSIPGNEERFDSYPMVLGAQHFHSGKHWEVDVTGKEAWDLG VCRDSVRRKGHFLLSKSGFWTIWLWNKQKYEAGTYPQ\TPSHLQVL PCQVGIFLDYEAGMVSFYNITD\HGSLIYSFSECAFTGPLRPFPSF\ GINDGGKNTAPSNPLVPLNIGSQGSTDYWMAFSGTLPLSPHWAPASS ATKPWPLFPHGTLPEPLSSAEASRDPQQASFSREVTSPINIPAPDGV V
6588	A	2	472	LKAVHRCCTGPEFPGRQRLRHEQGRLRGRCPPGRLPLHREALFQPSF LGMEACGIHETTFNSIMKGDVDIRKDLANTVLSGGTTMYPGIADRM QKEITALAPSTMKIKIIPPERKYSVWIGGYILGWLSTFHQMWISKQ EYDESGPFIHVHTTCF
6589	A	1	239	QCCSGGTHGNPAIGDR\MQKQILPWAPAQMIRFMAPPERKYSVWIA APILASLSTSSRMWISKQEYDESGPSIVHRKCF

6590	A	1	834	MDDDIAALVVDNSSGMCKAGFAGDDVPWAIFPSIVGCTRHQVMMHLV APEEHPVLLTEAPLNPKANCEKMTQIMFETFNTPAMYVAIQAMLSLY ASVRTAHVQGLHTTAEREIVRDIKKLCYVALDFEREMAMVASSSSLE KSYKLLDGQVITIGNERFHCPEALFQPSFLGMESCGIHKTTFFNYIMK CDVDICKDLYTNTVLSGGTTMYPGITNRMQKKITALAPSMMKIKIIA PPERKYSVWISGSILASLSTFQQMWISKQKYDQSGPSIVHECF
6591	A	1	702	LHVAPEEHPVLLTEAPLNPKANCEKMTQIMFETFNTPAMYVAIQAML SLYASVRTAHVQGLHTTAEREIVRDIKKLCYVALDFEREMAMVASS SLEKSYKLLDGQVITIGNERFHCPEALFQPSFLGMESCGIHKTTFFNY IMKCDVDICKDLYTNTVLSGGTTMYPGITNRMQKKITALAPSMMKIK I IAPPERKYSVWISGSILASLSTFQQMWISKQKYDQSGPSIVHECF
6592	A	1	1623	MVPSAAAAAGMRCILIKGVDSIGKTERTLQEI GSPCVALASPELLSS RDPVAVDSQGVVGLHSLLYRSFGICCAHYTQCNDHASHVWLKVPVS GSTAQLSLSCCKEKDILHENSTLREEIAMLRLLELDTMKHQSQLREKK YLEDIESVKRNDNLLKALQLNELTMDDDTAVLVDNNGSMCKAGFA GDDAPRAVFPSIVGRPRQQGMMGGMHOKESYVGKEAQSKRGILTLY PMEHGIITNWDDMEKIWHHTFYNELRVAPEEHPVLLTEATLNPKANR EKMTQIMFETFNTPAMYVAIQAVLSLYTSGRTTGIVMDSGDGVTHTV PIYEGNALPHATLRLDLAGRELDPYLMKILTEHGYRFTTMAEREIVR DIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRC PEALFQPCFLGMESCGIHETTFNSIMKSDVDIRKDLTYTNTVLSGGTT MYPGMAHRMQKEIAALAPSMMKIRIIAPPKRKYSVWVGGSILASLST FQQMWISKQYDESGPSIVHRKCL
6593	A	1	1132	MEEEDIAALVIDNNGSMCKAGFAGDDAPRAVFPSIVGRPRHQVMVGM GQKDSYVGDEAQSKRGILTLYPIEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLS LYASGRTTGIVMDSGDGVTHTVPIYEGYALPHAIRLRLDLAGRDLDY LMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSS LEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSI MKCDVDIRKDLTYANTVLSGGTTMYPGIADK\MQKEITALGP\STMKI KIIAPPERKYSVWIGGSILASLSTF\QQMWISKQYDESGPSIVHR \KCF
6594	B	635	646	MCDEDETTALVCDNGLVKGAGFAGDDAPRAVFPSIVGRPRHQVMV GMGQKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNE ELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAV LSLYASGRTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLT DYLKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENEMATAASS SLEKSYELPDGAGHHHRQALPLPGDPSFIGMEVGGHFTRPYNSI MKCDIDIQEGPFMPTTFMSGGTHDVPWESLTACRKEITRAGTPAPME DQDSFAPAGAQNTRVWIGGSILASLSTFQQMWITKQYDEAGPSIVQ PQMLDLTLHLQARDFSRITNLLNGGGG*
6595	A	1	1284	MGDTPRQFGGARPRSGGALRGCRSRGGGNRRGLCLSRALANGDRRLT MDDDIAALVVDNNGSMCKAGFAGDDAPRAVFPSIVGRPRHQVMVGM GQKDSYVGDK\AQSKRGILTLYRIEHGIVTNWEDMEEIWLHTFYSE LHVAPEEHPVLLTEASLNPKANHEKVNQIMFETFNTPAMYVAIQALL SLYASGRTTGIVMDSGDGVTHTVPIYGG\YALPHTILHLDLAGPDLT DHLKILTERGYSFTTTAKREIVHDIEENLCYVALDFEQEMAMVASN PPEKS*ELPDGQ\VITIGNE\RFRCEALFQPSFLGMESCG\IHET TF\NSIMK\CDVDIRKDLTY\ANTVLSGRTTPPCTLGIDRMQKEITAL APSTMKMKIIAPPERKYSVWIGGSILASLSTF\QQI\WISKQYDES GPS\IVHRKCF
6596	A	1	370	ETESRSVAQAGVQWHNLGSLQSPSGFKRFSCLSLPSNWDYRHPPSC PANFCIFVETRFHHVQAGLKLLTSGDPPTLAS* IAGITGMSHCAPW SLHIWTLILLFAKPRRWGTQVLLAAIFSQ
6597	A	2408	2810	IHTHTHTHTHTIFFLKR SFALVAQARVQWRDLCSLKPPPEFKQFSC LSLPSS*DYRCPPPCPANF/SFFFVFLVETGFHHVQAGLKLLTSSD

				SPTLASQNAGVTGMSHCAPQSNKYQNNFTMIQEQQQKE
6598	A	1	1157	APPVPANALGARGEAVRLQLQGEELRLQE\ESVRLHQINIYLSDRIS LHRRPLVRWNPLCKEKKYDYNLPRTSVIAFYNEAWSTLLRTVYSV LETSPDILLEEVILVDDYSDREHLKERLANELSGLPKVRILIRANKRE G\LVRARLLGASAARGDVLTFDCHCEHEGWLEPLLQRIHEEESAV VCPVTDVIDWNTFEYLGNSGEPQIGGFDWRLVF\RWHTVPERERIRM QSPVDVIRSPMTAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFR IWQCGGVLETHPCSHVGHVFPKQAPYSRNKALANSVRAAEVWMDFEK ELYYHRNPRARLEPFGDVTERKQLRDKLQCKDFKWFLETVPYELHVP EDRPGFFGMLQ
6599	A	1	1992	MGFRHVDQAGLELLTSGIQHELGHSEERLEATLRSKARGPVTTWQLT SKPAADTLRSRWPLGAEVLSPTTTRNEFCQKTCQPGLDPEFLKFRIC RCKEKKYDYNLPRTSVIAFYNEAWSTLLRTVYSVLETSPDILLEE VILVDDYSDRGCSAALVMDQAGFSPPTHSGQDKFQESHTLPPE GTAWKFSTHPIEQSVVAVWPQHLKERLANELSGLPKVRILIRANKREGL VRARLLGASAARGDVLTFDCHCEHEGWLEPLLQRLSVVPASLITS HQFLGELAFARGQLELAQQERRMDVLGAFRHEEESAVVCPVIDVID WNTFEYLGNSGEPQIGGFDWRLVFTWHTVPERERIRMQSPVDVIRSP TMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLET HPCSHVGHVFPKQAPYSRNKALANSVRAAEVWMDFEKELYYHRNPRA RLGLACDECSIKAGWWLEPFGDVTERKQLRDKLQCKDFKWFLETVPY ELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILYLCHG MGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPEN QKFILQEDGSLFHEQSKCVQAARKESDSFVPLLRDCTNSDHQKWF FKERML
6600	A	111	426	RIYKDRAGSPAHSQCQRDPLRTSPRGPHSLPWGQ\AAQSDAETEATH MGAPSCLGPAQLPLEPGGRSHTTSVDSRHSVEGFRDSRQTESPWN DEN*NLLDYGSL
6601	A	1	2219	MASILLRSCRGAPARLPPPPRYTVPRGSPGDPAPHLSCASTLGLRNC LNVFPFGCCTPIHPVYTSSRGDHLGCWALRPECLRIVSRAPWTSTSVG FVAVGPQCLPVRGWHSSRPVRDDSVVEKSLKSLKDKNKKLEEGGPVY SPPAEVVVKSLGQORVLDLKHYYHGFRLWIDTKIAARMLWRILNG HSLTRRERRQFLRICADLFRVLPFLVFVVPFMEFLLPVAVKLFPNM LPSTFETQSLKEERLKKELRVKLELAKFLQDTIEEMALKNAKAGSA TKDFSFFQKIRETGERPSNEEIMRFSKLFEDELTLDNLTRPQLVAL CKLLELQSIGTNNFLRFQLTMLRSIKADDKLI AEAGVDSLNVKELQ AACRARGMRALGVTEDRLRGQLKQWLDLHLHQEIPTSLILSRMYL PDTLSPADQLKSTLQTLPEIVAKEAQVKVAEVEGEQVDNKALEATL QEEAAIQEHREKELQKRSEVAKDFEPERVVAAPQRPQTEPOPEMPD TVLQSETLKDTAPVLEGLKEEITKEEIDILSDACSKLQEQKSLTK EKEELELLKEDVDYSEDLQEIIRKELSKTGEEKYVEESKASKRLTKR VQQMIGQIDGLISQLEMDQQAGKLAPANGMPTGENVISVAELINAMK QVKHIPESKLTSLAALDENKDGKVNIDDLVKVIELVDKEDVHISTS QVAEIVATLELEEKVEEKEKAEKAEKEVAEVKS
6602	A	1	221	LEMESHVSTQAGVQWRDLGSLQPPPPRFEQSSCLSLPSSWDHRHTPP RLAKCLLLNTQNALNQKQSPRSEEL
6603	A	2	218	PCGTWRTPGEGPDEGAGGRAHYHVLQKAYLMVAVPRGDLGSRAQE AERYISECKKRAEEKLGTERIERK
6604	A	101	456	GWERAHRLVQNYAANGGEAEAGANQGRGCLVVRGGEHACRRTAFAAAR YTRIWKNSAAICGPRGGGGPRPSPLPDTKASSKHAPRDRNDSRPN ATPEDPLPVPTLNPRAFPAPVLC
6605	A	62	558	PSCGLCRGRGTEGQEPWAPRGGGCIMDHLGASLWPQVGSCLLLLAGA AWAPPPNLPDPKFESKAALLAARGPEELLCTERLEDLVCFWEEAAS AGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSS FVPLELRVTSSLRRAISPCHPHQ
6606	A	2	178	QTPMPFLCRPSPAALLAARGPEELLCTERLEDLVCFLRSMRFSSSF

				FSSARFLHSLM
6607	A	1	194	PARPFVESIATQYMTNKQDHDRMASQWTKGIRSINGGFTILTFFCRS QKRAAYDFEGVREGGSW
6608	A	59	132	KAVDKKAAGAGKVTKSAQIAQKAK
6609	A	3	104	RNSWVDPPEAVDKKAAGAGKVSMSAQKAQKAK
6610	A	2	620	GFRPGDPRVRETGVLPKPGMLVTFAPVNVTTGGVKSVMHHEALSEALP GDNVGFNVKNVSVKDVRRGNVAGDSKNDPPEAAGFTAQVILNHPG QISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGD AAIVDMVP\ARPMCYESFSDYPLGRFAVRDMRQIVA\GVVIKAGDK KAAGAGKVTKSAQKAQKAK
6611	A	293	384	AAQRHETLTSLNLEKKARLKKEEAAMKAKTE
6612	A	39	543	QVAMGNLSGLRLAAGSCFRLCERDVSSSQRLT\RSSDWKG\INGFC\ TKPTGKVPGAPIPALTNRVFPNTKP\TDW\QKKRPLIWSRSPSKMED EIPQ\SLSPLEDALNACQRTKMPSESSLSQWICPDGGMDCI\FMVI EGQK\AA\QRHDDFTQA*TLEKKARLERGKQL
6613	A	1	194	YEPSCQNVNHGVLVVGYGDLNGKEYWLKNSWGHNFGEEGYIRMAR NKGNHCGIASFPSYPEI
6614	A	71	1145	NLRREPTNSRTLTVGATAGSITMKRLVCVLLVCSSAVAQLHKDPTLD HHWHLWKKTGKYGKYKEKNEEA VRRLIWEKNLKFVMLHNLEHSMGMHS YDLGMNHLGDMTSEEVMSSMLSSLRVPSQWQRNITYKSNPNRILPDSV DWREKGCVTEVKYQGSCGACWAFSAVGALEAQLKLKTGKLVLSAQN LVDCSTEKYGKNGCNGGFMTTAFQYIIDNKGIDSDASYPYKAMDLC QYDSKYRAATCSKYTELPHYGR*DVLKEAVANKGP\SVVV\ DARQP SFLPLQESGVYDPS\CTQ\NVNHGVLVVGYGDLNGK\EYWL*NSW GP\NFGEEGYIR/LWARNKGNHCG\IASFPSYPEI
6615	A	2	289	VLKELWPNKGQCLFGVDARHLPFFLYRSGVYEPSCQNVNHGVLV GYGDLNGKEYWLKNSWGHNFGEEGYIRMARNKGNHCGIASFPSYPE I
6616	A	2	125	PDQGYQCMKRPAYSGPGTAPGALDYPACTALYGESDLRC
6617	A	9	106	QSCSVAQAGVQWHELGLSLQSSLGKKSETPSQK
6618	A	2	505	THASDCLYRAVSKTVYGDQSLHRELREQTVHYIADHLDFSPLEIGD VGEPIIAAAQDGAWAGYPELLAMGQMLNVNIHLTTGGRLESPTVSTM IHYLGPEDSLRPSIWLSWLSNGHYDAVFDHSYPNPEYDNWCKQTQVQ RKRDEELAKSMAISLSKMYIEQNACS
6619	A	1	104	RCSRYLYTLVITDKEKAELKQSLPPGLAVKELK
6620	A	1	109	KVRCCRYLYTLVITDKEKAELKQSLPPGLAVKELK
6621	B	99	285	MPRKIEEIKDFLLTARRKDAKSVKIKKNKDNVFKVRCRSLYTLVI TDKEKAELKQSLPXX*
6622	A	239	449	NCGNQRTSLRHRPTKMPNSCQDPRKIRTLVKFKVRCRSLYTLVIT DKEKAE\KLKQSLPPGLAVKELK
6623	A	1	104	RCSRYLYTLVITDKEKAELKQSLPPGLAVKELK
6624	A	1	109	KVRCCRYLYTLVITDKEKAELKQSLPPGLAVKELK
6625	B	99	285	MPRKIEEIKDFLLTARRKDAKSVKIKKNKDNVFKVRCRSLYTLVI TDKEKAELKQSLPXX*
6626	A	239	449	NCGNQRTSLRHRPTKMPNSCQDPRKIRTLVKFKVRCRSLYTLVIT DKEKAE\KLKQSLPPGLAVKELK
6627	A	2	129	YGPTHASGAMLRSCAARLRTLALCLPPVGRRLP\EASRDPS
6628	A	1	289	MLRSCARRLRTLALCLQPPVGRRLPGSEPQPALRSFSSEEVILKDY SVPNPSWNKDLRLFLDQFMKKCEDGSKRLPSYKRTPTERIQDFKTH FL
6629	A	6	418	RRLMRDFKRLQEDPPVGVS GAPSENNIMQWNAVIFG\TFKLVIEFPE EYPNKPPTVRFLSKMFHPNVYADGSICLDILQNRWSPTYDVSPILTS IQSLLEPNPNSPANSQAAQLYQENKREYKRVSAIVEQSWNDS
6630	A	3	330	ARRRLMRDFKRLQEDPPVGVS GAPSENNIMQWNAVIFG\YADGSICL DILQNRWSPTYDVSSILTSIQSLLEPNPNSPANSQAAQLYQENKRE

				YEKRVSAIVEQSWNDS
6631	A	51	420	KLTAGQLRSMSTPARRRLMRNFKRLQKDPGGVRGAPFENNIMQNA VIFGPKGTPEKGTGPKLVKEFFEKYPNKPVPVRLSKRFHPNVYAEW SICLNILQNRWSPTYEGSSILTSIQPLL
6632	A	3	141	ECVTNFSIVFAVYADGSICLDILQNRWSPTYDVSSILTSIQVSV
6633	A	1	581	HSDSAAAPGGGAARDFFFQTDRRGSCGACSTPARR\RLMRDFKRL QEDPPVGV\SGAPSENNIMQWNAVIFGPG\GTPFEDG\TF*L\VIEF SEEYPN\KPP\TVRVFIPKMFPSPNVYA*WVGICL\DI\LQNRWESQ HMDVSFLSLTFNSVSGWDEPN\P*QSSPIAQAAQLYQENKREY\EKR VSAIVEQSWNDS
6634	A	2	266	YCGPL*SVVARNPPGFAFVEFEDPRDAAGVV*ELDGRTLCPG\PSW GHRP*DDYCRRLPPLRRRPPRRRNLSCSRSLYSPWTL
6635	A	3	164	GRSHLSNGEKSRNRGPPPSWGRRPRDDYRRRSPPPRRRYLRESLLR GIGVME
6636	A	1	947	IFLVFFITEMHRDSCPLDCKVYVGNLGNNGNKTTELERAFFGYGPLRS VWVARNPPGFAFVEFEDPRDAA*V*YLCPLRTLGCGRVRVELSNGEK RSRNRGPPPSWGRRPRDDYRFPMSLFSLSLLSNLQIGSSHLDRPHI PGQSAQLFIYQMSSQQLQQPSANKKAGKIHTPFANQLNPTATSGQ NLFRQILPGPSVRAGLTFTISSLLKPKTNLQEGEASLAAGAGPFLEI GEERDCLGREITSRDPDSLGLVVDLGQMKGNRRQFAREVYRKLH LTGVCTENFKCLRLHKLGAFLRCFSCSNLFS
6637	A	1	282	PLRSVWVARNPPGFAFVEFEDPRDAADAVRELDGRTLGCGRVRVELS NGEKSRNRGPPPSWGRRPRDDYRRRSPPPRRRYTIMSLTTLNLH
6638	A	116	561	PLDLEMRDSCPL\DCKVYVGNLGNNGNKT\ELERAFFGYGPLR\SV WVARNPPRPLAFVEFEDPPRMQLDAVPRS*DGKNTNVACPKEWELV RMGEK\RSR\NRGPPPSL\WGRRP\RDGFIRREGVPPTLFGSPRKG GRFLFAARSRLS
6639	A	126	376	VLLARLQANGANTVELSAEWTFPSGYVGSVLPQGHREPNA/CLSFS KFRVLGSAPFLINRRITASNCVNRRCRLAATWRAVLPL
6640	A	464	781	AFAFTKDRQLGSSKKRRMSSRFASSAAKCAVRPPLRSRRFPVPMP PGPWVSSTKLGSRLGRHQASCRG*SQRAR*SGLTGPTHMEPNKVRST GLKFLPAQQS
6641	A	201	318	EINLTNFIKFSSRSDVS*RESPFSRELHRISSISLEPG
6642	A	1	1714	MKLPEEGAGSNICCSAIFAVLQPLVPRQTVSGVDLQQTPTDLQLR VLTLLRRTSKQKGHTHQNPICMSPSSRTKGRQDKLEEILRGLTPRK NDIGDAMVFCNLNAEAAEEIVDCITESLSILKTPLPKACAPRVVSG AGPAGTWLALCAGAAFRPGLHGAAGGHPPGRGEVGGVTRTRTPPRA PDRATGVSSPPGPASAGNPPKSYRVHVHKVQVCYIGIHVPCWFAAAV KLSCITLDICPNAMVSAARQVPTGAGTPVRRQEGSIEVYEDAGSHYLC LLKAGPRDSGTYSCTASNAQQQLSCSWTLQVETHPSFLIPLSLRPS ATRNPGRFSSFSHRPRPLPLALGPRTTRHVPLSSLTLQVCFRWGRGR QVLSAGGLCVPRALLRWDLRGDTQSPEKLYMPKTIKETSLSTYHVP GITLNDRSIINKIDPGVEESPLDLHVCHGNNYVDEKPALLLSGKLG CPSLTSCYSNCLSYGNRCRLQLQELVNVQHVEQQPHYTHKPTLEYSPP PIPPQSPAYEPNLFDPESQFCPNQSLVSLLDQRESENIANPMQTS SSGQAAK
6643	A	1	789	MGFRHVQAGLKLTLSSDLPALASQVQCKLVVPASAERHISPLQRL IAFSLRDPDGLAGDRASLGVPPLCGYRIGNPRRSPKRTRHCARTAAVS CSAYSKCLYQFRPNVGHSASTPKAMCQTTAAGEGAHADEGYTQRVV GARRGTPQRYTGAETKNRAFRSYPKMETSWPRGGGSTPPVALDAQV ERECALGSGAQGHKSLAVRVVLIFCINEHYPTLTLYRLPFVPLRS GGTPTSWRALFFPSSSDSNCKLCGGTSS
6644	A	1	293	SPEMESHPIQAGVQWHNSSLQPEIPGLKQSSHLSPSSWDHR*EP L\WPKNIFKMLIL*IGFSHVIGNNGTYLYQSINNVEGPLKRSQKDR SCGN
6645	A	1	252	GLTLPPRLGCHATITAHYSLNLPGSSNPPTSASQVAGTTHSRPCPEI

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				TQTALQRGPTGLTTKASRPKARRGSKVSWTIAILPPQ
6646	A	1	1974	MERLETINILTLEKADLKTTLTYHTKRAARHFEEESKDLAGRLQYSLO RIQELERALCAVSTQQQEEDRGHCLSSPDQNFSLFTIQSSSCREAVL HRRLLQQTIKERALNAHVTVTESLKQVQLERDEYAKHIKGERARWQ ERMWKMSVEARTLKEEKKRDIHRIQELERSLSELKNQMGKMGLLQDE AKHLRQEVLEGKLSQVENNQALSLLSKEQKQRLQEQEMLREQE VQVRVEQERLCEQNERLREQQKTLQEQGERLRKQEQRLRKQERLRK EERLQKQEKRLWDQEERLWKKEERLQKQEERLALSQNHKLDKQLAE PQCSFEDLNNEKKSALQLEQQVKELQEKLDEVKEMQYVATYQQLTSE KEALHRQLLLQTLVDQLQQQEAWGKAHLEAASQONQOLETQLSLV ALPGEDPLMLLVSHLLIALAPHPFREPVRHFVTCDDQLGIYQKAFE HLGNALTYDPTNYKAISCLKRANYLAPFDWKILYNLGLVHVTMQQYA SAFHFLSAAINFQPKMGELYMLLAGLLSTCNPLVNLNYAVLLYNQGE KKNALAQYQEMEKKVSLLDKDNSSLEFDSEVCLLLAPKSHNQSNQTRE RKGIQISKEEVKLSLFPADDMIVYLENLKDSSKKLLELYLSEYWSFSV
6647	A	3	322	LLSTCNPLVNLNYAVLLYNQGEKKNALAQYQEMEKKVSLLDKDNSSLE FDSEVCLLLAPKSHNQSNQTRERKGIQISKEEVKLSLFPADDMIVYLE NLKDSSKKLLEL
6648	C	238	324	MADLPIFLVEFSCFIYFNGSFMFSQKK*
6649	A	1	1088	MQGFVYNHQNLETTKVLTSTGSTLQTSQSKEVLRPTGSTRKLAKG AQDQLHNALNLRHDLTYIMLGKIHLEGLDLDKAEVYKKAVEFSPE NTELLTTLGLLYLQLGIYQKAFELGNALTYDPTNYKAILAAGSMMQ THGDFDVALTKYRVVACAVPESPPLWNNIGMCFFGKKKYVAAISCLK RANYLAPFDWKILYNLGLVHVTMQQYASAFHFLSAAINFQPKMGELY MLLAVALTNLEDIENAKRAYAEAVHLDKCNPLVNLNYAVLLYNQGEK KNALAQYQEMEKKVSLLDKDNSSLEFDSEMVEMAQKLGAALQVGEALV WTKPVKDPKSKHQTTFNQQTWPVSSSLWALIKL
6650	A	1	368	GTSLKQEEAFRSYFEIFNGPGEVDAQSLKNILLMGFSVTLAQVEDA LMSADVNGDGREDFKDFLAVMTDTTRFFCFAEQNALSDMALSNPHTL LFEILHLPLYMLALPNARLCDIPDCILI
6651	A	3	243	HERNEYFRSEDLKLQISTETITLSHGSSTFSLSWSDTAQVTNQRVQI SVKKEKVVTITLDKEMSFTVVLTTRVWNHAIFI
6652	A	24	288	VLEIKKKEIIPSTSTPYSTLPPLKTDLPPLYPQVPPPSQCQTPAIHRM ATPPLKPQNFKALLRKWHHGLFIFPFFKGKSLKKFPSENS
6653	A	2	272	PDRPTRPAVPMSPSSHSPPEGRPPPLPGGPVCKAAASAPSSLLDQPC LCPAPSVRTAVALTTPDITLVLPPDVIQEEASALREETEAWAR
6654	A	965	2737	AASPGVLVCPQARTYIQSLPPALDVQLTPLPTTGFPAAIDLLGRMLV LDSDQRVSAEALAHAYFSQYHDPEDPEPEAEPPGPGGRHKLTLHL LELTYQEVLSWDEAAGRSPPPALPPRLRSPSGSGPPAAAASGFRR WAAPGPAMSSPPPARSGFYRQEVTKTAWEVVAGACAGCPAFPLSGPP RSSAVDGRGTAKVAIKKLYRPFQSELFANPARVLCCILNPMWPPQVI GHAEAGSVR*QRSGPSHSYLVMPFMGTDLGKLMKHEKLGALRGCAEA CHHAWEGGAQWPPFLCPRSLGVP*NPPPPQFFPQILDGFLARQADSE MTGYVVTRWSPVPLPTLSTRASISVDIWSVGCIMAEMITGKTLCS PGGGSGGPDLPWPPSCVPDLGADLDQLKEIMKVADLGLGVGPSFPLPT QAKNYMKGLPEWSVGPVVPDAPSPAAVNLLEKMLVLDAEQRTAG EALAHYPYFESLHDEDEPQVQKATTDGPSLSPDPHASPGHPGLGDVI AISSGATLTCGMAAVHTGPKVWAHRWPEDWGVAFALQTPRPRLSPQ VFLRPGRVGLGAALDPDPGWGAGRDL
6655	A	3	231	WAAPGPAMSSPPPARSGFYRQEVTKTAWEVVAGACAGCPAFPLSGPP RSSAVDGRGTAKVAIKKLYRPFQSELF
6656	A	27	144	QRSGPSHSYLVMPFMGTDLGKLMKHEKLGALRGCAEAC
6657	A	3	308	TKRAPAQYSGRTRLCTRSSGPTRGDQERVPLRGSWAAESLGAQPGG SRVLACTSTRSPGLTRGKCPRLPLSPPPSRHSRASVKSTRAGAPEIR HGNAGSA
6658	A	192	310	ARGSTKPKMQLRKPPVICGDSRAQLLIYGHLLAPWAGVL

6659	A	88	1506	ACGRFGFPEGPEGGRGRHVRAARGPVGPRAGEGPCAAWVGVPGSAP GTSLEGGGAGAPQRPAGGRASGRAARSREPEARAGAPSPVVGAPPA GSAGWAAPGPAMSSPPPARSGFYRQEVTKTAWEVRAVYRDLPVGS AYGAVCSAVDGRGTGAKVAIKKLYRPFQSELPAKRAYRELRLKMRH ENVIGLLDVFTPDETLDDFTDFYLVMPFMTDLGKLMKHEKLGEDRI QFLVYQMLKGLRYIHAAGI IHRDLKPGNLAVNEDCEKILDFGLARQ ADSEMTGYVVTRWYRAPEVILNWMRYTQTVDIWSVGCIMAEMITGKT LFGKSDHLDQLKEIMKVTGTTPAEFVQRLQSDEAKNMKGLPELEKK DFASILTNASPLAVNLLEKMLVLDAEQRTVAGEALAHYPFESLHDE DEPQVQKYDDSFDDVDRTLDEWK\RVTYKEVLSFKPPRQLGARVSKE TPL
6660	A	71	921	NPPQFFPQILDGFLARQADSEMTGYVVTRWHPVPLPTLSTRASIS VDIWSVGCIMAEMITGKTLCSCPGGGSGGPDLPWPPSCVPDLGADLDQ LKEIMKVADLGLGVGPSFPLPTQAKNYMKGLPEWSVGPPVWPDAPS PAAVNLEKMLVLDAEQRTVAGEALAHYPFESLHDEDEPQVQKATT DGPSLPSPDPHASPGHPGLGDVIAISSGATLTGMAAVHTGPKVWAHR WPEDWGVAFALQTPRPPRLSPQVFLRPGRVGLGAALDPDPGWGAGR L
6661	A	2	310	GDKVAHSVTKVGVQWHNHCSPQPRPSGLKRSSSLSLQSSWDHRRMPP CLAHFLIFCRDGVLLGLPRLGVALLGLKRSSHLGLPKVLRITGSEAT ILGPQGFS
6662	A	5517	5831	LPGNFFFFFFSDGVSLLLPRLGQWHHLGSLQPPPPGFQRFSCLSLPS SWDYRLLPRLARKFFVVMNTFGLISSFNSTSFVHKSQECFRQKTGF TLIIIRSVL
6663	A	1	625	CKFIRVMAHTRRLRLPLRRKKAHLMEIQVNEGTVAEKLDWARERLEQ QVPVNVQVFGQDEMIDVIGVTKGKGKGVTSRWHTKKLPRKTHRGLRK VAC\KDGLIKNNASTDYDLSDKSINPLGGFVHYGEVTNDFVMLKGC VVGTKKRVLTLRKSLLVQTKRRALEKIDLKFIIDTTSKFGHGRFQTM EKKAFMGPLKKDRIAKEEGA
6664	A	1	1261	MSHRKFSAPRHGSLGFLPRKRSSRHGKVKSFPKDDPSKPVHLTAFL GYKAGMTHIVREVDRPGSKVNKEVVEAVTIVETPPMVVVGIVGYVE TPRGLRTFKTVFAEHISDECKRRFYKNWHKSKKKAFTKYCKKWQDED GKKQLEKDFSSMKKYCQVIRVIAHTQMRLPLRQNAH\LM*IQVNG GHGPRSWDWPREGKQGGTVDPVSVLGRNMIDVIG\VTQGPKGK GGHPVVWHTQESCPRKD\HHPRACRKGHVLGAW\HPA\RVAFS VARAG\QKG\YHHRTEITKID\IYKIGPLSPLFRTAKVIKGTI ASTDYDLF*QEASTPPGGFVH\YGE\VTNDFVMLKGC VVGTKKRVLTLRKSLLVQTKRRALEKIDLK\FIDTTSKFGHGRFQ TMEEKKAFMGPLKKDRIAKEEGA
6665	A	1	168	PTRPATQSNICDEDSATETCYTYDRNKCYTAVVPLVYGGETK MVETALTPDACYPD
6666	A	3	203	SLCTELPPSSSAFSSSSSSPAFPFWSSSSSISRSTSSSSSPSSW SPLCTSFQPLDKAARDAS
6667	A	3	523	LQFFRRSEVKMKNHLLFWGVLAFFIKAVHVKAQEDERIVLVDNCKC ARITSRIIRSSDPNEDIVERNIRI\IVPLNNRENISDPTSP\LRTR FVY\HLSDLCK\CDPTEVEL\DNQIVTAT\QSNICGWMTPQSTCY TLSTGNKCYTAVVPL\VYGGETKMOVETALTPDACYPD
6668	A	3	276	EDSATETCYTYDRNKCYTAVVPLVYGALWPRRWRRLRSVPAAAAAG LLEDPAVPGLTALPAVELPERRRRQQRQAPGHQLLPRSGR
6669	A	2	152	FFFVFLVETEFYLVGQASLELVTSGDPAASASQSAGITGVSHACSPF QAF
6670	A	1	936	MAALYACTKCHQRFPPFEALSQGGQLCKECRIAPVVKCTYCRTEYQ QERLECNGTISAHCNLHLPSSSDSPASSRVAGITGIKTNTICKKAQ NVQLYGTPKPCQYCNIIAAFIGNKCQRCNTSEKKYGPYSCEQCKQ QCAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSRAGH QEKEQYSRLSGGGHYNSFSPDLALDSPGTDHFVIAQLKEEVATLKK

				MLHQKQDMILEKEKKITELKADFQYQESQMRAMNQMEKTHKEVTEQ LQAKNRELLKQAAALSKSKKSEKSGAITS
6671	A	1	1023	MAALYACTKCHQRFPFEALSQGGQLCKECLIAHPVVKCTYCRTEYQQ ERLECNGTISAHCNLHLPSSSDSPASSRVAGITGIKTNTICKKCAQ NVQLYGTGPKPCQYCNIIAAFIGNKCQRCNTNSEKKYGGPYSCQCKQQ CAFDRKDDRKKVDGKLLCWLCTLSYKRVLQKTKEQRKHLSSSSRAGH QEKEQYSRLSGGGHYNSQKTLSTSSIQNEIPKKKSKFESITTINGDSF SPDLALDSPGTDHFVIIAQLKEEVATLKKMLHQKQDMILEKEKKITE LKADFQYQESQMRAMNQMEKTHKEVTEQLQAKNRELLKQAAALSKS KKSEKSGAITS
6672	A	106	125	KYLEQCLKHGKSS*HSILQANFFASENDRAMK*KPCFYKCF*AITF LREDWDYRREPLRLAYPVYFLTCKIRIMYTHLKDYTGH
6673	A	3	155	GAISAHCNLRLPGSSSDSPDSASNLIQMSLLRVLLLEMLVTLRTRTKP SEI
6674	A	3	266	GAISAHNRNRLPGSSSDSSASSSQPGVVRGRWSPTSCSHGKHQRPG VRGAPRRQGCTLRGRRRPPCPGEGAQDHGGEYGRPQRVQPP
6675	A	5	160	RDLGSLQPPPPGFK*FSCRLRLPSPQVQRCCVPSPWLLEQMITAWGAS IHRN
6676	A	1586	2220	PSCSGISHATRSSFLLVSQANDTVDTAFICTAWTLFIPRASELV AVTWISSFGSLPHLLSSALSSMGTCPVDSYWTLMNSEEKSSSEPLVLC DLWYFIALPSPLVTFFCYLPYIGSCQGPSLSLSFFFFFFFFFFLRRRT ESCSVAQGVQWRDLGSLQPPPPGFKRFSCLSLPSSWDYRRAPPRPA NFYIFSRDGVSPCWPGWSRTPIS
6677	A	3	441	CGVGLHDRPWLPRNRCSPASALRSACVVNSPRARGALWPESACASTY PNPRGLSLGAAPTQSAPGPSGLCCSLCVGQPLSCLLWHHPGHSRAP HSPARLPSCCTQSPGAGAGSDLQGGTPGPAPCSTAAPSGPHAWRWAC IHIP
6678	A	1	91	SFATLLRLVNSWPMILLPRSPKVLGLQA
6679	A	2	226	FFEMESCCDAQARVQWHELSSSLKPLLCSPGSRDFSASASQVAGTTGM HRHAQLIFVFRVCVCFGIIVLEKQIKY
6680	A	3	187	EMGKGIDSLFNEIIAENFPGLARDIDIWKLETQGVPNRPNLKRSSQR QMIVKLSKVKNREF
6681	A	2	209	GEEGRTQKGERNGGGSERKEGEEHEARTGRGEGGGGEAKGRPRSA RRRGRGSRGSKSQTSPSRHLP
6682	A	2	702	FVSVPVSVLLGLQFWRSERD/TARLQSARWRVERGRKELLRSRQRRR REEVVVGREVCRTMEVRASLQKIVSNGDEQLEKAMEEILRDFEKRP SSLLVDCQSSSEISDHSFGDIPASQTNKPSLQLILDPSNTEISTPRP SSPGGLPEEDSVLFNKLTYLGCMKVSSPRNEVEALRAMATMKSSSQY PPVTLVVPNVPEGSVRHILSLLGGGEDVIASSGVELTVNSHCRHAE
6683	A	3	499	SFGLQRWRSERDSARLQSARRRVERGRKELLRSRQRRRREEVVVGR EVCRTMEVRASLQKIVSGSSDSVATMNSEEFVLVPQYADDNSTKHEE KPQLKIVSNGDEQLEKAMEEILRDSEKRPSSLLVDCQSSSEISDHSF GDIPASQTNKPSLQLIMDPSNTET
6684	A	1	224	RRLFFVVLIDMGFHHVQAGLKLSSSDPPTLASQSAEITSMHRA RPQCSPSTLHCIEKLINTLGDKLTYYL
6685	A	1	789	MGFRHVGQAGLKLTTSSDLPALASQVQCKLVVPAERHISPLQRGL IAFSLRPDPGLAGDRASLGVPPLCYRIGNPRRSPKRTRHCARTAAYS CSAYSKCLYQFRPNVGHASATPKAMCQTTAAGEGAHADEGYTQRVV GARRGTPQRYTGGAETKNRAFRSYPKMETSWPRGGGSTPPVALDAQV ERECALGSGAQGHSCLAVRVVLIFCINEHYPTLTLYRLPFVPLPRS GGTPTLSWRALFFPSSSDSNCKLCGGTSS
6686	A	1	7500	MLFTLNLAHAHQEIEYISPPLEHGSNQALRSTALETLHESALLSGELA LKTLCNKMDTGDTALGQKATSRSGETDKASGRWRQEQAIVKMSTFG SHEGQRQPQIEPEQIGNTASQAQLFGSGKLASPSSEVVQQAQYPPH RPSPYSCQHSLSFPQHSLPQGVMMHSTKPHQSLEGPPWLFPGPLPSVA SEDLFPFPIHGHSGGYPRKKISSLNPAYSQYSQKSIEQAEAAHKKEH

				KPKKPGKYICPYCSRACAKPSVLKKHIRSHTGERPYPCIPCGFSFKT KSNLYKHKRSHAHAIKAGLVPFTESAVSKLDLEAGFIDVEAEIHSDG EQSTDTDEESSLFAEASDKMSPGPPILPLDIASRGYHGSLEESLGGP MKVPILIIIPKSGIPLPNESSQYIGPDMLPNPSLNTKADDSHTVKQKL ALRLSEKKGQDSEPSLNLLSPHSGKSTDSGYFSRSESAEQQISPPNT NAKSYEEIIFGKYCRLSPRNALSVTTTSQERAAAMGRKGIMEPLPHVN TRLDVKMFEDPVSQILIPSKGVDPSQTSMLKSTKFNSESRQPQIIPS SIRNEGKLYPANFQGSNPVLEAPVDSSPLIRSNSVPTSSATNLTI PSLRGSHSFDERMTGSDDVFPYPGTVGIPPQMLRRQAAPFELPSVQEG HVEVEHHGRMLKGIISSSLKEKKLSPGDRVGYDYDVCRRKPYKKWEDS ETPKQNYRDISCLSSLKHGGEYFMDPVVPLQGVPSMFGTTCENRRR KEKSVGDEEDTPMICSSIVSTPVGIMASDYDPKLQMQEGVRSFGFAMA GHENLSHGHTERFDCRPQLQPGSPSLVSEESPSAIDSDKMSDLGGR KPPGNVISVIQHTNSLSRPNSEFERSESAELVACTQDKAPSPSETCDS EISEAPVSPWAPPDGAESGGKPSPSQQVQQQSYHTQPRLVQRHNI QVPEIRVTEEPDKPEKEKEAQSKEPEKPVVEFQWPQRSETLSQLPAE KLPPKKRLRLADMEHSSGESSFESTGTGLSRSPSQESNLSSHSSSFS MSFEREETSKLSALPKQDEFKGHSEFLTVPAGSYSLSVPGHHHQKEM RRCSSSEQMPCPHPAEVPEVRSKSPDYGNLSHAPVSGAAASTVSPSRE RKKCFLVRQASFSGSPEISQGEVGMDSVKQEQLEHLHAGLRSGWHH GPPAVLPLQQEDPGKQVAGPCPPLSSGPLHLAQPMHMSDQESLR NPLIQPTSYMTSKHLPEQPHLFPHQETIPFSPIQNALFQFQYPTVCM VHLPAQQPPWWQAHFPHFPAQHPQKSYGKPSFQTEIHSSYPLEHVAE HTGKKPAEYAHATKEQTYPCYSGASGLHPKNLLPKFSPDQSSKSTETP SEQVLQEDFASANAGSLQSLPGTVVPVRIQTHVPSYGSVMYTSISQI LGQNSPAIVICKVDENMTQRTLVTNAAMQGIGFNIAQVLGQHAGLEK YPIWKAPQTLPLGLESSIPLCLPSTSDSVATLGGSKRMLSPASSLEL FMETKQQKRVKEEKMYGQIVEELSAVELTNSDIKKDLSRPQKPQLVR QGCASEPKDGLQSGSSSSFSLSLSPSSSDYPSVSPSSREPPPSKEML SGRAPLPGQKSSGSPSESKESSDELIDETASDMSMSPQSSSLPAGD GQLEEEGKGHCRPVGMLVRMASAPSGNVADSTLLLTDMADFQOILQF PSLRTTTTVSWCFLNYTKPNYVQQATFKSSVYASISCNPNPSGL NTKTTLALLRSKQKITAEIYTLAAMHRPGTGKLTSSSAWKQFTQMKP DASFLFGSKLERKLVGNILKERGKGDHGDKDIGSKQTEPIRIKIFE GGYKSNEDYVYVRGRGRGKYICEECGIRCKKPSMLKKHIRTHTDVRP YVCKLCNFAFKTKGNLTKHMKSKAHMKKCLELGVSMTSVDDTETEEA ENLEDLHKAEEKHSMSSISTDHQFSDAEESEDGEDGDDNDDDEDED FDDQGDLTPTKRSRSTSPQPPRFSSLPVNVGAVPHGVPDSSSLGHSS LISYLVTLPSIRVTQLMTPTSDSCEDTQMTYQRLFQSKSTDSEPDKD RLDIPSCMDEECMLPSEPSSSPRDFSPSSHSSPGYDSSPCRDNPSK RYLIPKGDLSPRRHLSPRRDLSPMRHLSPTEKAALRREMSQRDVSPR RHLSPPRRPVSPGKDITARRDLSPRRERRYMTTIRAPSPRRALYHNPP LSMGQYLQAEPIVLGPPNLRRGLPQVPYFSLYGDQEGAYEHPGSSLF PEGPNDYVVFSLPLHSQQQVRAPIMVPVGGIQMVHSMPPALSSSLHP SPTLPLPMEGFEEKKGASGESFSKDPYVLSKQHEKRGPHALQSSGPP STPSSPRLLMKQSTSEDSLNATEREQEENIQTCTKAIASLRIATEEA ALLGPDQPARVQEPHQNPLGSAHVSIRHFSRPEPGQCTSATHPDLH DGEKDNFGTSQTPLAHSTFYSKSCVDDKQLDFHSSKELSSSTEESKO PSSEKSQLH
6687	A	1	8175	MKKENVSQGIKTASGSQKRQENDCPLPLELRRQPSSHLAFTPVRAVW GFRHLELMLVRQILVASVSFQCLQTYRSCGNFRVLFPQSATSVIIII ITVKFDVREKIAHGNLHLAFGWTFLOWRELCSYSPGPRTLANAHRLW CACGRFQREGAISKFADTLEHGSNQAALRSTALETLHESALLSGELAL KTLCNKMDTGD TALGQKATSRSGETDKASGRWRQEQAIVIKMSTFGS HEGQRQPQIEPEQIGNTASQALFGSGKLASPEVVQQVAEKQYPPHR PSPYSCQHSLSFPQHSPLPQGMHSTKPHQSLEGPPWLFPGPLPSVAS EDLFPFPIHGHSGGYPRKKISSLNPAYSQYSQKSIEQAEAEAHKKEHK

				<p>PKKPGKYICPYCSRACAKPSVLKKHIRSHTGERPYPCIPCGFSFKTK SNLYKHKRSHAHAIKAGLVPTTESAVSKLDLEAGFIDVEABIHSDGE QSTDTDEESSLFAEASDKMSPGPIPLDIASRGYHGSLEESLGGPM KVPILIIPKSGIPLPNESSQYIGPDMPLPNPSLNTKADDSHTVKQKLA LRLSEKKQDSEPSLNLSPHSKGSTDSGYFSRSESAEQQISPPNTN AKSYEEIIFGKYCRLSPRNALSVTTTSQERAAMGRKGIMEPLPHVNT RLDVKMFEDPVSQILIPSKGVDPSQTSMLKSTKFNSESROQPIIPSS IRNEGKLYPANFQGSNPVLEAPVDSSPLIRSNVPTSSATNLTIPP SLRGSHSFDERMTGSDDVFYPGTVGIPQRMRLRQAAPFELPSVQEGH VEVEHHGRMLKGISSSSSLKEKKLSPGDRVGYDYDVCCKPYKKWEDSE TPKQNYRDISCLSSSLKHGGEYFMDPVVPLQGVPSMFGTTCENRKRK EKSVGDEEDTPMICSSIVSTPVGIMASDYDPKLQMQEGVRS GFAMAG HENLSHGHTERFDPCRQQLQPGSPSLVSEESPSAIDSDKMSDLGGRK PPGNVISVIQHTNSLSRPNSFERSESAELVACTQDKAPSSETCDSE ISEAPVSPWEAPPDGAESGGKPSPSQQVQQQSYHTQPRLLVRQHNIQ VPEIRVTEEPDKPEKEKEAQSKEPEKPEVEEFQWPQRSETLSQLPAEK LPPKKRRLRLADMEHSSGESSFESTGTGLSRSPSLSHSSSFMS SPEREETSKLSALPKQDEFKGHSEFLTVPAGSYSLVPGHHQKEMR RCSSEQMPCPHPAEVPEVRSKSFYGNLSHAPVSGAAASTVSPSRER KKCFLVRQASFSGSPEISQGEVGMDSVKQEQLHLHAGLRSGWHHG PPAVLPPLQOEDPGKQVAGPCPPLSSGPLHLAQPIIMHMSQESLRN PLIQFTSYMYSKHLPEQPHLFPHQETIPFSPIONALFQFYPTVCMV HLPAQPPWWQAHFPHFPAQHPQKSYGKPSFQTEIHSSYPLEHVAEH TGKPAEYAHKTKEQTYPCYSGASGLHPKNLLPKFPSDQSSKSTETPS EQVLQEDFASANAGSLQSLPGTVVPVRIQTHVPSYGSVMYTSISQIL GQNSPAIVICKVDENMTQRTLVTNAAMQGIGFNIAQVLGQHAGLEKY PIWKAPQTLPLGLESSIPCLPSTSDSVATLGGSKRMLS PASSLELF METKQKRVKEEKMYGQIVEELSAVELTNSDIKDLSRPQKQPLVRQ GCASEPKDGLQSGSSSFSSLSPPSSSQDYPSVSPSSREPFPPSKEMLS GSRAPLPGQKSSGPPSESKESSDELIDETASDMSMSPQSSSLPAGDG QLEEEGKGHKRPVGMVLRMASAPSGNVADSTLLLTDMADFQOILQFP SLRTTTTVSWCFLNYPKPNYVQOATFKSSVYASWCISCNPNPSGLN TKTTLALLRSKQKITAEIYTLAAMHRPGTGKLTSSSAWKQFTQMKPD ASFLFGSKLERKLVGNILKERGKGDHGDKDIGSKQTEPIRIKIFEG GYKSNEDYVYVRGRGRGKYICEECGIRCKKPSMLKKHIRTHTDVRPY VCKLCNFAFKTKGNLTKHMKSKAHMKKCLELGVSMSTVDDTETEEAE NLEDLHKAEEKHSMSSISTDHQFSDAEESDGEDGDDNDDDEDEDDF DDQGLTPKTRSRSTSPQPPRFSSLPVNVGAVPHGVPSDSSLGHSSL ISYLVTLPSIRVTQLMTPSDSCEDTQMTQYQRLFSKSTDESPDKDR LDIPSCMDEECMLPSEPSSSPRDFSPSSHSSPGYDSSPCRDNPKR YLIPKGDLSPRRHLSPRRDLSPMRHLSPRKEAALRREMSQRDVSPRR HLSPPRPVSPGKDITARRDLSPRRERRRYMTTIRAPSPRRALYHNPL SMGQYLQAEPIVLGPPPIVTVGITGLPPKLVFDEGDVFPNLIKYKGD FVYVQNLNDSHTVKFPPFPAYEVVVTIVLMIAPFHSHFQENPCFOLA YDISQRRNLRRGLPQVPYFSLYGDQEGAYEHPGSSLFPEGPNDYVFS HLPLHSQQQVRAPIMVPVGGIQMVHSMPPALSSLHPSPTLPLPMEG FEEKKGASGESFSKDPYVLSKQHEKRGPHALQSSGPPSTPSSPRLLM KQSTSEDSL NATEREQEENIQTCTKAIASLR IATEEAALLGPDQPAR VQEPHQNPGLSAHVSIRHFSRPEPGQPCTSATHPDLHDGEKDNFGTS QTPLAHSTFYKSCVDDKQLDFHSSKELSSSTEESKDPSEKSQLH</p>
6688	A	3	598	<p>QCGGIRATTMAMSEFWPWQ\YRFPFFFTLQPNVDTRQKQLAAWCSLV LSFCRLHKQSSMTVMEAQESPLFNNVKLQRE\LPVESIQIVLEELRK KGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSVFTLYEL TNGEDTEDEEFHGL\EKPLLLRALQ/CPYSREHKAEIHHCSGDGRGV QVLLGRDLSPFTS</p>
6689	A	2	356	<p>SGQNNSVFTLYELTNGEDTEDEEFHGLDEATLLRALQALQOEKAEI</p>

				ITVKRWPRSSSSSRDLSPLYFLPPTFPGLSKGDQTPVSPKRLESVT PPELKKDSSPEGWGPWGMGFLKPP
6690	A	2	123	FCNVGQAGLKLLTSSDLPASASQIAGITVVIHHTWLECRF
6691	A	161	464	APPPCATQTAPHQHGHQSRDALLRFGCHCEILLFSSAGIYVQEMADM SMAKLYSGLLGVGDEILEVNGAKVAGLGLAHIKELLAHSESLSIRVL RQRPVPR
6692	A	3	86	HSAPRHFHTQTQSLQQSVRYLSLFCLF
6693	A	3	85	HSAPRHFHTQTQSLQQSVRYLSLFCLF
6694	A	2	201	RLAESLYDDRMFDIMRALDLTLKHHILPKELRTEYEEYFYLEPYLK QDIREGIEREEWAKKWSCK
6695	A	1	119	AVSRPAKAAESRLLTSPESLSRDLEDAPEVQESYRQOVPP
6696	A	1	3414	MEPNDSTSTAVEEPDSLEVLVKTLDSQTRTFIVGAQMNVEKFEHIR ASVSIPSEKQRLIYQGRVLQDDKKLQEYNVGGKVIHLVERAPPQTHL PSGASSGTGSASATHGGSPPGTRGPGASVHNRANSYVMVGTFNLP SDGSAVDVHINMEQAPIQSEPRVRLVMAQHMIRDIQTLLSRMETLPY LQCRGGPQPQHSQPPPQPPAVTPEPVALSSQTSEPVESEAPPREPME AEEVEERAPAQNPELTPGPAPAGPTPAPETNAPNHPSPAEYVEVLQE LQRLESRLQPFQRYEVLGAAATTDYNNNHGREEDQRLINLVGES LRLLGNTFVALSDLRCLACTPPRHLHVVRPMSHYTTMPVLQAAIP IQINVGTTVTMTGNGTRPPPTPNAEAPPPGPGQASSVAPSTNEVES AEGAPPPGPAPPPATSHPRVIRISHQSVEPVMMHMIQDSGTQPGG VPSAPTGPLGPPGHGQTLGQQVPGFPTAPTRVVIARPTPPQARPSHP GGPPVSGTLQAGLGTNASLAQMVSGLVGQLLMQPVLAQGTGPGMAP PPAPATASASAGTTNTATTAGPAPGGPAQPPPTPQPSMADLQFSQLL GNLLGPAGPGAGGPGVASPTITVAMPGVPAFLQGMTDFLQATQTAPP PPPPPPPPPPAPEQQTMPPPGSPSGGAGSPGGLGLESLSPEFFTSV QGVLSLLGSLGARAGSSSIAAFIQRLSGSSNIFEPGADGALGFFG ALLSLLCQNFMSVDVVMLLHGHFQPLQRLQPLQRLSFFHQHYLGGQEP TPSNIRMATHTLITGLEEYVRESFSLVQVQPGVDIIRTNLEFLQEQF NSIAAHVLHCTDSGFGARLLELCNQGLFECLALNLHCLGGQQMELAA VINGRIRMRSGVNPVSLVSWLTMMGLRLQVVLEHMPVGPDAILRYV RRVGDPPQPLPEEPMEVQGAKRASPEPQRENASAPGTTAEAMSRG S\PLAPEGG\SRDE\QDGASAEETP\WAAA\VPPEWVPIIQODIQ\S QRKLKQPPL\SDAYL\SGMPA\KRRKTPMG*GPPSCFSTEAVSRAA KAAGARPLTSPESLSRDLEAP\EVQESYRQQLRSDIQRLQEDPNYS PQRF\PNAQRAFADDP
6697	A	1	441	RKSFOKELGMALLKKDCQGLVVRLIQDFVLLTTAVEVAHRWRELAEK LANVSKQQMDAYESPHRDRNGVVDSEAMRKPAYDFLLTWSHQIGDSY RDVIQELHLGLDNMKNPITKRWKHLTGTLILVNSLDVLRAAAFSPAD QDDFEI
6698	A	2	180	DVWVNESERHQLKTKVVHLSKLPKDTALLDPNIYRTMPQRLKRTL IRKVFNLVLSKQ
6699	A	1	143	EVQEVQGGKKVARVANPGLDTFSREIFRNEKLKKCRRFLDELDVAKMD
6700	A	2	1069	SLVERLKMAASQAVEEMRSRVVLGEFGVRNVHTTDFPGNYSYDDAW DQDRFEKNFRVDVVHMDENSLEFDMVGIDAAIANAFRRILLAEVPTM AVEKVLVYNNTSIVQDEILAHRLGLPIHADPRLFYRNQGDDEGTE IDTLQFRLQVRCTRNPAAKSSDPNELYNHVKVYTRHMTWIPLGNQ ADLFPEGTIRPVHDDILIAQLRPGQEIDLLMHCVKGIGKDHA\KFSP VATASYRLLPDITLLEPVEGEAAEELSRCSFSPGVIEVQEVQGGKVAQ SCPTPRLD\FS\REIFRNEKLKKVRLARV\DHYIFSVES\TGV PPDVLVSEAIKVLMGKCRRLDELDVQMD
6701	A	197	310	WLCYIIYK*YDNWWHSMCFSKPLYPEIVSLNYILLKG
6702	A	3	67	GHRSDSSSHGCKANTAPQES
6703	A	3	517	DGSKPVKVPENPPSMVFKQMEQVAQFLKAAEDYGVIKTDMFQTVDLF EGKDMAAVQRTLMALGSLAVTKNDGHYRGDPNWFMKKAQEHKREFTE SQLQEGKHVIGLQMGSSSLCPQPQPNFLPESITALAPPSRLPPSPLL

				SPPWAKQGRSGLGVAWMWAKSTVLLGAKAH
6704	A	150	840	GSLLSPDMANKGPSYGMSREVQSKIEKKYDEELEEERLVEWIIIVQCGP DVGRPDRGRGLGFPVWLKNG\VILDRL*TTFTPDASKPV\KVPEKPPP SCSSSKTEPLPHFLKAAE\DYGVPRKSNIFQDL*TSLKKG\DMGSSS RGPLMAFGQLWQVTN\DGHYRG\DP\NWFYERKPQHKREFHRAQ LQKGKACPLALPDGAANRRGPPQARH*QGYGTTLGQIIKLEAERAKP
6705	A	3	842	TRAADPARPTRTRTRGRTRGRQHSLLKSRMENDMAQSLHSDTADDTA HRPGKSNLKLPGKILKKKVSASAEGVQEDPPELSPIPASPGQAAPLL PKKGILKKPRQRESGYSSPEPSESGELLDAGDVFVSGDPKEQKPPQ ASGLLLHRKGILKLNGMFFQTALALAAPTTFGSLDELAPPRPLARAS RPSGAVSEDSILSSEFDQLDLPERLPEPPLRGCVSDNLTGLEEPP SEGPGSCLRRWRQDPLGDSFSLTDCQEVATYRQALRVCSKLT
6706	A	1	570	CDGIWDMVSNEQLCEYVKSRLEVSDDLNVCNWWVDTCLHKGSRDNM SIVLVCFSNAPKVSDEAVKKDSELDKHLESRVEEIMEKS GEEGMPDL AHVMRILSAENIPNLPPGGGLAGKRNVEAVYSRLNPHRESGMAVL GTSICKPAESSGDKKGSWQTFQALRSTRTRKRFCKPERKINPALYN YK
6707	A	1	1437	MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHTAVVGIP HGLEDWSFFAVYDGHAGSRVANYCSTHLLHITTNEFDRAAGKSGSA LELSVENVKNGIRTGFLKIDEYMRNFSDLRNGMDRSGSTAVGVMISP KHIYFINGGDSRAVLRYNGQVCFSTQDHKPCNPREKERIQNAGGSVM IQRVNGSLAVSRALGDYDYKCVDGKGPTEQLVSPEPEVEYILRAEED EFIILACDGIWDMVSNEELCEYVKSRLEVSDDLNVCNWWVDTCLHK GSRDNMSIVLVCFSNAPKVSDEAVKKDSELDKHLESRVEEIMEKS G EGMPDLAHVMRILSAENIPNLPPGGGLAGKRNVEAVYSRLNPHRES DGASDEAEESGSGQKLVEALRQMRINHRGNRYQLLEMLTYSYRLAKV EGEESPAEPAATATSSNSDAGNPVTMQESHTESESGLAELDSSNEDA GTKMSGEKI
6708	A	3	286	CFSNAPKVSDEAVKKDSELDKHLESRVEEIMEKS GEEGMPDLAHVMR ILSAENIPNLPPGGGLAGNRNVEAVYSRLNPHRESGGAGDLEDPW
6709	A	172	364	FYLYLVMLCFIEPVKLLLVIGAYIL*LLKTIHEFHNQCFVDTKSLKG RHFKEYVFFTFILNMFHR
6710	A	1	683	KTGREPRGRFLLCLLFFTVITYFFVIGIAPIFILYELDSPLCWNEV FIGYGSALGSASFLTSFLGIWLFSYCMEDIHMAFIGIFTTMTGMAMT AFASTTLMFLARVPFLFTIVPFSVLRSMLSKVVRSTEQGTLFACIA FLETGGVTAVSTFNGIYSATVAWYPGFTFLLSAGLLTNQPSVYVL SSVPAGMREAMNFLYKKNPVKMLQTEPVKLLLVIGAYIL
6711	A	18	292	ELLVSPFLHPIIPPICGCFPRPPPKIDISYPVPLCDPRTQVSDCEQM WPCPETPAWPEGHASAYYFISPGSLPAVPRVSSSPTLGTRDATT
6712	A	1	687	PTRPVFDQVRTLVLCCECAHADRS GGAPSLCPHAAEPRGS PAPQACGS AAKCVRCASWLLCALSYGDTGGVGLDRYRSDYGDTGGVRLDRYRSD YGGTGGVGLDRYRSDYGGTGGVGLDRYRSDYGGTSGRGVDKVPVRLR WHRRRGVRQVLVRCTGSLNPCGFGSKDRTHPCHKRSTGRGVGVGAA LRVSRPQPHSHSSLGRKGRVPGVSWWVSQGAAPPVEVTGQE
6713	A	1	119	GTRSYTHLYRVFLELIKMSVYDLNHTVIMVISGHVRLAF
6714	A	1	339	GTRKFIPLTAWSNWAIVKAASEPFQSENEAYPPAERISAEEGDAAE GGEDSEEDFEENTDKPGDELISFEEHVGPSAAPKIEKPMPRCLKQR RALRSSRLIGIIRSGRLQ
6715	A	3	470	HERLEKNVKEVLEDFAEEDGEKKIKLLTGKRVQLAEDLTRTQHYTPGH HMAPHPALTLLLPCLGSDIRARLLFVMESLLLSSALTLCARVPLHLH PSHPLSLCPTPDRFLSSPGSQTMAFVGDTLFTLPVLRQPAPGHPPAQ ILSSVLDQATNSPM
6716	A	2	2942	TGAPAWPSRRLRDLPAAGMWRLRRAAVACEVCQSLVKHSSGIGKSLP LQKLHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS PIKYGYQPRRNFWPARLATRLLKRLYLILGSAVGGGYTAKKTFDQWK DMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPNSEDLVKLAPDFD

				KIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRKVSDKEKIDQ LQEELLHTQLKYQRILERLEKENKELRKLVLQKDDKGIHHRKLKKS IDMYSEVLDVLSYDASINTQDHLPRVVVGDQSAGKTSVLEMIAQA RIFPRSGGEMMTRSPVKVTLSEGP HHVALFKDSSREFDLTKEDLAA LRHEIELMRKNVKEGCTVSPETISLNVKGPGLQRMVLDLPGVINT VTSGMAPDTKETIFSISKAYMQNPNAIILCIQDGSVDAERSIVTDLV SQMDPHGRRTIFVLTKVDLAEKNVASPSRIQQIIEGKLFPMKALGYF AVVTGKGNSSIESIAIREYEEFFQNSKLLKTSMLKAHVTTNRNLSL AVSDCFWKVMVRESVEQQADSFKATRFNLETWKNYPRRLRELDNEL FEKAKNEILDEVISLSQVTPKHWEIILQQSLWERVSTHVIENIYLP AQTMNSGTFNTTVDIKLKQWTDKQLPNKAVEVAVETLQBEFSRFMTE PKGKEHDDIFDKLKEAVKEESIKRHKWDFAEDSLRIQHNALED ISDKQQWDAAIYFMEEALQARLKDTENAIENMVGPDWKKRWLYWKNR TQEQCVHNETKN\ELEKMLKCNEEHPAYLASDEITTVRKNLESRGVE VDP SLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRHFVDSELEC NDVVLFWRIQRM LAITANTLRQQLTNTVEVRLKKNVKEVLEDAEDG EKKIK\LLTGKRV\QLA\EDLKKVREIQEKLD AFIEALHQEK
6717	A	38	359	PVIDEILKPREVWKSFDRAVGPEWFPYAKAARHPFSSKITATTFLHL ASAALYRTAETSSTMQNYHQDWPTPGGIPETTLQGAYRKKIKRSDAA AAGTHSSPWCIP
6718	A	122	282	KPRSGASGAGWLPRGETKSLMCPSPGGCEIVEAWLRADRYAFWDVPL DSPPLA
6719	A	2	1010	ASGEWRVSGRPAGAGRPEEALAAGSDPRGAARLACSAPTGGGT PFDFRRFDIYRKVPKDLTQPTYTGAIISICCLFILFLFLSELGTGFI TTEVVNELYVDDPKDSDGGKIDVSLNLSLNLHCELVLGLDIQDEMGR HEVGHIDNSMKIPLNNGAGCRFEGQFSINKVPGNFHVSTHSDATAQ NPDMTHVIHKL SFGDTLQVQNIHGAFNALGGADRLTSNPLASHDYIL KIVPTVYEDKSGKQRYSYQYTVANKEYVAYSHTGRIIPAIWFRYDLS PITVKYTERRQPLYRFITTICAIIGGTFTVAGILDSCIFTASEAWKK IQLGKMH
6720	A	326	514	KPRSGASGAGWLPRGETKSLMCPSPGGCEIVEAWLRADRYAFWDVPL REETELSRVRPSGL
6721	A	1	1076	MSLCAQSPSPVLRGSYTCLSPSVNELYVDDPKDSDGGKIDVSLNLSL PNLHCELVLGLDIQDEMGRHEVGHIDNSMKIPLNNGAGCRFEGQFSIN KNQELQILSQVGERSALGRAEAPGGSWQGFQHVPAFLEARYCHSGA SQQRCEAAPFDRKLTSSQMSEFACFEQQRQPHQPHGDLVSSASPAG GGQDGVPGNFHVSTHSDATAQPIPDMTTHVIHKL SFGDTLQVQNIHGA FNLGGADRLTSNPLASHDYILKIVPTVYEDKSGKHRDSYQYTVANK EYVAYSHTGRIIPAIWFRYDLSPIITVKYTERRQPLYRFITTICAIIG GTFTVAGILDSCIFTASEAWKKIQLGKMH
6722	C	11	79	MLPILRHTFLRVTLRGKKACLL*
6723	A	3	198	YKSKLMITNLCLDNSRLGVVAHTYNPSTLEGPRQGDLSLPRGVQTS LGNARSCLYPKNIFFLN
6724	A	1	432	FRYSRGGSMEDYCDSPHGETTSVEDSTQDVTAEHHTSDDECEPIEAI AKFDYVGR TARELSFKKGASLLLYQRASDDWWEGRHNGIDGLIPHQY IVVQDTEGDVVERSSPKSEIEVISEPPEEKVTARAGANCPSGGHVAD IYL
6725	A	123	336	RCFLCCCCFPSSLPACPFSPSEDGVVERSSPKSEIEVISEPPEEKVT ARAGASCPSGGHVADIYLANINK
6726	A	1	227	FGFLVETGFLQVGQACLELLTSGDSPAPASQNGGITGRSHRAGPTIF LKKPFKNLHSLCSSNYIIGSFVNSNTY
6727	A	1	131	MPVLLTSDMHKSSVKAGFAKVDQQQAPKSVQLLTVKTRDSTSNRGN SGPRSQATDRICRTPYHFEDC*SGSTASPOVSSASDSEDKRLNK
6728	A	3	364	GSCSVAQAGVQWCDLSSQLLPPGSSSSPASACQIAGITGVYHHSQ LIFVFLVEMGFYHVGQAGLELLASGDPPALASQSAEITGVNYRAWPHV LYFFQVILKSTTRNVGMGFGMYNGNR

6729	A	2	197	QAGVQWLVLSSLQTLPPRFKPFSSCLRLPSSWDYRCLPPCLAKFCIFS RDGVSSCWPGWSQTPDVR
6730	A	2	422	NGMLGNMLKSSLIKFEDLQETAMETWSIDQVCSWLEEKNLRELVYRF QEEKLSGAALLALNDRMVQQLVKKIGHHAVLMDLIKKYKHTQGLKS PENPKKAAVVMQTEAARDYRDEESSSPARHGEQMPSFYPAENLDNG
6731	A	33	294	SQHFRGRSRWVDHLRSGVRDQPGQHGETPSLLKMQKFSQAWCWDYRHI TPHPANSCIFVEMGFRYVAQTGFKHLASSDPPASVSQML
6732	A	2	670	RSRGIKDFENDPPLSSCGIFQSRIAGDALDLSGIRISSVFASPALRC VQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLMSLEELK EANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQIVNTCPQDT GVILIVSHGSTLDSCTRPLLGLPPRECGDFAVRKIPSLGMCFCFEE NKEEGKWELVNPVKTLTHGANAAFNRNWIQGN
6733	A	1	171	GEEGTYKRSFFQTLSSLVQEEGYGSLYRGLTTHLVRQIPNTAIMMAT YELVVYLLNG
6734	A	1	789	MGRFHVQGAGLKLTLSSDLPALASQVQCKLVVPASAERHISPLQRL IAFSLRPDPGLAGDRASLGVPLCGYRIGNPRRSPKRTTHCARTAAYS CSAYSCKLYQFRPNVGHSASTPKAMCQTTAAGEGAHAADDEGYTQRVV GARRGTPQRYTGAETKNRAFRSYPKMETSWSRGGGSTPPVALDAQV ERECALGSGAQKHSCLAVRVVLIFCINEHYPTLTLYRPLFVLPLRS GGTPTSWRALFFPSSSDSNCKLCGGTSS
6735	A	3	363	FFFFFFFFLRQSLSLSPRLECRGTISAHCNLRLLGSINSSASASQVA GTTGACHHVQPIVFVFLGETGFHHVQAGLKLTLSSDPPASASQVRV ITGMSHQIWPKLSLIKSLSDAQIRE
6736	A	2	379	SCERFSTSQVLCSQALSSGKHYWEVDTRNC SHWAVGVASWEMSRDQV LGRTMDSWCVEWKGTSQLSAWHMVKETVLGSDRPGVVGIIWLTLAEGK LACDTEDDQDMLLSGVPHLSSYLGCIGMHV
6737	A	116	373	EIFGEQAVLRGSPGGPKDPGSFQCRLPVLQTWGGLRHDALDHAYGMP GGICVHASGYIGGHRRTREGALSMARATLAQRSYLPQIC
6738	A	1	164	RAKAKRRNTTVSCMRHLKIVYRRFRYRLYVGIIIGPGGLNETLVFT CKKITVP
6739	A	3	122	RIMKMRKVLKHHQQLGEVLTQLSSRFKPRVPVIKVQDFT
6740	A	83	2455	IRIAALDDFRTSLTMSSTRSQNPGLKQIGLDQIWDDLRAQIQQVYT RQSMASRYMELYTHVYNYCTSVHQSNQARGAGVPPSKSKKGQTPGG AQFVGLELYKRLKEFLKNYLTLNLLKDGEDLMDESVLKFYTQQWEDYR FSSKVLNGICAYLNRHWVRRECDEGRKGIYEIYSLALVTWRDCLFRP LNKQVTNAVLKLEKERNGETINTRLISGVVQSYVELGLNEDDAFAK GPTLTVYKESFESQFLADTERFYTRETEFLQONPVTEYMKKAEARL LEEQRVQVYLHESTQDELARKCEQVLEKHLIEFHTEFQNLDDADK NEDLGRMYNLVSRIQDGLGELKKLLETHIHNQGLAAIEKCGEALND PKMYVQTVL DVHKKYNALVMSAFNNDAGFVAALDKACGRFINNNAV KMAQSSSKSPELLARYCDSLLKKSSKNPEEALEEDTLNQVMVVKYI EDKDVQKFYAKMLAKRLVHQNSASDDAEASMISKLKQACGFYTSK LQRMFQDIGVSKDLNEQFKKHLTNSEPLDLDFSQVLSGSGSWPFQOS CTFALPSELEERSYQRTAFYASRHSGRKLTWLYQLSKGELVTNCFKN RYTLQASTFQMAILLYQNTEDAYTVQQLTDSTQIKMDILAQVLQILL KSKLLVLEDENANVDEVELKPDTLIKLYLGYKNKKLRVNINVPKTE QKQEQETTHKNIEEDRKLIIQAAIVRIMKMRKVLKHHQQLGEVLTQL SSRFKPRVPVIKKCIDILIEKEYLERVDGEKDTYSYLA
6741	A	83	2450	IRIAALDDFRTSLTMSSTRSQNPGLKQIGLDQIWDDLRAQIQQVYT RQSMASRYMELYTHVYNYCTSVHQFVGLELYKRLKEFLKNYLTLNLL KDGEDLMDESVLKFYTQQWEDYRFSSKVLNGICAYLNRHWVRRECDE GRKGIYEIYSLALVTWRDCLFRPLNKQVTNAVLKLEKERNGETINT RLISGVVQSYVELGLNEDDAFAKGP TLTVYKESFESQFLADTERFYT RESTEFLQONPVTEYMKKAEARLLEEQRVQVYLHESTQDELARKCE QVLEKHLIEFHTEFQNLDDADKNEDLGRMYNLVSRIQDGLGELKKL LETHIHNQGLAAIEKCGEALNDPKMYVQTVL DVHKKYNALVMSAFN

				NDAGFVAALDKACGRFINNNAVTKMAQSSSKSPELLARYCDSILLKKS SKNPEEAELEDTLNQVMVVKYIEDKDVQFKFYAKMLAKRLVHQNSA SDDAEASMISKLKQACGFYETSKLQRMFQDIGVSKOLNEQFKHLTN SEPLDLDIFSIOVLSSGSWPFQQSCTFALPSELEERSYQRFATFYASRH SGRKL TWLYQLSKGELVTNCFKNRYTLQASTFQMAILLQYNTEDAYT VQQLTDSTQIKMDILAQVLQILLKSKLLVLEDENANVDEVELKPDTL IKLYLGYKNKKLRVNINVPKTEQKQEQETTHKNIEEDRKLLIQAAI VRIMKMRKVLKHQQLLGEVLTQL\SSRFKPRVPVIKKCIDILIEKEY L\ERV\DGEKDTYSYLALTLSGKGLDLCDPQQIVHVGE
6742	A	3	318	EHNTPLTSGFVFQEWALTNYYSVKHMDLCLTVVDRAPGSLIKLQGCR ENDSRQKWEQIEGNSKLRHVGSNLCDSRTAKSGGLSVEVSGPALSQ QWKFTLNLLQ
6743	A	17	174	PPAVVPHEDRRFSPHFLDWAAGVMTLPSIGIPLLLWYSSKRKYDTP KTKKN
6744	A	3	711	LSSCLCGSGKAFGMPTMRLLSFVVLALFAVTQAEEGARLLVSKSLN RYAVEGRDLTLQYNIYNVGSSAALDVELSDDSFPPEDFGIVSGMLNV KWDRIAPASNVSHTVVLRPLK\AGYFNFTSATITYLAQEDGPVIGS TSAPGQGGMLV\QREFDRRFSP\HF\LDWAAGGHDPPFPSGIPLL\ LWYSSKRK\YDTPKTKKNLIWGFHKPSSPKSKAPLKKPQVLSQTP KGYF
6745	A	74	472	GDDETKLT LHGLQQYYVKLKDDEKNRKLFDLLDVLEFNQVVI FVKS QRCIALAQQFKDFQRRILVATNLFGRGMDIERVNI AFNYDMPEDSDT YLHRVARAGRFGTKGLAITFVSDENDAKILNDVQDRFE
6746	A	1	1371	MAENDVDNELLDYEDDEVETAAGGDGAEAPAKKDVKGSYVSIHSSGF RDFLLKPELLRAIVDCGFEPSEVQHECIPQAILGMDVLCQAKSGMG KTAVFVLATLQQLPVTGQVSVLMCHTRELAFQISKEYERFSKYP NVKVAVFFGGLSIKKDEEVLLKKNCPHIVVGTGPRILALARNKSLNLK HIKHFILDECCKMLEQLDMRRDVQEIFRMTPEKQVMMFSATLSKEI RPVCRKFMQDPMEIFVDDETKLT LHGLQQYYVKLKDNEKNRKLFDLL DVLEFNQVVI FVKSQRCIALAQLLVEQNFPAAIAHRGMPQEERLSR YQQ\FKDF\QRRILVATN\LFGRGMDIERVNI AFNYDMP\EDSDT\Y \LHRVARA\GRFGTKGLAITFVSDENDAKILNDVQ\DRFEVNISELP DEIGHLLPTLEQDTVEDSPILGMLTVCSFQGGGTPGWG
6747	A	2	139	AGSELGEGEEVGLSYL/DERTNSEEGGLRGEKRRDAENDGEEDE
6748	A	3	270	SYLMKEEIQDEEDDDYVEEGEEEEEEEGGLRGEKRRDAVKEEIQ DEEDDDYVEEGEEEEEEEGGLRGEKRRDAVKEEIQDEEDDDYV EEGEEEEDEEGGLRGEKRRDAEDDGEEED
6749	A	21	301	KVNFLKKYSWYRIFSKPLSEQEKKLQNSEQAPGKIIFDQLVVTYNML QKGPDENRGALPGGDQPRNTPVPSRPGSLELSSPIKLMVAPRKKG
6750	A	4	366	RHRVSLYPSE/WSAVAQTHSSL*P*APWELK*SF*LSPSS*K*RSI QLCPG*LRNFFFF/CGRDGVLMMLVFNWSWTQVMLLPQPPQVLGLR VELDDTFLKVSSLVFLCLKQGYKKRIWNP
6751	A	3	263	KMHARDFTVSALARGIDVQQVSLVINYLPTNRENYIHRIGRGRFG RKGVAINFVTEEDKRILRDIETFYNTTVEEMPNNVADLI
6752	C	54	161	MLPSIQITVEKRMNVFQYSQDAGFSPVNI VFTIGR*
6753	A	161	1122	RSLSFVASMLTVLRSLPLFSRELLFPVLKIQKVI LALGDYMGATCHA CICGTNVRNEMQKLQAEAPHIVVGTGPRVFDMLNRRYLSPKWIKMFV LDEADEMLSRGFKDQIYEIFQKLNTSIQVVLLSATMPTDVLEVTKKF MRDPIRILVKKEELTLEGIKQFYINVEREEWKDLTCDLYETLTITQ AVIFLNTRRKVDWLTEKMHARDFTVSALHGDMDQKERVIMREFRSG SSRVLITTDLLARGIDVQQVSLVINYLPTNRENYIHRIGRGRGRFR KGVAINFVTEEDKRILRDIETFYNTTVEEMPNNVADLI
6754	A	1	891	MDPDGVIESNWNEIVDNFDDMNLKESLRGIYAYGFEKPSAIQQRAI IPCICKGYDVIAQAQSGTGKTATFAISILQQLEIEFKETQALVLAPTR ELAQQVVLLSATMPTDVLEVTKKFMRDPIRILVKKEELTLEGIKQFY INVEREEWKDLTCDLYETLTITQAVIFLNTRRKVDWLTEKMHARDF

				TVSALHGDMDQKERVIMREFRSGSSRVLTITDILLARGIDVQQVSLV INYDLPTNRENYIHRIGRGGFRGKGVAINFVTEEDKRILRDIETFY NTTVEEMPMPNVADLI
6755	A	2	104	LITDILLARGIDVQQVSLVINYDLPTNRENYIHR
6756	A	957	1285	HGTRRRRDVIMREFRSRVKVRVLITDILLGSRGLMCNNVSLVIN/YM DLPTN\REN\YIHRIGRGGSNLGGKGVAINFCYLKKTRGFLRDIET LPILQWRRMPMKCGLTLF
6757	A	1	716	TPKRAPKKMAISGVPVLGFFIIAVLMSAQESWAIKEEHVIIQAEFY LNPDQSGEFMFDFDGEIFHVDMAKKEVVRLEEFGRFASFQAQAL ANIAVDKANLEIMTKRSNYTPITNDKFTPPVVNVTLRNGKPVTTGV SETVFLPREDFHFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHW FDAPSPLPETTENVVLCALGLTVGLVGIIIGTIFIIGLRLKSNAEERR GPL
6758	A	2	835	FLSVLPHSRALLTPKRAPKKMAISGVPVLGFFIIAVLMSAQESWAI KEEHVIIQAEFYLNPDQSGEFMFDFDGEIFHVDMAKKEVVRLEEF GRFASFQAQALANIAVDKANLEIMTKRSNYTPITNPPEVTVLNS PVELREPVLICFIDKFTPPVVNVTLRNGKPVTTG\VSET\VFLPR ENTLFR/KFHYFP\FLPPTEDVYDFRVE\HWGLDEPLLKHWFDAPS PLPK\TTENVV\CALGLTVGLVGIIIGTIFIIGLRLKSNAEERRGP L
6759	A	759	1022	PTQGQRKGTSHLGGGADAGCTAAEPPGGTAAASGAGAGRAGD*HPGT GAQHHPFAVPGEAPGEETQGGVQEEPAEAQGWQPHQPPF
6760	A	2	689	CISTSTGSDNMQVRKGTGPKIPWREREERGGGLVASAYQKDPLVH QKIVVLGEQELPSGVSSLLLLLWLSALQPVKPSFLTYKIETVIVP TLEYSEDIISNTCKTMRPASVQGHSTNIGHDGGDDDDDEEMMIA SACLLQAEVNYERVKEYCLKVLKKEGENFKALYRSGVAFYHLGDDYD KALYYLKEARTQQPTDNTVIRYIQLTEMKLSRCSQREKEAM
6761	A	2	1011	SGPRSPRSASPGPASTGPRHPQVAEGGRERAARSREAGEGPASEAA AAAAGAASGSSGENGSAGRQTAAGCHGRHEACEARGRRPRLNPGRR GGGGGGQIAARTRRRGGGRMERKGSAAAGAKGNPSPPAAGEGQRP PLCVPGGGGAPARGQVGAAPAEIIRRAHEFKSQGAQCYKDKKFR EAIKGYHRALLEKGLLPPGERERDSRAASPAAGALKPGRLLSEEQSK TVEAIEIDCYNLAACLLQAEVNYERVKEYCLKVLKKEGENFKALY RSGVAFYHLGDDYDKALYYLKEARTQQPTDNTVIRYIQLTEMKLSRCS QREKEAM
6762	A	2	151	KYLMKSKNLKGGFQEVAEHLELERIGPQHQAQSDSLLTGMAFFKMR EV
6763	A	3	740	RPIGEFSNADYQYQLLRNCVDDLKIIQLGLTFMNEQGEYPPGTSTW QNFNFKNLTEMDYAQDSIELLTSTGIFKKHEEETQYFAELLMT SGVVLCEGVKWSFHSYDFGYLIKILTNSNLPEEELDFFEILRLFF PVIYDVKYLK\SKN\LKGG\QEVAEQL\ELERIGP\QHQAGSDS L\LTGMAFFKMRMFFEDHIDDAKYCG\HLYG\LGSGSSYVQNGHRG MHMEEGSQGSPWTWK
6764	A	296	522	IWVFHNLKGLFEIFCCILKYFLEELLILF*KTKL*KHASFLKNPSI QDMESSTTVHRSLGGLCADVLSLQWL
6765	A	3	333	FFFFFLIPFFFIHQHFIHNKYKLFTATVKKAHHRGSLRALTCALWC WIPYPGWRGYFLKRRHVFTTLFFKIKLGSSSKKYFKNTTKGFQITLL RFVEKPKFKGQFGLG
6766	A	1326	1982	TSEASRQSERVDSAAALSLSLSRSSKCRPWGTARVARAGGCLTPLL SRRFLETRPFTGPWDPGLGVTWCPCPPKRLKSTPRPKFSVCVLGDQ QHCDEAKAVDATFEVCLGDQVLSNANGFLSLSAKHYDAFLASESLIK QIPRILGPGLNKAGKFPSSLREEGQAICYSSTNLT*SSLSSQVLCL AVAVGHVKMTDDELVYNIHLAVNFLVSLK
6767	A	11	713	EAMSSKVSRTLYEAVREVLHGTQRKRKFL\ETVELQISLKNYDPQ \KDKRF\SGT\VRKSHSPALSFVCVLGD\RQH\CD\EAKA\VDIP \HMDI\EALEKTSTKNKLV\KKAGQRKYDAVFGPQSLLIKQIP\RI

				PRAPGLNKAGK\FP\SLTHNENMV\AKVDEVK\SPIKF\QMKKVLC LAVAVGHVKMTDDELVFNIHLA\VNFL\VSLLK\KNWQKCSGALYYQ EAPMGQSPKRLY
6768	A	2	277	PRVRGRVGAFTYGTDLASLLSFEKLDRA SPYLWPEQLPGVAEFAA SFKSPITSSPPKMAEIERDDIDMLKATEMTRGKFLNILEKPKK
6769	A	1	336	MASPTDGTDLASLLSFEKLDRA SPDLWPEQLPGVAEFAASF SSPPKMAEIERDDIDMLKELGSLTTANLMEKVRGLQNLAYQLGLDE SREMTRGKFLNILEKPKK
6770	A	132	347	NAKQVGDRGKPCVCHYGLSLAWDPCMLKYCHSRDRPTPYKCGIRSCH KSYSFDFYVPQRQLCVWDEDPYPG
6771	A	3	109	CAPSPVRGAMASARLFAALLFFVGGVAESMTWKTP
6772	C	5	160	MGFEGGPKILNWKFVKVXSXSLXKGQXESIFLNTXKVIRAGDTXK SVLG*
6773	A	52	310	YIIRTQTQISHHPLHYILGSAKKKLCFGKSYFIRGSSFRKGGHEER GLKYKKKTGEGV**KRTKKQTKTKTKTIKYKLSRCCGNV
6774	A	149	333	EFMLKWIYRIFVNLFVVRFFNC SFLCAECISLPGQECGGAEVSSF SRTFPQHLLSLYLM
6775	A	1	1616	LLLLFFLESTRFY*FFFFFFFFFTIQTFGGGLSPFFFLFFIKPLP QFFFFIL
6776	A	2	138	ASGHREVQDSYEAYGQDDWNGTITSLK/APPARPVKGAYREHPYGRY
6777	A	1	1212	MQRDDPAARMSRSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGG GGGSRGGARAS PATQPPPLPPSATGP DATVGGPAPTLLPPSATAS VKMEPENKYLPELMAEKDSLDPSTHAMQLLTAEIEKIQKGSKKDD EENYLDLFSHKNMKMKERVLPVKQYPKEEELRKGDPKYAHLNMDL HVFIEVFGPPCEAYALMAHAMEEVKKFLVPDMMDDICQEQFLELSYL NGVPEPSRGRGVPRGRGAAPPPPPVPRGRGVGPPRGALVRGTPVRG AITRGATVTRGVPPPPTVRGAPAPRARTAGIQRIPLPPPPAPETYEE YGYDDTYAEQSYEGYEGYYSQSQGDSEYDYGHGEVQDSYEAYGQDD WNGTRPSLKAPPARPVKGAYREHPYGRY
6778	A	3	150	YYDYGHEVQDSYEAYGQDDWNGTRPSLKAPPARPAKAYREHPYGR Y
6779	A	2	1622	ASVATAPALPPPPTAARASVAAASLSRSLDR TSSQMQRDDPAARMS RSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGGGGGSRGGARASP ATQPPPLPPSATGP DATVGGPAPTLLPPSATASVKMEPENKYLPE LMAEKDSLDPSTHAMQLLTAEIEKIQKGSKKDDEENYLDLFSHKN MKLKERVLIPVKQYPKFNFVGKILGPQGN TIKRLQEETGAKISVLGK GSMRDKAKEEELRKGDPKYAHLNMDLHV FIEVFGPPCEAYALMAHA MEEVKKFLVPDMMDDICQEQFLELSYLN GVPEPSRGRGVPRGRGAA PPPPVPVTG\RGVGPPRGALVRGTPVRG AITRGATVTRGVPPPPTVR GAFC*RARTAG\IQRIPLPPPPAPETYEEYGYEDTYAEQSYEGYEG YYSQSQGDSEYDYGHGE\VQ\DSYEALWPRTNW\NGTRP\SLKAPL ARPVKG\AYREPPYGRLLKTKHEGENISYEQSLLLDFLYLP GIPVAL PTTDQGNWSKCFFRGSPSFSPTLIPFL
6780	A	1	76	RGFFFFFFFFFFFFFFFFFQQKSQIY
6781	A	1	287	CFL*DRVLLCHPGWSAVAHNHSSLQP*TPGIKQFSLRL/SSS*DYR CTSPYLAIFFFF*\FFCRKQSLATVPRTISNSWPQAILLSWSKHVEI TGF
6782	A	3	64	AASTFNFYFYFEIIVDLHAV
6783	A	2	69	FFFLCFFNFYFYFEIIVRFTCS
6784	A	1576	3458	KINLLNPKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEEVDLKP MKEKNAKEELIRWEEGKKWQAKIEGIRNKLKEKEGEVFTLTQNLNL KDLFAKADKEKLT LQRKLKTGMTVDQVLGIRALESEKELEELKKRN LDLENDILYMRHQALPRDSVVEDLHLQNRYLQEKHLALEKQFSKDT YSKPSISGIESDDHCQREQELQKENLKLSSENIELKFQLEQANKDLP RLKNQVRDLKEMCEFLKKEKA EVQRKLGHVRGSGRSGKT IPELEKTI

				GLMKKVVEKVQRENEQLKKASGILTSEKMANIEQENELKAELEKLK AHLGHQLSMHYESKTGTEKIIAENERLRKELKKETDAAEKLRIAKN NLBILNEKMTVQLEETGKRLQFAESRGPQLEGADSKSWKSIVVTRMY ETKLKELETDIAKNQSIDTLKQLVKEATEREQKVNKNYEDLEQQIK ILKHVPEGAETEGLKRELQVLRRLANHQLDKEKAEILHQIEANKDQS GAESTIPDADQLKEIKDLETQLKMSDLEKQHLKEEIKLKKKELENF DPSFFEEIEDLKYNKYKEEVKNILLEEKVKKLSEQLGVELTSPVAAS EEFEDEEESPVNFPIY
6785	A	3	841	GKRLGPPQWLDYDCDRAVIEDWVFRVPHVAIFLSVVICKGFLVLCSS LDLTTLVPERQVDQGRGFESILDVLSVMYINAQLPREQRHRWRLFS SELHGHFSQLCGHITHRGPCVAVLEDDHDKHVFGGFASCSEWVKKPQF QGDNRCLFSICPSMAVYTHGTGYNHYMYLNLHGQQTIPNGLGMGGQH NYFGLWVDVDFGKGHSRAKPTCTTYNSPQLSAQENFQFDKMEVWAVG DPSEEQLAKGNKSILDADPEAQALLEISGHSRHSSEGLREVDPDE
6786	A	1	960	MGKDFMTKTPTPMATKAKIDKWDNLNKLKSFCTAKDTIVRVNRQPIEW EKIFAIYPSDKRLIATIKELKQTYKKKINNLIKQTCGADLQQT ADLQQTGLSVRKKTDKQKGIASSTKRTSTQKPHPKITNMKTKEIQT TIKEYYEHLYTNKLENLQEMDKFLDTYTFPGLNQEEVQSLNRPITSS EIEAVINSLPTKKSPPGDRFTAIFYQORDMDEAGNHHSQQTNTGTENQ TLHILTHKWELENENTWTQGGYHTPGPVVRVWGNRGGIALGEIPNEC SSSPATDQSWMENDELKEEGFRRLVITNFSLEKEDV
6787	A	507	755	NKRGYKQMEHSMMLGRKNQYRKNGHTAQGNL*IQCHPHQATNDFLH RIGKNDPQVHMEPKKSPHRQVNPKEQSWRHAT
6788	A	274	882	PDQVDRGGAHWQTDADDPWLADHLQHCQRCGEILRHYSGGIRGNVSA VKCAEHHVPAFARLRNPQCGDFQRLDYRLFDSPGVKRREL*TAYRFC HVAP*LMDLRSGWAAGAVRYQSH*FTADRLRS\VDMDEAGNHHSQQ T\SQDQKIKQRTFSLISGS*TTTRTHGHREGNITHRGLSRPNTARILC ASKAHLGLPLRSSLP
6789	A	114	329	NKRGHIQMEKHSMLMDRKNQYHEYGHTAQSNLWICQYPHQATIDFLH RIRKNYFKVHTEPKKSPYSQDNPK
6790	C	1	1983	MGDGTSDFDPIGDIGIRQSNYSCGGCPRIPIVVRVTGRAHGTQTIVV FMAKVYYGNVMRREKDSGGAWGNPWAGILLPPPSTRNCTVHSSFSNE NIFPQHTSSCVVHNQYIGADFPWSNFSFVVEYNYVEDSCWTKHCKE LNIPYMAFKVILPDTVLERSTLLDRFGGFLLEIQIPIVVFASEGLLN TPDILQLLESKOMDEAGNHHSQQTIVRTENQTLHVLTHRWELNNENT WTQDGEHHTPGPVVGWRELIIAPGVEATALIIRQIADHSLMTSKRDP HEWLDKSWLKVPSEENRNQISTLSSQSSASDLDSVIEHNEYQYL GLGETVQEDKTTILNDNSSIMELKEISSFLPPVTSYNQTSYWKDSSC KSNIGQNTFPFLINIESRRPAYNSFLNHSDESDFSLGLTQMNCETI KSPTDTQKRVSVPVPRFINSQKRRTHEAKGFINKDVSDPIFSLEGTQS PLHWNFKKNIWEQENHPFNLOQGAQQTACNKLYSQGNLFTDQKCL SDESEGLTCESSKDETFWRELPSVPSLDLFRASDSNANQKEFNLSYF YQRAGKSLGQKRHHSESSFNSGDKESLTEEKTEAQEKMTTEDRGRGWG YATTNRMPRIAGNHQEPGERRGTPPPSEAPEGSNPANTLILDFPPP EL*
6791	A	190	486	FLHFFLHD*IISSNKLQKVNKSIPPTGPSLPCPCVLIVQLPLMSEN RCLVFCSCVSLLRMMVSSFIHVPLNFFNAFLLLNFFRFCPLLSCHMI KKSSS
6792	A	1	597	MDENLPSELKANPTQTSYMPISIKSYRGAGQLKIAQESGVSVQGHWSM KREGFQKLERTHKNFQMKFSRWGIAVGKLEQHDCHKEEAVTGTSCM KELKDKSYRRIQQRDMDEAGNHHSQQTIRRTENRTLHALTHKWEIN NENTWTQEDPSTPVNSTATNRIQVTSSGLWQKASSVSPLLPVPTLPW SRFHIIAQGIF
6793	A	1	721	MTSYNEQNKKPVTDPNEMAIHEDSNQEFKIAVVNETQRSRSPSTE LMTPPPLPTREQQPPLTVIFHYLPKSYKTAPPLSPFPDSLFGLSQPA PRDMDEAGNHHSQQT\KQEQTTHCMFSLTSGS*TMTRTHGHREGTVI

				HRGLLGQFSQQLINKSEFSNTVCREKSGRVLQVNMESPL*MIQDALQ DQTPPKGPITVFL*LFYLDHLLRSSHKVASYLSTESRSGSITVLF RCSEP
6794	A	417	698	DRNRKANTACFQHSQVGVEQ*EHMDTGKV*SI*YGNYEHTSTCERME IQKATTEHLNL*S*SGSFLRFTWKMLQFSKISRSTFYQVLKHQQKIM
6795	A	325	1489	RSPTLLMHVHYIKVISWRELLLIWLRAANASINPGVEQSPSGDPKTV TGFPFLRLEAADWVEEASVPKGVHIALSSQEQRAGDPRDLEAPSNLV ISERTHRFRVSWTPPSDSVDYKVEYYPVSGGKRQEVVTPGVVDL RLPAIIPOAAWLLAHLPAAPSAPPTLPTKHTEAQSQRCSLLCSVT EVAAPSQVVKAPPSTHTGTENGYQGEESLFNKAYYGGGTNFFRKES QKLQQSAAKRDALANGALGIIELNNDYTLKKVMKPLITSNTVTDEI ERANVFKMNGKWYLF TDSRGSMTIDENKIPRNPTYKREGPLQGE QTTAQGNKRGYQMEEHSMMLDRKNQYRENGLTAQA\QPPPSGI*G YTAPCFPWENLI
6796	A	274	718	QACYIYTTEYYAAIKNDEF/TVLCRDMDEAGNHHSQQTVTTRTKNQTP HVLTHRWELNNENTWTQGEHHTPGPVMLDSAPPTLGHQTPGSSAFG LWDLHQRLRLPRPQTKGSTVGFPGSEAFKLGLGHYWLSFPPSLQTAY RGTLPPFNH
6797	A	1	870	MDEAGNHHSQQTITRTENQTMHVLTHKWELNNENVWTVQVYKESSPHK AAAAQGAGKKKGFFVNYGPGQRFKGRKVHTDQIGLALLKNEMDAKGT LSLMPEFKVRERALLEALHRFGMTEEGCIQAWFSLPHSMRIFYVHAY TSKIWNEAVSYRLETYGARVVQGDVCLDEDIDENFPNSKVVLPLV GYNIQYPKNKVGQWYHDILSRDGLQTCRFKVPTLKLNI PGYRQILK HPCNLSYQLMEDHDIDVKTGSHIDETALSLLISFDLDASCYATVCL KEIMKHDV
6798	B	328	2283	MKLEAILSKLTQEQKNQTLHVLTHRWELNNENTWTQGGEYHTLGPV DGFQKKEEAAIGAILQPLLVIQTVLGVDLQQTADLQQRGLLEEKLT NRKKIAHTVRDHIQREHNSSPAREQNWMENTFDELTVGVFRRWVINS SELKEHDLTQCKKGTMMLETIIFSKLTQEQKNQTLHVLTHKWELNN ENTWTQGGEHTLGPVWRMFQIYVVAERMLDKIPSLAFGLDLRQWF ARGCWSFGHRLKAARITAPRLAREQNWMEFEKLTTEVVFRWVITK SKLKEHALTQCKEDKNLEKKELATQQKMSSRTASEASSVFTATPHCY HYLLSSASYHISGSIRFPVLEKIRLHMGLENKCKVLLSGGSSSQMY GDLEGGWNGKVFPWSWAVQEPASPPTTLGQISLTVCCSTVNGLPAS VDVFFCREALPRNLQKFPKADLGCILLQYIDNLLLGYSTAVGCARRM DALLRHLEDGCGYKVSKKKAQICRQQTGEQTI RERWIKLSDGRIAVP QLLGAAVVLAVHKT IHLGQESLEKLLGQYFYI SHLPALAKTVAQQCV TCQQRHAKQGPSVPPGIQAYRVASFENLQVDFTEMPKCGDQGLERGS TVALVEGTPDHYPDHSYSYKGRRNPKLDSHSCVKPATAKT*
6799	A	2	472	LKAVHRTGPEFFGRQRLRHEQGRLRGRRCPPGRLPLHREALFQPSF LGMEACGIHETTFNSIMKGDVDIRKDLANTVLSGGTTMYPGIADRM QKEITALAPSTMKIKIIAPPERKYSVWIGGYILGWLSTFHQMWISKQ EYDESGPFIHVHTTCF
6800	A	1	239	QCCSGGTHGNPAIGDR\MQKQILPWAPAQMKIRFMAPPERKYSVWIA APILASLSTSSRMWISKQEYDESGPSIVHRKCF
6801	A	2	441	TGIVMDSSDGITHMPIYEGYTLPHAILPLDLAQDLTDYFMKILKE GGYSFTTTAEREIMLDIKEKLCYITLDFEQEMATAASSSSLEKS*EL LNGQVITISNQWFHCP/EYLFQPSF\FTSIMKCDVDICKDLANTVL SGGTTMY
6802	A	2	212	PGSTHASTRREITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTF QQMWISKQEYDESGPSIVHRKCF
6803	A	3	445	IVFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSF LGMESCGIHETTFNSIMKCDVDIRKDLANTVLSGGTTMYPGIADRM QKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQ EYDESG
6804	A	1	1470	MSTRPRRPPQLGRSTGRARLASRVAAAAGPPGARAPLAGDRAPAAGA

				PRRAGAGPCRDPDFPPAAGPTRGSPREGGKTGNRGKEREKGRRRAQSL AFADPPPVATRRQLTMDDDDIAALVVDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHQGMVGMGQKDSYVGDEAQSQRGILTLKYPIEHGIVITNW DDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFET FNTPAMYVAIQAMLSLYASGRTTGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVA LDFEQEMATAASSSSLEKSYELPDGQ\ VITIGNE\RFRCPALFQPS FLG\MESCG\ IHETTFNSIMKCDVDIRKDLY\ANTVLSG\G\ TMYP G\ IADRMQKEITAL\APSTMK\ IKIIAPS*RKYSVWIGGSILGL\ LS TF\ QQMW\ ISKQEYDESGPSI\ VHRKCF
6805	A	171	393	GKPKPKPKPLPKPKSREISHIP*GL*KAGPFRAPGRPGCKPCWLGPS \ GPGR*GCP*KASPEKVLGENLTLKNP
6806	A	3	264	SRRGSSPAQGSLLGRPQLLSAQYKWVGVDVSL* TMDPSLAPKTNQ RASQSKLDLQPA*APWP/PQLCGHPVPSPASCPSPTFKPT
6807	A	1	632	DHYARALELQIFKTLHYLSNLIQSIMTPLGTENPARVCRDLMDCQEQ TMVDGTYWVDPNLGCSSTIEVSCNFTHGGQTC KPITASKVEFAIS RVQMNFLHLLSSEVTQHI IHCLNMTVWQEGTGQTPAKQAVRFRAWN GQIFEAGGQFRPEVSMGCKVQDGRWHQTLFTFRTQDPQQLPIISVD NLPPASSRESSTAWEVGPACFL
6808	A	1	591	MTSVHSADDGNIWQHPLQCGDDRD LVEFNLGSPKNVGPFLAVDQKH NILLKYRCHGPP IRFTTVFSNELHYVANELNGIVGGKTQCTFPLEVY IRRLRNIRRAVRL LDRSPQTVVIRTANAQELGPEVSLFNSDWYNF QLDTILRRMFSGVGVY LDAWEMTLAHYLPHKLHPDEVIVKNQLDMF LSFVCPLET
6809	A	783	1516	RNHISSNFRETSHDFNPEILL LLGQDKVALQKLNDAA TKLQACGLV EFNLGSPKNVGPFLAVDQKH NILLKYRCHGPP IRFTTVFSNELHYVA NELNGIVGGKNTVVA IAVWSHFSTFPLEVY IRRLRNIRRAVRL LDR SPKTVVIRTANAQELGPEVSLFNSDWYNF QLDTILRRMFSGVGVY L DAWEMTLAHYLPHKLHPDEVIVKNQLDMF LSFVCPLETYPVLEGTG G IFNDLLN
6810	A	1	951	GTRQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEE HHFYFNLSVEDTNSSFTI DNQDNTAVILTNRTGFNLQEEPVFYIS ILIADNGIPSLTSTNT LTIHVCDGDSGSTQTCQYQELVLSMGFKTE V IAILICIMI FGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDD EGGGEEDTEAFDIAELRSTIMRERKTRKTTSAEIRSLYRQSLQVGP DS IFRKFILEKLEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLE SAVSDQDES DYLNELGPRFKRLACMFGSAVQSN
6811	A	122	271	FAPSDLFHYLLQLHL LILWPLQMPRQGETSGNEPQESGHLRVPGDD AS
6812	A	3	132	VWND DTQSYVLNFHGRVTQASVKNFQ IHGNDQTQRCDTILI
6813	A	3	302	GAHPASSESRGVPGARWHRGRSGRPGSQEGEAAAPSGPDWSSKSGGY PRSSGPGRWLQPREGIAGSNSGKGKQRHGTSAHWMRIHL PFELGIDF VKDIM
6814	A	2	2158	STGGQEEQEQQEEQEQQEEQEQQEEQEQQEEQEQQEEQEQQEEQE QEQQEEQEQQEAA TPSGGRNRSASSSWVGT MAGITTIEAVKRKIQLV QQQADDAEERAERLQREVEGERRAREQAEVASLNRR IQLVEELD RAQERLATALQKLEEA KADESERGMKVIENRALKDEEKME LQEIQ LEEAKHIAEEADRKYEEVARKLV IEGDLERTEERAELAESRCREMD EQIRLMDQNLKCLSA AEEKYSQKEDKYEEEIKILTDKLKEAETRAEF AERSVAKLEKTID DLEDTNSTSGDPVEKKDET PFGVSVAVGLAVFAC LFLSTLLLVLNKCGRRNKFG INRPAVLAPEDGLAMSLHFM TLGGSSL SPTEGKSGLQGH IENPQYFSDACVHHI KRRDIVLKWELGEGAFGK VFLA ECHNLLPEQDKMLVAVKALKEASESARQDFQREAE LLTMLQHQ HIVRFFGVCTEGRPLLMVFEYMRHGD LNRFLRSHGPD AKLLAGGEDV APG PLGLQLLAVASQVAAGMVYLAGLHFVHRDLATRNCLV GQGLVV KIGDFGMSRDIYSTDYRVGGRTMLPIRWMPPESILYRKFTTESDVW

				SFGVVLWEIFTYGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYA IMRGCWQREPSNATASRMCTPGCKPWPRHLLSTWMSWARGPAQGLGV VSRNTGACPOHPP
6815	A	2	186	HELKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDH ALNDMTS IASLOPT
6816	A	1	866	MMEAIIKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAM QKKLKGTEDELDKYSEALKDAQEKLELAEKKAADAEVASLNRRIQ LVEEELDRAQERLATALQKLEEAKADESERGMKVIENRALKDEEK MELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAE SKCSELEEL\KNVTNNLKS\EAQAEKYSQKEDKYEEEIKILTDKL KEAETRA\EFA\ERSVAKLEKTI\DDLEDELFAQKL\KYKAL\SEE LDHALNDMTSI
6817	A	1	639	MLSIQSTHAEKELENFFQNTEDWYFHTSHHLATWIKQKSEKDPVHLQ KGKNGPSCTKGQCNPLELVITNPLDPCWKKEERVTLGIDGAGLDPOV HILVRGEVYKHSPEPVFQTFCDELNVPVPEIPGKTRNLFLQLAWHVA QCLNVTSCYVCGRTIIGDQWPQEAQELVPTDPVPDEFLLAQKNHPDNF WVLKPSIIGQYCIAREGKEFTHPIG
6818	A	1	1710	MAVGVLQTQVRLWPRPVAYLSKQLDGVSKGWPPCLRALAAMALLAQE ADKLTGQNLNIIKAFHTVVTLMNTKGHHWLTNARLTKYQSLLENPR IITDVCNTLNPATLLPVSESLVKHNCVDMLDVYSSRPDLRDQPWAS ADWELYMDGSNFINPHGERCAGYAVVTLNVAIEAKPLPQGTSAQKAE LIALTRALELSEVHGALYKEKGLNSRGKDIKYQOEILQLEAVWKP QKVAVMHCGRGHQRASTSVAGNSQTDSEARKAASTPYCASVAAPLLP QTPDLVPTYSKKEKDFHTEVGQVIKEGWIRLPDGKVAVPQLLRATV VLAMHETTLGQESLEKLLGRYFYISHLPALAKAVAQCIQAYGAAPF EGLQVDFTEMPKCEGNKYLLVLVCTYSGWVEAYPTQTEKAYEVRVL LRDLIPRFGPLRIGSHNGPVFVADLDCVEINVDIGVIWATWIKNEK DPVQLQKGKSGPSCTKGQCNPLELVITNPLDPRWKKGERVTLGINGA GLDPRVNILVRGEVYKHSPEPVLTQTFYDELNVPVPEIPGKTRNLFLQ LAKHVA
6819	A	764	1203	FWLWVSFWVPCNTHTSKSTSFSSPSTQATRFVGL/WFVIKASIIQ YCIARERKEFTHPVGRLSCLRQKLYNGTTETVTSWSSNHTERNPF FPKLRTVWTHPESHQDWTAPTGLYWICGHRFAKLDPDESAGIGGPKQ GAIGIKE
6820	A	24	225	ARQAQAWFWAWRAACLWFYFLVVS*NRY*VSNN\KNNIRRLSSL NSSCKF/WSTRQK*IPKMLS
6821	A	1	1752	MLSIQSTHAEKELENFFQNTEDWYFHTSHHLSSLRFFSARESNCSMK LYEEAYMERYRDFLPATMWSAHEVDVPGQATWIKQKSEKDPVHLQK GKNGPSCTKGQCNPLELVITNPLDPCWKKEERVTLGIDGAGLDPOVH ILVRGEVYKHSPEPVFQTFCDELNVPVPEIPGKTRNLFLQLAWHVAQ CLNVTSCYVCGRTIIGDQWPQEAQELVPTDPVPDEFLLAQKNHPDNF VLKPSIIGQYCIAREGKEFTHPVGRLSCLGQKLYNGTTETVTVWSSN HIERNPFSKFPKLQTVWTHPESHQDWTAPTGLYWICGHRAYAKLPDH WAGSCVIGTIKPSFFQLPIKTGELLGFPVYASRKKRSIAIENWKDDE WPPERIIQYYPVTAQDGLWGYQTPYVLNRIIRLQAALBIITDK ISRALTILAWQETQMRNAISONRLALDYLLAAEGGVYGFNLNCCCL HVDDQGVVEDIVRDRTKLAHPVQVWHEFDPGAMFGKWF PALGGFK TLIIGVLIVIGTCLLLPCLLPVLLQMIKSFIATLVHQNASAQVYYVN HYQSIAQKDISSKNKSENSH
6822	A	110	203	GTPNSANTQGNSTPNPQVIFPCRAYLKIRL
6823	A	76	353	FFSLSSVSLPLAKIIPVNGQIHVCSETPSHFVQVRRKLGSVIKSK LYLWWWSCLSNIIKLHSLLRGFFKKSQNLHVEYGRVSHESSNNGP
6824	B	64	930	MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQERAAE YIAQARRQYHFESNQRCTNMVLSMLPTLREALMQQLNSESLTALLK NRPSNKLIEWEDLKIIISFTRSTVAVYSTCMLVLLRVQLNIIIGYIY LDNAAVGKNGTTILAPPDVQQYLSSIQHLLGDGLTELITVIKQAVQ

				KVLGSVSLKHSLSLLDLEQKLKEIRNLVEQHKSSSWINKDGSKPLLC HYMPDEETPLAVQACGLSPRDITTIKLFHKTEDMLGSPDFRQFLNT CFKPRF*
6825	A	385	666	LSANPVWSTLYIHRDKTNTSTCSFFSCLSLSRPCLAYCSFSLHFFCV HTCSAAHPHWQWRYHDHEGGFPRARLIHRTPDMLTPAIFPNVGNSTA
6826	A	701	930	VAERQTGTGQGTVDITDRATSM*MRQRRGCCFATCC/FRHEGVVPV WQGRYHDHEGGFPRARLIHCTPDVLTYPYHVP
6827	A	248	719	TDEPSLLSHTFCPKGALLSACSGACPLSSGTOAGMPPSTEALQPCRG LTVPHQQDKGHRACC/VWKALAADWSVEWQKGRRGLGKALSVTSR/I RATSM*MRQRRGCCFATCC/FRHEGVVPVWERGYHDHEGGFPRARLI HCTPDVLTPAISPNNVGNSTA
6828	A	1	2489	MTVPELAGETEHCQCLINNVLMYGQPYRVLTLELELPESPVNQDLGMF LVTISCYTRGGRIISTSSRSCNVYNSGQRRKLLLFKTFSRKVVVVVP NEEDWKKRLELRKEVEGDDVPESIMLEMKAPVPSQAPAPAEALVQV KVEAIVISDEETDVSDEQPQGPERRAFPSGGAVYGAQPSQPEAFEDPG AAGLEEVGPSDHFLPTDPLPHYLLPGAGQYHRLVTSPLPAPASLH EPLYLSSEYEAAAGPSFGVFTEDVPTCKTCGKTFSCSYTLRRHATVHT RERPYECRYCLRSYTSQGDLYRHIRKAHNEDLAKRSKPDPEVGPLLG VGLFTEIGPMSCFISRHDIVIQDDDEIRLKIVGTRVDKNDILHLLH FPVPQEPWATVMEKRLQEAQLYKEEGNQRYREGKYRDAISLEHILL HPRYFGPNLLNTVKQKLFTEVEGTCTGKYGFVIAVTTIDNIGAGVIQ PGRGFVLYPVKYKAIVFRPFKGEVVDVAVVTQVNKFQDPCAGYAGSLA DSCLADRCLWDRHLHAQPRLGTVPTFDWFFGYDEVQGLLLPLLQEAQA ASPLRVLDVGCCTSSLCTGLYTKSPHPVDVLGVDFSPVAVAHMNSLL EGGPGQTPLCPGHPASSLHFMHADAQNLGAVASSGSFQLLLDKGTWD AVARGARGPAPELRLARGRPGRSPADPALSGSTDRELEWNRDYSSG GKDQAPANGDCVGAATLFPQAFLSPFISHEMGSELKKKLFKRRRVLN RERRLRHRVVGAVIDQGLITRHHLLKCRANHQLLHPMARGGVQVAEQL GTQGLNLGPDITLLSRPWSTTLQYLPYCGPR
6829	A	227	548	FHNKCPRRLES LRQQISIFGMPENHLLKMQILRSAPDSLDFPCAGPL HLGEELLLHRVEQVGAEEVARVQQDFVL*GDMVEHLPRPGRQAESTPP TVPGNPPETLRRR
6830	A	3	435	FQVSKDRYGGQPLFSEKFPTLWSGARSTYGVTKGKVCFEAKVTQNL MKEGCTEVSLLRVGSVDFSRPQLGEDEFSGYGFDRGLKAENGQFEB FGQTFGENDVIGCFANFETEEVELSFSKNGEDLGVAFWISKDSLADR LS
6831	A	37	360	VFPVDSQGLPEVWTLPAYLVWEDVLPCEQSGSWRQGLGGKEEQQAP ARDSPCRPITCQRLAWSPSHFSPQISLEHEILLHPRYFGPNLLNTVK QKLFTEVEGTCTGK
6832	A	280	1816	KPRFPRKIHATSVGHAVLPGVPLFSDSSLWPPVCLRLNREDTEIQIS GLQGAGPGLVRAGAAILRPEGGRDHIEENAGCLGAAILREALYGLR DVGAAMLVRPSWNGSGGRSHLRYKIGSSRGEDEFSGYGFDRGLKAE NGQFEFEGQTFGENDVIGCFANFETEEVELSFSKNGEDLGVAFWISK DSLADRALLPHVLCCKNCVVELNFGQKEPFFPPPEEFVFIHAVPVEE RVRTAVPPKTIIECEVILMVGLPGSGKTQWALKYAKENPEKRYNVLG AETVLNQMRPRSNTVKVHCRPPMKANCSRLSVDCLSSVVKWSIKSVT DSTAAEPCCKTSAPGVSSSEKALHFRQLQRVLFEELELLGRTGLRSNVLL PNDLQDWACTSHQSHKRPSDSAAYFVSLCTSRCSFSSFTLMGDQ CTVSHVSTGTHPSSTTATRSCGQPAHAEEVRGEWVNEQKEHSGSRRO ISLEHEILLHPRYFGPNLLNTVKQKLLHRGGRPGTGKYGLC
6833	A	3	251	GGALRLHQVPPALPLRGAVSGAAAVQGMSDCTPCCEVHLLQD*VPAG EARVQWHDGLSLQPPPPRFKRFSCILPSSWDYRH
6834	A	3	251	GGALRLHQVPPALPLRGAVSGAAAVQGMSDCTPCCEVHLLQD*VPAG EARVQWHDGLSLQPPPPRFKRFSCILPSSWDYRH
6835	A	2	340	SFTLVAQAGVQWHDGLSLQPPPPRLKQFSCFNLPSWDYRCPPRLA NFCIFNRDGFHHVQAGLKLTTSSDPPTSASQSARTTGMSHHTRPSI

				FFFKRWGLTMLPRLVSN
6836	A	220	412	LQTFWAVAVGSSRYLCFHVPFVCLEFVAVISLPKNHLLQSLDGEHSP ARHPVLAVLPVPIPSFW
6837	A	425	619	LCFHLHFVCLFEFVEVISLPKNDLLQRLDALVAEEHLLTVDARVYSYAL ALKHANAKPFEVPFLKF
6838	A	1	684	MESQEPTESSQNGKQYIISEELISEGKWVLEKTTYMDPTGKARTWE SVKRTTRKEQTRDGVAVIPVLQRTLHYECIVLVKQFRPP\MGGYCIE SPA\GL\IDDGETPRKQLLSRELEETGLQRGPLPEC/SLPAVCMGP QACPNT\IHIVTV/TPINGDDAENARPKP/KSPGDGEFVE\VISLP \KNDLLQRLDALVAEEHPHSGTPRVYS\YALAL\KHANAKP\FEVPF LKF
6839	A	3	194	EMESHYVAQSGKLKLLSSSKAPTALFQSAWITDLNHDTPWALLFIKE HILDFKSKPRNYLNKS
6840	A	1	168	PLSEDQRTALQEVYTLAEHRRTVAEAKKKIEQQGGFTFENKGVLSAF NFGTVPSNN
6841	A	3	191	RIFHIVENDLYIDFGGKFHVCRRPEVDGESPISWYAVWRRFSQVMI TCFSSNSDFGKHKR
6842	B	15	377	MAALCRTRAVAESHFLRVFLFRPFRGVGTESGSESGSSNAKEPKT RAGGFASAYGAARRSFYRRWSPYRKVEPGRGSPKKCGILCIYAETIL PLTTDGTQLTKLVHWTGSPFIVENDL*
6843	A	2	205	TFLRRWGFTILPRLFNSWAQEICLPWPPACLGITGMSHCAQSSWLF KNNFKFLWFQARADHKPSHS
6844	A	1260	1628	SFLCLVSCFSNFS*NCSRPFVSLSLKDFVFLPCDGVLLCHPGWIA VAQSRLTTASTRI\KRFSCLTIRSSWDYRRPPPCPADFCIFSR/DR GFTMLARLVWNS*PQVICPPPPPKVLGLQA
6845	A	3	629	NSTTIMSRHSLVSIIEEGLDMVNRETAHEREMQTAMQISQSWDESLS LSDSDFDKPEKLYSPKRIDFTPVSPAPSPTRGFGKMFREQQWIATKS SSQSKTDFQAGEVRVQVKIKTQVFLGPLKKKKVKWRPESQPQETLS KGTNMLSPDAAQLSDLSSCSIDLGSSSSSGLSSDPLAKGSATAES PVACSNSSCSFILMDDLSPK
6846	A	15	241	ILNVLTTTKNDKYVRFLTTVDPHRKSFSSFKMCSCPMGSSCPLHKKI SSWRPWQNSFQIQEKSGREKQICKFCS
6847	A	93	172	DRVSQCCLGWCQTPRLKRSSGPHPP
6848	A	3	82	KGREGVHQIRREKRRWERRERERGS
6849	A	2	237	GTRVLLSEGWRQKYCLNPGGRGCNELRSHHCTQAWATEQDCVSKKP NQTKTKIHEQVDLPSSNHCCSKGSIVYYFHW
6850	A	407	529	YLPVMKTGAKKLSILATFKSKLVNSPRDWLGWFLGSCGNS
6851	A	2	383	DFADFGTTIKQDFRLLGQTSVDRLLQLSQQAVKGNQLLPVSLFVTL FVGVRGFSILLSAEVFKHDSAVWYLDGSIGVLI GLTIFAYGVKEFM STELGQLDQLWKFDQLPKGHSMVNFTRGPNDGR
6852	A	1	444	AAAVHSAHREYIACVILGVIFLLSSICIVVKAHDLSTRLLPEVDDF LFSVLSILSGILCSILAVLKFMLGKVLTSRALITDGFNSLVGGVMGFS ILLSAEVFKHDSAVWYLDGSIGVLI GLTIFAYGVKLLIDMVPRVQT RHYEMFE
6853	A	1	279	RWIAADAANALLPANRAMAYLKIQKYEEAEKDCTQAILLDGYSKAF ARRGTARTFLGKLNEAKQDFETVLLLTWEIRQAVTELSKIKKGIN
6854	A	3	991	LEEFPAKKDYERVELEPNNFATNELRKISQALASKENSYPKEADI VIKSTEGERKQIEAQNKQQAISEKDRGNFFKEGKYERAIECYTRG IAADGANALLPANRAMAYLKIQKYEEAEKDCTQAILLDGYSKAFAR RGTARTFLGKLNEAKQDFETVLLLEPGNKQAVTELSKIKKKPLKKVI IEETGNLIQTIDVPDSTTAAAPENNPINLANVIAATGTTSKNSSQD DLFPTSDTPRAKVLKIEEVSdTSSLQPQASLKQDVCQSYSEKMPIEI EQKPAQFATTVLPPIPANSFQLESDFRQLKSSPDMLYQYLKQIEPSL
6855	A	1	318	DIVMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFALTISSLPQDDFATYYCQHRGAF

				GQGTKVEIKRAA
6856	A	1	397	VPAQLLGLLLWLPGAKCDIQMTQSPSTLSASVGDRVTITCRASQSI SSWLAWYQKPGKAPKLLIYKASSLESQVPSRFSGSGSGTEFTLTIS SLQPDDEFATYYCQYNSYSRITFGQGTRLEIKRTVAAP
6857	A	15	95	SVTSIEERTRPILSKTLKGILHKGIIY
6858	A	3	350	GRHTLGENIADNGGLKAAAYRAYQNWVKNGAEHSLPTLGLTKKKEKR NSCHLPQDPNPLSEHRHPPHGWAWLPGPVQSSSALSEAAAAQSPPGQ RTAPAPRMPLASAVQPPGVLY
6859	A	118	325	PSREKEKFLQDITDAEKYFIGLIYHREEKRWRWINNSVFNGKYVNMP QFPDGLGLLQKTKPEIAGFTLE
6860	A	1	135	PRVRCHYDAGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEENQ
6861	A	1009	1140	RQGLPLVAQDGLLELSSNPPTLASQSAEITRHEPLCPNLSRMT
6862	A	3	416	HASETLFISNDKKVVGCLIAEHQWGYRVEEKLPIRSEEEKVRF ERQKAWCCSTLPEPAICGISRIWVFSMMRRKKIASRMIECLRSNFIY GSYLSKEEIAFSDPTPDGKLFATQYCGTGQFLVYNFINGQNST
6863	A	4	252	NSSLRKLYPNSGKAQFLLNHTLVPGLCIGLLLVNLLLLPGNVDTWL PGVQRPWHLGGFELDRSLETASRSSGCRESQKGR
6864	A	3	130	TTTALGLLTPII IHPIDRSVDFLLDSSLRKLYPTVKGPPSS
6865	A	1	1590	MVTVTQCSVRPQWPESEVGIMAPVYISEREAQRGYANEVGEAFRSLV PAAVVWLSYGVASSYVLADAIDKGKKAGEVPSPEAGRSARVTVAVVD TFVWQALASVAIPGFTINRVCAASLYVLGTATRWPLAVRKWTTTALG LLTIPII IHPIDRDHPLSSDESGLSSQVGGFPPGLQPAQALPNSGE AQLLLIILWYLACASACFMSTSYSCQGMWTPGSLVSKDPGTWLREV ERWEHRAEADLGPSQPCPKHQISSHQDPGPIPCSPVPAIPGYEVFTA PFKAYGFIQLVRGLLEAHEDKAAKSQGVPGFRFGGEELGCLGWKEGCL VNGKNFHSFVFPQEVPRLELSFQAFSFTGTTPADVPSDATKKACSFH RGTHGWYTCTLSHVNMVVLGNGGCHPVSSPLLVHFLPLLHVHFLPLL VYLLPLLGRFLPRLVYLLPLLHVHFLPPLMHFLPLLHVHFLALLAHFLP LLVHFLALLAHFLPLLVYFLPLLVYFLPLLHVHFLPLLAHFLPLQALP SLSLLYMEVFPVH
6866	A	1	595	GTRRLAPTAQRKRDENQSVKPEPGRGASVRGGNLTLPAGGDFLTCP SARDFRRVPAQQTQVPAETAPEVPAVAVAGARGGRVMSEPQPRGAE RDLYRDTWVRYLGYANE\ VGEAFRSLVPAVVWLSYGVASSYVLADA IDKGKE/ELERCPALEASRSARVTVAVVDTFVWQALASVAIPGFTIN RVCAASLYVLGT
6867	A	2	453	GGDCSGASTGCSGRGRGGRVMSEPQPRGAERDLYRDTWVRYLSYANE VGEAFRSLVPAVVWLSYGVASSYVLADAIDKGKKAGEDGGFPPGLQ PAQALPNRWGSPAPPDHTLVPGLCIGLLLVNLLLLPGNVDTWLPGV QRPWQPGWV
6868	A	1	265	EEGKAGAAGGGGSGGAGSREQPSSHNCGGGVRESGRDSSPPSSPP RLRGASAHRRDPFPRFLRLLSPLLGDGPTRPPPCAAAALRS
6869	A	46	194	KDHAAFFTIPKRWRQPSPSIDWRNIMWSSHTVEYYTAMKRNKQLY SQ
6870	A	4	228	DRFCVAEAEVQRYDHSSVQKPRPPMLKLSSCLSLPSNWDYEITGAPP HPANFLTFCRDKGLTLCCPGWSQTRGLQ
6871	A	1	288	ALIYWQRKISIWPAITQVAIQYLSCPMCSWQSECIFTKNSHFHPRQI MSLDFDNIEQLMFLKMNKLVNNDYSTLVLSWDPEQNEVVQSSEKEI LP
6872	A	1	885	MDDFLQKLQKIKIGVVGGSDFEKVQEQLGNDAFKQSDRSSYCPSP SPPHLPITETESPAQDPEKPERLIDPFTGESDLIGLYLQSYSLYDVN DDDASATRVMRQTRYDSVLLLEIVSYKIGVHQEDELLECLSPATS RTFRIEEIPLDQVIDKENEMLVTVAHFHKEVFGTFGIPFLRIHQF KIAIVMDRHQYINEDEYEVNLKDFEPQPVCSAKETGLSAQLCSTMQ VEVAARTGRNRAAQMLGQGMPLPGWRSVTHKSQRINTENAGPQCHE KHKRLTNRLHLP

6873	A	532	687	GVPGLLCGLTCFSSSPPGNMSHPRPWLGLDHFNKAPKRSRYTYLEKA IKIHN
6874	B	158	3331	PRPPAAGEAQAAADMNHQQQQQQKAGEQQLSEPEDMEMEAGDITDDP PRITQNPVINGNVALSDGHNTAEEDMEDDTSWRSEATFQFTVERFSR LSESVLSPPCFVRNLPWKIMVMRPFYPDRPHQKSVGFFLQCNAESDS TSWSCHAQAVLKIINYRDEKSFSSRISHLFFHKENDWGFSNFMWS EVTDPKGFIDDDKVTFEVQADAPHGVAWDSKKHTGYVGLKNQGA TCYMNSSLQTLFFFTNQLRKAVYMMPTGDDSSKSVPLALQRFVYELQ HSDKPVGTTKLTKSFGWETLDSFMQHDVQELCRVLLDNVENKMGTC VEGTIPKLFGRKMVSYIQCKEVDYRSDRREDYDIQLSIKGGKNIFE SFVDYVAVEQLDGDNKYDAGEHGLQEAEGVKFLTLPPVLHLQLMRF MYDPQTDQNIKINDRFEFPEQLPLDEFLOKTDPKDPANYILHAVLVH SGDNHGGHYVYVLYNPKGDGKWKCFDDDVVSRCTKEEAIEHNYGGHDD DLSVRHCTNAYMLVYIRESKLEVLQAVTDHDI PQQLVERLQEEKRI EAQKRKERQEAHLYMQVQIVAEDQFCGHQGNMDEEKVKYTVFKVL KNSSLAEFVQSLSQTMGFPQDQIRLWPMQARSNGTKRPAMLNDEADG NKTMIELSDNENPWTIFLETVDPELAASGATLPKFDKDHVMLFLKM YDPKTRSLNYCGHIYTPISCKIRDLLPVMCDRAGFIQDTSLLIYEEV KPNLTERIQDYDVS LDKALDELMDGDIIVFQKDDPENDNSELPTAKE YFRDLYHRVDVIFCDKTI PNDPGFVVTL SNRMNYFQVAKTVAQRLNT DPMLLQFFKSQGYRDGPGNPLRHNYEGTLRDLLQFFKPRQPKLYYQ QLKMKITDFENRRSFKCIWLNSQFREEEITLYPDKHGCVRDLLIECK KAVELGEKASGKLRLLEIVSYKIIGVHQEDELLECLSPATSRTFRIE EIPLDQVDIDKENEMLVTVAHFHKEVFGTFGIPVFAEDTPGRAFSRS DEANPEPAGHQEGVLRSLNLQL*
6875	A	589	732	GWDPRLRPHNFLPRWTCTQSSISPQYNICEQMVTSDDLLRFIFQLAR S
6876	A	1	799	GRLNVKLLYNSSVEQIWIITVLQCRDL SWPSSYGDTPTVSIKGIITLP KPVHFKSSAKEGSNAIEFMETVFVFAIKLQNLQTVRLGFKIQQTQPRK KTIGECMSLRTLSTQEMDYSLDITPPSKI SVCHAELELGTCFQAVN SRIQLQILEARYLPSSSTPLTSLFFVKVGMFSSGELIYKKKTRLLKA SNGRVKWGETMIFPLIQSEKEIVFLIKLYSRSSVRKHFVGGIWISE DSNNIEAVNQWKETVINPEKVIRWHKLNPS
6877	A	2	470	PRVRPRVRS LAALLVLI LRGNELRSLHGLKQLRNLRLHLDLAYNLLG HRELSPLWLLAELRKLYLEGNPLWFHLEHRAATAQYLS PRARDAATG FLLDGKVLSTDFQHTSLGLSPMGPPLPWPVGSTPETSGGPDLSDS LSSGGVVTQPLGAGQ
6878	A	3	204	GEQACTHTWGARTHMRPHMCTHTHTGTCTHAHARTHMHYTHMCTHA WLGRHLRLVMNAPFSLVHS
6879	A	367	551	EHSTLKLPHYTQEAGAAPGPTGTDSHEVDHLEGGAGKEAGPCA*SLG TMVAPVRSNSGSPE
6880	A	24	547	VLSFSFVYTFGNIILRIVHRLNQTAGTMAPKWLQAMVQRDHWREP WRLLSLHVPAHLGADLPTLVTRVYISLYASHQLTLLRGPLLSWFLY PSGNVYKFQTSRFAILWHKHLDDACKSNRPQEAGAAPGPTGTDSH EVDHLEGGAGKEAGPCALKAWAPMVAPSQEQW
6881	A	1	828	MKDWRPRRKKWPGPGPGPHCCPEPRDLVSYILAAPAMAKRGQGRAR VVVSEGAAWQLPHGVEPVGAQKSRTKLNTVQEFHNAITSINSRINQ AEERISELENWLSEIRQSDKNKEKRIKRNEQNLQEVGDYVKKPNLQI TVIPERKGEKANLENVYQYIVHENFHNLAREDNWSIQEIQTTPARF YTGRSSPRHIIVRFSKDPDSLEGDLHRLRINLLWHSATHKYRLHLGF SSVGLLAASDEGLFKGFHGGPLTLTLGFKLVNRFDPGIYT
6882	A	2	270	NMPTKLQKLDLSSYPEATEKNVERILGLLQTYFRKYPDTPVSYFEFV IDPNSFSRTVENIFYVSFIVRDGFARIRLDEDRLPNIRADEC
6883	A	2	114	KGLLDVTCKTVANMIKGTPEEIRKTFNIKNDFFPSFL
6884	B	75	293	MPSIKLQSSDGEIFEVDVEIAQSVTIKTMLEDLGMDDEGDDDPVPL PNVNAAILKKVIQWCTHHKDDPPSS*

6885	A	446	639	NGYLVFPRKNSFLLIFGLFVYLETNLDSLPLVDTHSKRTLLIKTVET RDGQVINETSQHHDDLE
6886	A	3	1503	ARQRRSRAPTTHTHRALVRLFSGSQSAPPPPPRSPSPSAAMSTRSVS SSSYRRMFGPGTASRPSSSRSYVTTSTRYSLGSALRPSTSRSLYA SSPGGVYATRSSAVRLRSSVPGVRLQLQDSVDFSLADAINTEFNTRT NEKVELQELNDRFANYIDKVRFLQEQNKILLAELEQLKGQGSRLGD LYEEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQ REEAENTLQSFQDQVDNASLARLDLERKVESLQEEIAFLKKLHEEEI QELQAQIQEQHVQIDVDVSKPDLTASLRDVRQQYESVAA\KNLQEA EWYKCQVC*PLLRASNRN\NEPLRQAK\QES\TELPENRVQSLTC\B VDAL*RKPMSSLER\QLREMEENFC/AVKAANYPRPLLARL\QDEIQ NY*RREMASLTFVEYQ*PALNVKMAP*HLRFATLQE/MLLGRRGERG FPLASFNFSLP*TLRGNLIWDSLPSGLIPHSKRDT
6887	A	3	232	FEAESYSVTQAGVQWHDLSLQPPPPRIKQLSYLSLQSSCDYRHLPP CPANFCIFSRNGASPCWPCWSRTPARWIH
6888	A	252	384	DSWSEQVIKPPFQRGSCPIPRRKECCSERPRRIWTRPCVVFS
6889	A	3	196	LIMICFSFFLLSVLENKNSGPYLFQRFQFSSVVKVRVHRLSKRLRPR LTSYITFRVFCFLTP
6890	A	1	2994	MAQVAMSTLPVEDEESSESRMVVTFMLSALESCKELAKSKAEVACI AVYETDVFVVGTERGRAFVNTRKDFQKDFVKYCVEEEEKAAEMHKMK STTQANRMSVDAVEIETLRKTVEDYFCFCYKALGKSTVVPVPEYK LRDQSAVVVQGLPEGVAFKHPENYDLATLKWILENKAGISFIIKRP LEPKKHVGGVRVMTDADRSILSPGGSCGPIKVKTEPTEDSGISLEMA AVTVKEESEDPDYQYNIQAGPSETDDVDEKQPLSKPLQGSHHSE NEGTEMEVPAEDSTQHVPSSETSEDPEVEVTIEDDDYSPPSKRPKANE LPQPPVPEPANAGKRKVRREFNFEKWNARITDLRKQVEELFERKYAQA IKAKGPVTIPYPLFQSHVEDLYVEGLPEGIPFRFPSTYGIPLRLERIL LAKERIRFVIKKHELLNSTREDLQDKPASGVKEEWYARITKLKRMV DQLFCKKFAEALGSTEAKAVPYQKFEAHPNDLYVEGLPENIPFRSPS WYGIPLREKIIQVGNRIKFVIKRPPELLTHSTTEVTQPRNTNTPVKEDW NVRITKLKQVEEIIFNLFKAQALGLTEAVKVPYPVFESNPEFLYVEG LPEGIPFRSPTWFGIPRLERIVRGSNKIKFVVKKPELVISYLPFGMA SKINTKALQSPKPRSPGNSKVPPEIEVTVEGPNMNPQTSAVRTPT QTNGSNVFPKPRGREFSFEAWNAKITDLKQKVENLFNEKCGEALGLK QAVKVPFALFESFPEDFYVEGLPEGVPFRFPSTFGIPRLEKILRNKA KIKFIIKKPEMFETAIKESTSSKSPPRKINSSPNVNTTASGVEDLNI IQVTIPDDDNERLSKVEKARQLREQVNDLFSRKFGAIGMGFPVKVP YRKITINPGCVVVDGMPGVSFKAPSYLEISSMRRILDSAEFIKFTV IRPFPGLVINNLVDQSESEGPVQIESAEPSSQLEVPATEEIKETDGS SQIKQEPDPTW
6891	A	75	350	TGIPVNSYRVKINWYTLQFVSLFRFPFGLVINNLQADQSESEGPVQ ESAEPSQL\EVPATEEIKETDGSSQIKQEPDPTWETSFLGGEISF
6892	A	1	2935	MAQVAMSTLPVEDEESSESRMVVTFMLSALESCKELAKSKAEVACI AVYETDVFVVGTERGRAFVNTRKDFQKDFVKYCVEEEEKAAEMHKMK STTQANRMSVDAVEIETLRKTVEDYFCFCYKALGKSTVVPVPEYK LRDQSAVVVQGLPEGVAFKHPENYDLATLKWILENKAGISFIIKRP LEPKKHVGGVRVMTDADRSILSPGGSCGPIKVKTEPTEDSGISLEMA AVTVKEESEDPDYQYNIQGSHHSENEGTEMEVPAEDSTQHVPS TSEDPEVEVTIEDDDYSPPSKRPKANLPQPPVPEPANAGKRKVR NFEKWNARITDLRKQVEELFERKYAQAIAKAKGPVTIPYPLFQSHVED LYVEGLPEGIPFRFPSTYGIPLRLERILLAKERIRFVIKKHELLNST EDLQDKPASGVKEEWYARITKLKRMVDQLFCKKFAEALGSTEAKAV PYQKFEAHPNDLYVEGLPENIPFRSPSWYGIPLREKIIQVGNRIKFV IKRPPELLTHSTTEVTQPRNTNTPVKEDWNVRITKLKQVEEIIFNLFKA QALGLTEAVKVPYPVFESNPEFLYVEGLPEGIPFRSPTWFGIPRLER IVRGSNKIKFVVKKPELVISYLPFGMASKINTKALQSPKPRSPGNS

10545

				SKVPEIEVTVEGPNNNNPQTSAVRTPTQTNGSNVPFKPRGREFSFEAWNAKITDLKQKVENLNFNEKCGEALGLKQAVKVPFALFESFPEDFYVEGLPEGVPFRRPSTFGIPRLEKILRNKAKIKFIIKKPEMFETAIKESTSSKSPPRKINSSPNVNTTASGVEDLNIIQVTIPDDDNERLSKVEKARQLREQVNDLFSRKFGAIGMGFPVKVPYRKITINPGCVVVDGMPPGV SFKAPSYLEISSMRRLD SAEFIKFTVIRFPFGLVINNQLVDQSESEGPV IQESAEP SQLEV PATEEIKETDGSSQIKQEPDPTW
6893	A	214	301	LIGTVLFLLEIKETDGSSQIKQEPDPTW
6894	A	1	2879	MAQVAMSTLPVEDEESSES RMVVTFLMSALES MCKELAKSKAEVACI AVYETDV FVVGTERGRAFVNTRKDFQKDFVKYCV EEEEEKAAEMHKMK STTQANRMSVDAVEIETLRKTVEDYFCFCYKALGKSTVVPVPEKM LRDQSAVVVQGLPEGVAFKHPENYDLATLKWIGENKGGISFIIKRPF LEPKKHVGGRMVMTDADRSILSPGSGCGPIKVKTEPTEDSGISLEMA AVTVKEESED PDYYQYNIQGS HHSSEGNEGTEMEVPAEDDDYSPPSK RPKANELPQPPVPEPANAGKRKVREFNF EKWNARITDLRKQVEELFE RKYAQAIAKAGPVTIPYPLFQSHVEDLYVEGLPEGIPFRRPSTYGP RLERILLAKERIRFVIKHELLNSTREDLQLDKPASGVKEEWYARIT KLKRMVDQLFCKKFAEALGSTEAKAVPYQKFEAHPNDLYVEGLPENI PFRSPSWYGIPRLEKIIQVGNRIKFVIKRPPELLTHSTTEVTQPRNT PVKEDWNVRITKLKQVEEIFNLKFAQALGLTEAVKVPYPVFESNPE FLYVEGLPEGIPFRSPTWFGIPRLERIVHGSNKIKFVVKKPELVISY LPPGMASKINTKALQSPKRPRSPGSGNSKVPEIEVTVEGPNNNNPQTS AVRTPTQTNGSNVPFKPRGREFSFEAWNAKITDLKQKVENLNFNEKCG EALGLKQAVKVPFALFESFPEDFYVEGLPEGVPFRRPSTFGIPRLEK ILRNKAKIKFIIKKPEMFETAIKESTSSKSPPRKINSSPNVNTTASG VEDLNIIQVTIPDDDNERL\SKVEKASQL/REDQVNDLFSRKFGA I\GMGFPVKVPYRKITINPGCVVVDG\MPPGV SFKAPSYLEISSMRRLD SAEFIKFTVIRFPFGLVINNQLVDQSESKGPV IQESAEP SQLEV PATEEIKETDGSSQIKQEPDPTW
6895	A	1	334	PTRPPTRPPTRLFSPLVKDWAPKAFIISFKLETDP AIVINRARKAL EIIYQHVGGANILESRSQSFVFI VTKDSETKLLLSEEEIEKGVEIEEK IVDNLQSRHTAFIGDRN
6896	A	3	444	VIVHARPIRTRASKYIPEAVYGLPAYPAYAGGGGVLSGATLHRLA GACAQVELFPIDDVFLGMCLQRLRLTPEPHPAFRTFGIPQPSAAPHL STFDPCFYREL VVHGLSAADIWLMWRL LHGPHGPPCAHPLPVAAGP FQWDS
6897	A	117	1009	REPGAFSVLFKEPQAIINYFSSLMQQRVQEKGETAEVNEENRIQSTE KKNLAQKNDKPGTPGVKRSSHLSLSVLGLRTRSTSRRI PAFKADGR EQGGDIPTFYTYEGLSHLTAEGQATLERLEGMLSQSVSSQYNMAG VRTEDSIRDYEGGWSPGPRETC DPCRRENFSPEGKSALRDPAPLPS SATDPERSYRMILETAHFRNHGWFRGGTSILISHTGSEVRGEEQLAG SRSFEGAEPETNTFCPSQGLPLVAIVGGGPAHSHHTLNHGATGALDD GPFCQGPLDRPLREI
6898	A	5	808	LPLPGRAVWCTHCCAPTSPGPVLP HSAAMSFLKSFP PPGPAEGLLRQ QPDTEAVLNGKGLGTGTLYIAESRLSWLDGSGLGFSLEYPTISLHAL SRDRSDCLGEHLVVMVNAKFEEESKEPVADEEEEDSDDDVEPITEFR FVPSDKSALEAMFTAMCECQALHPDPEDESDDDYDGEEDYVEAHEQG QGDIPTFYTYEGLSHLTAEG\QATLERLEGMLSQSVSS\QYNMAG\ VRT\EDSIRDY\EDGDGRLD TTP\TVCLGQF\EDADV
6899	B	233	411	XALNGLSAQDNWAKLQRDYPDALITNYLWPAVQLANFYLVPLHYRE DPASTTLVSDPT*
6900	A	109	435	HGKPFWRDYSFIPRMGTINREAITQLFTFFLCAEVGVGPGKTVSLGS GGGAAIQPLHLQLWPAVQLANFYLVPLHYRYVAPLPHPSRKTHVT NSWRQND SHFNLELP
6901	A	34	408	RQWLQEEAYITKEQKYSFLHDSQTSFCFSDSIPTSSNMEETQQ/KSN LELLHISLLN\QSRLEPVRFLRSTFTNNLVYDNSDSDDYQLLKDLE

				GGIQMLMGRLEAATN*LGGPQANYNKFDKTRTT
6902	B	80	495	XPGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLFDHAMLQAHRAHQ LAIDTYQEFEETYIPKDQKYSFLHDSQTSFCFSDSIPTPSNMEETQQ KSNLELLRISLLIESWLEPVRFLRSMFATTWCMPRTAMTITS*
6903	A	1	597	MAAGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLPFKEAMLQAHRAH QLAIDTYQEFISSWGMDSIPTSSNMEETQQKSNLELLHISLLLIESR LEPVRFLRSTFTNNLVYDTSDDYHLLKDLEEGIQMLMGRLEDGSH LTGQTLKQTYSKFDTNSHNDALLKNYGLLHCFRKMDDKVETFLRMV QCRSVEGSCGF
6904	A	3	552	QTSFCFSDSIPTSSNMEETQQKSNLELLHISLLLIESRLEPVRFLRS TFTNNLVYDTSDDYHLLKDLEEGIQMLMGVRVAPGVNPGSPLAS RAGGEKHCCPLFSSQALTQENSPYSSFPPLVNPPGLSLHPEGEGGKWI NERGRELGPSAGPLLLFLHFAEAGRRQPPDWADPQADLQVQ
6905	A	3	716	DPKAQLPEPLRVLWTAHLAAMATGSRTSLLLAFGLLCLPWLQEGSAF PTIPLSRFPDNAMLRHRLHQLAFDITYQEFEETAYIPKEQKYSFLQNP QTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRS VFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQT YSKFDTNSHNDALLKNYGLLYCFRKMDDKVETFLRIVQCRSVEGSC GF
6906	A	359	648	WIPRPNSPNHSGSCGQAHVAMAPGSRT\ SLLLAFALLCLPWASRRL GAVPKPFRISRLF\ DHA\ MLQAHRAHQLAI\ DTYQEFEET\ YIPKDQ KYSFLA*\ POTSFCFSDSIPT\ PSN\ RRI\ TQKSNLELLRI\ SLLL\ TESWLEPVRFPQEYCSANNLGVLTPTAIDYHLLKDLEGHPTV*WN ICREVCFSACFSRGIRDDIEEEDDQEAYFRYMAENPTAGVVQEEEEED NLEYDS DGNPIAPT KKI IDPLPPIDHSEVDQHGLRPEGTHLTLKERT SWVESVADTLCTILTTLVMDPKAQLPEPLRVLWGTSPSGNGSRLEPDV PCSWLLPCSACPLQGGWVPCQNRSVYPGFFDHAIA PPSRAPAGHC TPTRSLKKPHIPKDQKYSFLA
6907	A	113	412	GSSQGA KPQDRGWGPRTLWTPVFFMRGPQHATCLLWQAGRVEAFCK FHMWPQGMTSLMKAALDLTYPITSMFSGAGFNSSIFS VF KDQQIEVH PHPRK
6908	A	3	1162	GGGARGCAHVVLKALAECCIRVDMVGGTSIGAFVGALYSEERNYSQ MRIRAKQWAEGMTSLMKAALDLTYPITSMFSGAGFNSSIFS VKDQQ IEDLWIPYFAITTDITASAMRVHTDGLWRYVRASMSLSGYMPLCD PKDGHLLMDGGYINNLPADVARS MGAKVVAIDVGSRD ETDLTNYGD ALSGWWLLWKRWNP LKVKVNLMAEIQTRLAYVCCVRQLEVVKSKD YWEYL RPPIDSYSTLDFGKFNEICEVGYQHGRVTFDIWGRSGVLEKM LRDQQGPSKKPASAVLTCPNASFTDLAEIVSRIEPAK PAMVDDSDY QTEYEEELLDVPRDAYAD FQSTSAQQGSDLEDESSLRHRHPSLAFPK LSEGSSDQDG
6909	A	2	265	RLMQCVSSFSKNGALQARLEICALRDTVAVYLTPEKSSFKQALEAL PQLSSGADKLLLEELLNKVKSSMHLQLNCFQAASSTMMKT
6910	A	3	151	ILPLPLQONATVEAGTRCQVAGWGRKWSQGRVALVTGASWGPLGAEKS AT
6911	B	58	359	SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLISTKVQ DKLLLSACHLLVSLATTVRPVFLISIPAVQKVFN RITDASALRLVDK RMSSSGP*
6912	A	4	329	SSRPATAWGHGLLLLPPAPALPSTWKS RGV AHADQAHVAHGAE L PRT AHD SATFSPFQPRRDVTLELLWHFCQAS PAPIALRSLLFVRDLQRLT FLLFSHHSIVILRN
6913	A	2	257	YEDALVLLLTEVLNRIQFRYNQAQLEELDD ETDLDDDVQDKLLLSACH LLVSLATTVRPVFLISIPAVQKVFN RITDASALRLVDK
6914	A	1	350	AQVLVCRALSNILLPWPNL PENEQWPVRSINHASLISALSRDYRN LKPSAVAPQRKMPLDDRHLNITAENDCRR LHCSLRDLS SLLQAVGR LABYFIGDVFAARFNDALTVEE
6915	A	257	2659	VDCRMS/FSYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFKY

				TFHQPTHEGYFSCLDIWTFLDYLTSKIKSRLGDKEAVLNRYEDALV LLLTEVLNRIQFRYNQAQ\LEEL\DDETLDDDDQQTTEWQRYLRQSLEV VAKVMELLPTHAFSTLFPVLQDNL\EVYLGGLQQFIVTSGSGHRLNIT AENDCRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR\FNDALTVVE RLVKVTLYGSQIKLYNIETAVPSVLKPDLDIVHAQSLAGGCRLSAHW LAQYCSEIHRQNTQQFVTLISTTMDAITPLISTKVQDKLLLSACHLL VSLATTVPVFLISIPAVQKVFNRTDASALRLVDKAQVLVCRALSN ILLPLPWNLPENEQWPVRSINHASLISALSRYRNLK\PSAGAPQR KMPLDDTKLIHQTLQRLRKILWENISG\ESTKSSTDFAYQFGCRES V\QVSLGLFPAP\IHQSDVTDEMLSFFLTFLRGLRVQMGVFP\TEQI IQTFNLMPFREQLAESILHEGSTGCRVVEKFLKILQVVVQEPGQVFK PFLPSIIALCMEQVYPIIAERPSPDVKA\ELFELLFRTLHNNWRYFF KSTVLASVQRGIA\EEQMENEPQFSAIMQAFQGSFLQPDHILFKQNL F\YL\ETLNTKQKL\YHKK\IFR\TAM\LFQFVNVLLQ\VL\VKSH DLL\QE\EIGHRHSYNMASVDF\DGFFAAFLPEFL\TSC\DGV\ DAN QKSVLGRNF\KMDRVRRERGRAKRAEWARKPGTCAARRGHIEASGR GLCPPCSLAAAHEMPADLVL
6916	A	1	321	NSKIMELLQVVPSCVASLDDVAETDRKEYVTVKIRKKWRQSVTLRQN NLPAQSGSHAAEKGNSDWPERPGLTQTGPGHRRMLRRHTVEDAVVSQ GPEAAGPLSTPQE
6917	A	1	259	HGASINASNNGNTALHEAVIEKHVFFVVELLLLHGASVQVLNKRQRT AVDCAEQNSKIMELLQVVPSCVASLDDVAETDRKEYVTG
6918	B	1	3045	MPDCTSKCRSLKHALDVLVSVTKGSENQIKAFLLSHCYNAATIKDVF GRNALHLVSSCGKKGVLDWLIQKGVDLLVKDKESGWTALHRSIFYGH IDCVWSLLKHGVSPLYIQDKEGLSALDLVMKDRPTHVVFKN TGCLLDP NGEKCVTAPRQVSALHHKDIALSLVAASDGATVCVTTTRGDIYLLADY QCKKMASKQLNLKKVLVSGGHMEYKVDPEHLKENGGOQKICILAMDGA GRVFCWRSVNSSLKQCRWAYPRQVFISDIALNRNEILFVTQDGEGR GRWFEEKRKSSEKKEILSNLHNSSSDVSYSVDINSVYERIRLEKLT AHRVSVSTDPGSCNFALQSDPKTSLYEIPAVSSSSFFEEFGKLLR EADEMDSIHDVTFQVGNRLFPAHKYILAVHSDFFQKLFLSDGNTSEF TDIYQKDEDSAGCHLFVVEKVHPDMFEYLLQFIYTDTCDFLTHGFKP RIHLNKNPEEYQGTLSHLNKNVNFHEDDNQKSAFEVYKSNQAQTVSE RQKSKPKSCKKGNIREDDPVRMLQTVAKKFDNLSRLDGVRFEN EKINVIKNTGNKLSQKKWYNVYKEKVMVFFLFLESQNVDFICS VLVADQLLITRLKEICEVALTEKLTAKNAAMLEFAAMYSQKQLK SCLQFIGNMAALLEARSLDVLSDGVLDLSEFYRKMI PAMDRRVT PYQDGPDISYLEVEDGDI FLKEEINMEQNHSETMFKAKTKAKKKPR KRSDDSSGGYNLSDIIQSPSSTGLLKSGKTNVSVESLPELLTSDSEGS YAGVGSPRDLQSPDFTTGFSKIEAKVKPYVNGTSPVYSREDLKPWE KSPILKISAPQPIPSNRIDTSSASWVAGSFSPVSPVVDLRTIMEI EESRQKCGATPKSHLGKTVSHGVKLSQKQRMIALTTKENNSGMNSM ETVLFTPSKAPKPVNAWASSLSHVSSKSFDRFLLEBKSVTSHSSGD HVKKVSFKGIENSQAPKIVSFVGGERR*
6919	A	1	1149	GETMFKKAKTKAKKKPRKRSDDSSGGYNLSDIIQSPSSTGLLKSGKTN SVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFSKIEAKVKPY VNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTSSASWVAGS FSPVSPVVDLRTIMEIEESRQKCGATPKSHLGKTVSHGVKLSQKQ RMIALTTKENNSGMNSMETVLFTPSKAPKPVNAWASSLSRVSSKSF DFLLEBKSVTSLSSGDHVKKVSFKGIENSQAPKIVRCSTHGTPGPE GNHISDLPLLDSPNPWLSSSVTAPSMVAPVTFASIVEEELQQEAALI RSREKPLALIIEHAIQDLLVFYEAFGNPEEFVIVERTPQGPLAVP MWNKHGC
6920	A	426	2967	HSAPPAVLRRGGMSEAGGAGPGGCGAGAGAGAGPGALPPQPAALPPAP PQGSPCAAAAGGSGACGPATAVAAAGTAEGPGGGGSARIAVKKAQLR SAPRAKKLEKLGVSACKAEESCKCNGWKNPNPSPTPPRADLQOIIV

				SLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFCTVHK EEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKPPFEKPSIEQG VNNFVQYKFSLPAKERQTIVELAKMFLNRINYWHLEAPSQRRLRSP NDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLRLSVFTV MRRQLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIW DQDFLSASSRTSQLGIQTVINPPPVAGTISYNSTSSSLEQPNAGSSS PACKASSGLEANPGEKRMKTDShVLEEAKKPRVMGDI PMELINEVMS TITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNLSNQK PNKKILMWLVGLQNVFSLHQLPRMPKEYITRLVFDPKHKTALIKDGR VIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH D\ILNFLTyaDEYAIGYFKKQG\YCKEIKIPITKYGGYIKDYEGATL MGCE\LNPR\IPYT\EFSVIIKKA/EIGIKKLIERKQAQIPKKFTL GLSCFKDQVRQIPIESIPGIKKA\GWNPSGKEKSKEPRDPD\QLYST \LKSILQQVKSHQSAWAFMEPVKRTAPGYEYEVIRFPMDLKTMSERL KNRYVSKKLFMADLQRVFTNCKEYNAAESEYYKCANILEKFFFSKI KEAGLIDK
6921	A	1	184	GKEKSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTAPGYEY EVIRFPMGNTINIF
6922	A	114	384	FWHEYTKAFFFFFFSMCFLFLGSLCIYYFSLFLVFFFLFLFCLVFC CLHCFRYFFTPLDSPRAGSRWSSYAQLLPPPPPLVEHSCDC
6923	A	141	1741	WEPAQFPPEQQWAGWGHRSRCQQLGTPWQGRWGLRAEPPPGLVYPCGA CRSEVNDQDAILCEASCQKWFHRECTGMTESAYGLLTTEASAVWAC DLCLKTKETIQSVYIREGMGQLVAANDGPSVAHYTPCVLQLSAPLFP LPGLIEGKLEKAQSPIPHFLHDKRIQSLPVETLGPASRMDPESERL QAPHSPSKTDGKELAGTMDGEGTLFQTESPQSGSILTEETEVKGTLE GDVCGVEPPGPGDTPVQGDLOETTIVTGLGPDTPDLEGQSPQSLPS NPKAVNYAKGAGKGRVRAGAAATAAPDSRRPRAGAAKGVGQGLFQL LVNPMNIYEEQKIMFLYSLVPSTQDPLFPYGPQCPVDLAGPPCLRP LFGGLGGYWRALQREGRTMTSRASELSPGRSVTAGIIIVGDEILK APCMKSNALIVILGTVTLDVAVGIGLVMPVLPGLLRDIVHSDSIASH YGVLLALYALMQFLCAPVLGALSDFRGRPVLLASLLGATIDYAIMA TTPVLWIYPLVNSPSC
6924	A	1	153	RECTGMTESAYGLLTTEASAVWACDLCLKTKETIQSVYIREGMGQLVA ANDG
6925	A	1	200	IDNYGTPKGNIFLCVFLTLGAALTAFIKADLRRQKANKETLENKLOE EEEESENTSKVPTAVSEDHL
6926	A	2	242	WIKDTNLKPATIKILKDDIGNTLLDNLGKDFMTKNPKANATKTKVA KENNAVKHWVEHTLLTYRRDRARSASLVDFSLP
6927	A	132	251	VPAGEARVQWHDGLSLQPPPPRFRKRFSCILPSSWDYRH
6928	A	132	251	VPAGEARVQWHDGLSLQPPPPRFRKRFSCILPSSWDYRH
6929	A	2231	2578	PLPPGSRTLHWMAPDEEDFRIGN*TMNAIFFFLFLFFFFFLRQSF ALVVQAGVQWHDLSLQPPPPRFRK*FSCSLPSGWD*RHAPPRPAIF VFLVEMGFHHVNQDGLDLLTW
6930	A	2	94	WRDLGSL*PPPPGFKRFS*LSLKSHPNVTS
6931	A	130	295	GIISNADFVSFFFF*DGVFALVAQAGVQWRGLGSLQPLPPGFKRF\S CLSLPSTW
6932	A	3	403	TYKILDFIVNSIRHRRGTPRFPGHTEVTSMTLDFIGAG*/SNLQ*PA ST*PGDQY*I*LLQST*NYVLHKFQLPTWKGRSEISEQAVSAKEKT* KS/T*LALVK*ARTLESNWP/L*ILILISLSMIWTNDNLNLF
6933	C	78	335	MWSPLTKEIFSCPTPQTCGAFKGTALKRAPXXXXXXXXXVKIGXXXXXX XXXXXXXXXVSPRLSARVLAPCLGCDFFVSFNRTTVWK*
6934	A	1	143	GFRWFSCGLPSCWDYRHAPHPANFCIFSDRVSPCWGWSQTPDLE
6935	A	1	1676	MALKGQEDYIYLFKDSHPVDFLDAFRTFYLDGLFTDITLQCPSGII FHCHRAVLAACSNYFKAMFTADMKEKFNKIKLSGIIHDI LEGLVNY AYTSQIEITKRNVSLEAADLLQFLSVKACERFLVRHLIDNCIG MHSFAEFHVCPELEKESRRILCSKPFKEVWQEEFLEISLEKFLFILS

				RKNLSVWKEBAIIEPVIKWTAHDVENRIECLYNLLSYINIDIDPVYL KTALGLQRSCLLTENKIRSLIYNALNPMHKEISQRSTATMYIIGGYY WHPLSEVHIWDPLTNVWIIQGAIEIPDYTRESYGVTCGLPNIIYVTGGYR TDNIEALDTVWIYNSESEDEWTEGLPMLNARYYHCAVTLGGCVYALGG YRKGAPEEAIEFYDPLKEKWIPIANMIKGVGNATACVLHDVYIYVIGG HCGYRGSCYDKVQSYNSDINEWSLITSSPHPEYGLCSVPFENKLYL VGGQTTITECYDPEQNEWREIAPMMERRMECGAVIMNGCIYVTGGYS YSKGTYLQSIKDYDPLNKNWEIVGNLPSAMRSHGCVCVYNV
6936	A	1	161	YILLVFLTLWLLIEMIYCYRKVSKAEAAQENASDYLAIPSENKENS AVPVEE
6937	A	61	742	RLKRKSKKATKQSLQDSFLDLKSPPSFPVEISDRLPAASWEGQESC WNKQTSKSEGTQEGTYGEQLVPELCNQSESSGEDFFLKSKLQEQDV WRRSTSFYTHMCNPWGLLVGAGGSLIMFVIQWVYTLVNMGVAAIVY FYIGRASPLHLGSASNFSFRWMRSLLLPSCRSRLSPQEQIILAPS LAKVDMEMTQLTQENADFATRDRYHSSLVNREQLMPHY
6938	A	7	238	PGGSQGVPAAGRGSGRWSSALPGPLPRPGSVGSPTLLATWLPAGPGR GPARGTVRKTPIPPPRCWVPGPPWFLSQTG
6939	A	1	213	RNTDNAWIETAGGTVHLQDQNDGELNRLNSNLHTCEWRASIPWQGGD RRIFLYANHKTLLHMAAABIGANY
6940	A	1	257	RRSFALVAQAGQWRNLSSPQPPPLGFEQFSCLSLSSSWDYRHVPPR PANFVFLVEMGFLYVVQAGNPPALASQSAEITGTSHHA
6941	A	3	279	GSGWDGRGQSGRVADSS*ARVLSAL\REVNK\RLQDLRSLSPKPPQ GQEQQGEDEVVLVEGPTLPETPRLFPKIRCRADLVRLPLRMVSA
6942	A	73	816	FLGFVGPVSLHCLRPVSCFYRDLDNSPLSPSPRTKSRTHTRALKK LSEVNKRLQDLRSLSPKPPQGEQGEDEVVLEEGPTLPETPRLF PLKIRCRADLVRLPLRMSEPLQSVVDHMAHLGVSPSRILLFGETE LSPTATPRTLKLGVAIDICVVLTSPEATETSQQLQLRVQGEKHQ TLEVSLSRDSPKLTLMSHYEEAMGLSGRKLSFFFDGTKLSGRELPAD LGMESGDLEIENVG
6943	A	1	484	MEPTQMPINQMDKETILKLLKGKVVVGHALHNDFQALKYVHPRSQT RDTTYVPNLFSEPLHTRARVSLKDLALQLLHKKIQVGQGHGSSVED ATTAMELYRLVEVQWEQQEARSWTCPEDREPDSSTDMEQYMEDQYW PDDL AHGSRGGAREAQDRN
6944	A	1	1758	MDFQLKKKQVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLEREL ESLRIQQRQNCQPTNVSEYNAAALMELLREKEERILALEADMTKWE QKYLEENVMRHFALDAAATVAAQRSIFEGHILYVHNLIVRERSHFIW DTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHA QIIEKDAMIKVQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLS HSSTLTGSPIMEEKRDDKSWKSLGILLGGDYRAEYVPSTPSPVPPS TPLLSAHSKTGSRDCSTQTERGTESNKTAAPVAPISVPAPVAAAATAA AITATAATITTTMVAAAPVAVAAAAAPAAAAAPSPATAAATAAVSP AAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAPVPAPALVPVP APAAAQASAPAQTAQTSAPAVAPTAPPTPTPAVAQAEVPASPATGP GPHRLSIPSLTCNPDKTGNEREYADFYSHFDIANDLVYICSLLYLQS PEECLMQTMFLRPETQMRDPARSLLFQTRAQKLVTQLRQCDGKRAVI KNHTTPEPECLELYLLYLHLQAV
6945	A	1	1420	QLQAACEKREQLEHRLRTRLERELESLRIQQRQNCQPTNVSEYNAA ALMELLREKEERILALEADMTKWEQKYLEENVMRHFALDAAATVAAQ RDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLH AQIIEKDAMIKVQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLL SHSSTLTGSPIMEEKRDDKSWKSLGILLGGDYRAEYVPSTPSPVPP STPLLSAHSKTGSRDCSTQTERGTESNKTAAPVAPISVPAPVAAAATA AAITATAATITTTMVAAAPVAVAAAAAPAAAAAPSPATAAATAAVS PAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAPVPAPALVPV PAPAAAQASAPAQTAQTSAPAVAPTAPPTPTPAVAQAEVPASPATG GPHRLSIPSLTCNPDKTGDPVFSNTLERKTPIQILGQEPDAEMVE

				YLI
6946	A	186	209	QLWPN*LLSRNKEATLRYSQLPTCHSICY*MPAF*HTISDLSFNKNI NCKSYHLRVFYKYV*IVCHF*VPKVYWTXYQTSCRT*WR*SGVE*P PIISSSSSACCLLRRLPTEGTCPEIFWNPRLGISAECRDS CGPTSF
6947	A	2	2948	CLWRKWSVALGCRYFFGLLRGARIQLLPSGAFSCLRVSLSPSPPGT PLSTMRKGLRATAARCGLGLGYLLQMLVLPALALLSASGTGSAAQDD DFFHELPETFPSPDPPEPLPHFLIEPEEAYIVKNKPVNLYCKASPATQ IYFKCNSEWVHQDHIVDERVDETSGLIVREVSI EISRQQVEELFGP EDYWCQCVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEV LLQCRPPEGIPVAEVEWLKNEDIIDPVEDRNFYITIDHNLI IKQARL SDTANYTCVAKNIVAKRKSTTATVIVYVNGGWSTWTEWSVCNSRCGR GYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC PVDGRWTPWSKW STCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQTAP DSDDVALYVGIVIAVIVCLAISVVVALFVYRKNHRDFESDIIDSSAL NGGFQPVNIKAARQDLLAVPPDLTSAAMYRGVPVYALHDVSDKIPMT NSPILDPLPNLKIKVYNTSGAVSPQDDLSEFTSKLSPQMTQSLLENE ALSLKNQSLARQTDPSCTAFGSFNSLGGHLIVPNSGVSLLIPAGAIP QGRVYEMYVTVHRKETMRPPMDDSQTLTTPVSCGPPGALLTRPVVL TMHHCADPNTEDWKILLKNQAAQGWEDVVVGEENFTTPCYIKLDA EACHILTENLSTYALVGHSTTKAAAKRLKLAIFGPLCCSSLEYSIRV YCLDDTQDALKEILHLERQTGGQLLEPKALHFKGSTHNLRLSIHDI AHS LWKSKLLAKYQEIPFYHVWSGSQRNHCTFTLERFSLNTELVLC KLCVRQVEGEGQIFQLNCTVSEETGIDPLLPDANTITTVTGPSAF SIPLPPIRQKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPT GVILDLWEAQNFDPDGNLSMLAAVLEEMGRHETVVS LAABEQY
6948	A	1	616	MREVEEDSPHESPLVLVSDWDVGI VTLWPCLLGSFLHHVTTRGYRRL SFVLEKAAAFQDVVVVGEENFTTPCYIQLDAEACHILTENLSTYALV GHSTTKAAAKRLKLAIFGPLCCSSLEYSIRVYCLDDTQDALKKLVGP QLSRHSAEIPNLGFQKISGQVPSVGKRLSRQQADEELLIIGGLAVPS TLAEYLLVCPADAPQPC
6949	A	1	1913	EPSIGEFNEQVLRMLHSLGIDQQKTIESLQNKSYNHFAAIYFLLVER LKSHRSSFPVEQRLDGRQRRPSTIAEQTVAKAQTVGLPVTMHSPNMR LLRSALLPQASNVFAFSFPASGCQAEAAFMEEECVDTPKVNGCLLDP VPPVLVRKGCQSLPSNMETS IDEGLETEGEAEEDPAHAFAEFQSTR SGQRRHTLSEVTNQLVVM PGAGKIFSMNDSPSLDSVDSEYDMG SVQR DLNFLEDNPSLKDIMLANQPSPRMTSPFISLRPTNPAMQALSSQKRE VHNRSPVSFREGRRASDTSLTQGIVAFRQHLQNLARTKGILELNKVQ LLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVSTLPASV HPQLSPRQSLETQYLQHLRQKPSLLSKAQNTCQLYCKEPPRSLEQQ QEHRLQQRKRLFLQKQSLQAYFNQMQUIAESSYPQPSQQLPLPRQETP PPSQQAPPFSLTQPLSPVLEPSSEQM QYSPFLSQYQEMQLQPLPSTS GPRAAPPLPTQLQQQPPPPPPPPPPRQPGAAPAPLQFSYQTCELPS AASPADYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL SELPGLFDCEMLDAVDPQHNGYVLVN
6950	A	3	185	EFFGDPSPASSRRYPGGLGDIGRLPPAPPPRPQPLVTAKPPFLLPKS RRRKLQCQLEGCS
6951	A	112	569	KVTLGSTACGRWNSKMAPQGLPLPPAVNMPCINIISGTGTQRDFIYL FYFYFLRWSFTLVAQAGVQWRDLASLQPPPPGFKQFSCLSLSNCWDY RNAPPRPANFVEMGLHVGQAGLKLLTSGDPPTSALQNAGITGMSHH AQPCGLGYFIS
6952	A	1	1210	NHITKGTSHGWDEDTSPCKVYHAGSTTSPSTACNRLAGKCSCSWAR EGGAGDKSEAQSGQTSVGGSTALRCSSSEGAPKPVYNWVRLGTFTPT SPGSMVQDEVSGQLILTNLSTSSGTYRCVATNQMGASCELTL SVT EPSQGRVAGALIGVLLGVLLLSVAAFCLVRFOKERGKKPKETYGGSD LRCEAKEERKRDIMQNI VQILES VQLKWELFQSWTDFSRHLHLSNKLA IFGIGYNTRWKEDIRYHYAEISSQVPLGKRLREYFNSEKPEGRIIMT

				RVQKMNWKNVYKFLITISEARCLELHMEIDWIPIAHSKPTGGNVV QYLLPGGIPKSPGLYAIGYEECIERPLSPHMSDKFPGTQGKEGRVDL GNPFSTSLIYRWEIGHTHPNYLLLPDC
6953	A	75	333	HCAVSSSLPLSLSCVHTRTTRTHTRYAHIMQVRAHTHIWFPCLLR QQKGVPSSPSSFTSQGALGPQVPKTQPOAWHALAFPGF
6954	A	271	512	GAVGRPRSQQKSIGVPGWVSPGF*ECGKRRMTFVLLKHIMLLFPARF QQIMRNIPRRLAEHMQQLFSSCPSLMRAFEVT
6955	A	2	184	FCSEPRSCHCTPAWATRACLCLKNKNKQTKNALKEEKGDNNIATTSK VLPGPSNPNTALS
6956	A	13	163	LQVSSSTYSRADPRVRQVALGDPLLPASLPPIAQPTGLLQAVATGSSR KGK
6957	A	627	849	WECPSVFTTMIPTCSLLASAVAFSVSSNLCPGWSAVVQSRLTVALTS WAQAISPLQPFPTDPVAPRSEHLASP
6958	A	3	144	FPTIYFAPSGDKKNPVKFEGGDRDLEHLSKFIEEHATKLSRTKEEL
6959	A	1	2008	PAAADARRPRAPATMRPRKAFLLLLLLGLVQLLAVAGAEGPDEDSS NRENAIEDEEEEEEDDDDEEDDLEVKEENGVLVLNDANFDNFVADK DTVLLEFYAPWCGHCKQFAPEYKIANILKDKDPPIPAKIDATSAS VLASRFVDVSGYPTIKILKKQAVDYEGSRTQEEIVAKVREVSQPDWT PPPEVTLVLTKEFDEVNDADIILVEFYAPWCGHCKKLAPYEKAA KELSKRSPPIPLAKVDATAETDLAKRFDVSGYPTLKI FRKGRPYDYN GPREKYGIVDYMIEQSGPPSKEILTLKQVQFLKDGDDV I IIGVFKG ESDPAYQQYQDAANNLREDYKFHHTFSTEIAKFLKVSQGLVVMQPE KFQSKYEPRSHMDVQGSTQDSA IKDFVLKYALPLVGHKVSNDKR YTRRPLVVVYYSVDFSF\DYRAATQFWRSKVLEVA\KDFPEYTFIAIA DEEDYAGEVKDLGLSESGEDVNAAILDESGKKFAMEPEEFDSDTLR\ ELVTAFKKGKLKPKVKSQP\VPKNNKGP\VKVVVGRTFDSIVMDPKK \DVLIE\FYAP\WCGHCKQLEP\VYNLA\KKYKGQGLVIAKMEAP \ANDVPQRPAPRVEGFPT\IYFRPPVGDKKOPS/VKFEGGD\RDLEP FEPSFIEEHA\TKLSRT\KEEL
6960	B	137	214	ASQFPIEWRPVKDAATVDSEPALPQQ*
6961	A	1	625	PSLKGQKLELRGAAALELVDPGCRSGLVHARGCTYSQLSRSHPF CCSRGPLAMAGILFEDIFDVKIDIRKAKKF\DRV\SRHCESESFKM DLILDVTIQIYPVDLGDKFR\LVIASTLYEDGTLDGEYNPTDDRPS RADQFEYVMYGK\YVRIEGD\ETSTEAAATR\LSAYVS\YGGLL\MRL QGDANN\HGFEVDSRVYLLMKKLAF
6962	A	1	273	AAAARAGTPGRVCAAQEVPLSPHNRPLQPLPPPPPPPPYSGSGPG LRRATLTSFIPVKAQWLPDPVVSNSVSPVKQSRSLGSRHH
6963	A	135	233	PRDLCSRVYLLTFSPLLSYDPDTPSPRNTPE
6964	C	198	449	MGPSPAFYKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXSPNRFSGLGCLGSFFRIPPDW
6965	A	1	1278	MGDFNTPLSTLDRSTRQKVNKDTQELNSAQHQVDLIDIYRTVHPKST EYTFFSAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSDHSAIKLE LRIKNPTQSCSTTWKLNLLNDYVWHNEMKAEIKMFFETNENKDTT YQNLWDAFKAVCRGKFIALNAHKRKQERSKDTLTSQLKELEKQEQT HSKASRRQEITKIRAEKIEVTQKTLQKINESRSWFFERINKIDRPL ARLTKKKREKNQTDAIKNDKGDITDPTIEIOTTIREYKHLIYANKLE NLEEMDKFLDTYTLPRLNQEEVESLNRPIITGAEIVAIINSPLTKRVQ DQMDSQPNSTRENKIPRNPTYKGCEGPLQGELOTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQGKPPASAEVIAEERGFRETQDEYRG AAP
6966	A	1	325	KTFEEEEFFQTNRSVAQAGVQWRDLGSLQPLPPGFQRFSCSLLS WDYRRRLPRANFCIFRGFRHVQAGLELLTPGDPPASASQSAGITG VSHRAGLFHSVFIF
6967	A	525	661	TEILSGSLGSEIPTTSES*RPGLGPSFVIFLSSSVCLNIFFRVL
6968	A	1	293	MAGTPPPALLPPCSLISDCCANNQRDSVGVGPSEPGAGYNLVRSFL SPSEKRSVRVGVTRLFQGRPSPLSLTQKGNP\LTPCASQFTSTISDG

				RIMV
6969	A	1	1372	MKSPFPLVSTKAEWGTWIFNPEABESLEPRSLISDCCANNQRDSVGV GPSEPGAGYNLVVRSFSLSPSEKRSVRVGVTRLRRCRPSPLSLTQKGN PLTPCASQVRQCLALLRLRHVYFYNFGWKDYGVASLTITLDMVKVMT FALQEGKVAIHCHAGLGRTGVLIACYLVFATRMTADQAIIFVRAKRP NSIQTRGQLLCEAQSGAFSADVSGSHSPGEPVSPSFANVHKDPNPA HQQVSHCQCKTHGVGSPGSRVQNSRTPRSPLDGSSPKAQFLVEHET QDSKDLSEAASHSALQSELSAEARRILAAKALANLNESEVEKEELKRK VEMWQKELNSRDGAWERICGERDPFILCSLMWSWEQLKEPVITKED VDMLVDRRADAEEALFLEKGGHQTILCVLHCIVNLQTIPVDVBEAF LAHAIKAFITKVNFDSENGPTVYNTLKKIFKHPL
6970	A	2	277	KNEMTLDAYIFLADMAAYQEEQMQLPRADAIRSLIDTFSLEIHLQ GLSQAVPRHTIRELLGQQPISSLI*I*DSYPHPLHLRVENSGEV
6971	A	434	564	ETTFYNEQGRGPQPHLPEVKKKYRGN*EAKTK*LRPENWKGDI
6972	A	197	1247	ALVRLDSWMGLNTTANLGGGEMTEARGVTPWICPRSSAERARSGIPA AMVPISVKISGPQLLIGPNPPGSTKRWARNSSCSSEHCR/SQGAQEE SCLAQHH/TPSAPSQMT*TPNC*CAGAPLAÄVHR\GITQRCQMNEVQ VAHMPPTLP*ETGDHNAELSGAPAIYLPQGAQHSPVH*DQLL*FPIS *TY*EPTKLQDLLRTKSPGGTPQLFCFAH/ALPAVPAQVVLGLLQIM SGSPQSLRAPSLQSLQQLTRLLGMSLVHLHNLAQVLEDPQQLVAPP/T /DYQGCFLGSKLWLPTQLSN/VCSAPSSAAFLAAGSLDPRPPGFV VPSPPLPGGGGSPAAALELFAPAPPPT
6973	A	232	476	IFVSSYYHVNLFRRFT*AHSSSH*TNPQDLYPYQHGNKVKDIPGTL PENRKVG*PLKKDLQDENKQDKPSCHLQGLQWP
6974	A	442	698	DVNEWHQLGEAASALLVGKRPCLSPGSLRPLSPDFTLPPPAQAPPEP GYPYAGRAQGRPLPASLRPISRPARPPGFGSPRDPALAP
6975	B	546	1820	LLNCPFCYGLTSVLHVTCFFSHHGYDTSKDNAGKQQPKDEIDAA EDATDFRHLDPVLKQCIPMIQASQPADSAVPATSGKVYGTPELTQ PTNIEAAPLAEEHASSATSITECDKLSSFATSAEDQSVASLTAPQ TEETGKSSLLDVTSTIPSSRTEATQGLDYVPSAEDKGFKSPPCEDF SVTGESEKRGIEIGKGLSGERAVEEEEEETAHVEMSEKLCSEQYGTVP FSAPGHALHPGEPALGEAEERRLSRDDSTVKMASPAPSGPPSGTHTP FHESPVEEKSEPQDFQEADSWGDTQRTTSVGKRAAEELRCLVTRGR SIRGLSLPPACTRAERREVERVVVDALSGKGLAGRYRLSEMTEA EQQLIDDHFLFDKPVSPLLTAAGMARDWPDARGIWHNNEKSFLIWN N*
6976	A	2	480	YFLAETGFHAGQAGLELPNSGDLASVSQSAGITGVSHRARPRHLY FFNFNEQILFYLVNVIIFNSLFPTIPFIIFCWAQGYWKPIHCFTCLPS SSVPALQTLVTSYVPLGYTEAFLATQNIQGRVSLWAKHGHPDPFPLAR ADFRAQESPSPPNDPSWLL
6977	A	1	2043	MVSISRPHDPPASASQSAGITGVSHRLRFYFDHQDVAPECCGAYFFHE LAKEKRKGVERLLKMQNQRGGPAVFQDILKPGQDEWGKTEAMEAAM APGKNLNQSLDLHALGSAPTDPHLCDFLSHFRDEEVTFMPRKSAD LHAAGEAASLGGVSLNVMKGASLHALCLRLNLSFGPGVATLCGERVV HKNNRASALRKCIFWPVSLNSSRARPRQRTTAGGAVPTAALQRVIPA SSQCLFPAPMGTTTEATLRMENVDVKEEWQDEDLRPLPEETGVLELLG SPVEDTSSPPNTLNFNGAHRKRKTLVAPEINISLDQSEGSLLSDDFL DTPDDLDINVDDIETPDETDLSLEFLGNGNELEWEDDTPVATAKNMPG DSADLFGDGTTEGSAANGRLWRTVIIIGEQEHRIDLHMRPYMKVVT HGGYYGEGLNAIIVFAACFLPDSSLPDYHYIMENFLPPGQQTTPGP VGLTQPAAGVEAGRVGTAGVLTLDPSMLGPCLLCPVSRYVISSLELL VAEDYMIYVLNGATPRRRMPGIGWLKKCYQMLDRRLRKNLKSIIIVH PSWFIRTVLAISRPFISVKFINKIQYVHSLEDLQIPMEHVQIPDC VLHQRQIILTTLCAYGEGEALASHLFHVILPFIHSCFPSSTETSDP PCGPGDLAYTTPFSTHFAQRGK
6978	A	1259	1497	DYRHLPLLLANFVFLVEMGFHHIGQAGLKLPTSGDPPASASQIARIT

				GVSHRARQVLFIFVSPDSSTRMEAWDVLCEGC
6979	A	2	425	SKNDPPDHPILSSLSILFFYHQGTIVKGSFLISVVRIPRIIVMYMQN ALKEQHGAISRYLFRCCYCCFWGLDKYLLHLNQNAITTTAINGTDFC TSAKDAFKILSKNSSHFTSINCFGDFIIFLRKGLRVCFGTGFGRTQCF
6980	B	259	329	XPRKKEQQIKQCKGTAGQALIKE*
6981	A	1	1251	MFVFETLGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILAC QQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTIVKGSFL ISVVRIPRIIVMYMQNALKEQRQSWEIPGVCEEERGRKGEGLNESVY QHGAISRYLFRCCYCCFWGLDKYLLHLNQVRLYLLPQEHTEGSKGGG GGSQSPAPAGERTMHCLGAEYLNAYTTTAINGTDFCTSAKDAFKILS KNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAV PLLLVAFAYLVAHSFLSVFETVLDALFLCFAVDLENDGSSEKPYF MDQEFLVSKHFISNCNLHARNLESFVKLHTRKRLIPSLSLLEGSEAS TTPGPESGICAELSKAEPTSLSENLLPEEVKLNKNADQMDS
6982	A	1	421	AINGTDFCTSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFT VFGGLMAFNYNRAQVWAVPLLLVAFAYLVAHSFLSVFETVLDALF LCFAVDLENDGSSEKPYFMDQEFLSVFKRSNKLNNARATAGTSTH
6983	C	120	371	MSAHSHPCTCINGHTPVSIYXXXXXGGPFKRTLGGPKFNGGGQGKI FFFMGGLEKPSLGFLKLNLFXXXXTYGATPPPKFKP*
6984	A	76	251	ALKFCRGVFFIFSPPPQKKFLFQNSPGGFFFPPLKEKNFSFPP*KSSS PPKPLNFVGGFFFPFPPP/NKKFLFQNSPGGFFFPPLKEKNFSFPPP VKFGPPQGSF*TPPP
6985	C	193	315	MGGQLKPSLGFLKLNLFPGGEKNGHXXXXKFKPLGXXXXF*
6986	C	363	413	MKVICGVILPKQGGNSA
6987	A	1	1088	YKLVCIYTSWSQYREGDGSCFPDALDRFLCTHIIYSFANISNDHIDT WEWNDVTLYGMLNTLNNTNPNLKTLLSVGGWNFGSQRFSKIASNTQS RRTFIKSVPPFLRTHGFDGRDLAWLYPGRRDQKHFTTLIKEMKAEFI KEAQPGKKQLLLSAALSAGKVTIDSSYDIAKISQHLDFISIMTYDFH GAWRGTTHGHSPLFRGQEDASPDERSNTDYAVGYMLRLGAPASKLVM GIPTFGRSFTLASSETGVPAISGPGIPGRFTKEAGTLAYYEICDFL RGATVHRTLGGQVPYATKGNQWVGYYDDQESVKSQVYKDRQLAGAM VWALDLDDFQGSFCGQDLRFLPLTNAIKDALAAT
6988	A	64	1279	LAPGAVGKGRGHTLPCSAARMGVKASQTGFVVVLVLLQCCSAYKLVC YYTSWSQYREGDGSCFPDALDRFLCTHIIYSFANISNDHIDTWEWND VTLYGMLNTLNKRNPNLKTLLSVGGWNFGSQRFSKIASNTQSRRTFI KSVPPFLRTHGFDGLDLAWLYPGRRDQKHFTTLIKEMKAEFIKEAQP GKKQLLLSAALSAGKVTIDSSYDIAKISQHLDFISIMTYDFHGAWRG TTGHSPLFRGQEDASPDERSNTDYAVGYMLRLGAPASKLVMGIPTF GRSFTLASSETGVGAPISGPGIPGRFTKEAGTLAYYEICDFLRGATV HRTLGGQVPYATKGNQWVGYYDDQESVKSQV\QYKDRQLAGAMVWAL DLDDFQGSFCGQDLRFLPLTNAIKDALAAT
6989	A	3	174	FPGRRFRGIPTFGRSFTLASSETGVGAPISGPGIPGRFTKEAGTLAY YEVMELGRR
6990	C	116	181	MCSTSRSRFTNILKSCNLLKY*
6991	A	20	111	TPGLEQSACLSLPKCWDYRCEPLCPACYLI
6992	A	120	426	EVFSLNLVLCCKSTVGHKLTSLQHLLTPSAVIQSPSSLLDTSFLLFA RHQHWPFVAVPLDFLHSLVAVPFGCFLEVFFFSYRCLASLCLGFIFL CIIQGES
6993	A	2	112	RRSLALSPKLECSGVILAHCKLCLPGSRHSPAPARD
6994	A	24	316	FLFLFFETESCSVA\RLECSGAI SAHCKLCLPGSRHSPASASSQVAG STGACHQA/QANFVFVFLVETGFYRVSPG*SG/LSLELVIRPPRPPK VLGLQV
6995	A	80	326	KKFSLGSQGRAGVFP RPPLGKLQTTALNSGAKGTPPFLFPEPRKRG GPPAPGWEGIFCPHFFPMGQKGEGLWHTGEGPH
6996	A	1	233	QNFSLVQAVAQWRSLSLQPLPPRFKQFLCLSLPGSWDYRRMPPCA

				NHLRLMSMWARVCTQQKVAGKAPSLLLKSP
6997	A	1941	2223	RTPRMKQSPAPIPCQPTTCSGCMASRATRTGWTSVCAY\CRLFRAHA \CVPVALPEMVRALSAQQQTLKQIVICGDRQAKDTKALGAVRPLCLH S
6998	A	211	544	WGPLELPVPPAAFPEYPPTVGRPRPLHMCVRIKPCSVPIITDPCELRK TTTSIDMPIPLGVGLEGEASQLDVETPRPCRAVVEPCGHPWSTLPLR LTLGQYVTCPLGTHSP
6999	A	31	230	CPPSSAVSPAGAAAGPPPGLSSAESRNTATSLPLPECPLIKPIAA LSALGPPDFHNEQGKGLRT
7000	A	1	861	EIGVNHTHLLFHTEVRWLSQGVLSRVYELRNEIYIFLVEKQSHLAN IFEDDIWVTKLAYLSDIFGILNELSLKMQGNNDIFQYLEHILGFQK TLLLWQARLKSNRPSYMFPTLLQHIEENIINEDCLKEIKLEILLHL TSLSQTFNYFFPEEKFESLKENIWMKDPFAFQNPESIIELNLEPEEE NELLQLSSSFTLKNYKILSLSAFWIKIKDDFPLLSRKSILLLLPFT TTYLCELGFSILTRLKTKRNLNSAPDMRVALSSCPVDWKELMNRQ AHPHSH
7001	A	55	406	PEMLFCATSQCQLTGGGAWLSSTARSVGTSDGVPVPLLRVRLPRVS NTDPPPALGPVPGSPQNPBSLLSCLRLQPARAPRAWDILCSPQPEPE AEPQAQSAPOQPSHYQGLHCGH
7002	A	1	361	CSGFLTFLPCQAGFGRPDGEYWLGLEPVYQLTSRGDHELLVLLEDWG GRGARAHYDGFSLPESDHYRLRLGQYHGDAGDSLWHNDKPFSTVD RDRDSYSGKENSYSGERIGEAGLLFW
7003	A	1	1725	ARAKTNSWGCERPRPGPESTPAQSPTWGARLPTMRKIRANAIAITLV AWILGTFYYLWQDNRAHAASSGGGGAQRAGRSEQLREDRTIPLIVT GTPSKGFDEKAYLSAKQLKAGEDPYRQHAFNQLESCLKSPDRPIRDT RHYS CPVSYSDDL PATSVIITFHNEARSTLLRTVKSVLNRT PANLI QEIILVDDFSSDPEDCLLLTRIPKVKCLRNDREGLIRSRVRGADVA AATVLTFLDSHCEVNTWEWLPMLQVRKEDHTRVVSPIIDVISLDNFA YLAASADLRGGFDWSLHFKWEQIPLEQKMTRTDPTRPRTPIVAGGI FVIDKSWFNHLGKYDAQMDIWGGENFELSFRVWMCSSLEIVPCSRV GHVFRKRHPYNFPEGNALTYYIRNTKRTAEVWMDEYKQYYEARSAPAI GKAFGSVATRIEQRKKMNCKSFRWYLENVYPELTVPVKEALPGI IKQ GVNCLESQGGNTAGDFLLGMGICRGSAKNPQPAQAWLFSDDLIIQQG KCLAAATSTLMSSPGSPVILQMCNPREGKQVSLASGPEAQOPEGPCL RVADLGRRAPD
7004	A	1	1271	MRRLMKGDEV LHVVYDI IYHPKKEASKINI IHQGF GFGFVFW EVMRG VDHTRVVSPIIDVISLDNFAYLAASADLRGGFDWSLHFKWEQIPLEQ KMTRTDPTRPRTPIVAGGIFVIDKSWFNHLGKYDAQMDIWGGENFE LSFRVWMCSSLEIVPCSRVGHVFRKRHPYNFPEGNALTYYIRNTKRT AEVWMDEYKQYYEARSAPAI GKAFGSTTPAKYEV LNVEETE AQIAGD EGRQPVAIVGVPEEGQSPSPASSYSVATRIEQRKKMNCKSFRWYLE NVYPELTVPVKEALPGI IKQGVNCLESQGGNTAGDFLLGMGICRGSA KNPQPAQAWLFSDDLIIQQGKCLAAATSTLMSSPGSPVILQMCNPREG KQKWRRKGSFIQHSVSGLCLETKPAQLVTSKQADAAQOQWQLLPH
7005	A	3	329	LIKLC SKAKSCENDLEM GMLNSKFKKTRYQAGMRNSENLTANNTLS KPTRY/QGELKEIKQDISSRLRYELLEKSQATGELADLIQQLSEKFG KNLNKDHLRVNKGKDI
7006	A	1	801	MPIRHPSGDIKLVIGYGEERVEESFKTLFWSIFGLSEVISVVLKYDH KFIENIGYVLYGVYNTMVVLLNMLIAMINNSYQEI EEDADVEWKF ARAKLWLSYFDEGR TLPAFNLVPSPKSFYYLIMRIKMCLIKLCKSK AKSCENDLEM GMLNSKFKKTRYQAGMRNSENLTANNTLSKPTRYQKI MKRLIKRYVLKAQVDRENDENVNEGELKEIKQDISSRLRYELLEKSQA TGELADLIQQLSEKFGKNLNKDHLRVNKGKDI
7007	A	21	373	AERLEAGAPTICMPGRWTFILRSEPHFCPLRPAAQEPRI GADRG PGR NEAPAPDLPGLPRLLRSGSGVLPKGGLGAKWKGM LSGRPSPCSGALG PLGPENPFPWQVLTESWPSRQLA

7008	A	3	63	LIKKAVAVRKHLERNRKVS
7009	B	374	447	XFCFLADMIMQSGDAISGFPVCL*
7010	A	1	860	MELCRSLALLGGS\GLMFCLIALSTDFWFEAVGPTHSAHSGLWPTGH GDIISGYIHVTQTFSIMAVLWALVSVSFLVLSCFPSLFPFGHGPLVS TTAAFAAAISMVMAVYTSERLSGMGVKRSLQSGGILLSLVANVLM VLSTATNYWTRQQEGHSGLWQECNHGICSSIPCQTTLAVTVACMVLA VGVGVGMVMGLRIRCDEGESLRGQTTSAPFLFLGGLLLLTALIGYTV KNAWKNNVFFSWSYFSGWLALPFSILAGFCFLADMIMQSTDAISGF PVCL
7011	A	1	691	KPASCDAQDPSLPQLLAVLSFLGSKDPGVVHSHLLSEIQESDQOP LPPPGPRSPELIPMELCRSLALLGGS\GLMFCLIALSTIFWFRAG GPTHLA\HSGLWPTGHGDIISG\YIHV\TQTFSIMARSVGPVWSVSF PGSLSCFPSL\FPPGHGPLV*T\TEAFAAAISMVMAVYTSEWRDQ PPHPQIQTFSSWSFYLGWVSAILLLCTGALSGLAHCGGPRPGYETL
7012	A	1	521	MSSKRTKTKTKRPQRATSNVFMFDQSQIQEFKEAFNMIDQNRDGF IDKEDLHDMLASLGKNPTDEYLDAMMNE\APGPINFPQWFSPMLVRS LNAPDP\ENVIRNAFACFDE\EAPGPIQEDYLRELLPTMGDRFTNEE VDELHREAPIDKKGNFNFIYIGFTRILEHG\AKDKDD
7013	A	106	693	TTTMSKKAKTTKTKRP\QRATSNVFMFDQSQIQEFKEAFNMIDQ NRDGFIDKEDLHDMLAS\LGKNP\TDAYLDAMMNEAPGP\INSTMF\ LTMFG\EKFKSHRSPEDVI/RANGLCFCSDDEEATGHFPQED/YTLRE LLTNPWGD\RFPDGGKWMNLYQRKHLIGPKKGEFSNYIGVHHGILT RPPKHKDDLKELLA
7014	A	78	188	ALMAPSHSSLGNVRPFPFKLTKPGRAQWLTPVIPAL
7015	A	2	93	GGSCS*SQHFGRPRWADHEVRRSRPSWLTR
7016	A	2	93	GGSCS*SQHFGRPRWADHEVRRSRPSWLTR
7017	A	2	93	GGSCS*SQHFGRPRWADHEVRRSRPSWLTR
7018	A	2	93	GGSCS*SQHFGRPRWADHEVRRSRPSWLTR
7019	A	2	94	GGSCS*SQHFGRPRWADHEVRRSRPSWLTR
7020	A	1	418	RRLRTAMKLRSRHPDQTDWHDQYKNAHLGAALQANPLGGAHAHAKGIV LEKVRVEATQPK\SAIMK/CVRVQLIKNGKKITAFVPNDGCLNFIEE NDEVLVAGFGRKGHAVGDI PGVRFKVVKVANVFILALYKGGKERPRS
7021	A	2159	2334	SATNYRNLTVLELGNSTHRHSHKTNST*KNCTRIPOTSQNLK*VKKH QSHICQSNCPF
7022	A	1748	1821	SQHFGRPRWADHEVWSLRPSWLTO
7023	A	2179	2485	PPHLQDRGKPVRRAPPDVTRRNQOEGSPSSLLGRPPGPAEPCPTQLH RAVLPPHGRRAEETTRSGEQGHEGDLSTQVFRGTLSSSGSASGGHL PPCGSRRRA
7024	A	3	502	TARAWLLGPVWPVCVSEWSKKPSPRGGRDPSDRDPAFAARSTVPP RISAYERPVWPGEWNPGRPGRRASAVVSPREGNWGVLDRPRLQAR KPRMVRSRQMCNTNMSVPTD/GCCNHLTDSSFGTRDPG*TKALAFEV IKVCWCTKRHLYYERGSFLSWPVYYD
7025	A	89	291	CKGVSSHESIFVIATNTRNKLLILFQENDEVLVAGFGRKGHAVGDIP GVRFKVVKVANVSLALLIF
7026	A	1295	1429	GQLYEKLGRRGPGAVAHAYNSQHFGRLRWADHEVRRWRPSWLTO
7027	C	332	763	MTGCLNFIENDEVLVAWIWSQKVMMLLVIFLESXFKVQSSPMVSL ALYKWLYGETKIINMNGENTVVINFHMPKNVCILLSPVLTTKIMFIT TTTTPPYFFYPKPVNAGPVPI LGNNKTGLFQDSLELITFVTWHSFPH VE*
7028	A	89	184	IHILTLQELLKEALNMERDKQYEPLGKHTKL
7029	A	2	275	LDLDKSIKIVKLLKTGFPYKIFKNTSFI/KDIVFMRTWYPVSI YNPVTSLLKP/VGEKDTWSGMWTGHLGL/AHGVRLKTNKDSLYKGL V
7030	A	178	621	PPRHVQLNHAEFEDQDDEARVQYEGFRPGMYVCVEIENVPCFV*NF DPRIPIILGGLGNSEGNVGVVQ/IPITPQGTGFLAIQSVSGIMPDR

				IAATGVVLDLDSIKIVKKLKTGFPPYKIFKNTSFIKGMFNSALEVA KFEGAVF
7031	A	159	486	DPITPQGTGFLAIQSVSGIMPDFRIAATGVVLDLDSIKIVKKLKT GFPPYKIFKNTSFIKGMFNSALEVAKFEGAVIRTISGIRGQIKKAL*A PEGAFRASFEKLL
7032	A	19	3881	IATMEAKDQKQKHKRKNKSGPKAAKKKKRLLQDLQLGDEEDARKRNPKA FAVQSAVRMARSFHRTQDLKTKKHHIPVVDRTPLEPPPPIVVVMGPP KVGKSTLIQCLIRNFTQKLTEIRGPVTIVSGKKRRLTIIIECGCDIN MMIDLAKVADLVMLIDASFGEFEMETFEFLNICQVHGFPKIMGVLT LDSFKHNKQLKTKKRLKHRFWTEVYPGAKLFYLSGMVHGEYQONQEI HNLGRFITVMKFRPLTWQTSHPYILADRMEDLTNPEDIRTNIKCDRK VSLYGYLRGAHLKNKSQIHMPGVGDFAVSDISFLPDPCALPEQQKKR CLNEKEKLVYAPLSGVGVLYDKDAVYVDLGGSHVFQDEVGPTHELV QSLISTHSTIDAKMASSRVTLFSDSKPLGSEDIDNQGLMMPKEEQM DLNTGRMRRKAIFGDEDESGDSDEEDDEMSEDDGLENGSSDEEAAE EENAEMTDQYMAVKGIKRRKLELEEDSEMDLPADFADSDDLERSAE EGEAAEADSESEEDCTAGEKGISGSKAAGEGSKAGLSPANCQSDRV NLEKSLMKKAALPTFDSGHCTAEVFASEDESEESSLSAEEDSE NEEAIRKKLSKPSQVSSGQKLGPNFIDETSDIENLLKEEEDYKEEN NDSKETSGALKWKEDLSRKAAEAFLRQQQAAPNLRLKIYGTVTEDNE EEDDDTLEELGGLFRVNQPDRECKHKADSLDCSRFLVEAPHDWDLEE VMNSIRDCFVTGKWEDDKDAKVLAEDEELYGDFEDLETGDVHKGS GPNTQNEDEIEKEVKEEIDPDEEESAKKKHLDKKRKLKEMFDAEYDEG ESTYFDDLKGEQKQAQLNRAEFEDQDDERARVQYEGFRPGMYVRIE ENVPCFVQNFDPHPYIILGGLGNSEGNVGYVQMRLLKQHRWYKILK SRDPIIFSVGWRRFQTIPLYIEDHNGRQRLKYTPQHMHCGAAFWG PITPQGTGFLAIQSV\SGIMPDFRIAATGVVLDLDSIKIVKKLKT GFPPYKIFKNTSFIKGMFNSAL*VAKFEGAVIRTVSGIRG\QIKKALR APEGVFR\ASFE\DKLL\MSDIVFMRTWYVPSIPAFF\NPVTSLL\K PVGEKDTWSGMRTTGQLRLAHGVRLKANKDSLYKPIRLQKKHFNLSLH IPKALQKALPFKNPKTQAKAGKVPKDRRRPAVIREGFRKILALLD ALSTVHSQKMKKAKEQRHLHNKEHFRAKQKEEBEELKRQKDLRKKLF RIQGGKERRNQKSSSLKGAEGQLQ
7033	A	182	374	PDFRIAATGVVLDLDSIKIVKKLKTGFPPYKIFKNTSFIKVCISY SHIYKSPYWLKGMKYL
7034	A	2	198	QARLCLKKKKKMWHIYTMEYYAAIKKNGIMSCAATWMELEAILNE LTQKQKTKYHMFSLISRS
7035	A	1	457	IFLRQFLSPRLEYSQVIAHCSLNLGSSDPPASAFKVAGTTGIRHH AWLIFVFFFAETGFHYVAQGGLELLNLRNLPATAFQSAGIIGISHHD LLGIQITTWLLQKLSYLLQKKICKDQETGLLHAFHLYPYPYMPSSPQ LLQGPDIITNG
7036	A	2	145	VETGFHHVGGAGLELLTSDPPASDYQSAGITGISHCARPMAPFLTL
7037	A	55	193	MLSFSFLSFFFFRGMVLTMLLPRVVLNCWPQAILPPRPPKVLGLLA
7038	A	564	884	GLLMSPITLCLVDLLPLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL LLPPPPPPPPPPPPPLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL GSLQALPPRFAP
7039	A	257	515	KFFSFLSSACCLEQVLCFVLFVFFVFLLLIIFSFFFSFSFSSFFSS SSSSSSSSSSSSFFFLRWS/PRSVAGVQ/WS*FGSLQPP
7040	A	936	1317	ILVLHGCFCIWYYLCLSMYFFFNFFEMESRSVAQAGVQWCA/DLCSL QAPPAGFTFPFSLSPSSWDYRHPPRLAKFFVFLVETG\FHRVSQD GLDLLTSGDPPTSASQSAGITGVSHRARPLKHL
7041	A	1	1218	MKGVKWQQMYPQYATYYYPQYLQAKQSLVPAHPMAPPSPSTSSNN SSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAI LDKTTNKCKGYGFVDFDSPAQAQKAVSALKASGVQAQMAKQQEQDPT NLYISNPLSMDEQELENMLKPFQVISTRILRDSSGTSRGVGFARM ESTEKCEAVIGHFNKFIKTPPGVSAPTEPLCKFADGGQKKRONPN

				KYIPNGRPWHREGEVRLAGMTLTYPDTTAAIQNGFYSPYSIATNRM ITQTSITPYIASPVSAQVQSPSWMQPQPYILHDPGAVLTSPMEHTM SLQPASMISPLAQQMSHLSLGSTGTYPATSAMQGAYLPQYAHMQTT AVPVEEASGQQQVAVETSNDHSPYTFQPNK
7042	A	1	1169	MAPPSPSTSSNNSSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVK LCQPYGKIVSTKAILDKTTNKCKGYGFVDFDSPAQAQKAVSALKASG VQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKFPQVISTRILR DSSGTSRGVGFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLC KFADGGQKKRQNPKNKYIPNGRPWHREGEVRLAGMTLTYPDTTAAIQN GFYSPYSIATNRMITQTSITPYIASPVSAQVQVAKETRENKYRGS KVQSPSWMQPQPYILHDPGAVLTSPMEHTMSLQPASMSPLAQQMSH LSLGSTGTYPATSAMQGAYLPQYAHMQTTAVPV\EEASGQQQVAVE TSNDHSPYTFQPNK
7043	A	1	743	VFLVEMGFHHVQGQPSLELPSSSDAPASASQTAGITGVSHCSRPFVRF FAGMLLTCCISWRCFASRALCRLQHPISSSSQPLAFQCFWSTDVVK TRVYQIGTILPLPSKLLDSWAEGYPATFESHVPGIYSRVGVSSIWHL GCVWSEPGVSRFLPMRWGPSAREWMVLCHARKAAPACSRFPAQPV LSQAPPPATVALCHVLTSLIPLFNLQVLSYWLPSRDEVGVSAWSE AWLLHSAPKPQ
7044	A	2	171	YIGGWWDKAGAHSILNGVWYRGGHYKIKHQDGI FWAEPGGSYSLRA AHMMIRPID
7045	A	1	350	EGGTGVRSLSFYQHII TVGTGHGSLLFYDIRAQKFLEERASSSLDSM PGPAGRKLKLACGRGWLNDQDDVWVNYFGGMGEFPNALYTHCYNWPEM KLFVAGGPLPSGLHGNAGLWS
7046	A	2	1685	QTYDDGAATRLMSTVKPLREPAPSEDVIDIKPDPDDLIDEDLNFVQE NPLSQKKPTVTLTYGSSRPSIEIYRPPASRNADSGVHLNRLQFQQQ NSIHAQQLDMQSSWVYETGRLCEPEVLNSLEETYSPPFRNNSEKMS MEDENFRKRKLPPVSSVVKVKNHDGEEEEEDDDYGSRTGSISSSV SVPKPERAFYSGASTHRCFLRGSCCCFSPEGKALPEVSTEWKFFK GKCRYSRGSVFFSSQKRYDFRYSIFTWSKEGGAVKLWDQELRRCRAF RLETGQATDCVRSVCRGKGKILVGTNRNAEIEVGEKNAACNILVNGH VDGPIWGLATHPSRDFFLSAAEDGTVRLWDIADKKMLNKNVNLGHAAR TVCYSPGDMVAVGMKNGEFIILLYCFGYLEPLAGPCEFEWLFISM KKHIGIVIATAPSIHIWDAMNKQTLNILRCYHSGVCSVSFSATGKL LLSVGLDPEHTITIWRWQEGAKIASRAGHNQRI FVAEFRPDSDTQFV SVGVKHVKFWTLAGRALLSKKGLLSTLEDARMQTMIAIFGAVA
7047	A	47	218	GHMEGEVWGLATHPYLPICATVSDDKTLRIWDLSPSHCMLAVRKLKK GKRLSHLNVD
7048	A	3	1716	GRCCCFSPDGKALAVGLNDGSFLMANADTLEDLVSFHHKDMISDIR FSPGIWPFVIGVTDV TASCLTSDKMVLATGDDLGFVKLFRYPTKASS EQGPTTARETPDKQCRQEKETYRATAPSIHIWDAMNKQTLNILRCYH SKGVCSVSFSATGKLLSVGLDPEHTITIWRWQEGAKIASRAGHNQRI FVAEFRPDSDTQFVSVGVKHVKFWTLAGRALLSKKGLLSTLEDARM QTMIAIFGAGKILVGTNRNAEIEVGEKNAACNILVNGHVDGPIWGL ATHPSRDFFLSAAEDGTVRLWDIADKKMLNKNVNLGHAARTVCYSPG DMVAIGMKNGEFIILLVSSSKIWGKKRDRRAIHDIRFSPDSRYLAV GSSENSVDYDLTLGPTLNRISYCKDIPSFVIQMDFSADSSYLQVSS GCYKRHVYEVPSGKHLMS\SAIDRITWATWTSILGDEVLGWISRA EKADVNCACVSHSGISLVTGDDFGMVKLFDFPCPEKFAKHKRLGHS PHVTNIRFTSGDRHVVSAGGDDCRLVTFSAEHQTMILLVKRLNTTTP TALVYEIS
7049	A	1	5853	MPLKLQNCALALHPERVLVATGQVGKEPYICIWDSYTVQTTISVLKDVH THGIACLAFDLGQCSVKAVIDNARNNECGYIPVKLYLQKHSFSLIC LPFYSFLDFLDINQRLVSVGLDSKNAVCVWDWKRGMKLSMAPGHTDR FWSLCGNALTPKRGVFGKTGDLQTLCLACARDELTYSGALNGDIYV WKGINLIRTIQGAHAAGIFSMNACEEGFATGGRDGCIRLWDLTFKPI

				<p>TVIDLRETDQGYKGLSVRSVCWRGDHILVGTQDSEIFEIVVQERNKP FLIMQGHCEGELWALAVHPTKPLAVTGSDDRSVRIWSLVDHALIARC NMEEP IIRCAAVNADGIHLALGMKDGSTVLRVRDMTEVVHIKDRKEA IHELKYS PDGTYLAVGCNDSSVDIYGVAQRYKKVGECLGSLSFITHL DWSSDSRYLQTNDSNGKRLFYRMPGGKEVTSTEEIKGVHWASWTCVS GLEVNGIWPKYSDINDINSVDGNYIGQVLVTADDYGIKLFYRYPCLR KESLADSHSDESDSDLSVPELDSEIEQETQLTYRRQCSAGCTSRAP ASAQLLVKPQEAFTHGRRQRGSSYRGYDCRSNLFYTQIGEIVYHVAA VGVIYNRQONTQRFYLGHDDILCLTIHPLKDYVATGQVGRDPSIHI WDTETIKPLSILKGHHQYGVSAVDFSADGKRLASVGIDDSHTVVLWD WKKGEKLSIARGSKDKIFVVKMNPYVPDKLITAGIKHMKFWRKAGGG LIGRKGYYIGTLGKNDTMMCAVYGWTEEMAFSGTSTGDVCIWRDIFLV KTVKAHDGPPVFSMHALEKGFVTGGKDGIVALWDDSFERCLKTYAIKR AALAPGSKGLLLEDNPSIRAIISLGHGHILVGTKNGEILEVDKSGPIT LLVQGHMEGEVWGLATHPYLPICATVSDDKTLRIWDLSPSHCMLAVR KLKKVQKGNVLEPPYRVPTGAPPSGVMRRGQPSFRPQNGRTTDSLH HVPKGATGTECQPVKAARKGAILCKTTGAELPKTMGTHLLHQCGLDL RFAGGPLQTFFAWVPPTPRGITSGGCKTVKRVTELIPVETPLYKVSS NPCWGGLTQSGGTGSRTHLMKHS DYPLAEGVHYTGGNPTCPDCPDSS ELGAQSSEAAADSQSDSDSRPFPQELGSLRQSVAKWPLRICAALCLGLK ELVAWAHGGDLLIHQLHRSMEKVVWPGQDSTITHCLSWLGVGAPLVL CSSQKAATLVLRSESEQVKGSDSLFGNGVAATRFSELVAKKLARGCS PQWNSESSHLVKEKLARGSRPELNGGRCCCFSPDGKALAVGLNDGSF LMANADTLEDLVSFHHRKDMISDIRFSPGIWPIGEVTDVTASCLTS DKMVLATGDDLGFKVLFYRPTKKGKFGKFKRYVAHSTHVTNVRWTYDD SMLVTLGGTDMSLMVWTNEMEGYREKRPCDSEESDIDSEEDGGYDSD VTRENEISYTI RALSTNIRPMLGIKPHLQQKEPSIDERPPVSRAPPQ PEKLQTNVVGKKRPIEDLVLELIFGYRGRDCRNNVHYLNDGDDIY HTASVGILHN VATGSQSFYQEHNDILCLTVNQHFKFINIVATGQVA TAPSIHIWDAMNKQTL SILRCYHSKGVCVSFSATGKLLLSVGLDPE HTITIW RWQEGAKIASRAGHNQRI FVAEFRPDSDTQFVSVGVKHVKF WTLAGRALLSKKGLLSTLEDARMQTMLAIAFGANNLTFTGTISGDVC VWKDHILCRIVARAHNGPVFAMYTTLRDGLIVTGGERPSKEGGAVK LWDQELRRCRAFRLETGQATDCVRSVCRGKGKILVGTRNAEIEVGE KNAACN ILVNGHVDGPIWGLATHPSRDFFLSAAEDGTVRLWDIADKK MLNKVNLGHAARTVCYSPGDMVAIGMKNGEFIILLVSSLKIWKKR DRCIAIHDIRLVNKWNRVSSIYLI</p>
7050	A	1	426	<p>LKQQIEEQRVQVQVVERAQVAVQEQEIARAEAEQMAKAE/AFQLY QEAAQLDMLLEKLPQVA\EEISGPLTSANKITLVSSSGSGTMGAAKVT GEVLDILTRL\ESVE\RLTG\VTILPRLNHKAF*RTALSLQPSQMP SLIAE</p>
7051	A	162	1449	<p>TMFFTCGPNEAMVVSGFCRSPPMVAGGRVFLVPCIQQIQRISLNTL TLNVKSEKVYTRHGVPISVTGIAQVKIQGQNKEMLAACQMFLGKTE AEIAHIALETLEGHQRAIMAHMTVEEIIKDRQKFSEQVFKVASSDLV NMGISVVSYTLKDIHDDQDYLHSLGKARTAQVQKDARIGEAEAKRDA GIREAKAKQEKVSAQYLSEIEMAKAQRDYELKKAAYDIEVNTRRAQA DLAYQLQVAKTKQIEEQRVQVQVVERAQVAVQEQEIARREKELEA RVRKPAAEAERYKLERLAEAESQLIMQAEAEASVRMRGEAEFAIG ARARAEAEQMAKAEAFQLYQEAAQLDMLLEKLPQVAEEISGPLTSA NKITLVSSSGSGTMGAAKVTGEVLDILTRLPEVERLTGVSISQVNHK PLRTA</p>
7052	A	57	389	<p>GWELLVTKVRKDDQWNEDLKTQSKLFYECCQIMGTEWVSLSCQVAE BISGPLTSANKITLVSSSGSGTMGAAKVTGEVLDILTRLPEVERLTG VSISQVRSQVGAEENC</p>
7053	A	162	1581	<p>TMFFTCGPNEAMVVSGFCRSPPMVAGGRVFLVPCIQQIQRISLNTL TLNVKSEKVYTRHGVPISVTGIAQVKIQGQNKEMLAACQMFLGKTE</p>

				AEIAHIALETLEGHQRAIMAHMTVEEIKDRQKFSEQVFKVASSDLV NMGISVVSYTLKDIHDDQDYLHSLGKARTAQVQKDARIGEAEAKRDA GIREAKAKQEKVSAQYLSEIEMAKAQRDYELKKAAYDIEVNTTRAQA DLAYQLQVAKTKQIEEQRVQVQVVERAQQVAVQEQTARREKELEA RVRNPAAE\AERYKLERPAEAEKSQLIMQAEAK\AASVR\MRGEAEGL CP*GPEPRAE\AEQMA\KKAFAF\QLVPRGVAQLDMLRRESCPRWQE EI\SGPLNFSPIRSLVSSG\SGTMGAA\KVT\GEVLDILNSPCP\E SVER\LTGREHLPRVNH\KPLKNSLEPSALHRCPASLAEVALNDPPV ACNPLGLPEHVH
7054	A	1	327	FFFFFFFFERESYSLAQAGVQWHNLSLQPLPSGFKRFSCSLPSSRDH ERAPSHLAVVFLVEMGFHHVGQASLELLTSSDPPALASQSSGITVVS HHARPGILNSINRFT
7055	A	1	202	MELRLSANANWPALTGGAWPRRSHQASSLGYCCVSSSAVCSASLSGR RRGRHEPLVSPPPYRHLTML
7056	A	1	493	FPASRLVTLCSEPEDAAMERSAFMELDAGSRLVMHLREWPAALLVSST GWTEFEQLTLDGHNLPVLCVITGSDVLGVCLHMSSSGLDLPKMKVVD MFGCCLPVCVAVNFKCLHELKHEENGLVFEDSKELAAQMFFSHFPD PAGKLNQFWKDLRESQQLRWDES
7057	A	409	521	ALLFILOQLFSNFPDPAGKLNQFRKNLRESQQLRWD
7058	A	296	869	PYSSCPMTRASSPKELQQFVVGSPMRAPBEEPDPDTERSAFMERD AGSGLVMRLRERPALLVSSTGWTGSDVLGVCLHTSCSGLDLPKMKVVD MFGCCLPVCVAVNFKWQEQNPNSGDSFTDPPLRRKQCRASCPLHEL VKHEENGLVFEDSEELAAQLQVLFNSNFPDPAGKLNQFRKNLRESQQL RWD
7059	A	1	848	MPGLRVKMPGPGISQDEAVWSMDDNFEVKNQHPVWRAATLAKDCKN QSAQAVTVYNKPASFFKEAPLDLQHRLFMKLGSTHSPFRARVFFCSF ISEPEDPATERLAFTERDAGSRLVTLLHERPALLVSSTSWTGKGPLR EYYSRLIYQKHPQHIQVCTPWL\GAEDYPLLIGSADLG\VCLHTSS\ SGLDLP/L*KVVD MFGCCLPVCVAVNFKVFT\ELVKHEENG\LVFEDS EELAAQLQMLFSNFPDPAGKLN\SPRKNLPESQQL*WDES WVQTVLP LVMDT
7060	A	738	1902	FHHLTETNSPNYFITMALNVAPVRDTKWLTLEVCRQFQRGTCRSRDB ECKFAHPPKSCQVENGRVIACFDSLKGRCSENCKYLHPPTHKTQL EINGRNLIQQKTAAMLAQQMQFMFPGTPLHPVPTFPVPGAIGTNT AISFAPYLAPVTPGVGLVPTTEILPTTPVIVPGSPVTVPGSTATQKL LRTDKLEVCREFORGNCCARGETDCRFAHPADSTMIDTSDNTVTVCMD YIKGRCMREKCKYFHPPAHLQAKIKAAQP/QAAATVMTQSTAKAMKR PLEATVDLAFPPGALHPLPKRQALEKSNGTSAVFNPSVLHYQQALTS AQLQQHAAFIPTGSLCMTPTSIVPMHSATSATVSAATTPATSVP FAATATANQIILK
7061	A	1	240	ALHPLPKRQALEKSNGTSAVFNPSVLHYQQALTS AQLQQHAAFIPTG MCPYCPTSCALLVMCFLLISLSCLVASSLLLKV
7062	A	3	354	AARVMTQSTAKAMKRPLEATVDLAFPPGALHPLPKRQALEKSNGTSA VFNPSVLHYQQALTS AQLQQHAAFIPTDNSEIISRDMECQESALRI TRHCYCTYYPVSSSVELPRTAC
7063	A	1	621	MTAFFVKPANVCQLPHWNDIISNSLYWERYKKRENASSSSTCSSGQV SFLEKKVLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIIELEKKIV TATVNNSVLQKQHDLMETVNNLLTMMSTSNYLQIVMEMSQAFFQKH CRTPNKEWKFSGGGVNRGQRCRVKPTAVTPEAHPSPRVGTNVENL GNGEQASFGTYPCFRFTPE
7064	A	362	720	SDVTFSGKPSLVTLFPLYPPGKFSFSSVDVSMQLSTIKHGSCSLWAS PSEEFDILEVVPLFCVLFRTASFISSRLPSKGVKSSSCPFGKEAGV LNGCKEKAIFPLGACVFFPSLSTTP
7065	A	1	2610	MAETAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIR KSDGTLQEHGICEIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPWFIKRAHSPSRGLYSVINPYLIPFFIG

				LQNRFTQFRLSETKEITNPNYAMRLYESLCQYRKPDGSGIVSLKIDWI IERYTATIATTQRCQIQTKRGVRELPAEEAFRIELGGHYTGSNLE HVGVPVSTEHTPSVVEEDTVRSRDFQCTGLKSLKIVRDSSAYNNFRK SMDSIGKKQYQVQHGCSTYFLLPEMDNCRSSSSPYVSNVQORDAPL EYDDSVQRLQVGDNSIDSWKNAGRVFKDSKWDANDPILKDOTQEWS GSATFTSDGKIRLFYTDYSGKHGKQSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFIDEGNYTSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQOSAKKRD AELANGALELEKTTLKFIVNQKRARIAKSILSQKNKAGGIKLPDFKL YYKATVNTAWCAQIQTKRGVRELPAEEAFRIELGGHYTGGCSETL SQGSLGDPVGLLTSQRGGRSLSPRVRTTLRRPCLPRLFGMAALWDHC LNKLPACLPPLSQALLLGKPKLRQCENLLVPLRRGLRTACEPRNFVG VVEAKAERVNSIYNHGVPRKKRSQSNMHVFPANDPTVAKEEQISFRD CAEVFKSGHTTINGIYTLTFPNSTEEIKPTAVTPEAHPSPRVGTNVEN LGNGEQASFGTYPCFRFTPEGRACGALSPLPLTFQQVLEFDSHQTEI AKICKNSIGQLFCINDCTGSKGQK
7066	A	122	1840	AGLFFPLQSDSLLHAWREHSSKNQVCYWKKRKEKTFIDGPSHGSVAA LRFRRRQQLGTLDVCLPSSLLSCWFITEERMWQIVFFTLSCDLVLA YNNFRKSMDSIGKKQYQVQHGCSTYFLLPEMDNCRSSSSPYVSNV QRDALEYDDSVQRLQVLENIMENNTQWLMKLENYIQDNMKKEMVEI QQNAVQNQTAVMIEIGTNLLNQTAEQTRKLTDEVAQVLNQTTRELEQ LLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKKVLAMEDKHIIQL QSIKEEKDQLQVLVSKQNSIEELEKKIVTATVNNSVLQKQHDLM TVNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTINGIYTL TFPNSTEEIKAYCDMEAGGGGWTIIQRREDGSDVDFQRTWKEYKVG NPSGEYWLGNFVSQLTNQRYVLKIHLDKWDGNEAYSLEYHYLSS EELNYRIHLKGLTGTAGKISSISQPGNDFSTKGDNDKCICKCSQML TGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKGSGYSLKATT MMIRPADF
7067	A	1	1433	MPNRRGRQRRRVVTRGLMRPPPRWLPTAVTPEAHPSPRVGTNVEN LGNGEQASFGTYPCFRFTPEGSFLEKKVLAMEDKHIIQLQSIKEEKD QLQVLVSKQNSIEELEKKIVTATVNNSVLQKQHDLMETVNNLLTM MSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTINGIYTLTFPNSTEE IKAYCDMEAGGGGWTIIQRREDGSDVDFQRTWKEYKVM TDVSRIFAIQ LTMVQLKIFRLYDVICGTMPLPHDARQRQRATGPSQSCDPQGEQQLR APCCQMALSDCGLMIHLKGLTGTAGKISSISQPGNDFSTKGDNDKC ICKCSQMLTGDEYFAGGLHSSFDLDCGNSGCGNQERKLEGSINDIKS DVCISSVLKANNIHSSPSFTHLDKSSPQEISEVIFQREEINLAKEI LQGVVHPSPKRQGRVCLQGRLEERYPFVFLPLFFQKQGHLLDTF QDPGVPO
7068	A	3	326	HSLHSALSLEVTGSTKLPKPYITINNLNPRENKDVLNFTCEPKSENY TYIWWLNGQSLPVSPRVKRPIENRILILPSVTRNETGPYQCEIRDY GGIRSDPVTNLNL
7069	A	3	423	ETPKPSISSNLNPREVMEAVRLICDPETPDASYLWLLNGQNLPMTH RLQLSKTNRTLYLFGVTKYIAGPYECEIRNPALLNDCHNTNTEKKKQ PEKVESDDIENSNPFSHPKAFKNIRVQHGHIHRKLITKLET
7070	A	3	554	SLLNFWNLPTAQVTIEALPPKVSEKDVLLLVHNLQPONLAGYIWK GQLMDLYHYITSYVVDGQINIYGPAYTGRETIVSNASLLIQNVTR AGSYTLHIKRGDRTRGVGTGYFTFNLYHTSYLWWMNGQSLPMTHRLQ LSKTNRTLFI FGVTKYIAGPYECEIRNPVSASHSDPVTNLNL
7071	A	3	602	SLLNFWNLPTAQVTIEAQPVKVSEKDVLLLVHNLQPONLTGYIWK GQIRDLHYITSYVVDGQIIYGPAYSGRETAYSNASLLIQNVTR AGSYTLHIKRGDGTGRVGTGYFTFTLYREAMETVILTCDPETPDTSY QWWMNGQSLPMTHRFQSLSETNRTLFLFGVTKYTAGPYECEIRNSGSA SRSDPVTNLNL
7072	A	3	550	ETPKPSISSKLNPREAMEAVSLTCDPETPDASYLWWMNGQSLPMTH

				RLQLSETNRTLFLLVTKYTAGPYECEIRNPVSASRSDPFTLNLLHG PDLPRIYPSFTYYRSGEVLYLSCSADSNPPAQYSWTINGKFQLPGQK LFIPQITTKHSGLYACSVRNSATGKESSKSMTVKVS DWTL P
7073	A	1	102	AGSYTLHIKGGDGTGRVGTGRFTFTLHRIQTSEE
7074	A	3	1451	GAVRTWGRGFQTEKQASLLNFWNPPTTAQVTIEAEPTKVSKGKDV LLVHNLPQNLAGYIWKYQGMKDLYHYITSYVVDGQIIIIYGPAYSGRE TVYSNASLLIQNVTRDAGSYTLHIVKRGDGTGRGETGHFTFTLYRHS LDSALSLEVTGSSQPL*DTWENCPTLWLHCLMTELTSGLD SVLP CVI SAEVPSPRSGFPVSKGFKDNWKFHHPSLGCPWQGLQRKHTSGGKVR LKLRRFQHCLMQVRTTS\ETPKPSSISSNLYPREDMEAVSLTCDPET PDASYLWWMNGQSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIR NPVSASRSDPVTLNLLPKLPKPYITINNLPNRENKDVLAFTCEPKSE NYTYIWWLNGQSLPVSPRVKRPIENRILILPSVTRNETGPYQCEIQD RYGGIRSYPTLVNLY\TTKHSGLYACSVRNSATGMESSKSMTVKVS APSGTGHLPLNPL
7075	A	3	437	ETPKPSSISSNLYPREDMEAVSLTCDPETPDASYLWWMNGQSLPMTH SLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPVTLNLLQH SWLIDGKFQQAQVFFIPQITKTYRGVYVCFIHNSATAGTNLI IKRI IVP
7076	A	79	1516	EASLLEDDDMVYLRLPLTSHQYRTAQLRAMLRKFLDPRLSSTEENTQ AAETMGPLSAPPCTQRITWKGLLLTASLLNFWNPPTTAQVTIEAEPT KVSKGKDVLLLVHNLPQNLAGYIWKYQGMKDLYHYITSYVVDGQIIII YGPAYSGRETUVYSNASLLIQNVTRDAGSYTLHIVKRGDGTGRGETGH FTFTLYLETPKPSISSNLYPREDMEAVSLTCDPETPDASYLWWMNG QSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPV TLNLLPKLPKPYITINNLPNRENKDVLAFTCEPKSENYTYIWWLNGQ SLPVSPRVKRPIENRILILPSVTRNETGPYQCEIQDRYGGIRSYPT LVNLYGPDLPRIYPSFTYYHSGENLYLSCFADSNPPAEYSWTINGKF QLSGQKLFIPQITTKHSGLYACSVRNSATGMESSKSMTVKVSAPSGT GHLPLNPL
7077	A	9970	11210	MKDACGGIKGATQDNLLLSTQ/PKLPMPIYITINNLPNRENKDVLAFT CEPKSRNYTYIWWLNGQSLPVSPRVKRPIENRILILPSVTRNETGPY QCEIRDRYGGIRSNPVTLNVLCEYPLFLCGPGHQLNSKRPEARPLSL SPVQV*TTLLDIRPGHDSLPEILGRHSLNQEYKGRGALVMGH*GP TACNERNRGIPQAWA**T*MGFGCHLRCLGSEGHCVPLRDQEHPLP LDDITCGFILFPDGPDLPRIYPSFTYYRSGENLDLSCFADSNPPAE YSWTINGKFQLSGQKLFIPQITTNHSGLYACSVRNSATGKEISKSMI VKVSGKWIPASLAIGF*VESIWLSEKSQENICIPRLCPMGTSKSQL LLNPPNLSLQTLFCLFFCFLMADLVSGLRKVGRGLYQP
7078	A	460	1832	QPVLREFLDPRLISTEENTQAAETMGTL SAPPCTQRIKWKGLLLTAS LLNFW\NLPTTAQVTIEAEPTKVSEGKDVLLLVHNLPQNLTRATI W\ YK\QMRHLYHYITSYVVDGEIIIIYG\PAYSGRETAYSNASLLIQNV \TRED\AGSYTLHIK\RGDRTRGVGTGYFTFNLYLETPKPSISSNL NPREAMETVILTCNPETPDASYLW*LNGQ\NLPMTHSLQLSKANRT LYLFG\VTNYTAGPY\ECEIWELRECQARS DPVTEPFSSRKL PKPYI TINNLPNGEE*GCL*TFIC\EP\KSENYTYIWWLNGQKPP/VSSPRV KRPH*KTGSLIPTPVFTRKWKQGPYSMWNYGDRYGG\IRSLPSSPLN CSSYGSRTSPRILPFHFTY\YRFREENLDLFLGFTGIFNPP\AQYSW DN*WKSQFQTRGQKLFYSGHITTKHSGLYVC\SVRNSATWQ GKAPNP
7079	A	2	315	RWSLCPLQAGVQWRDLCSLKPPEFEKQFSCSLSPSS*DYRCPPPCP ANF/SFFFVFLVETGFHHVGQAGLNLTSRDLLTSASQSAEITGM SH CPRPTLSNSRVL
7080	A	1	534	MSWLEENVHEVLQAVDAGDPAVEACENRRKVLYQRAPRNIHRH VILS EIKEAVALPPHPKLMRPHGPPGESRACAQLLLCPLAAPP CPCE GGSWQAAPLSPISHGNTIALFFRSLLPNYTMEGERPEEGVAGGLNRN HGLNRLMLAVRDMANFHLNDLEAPHEDDAEGEGEWD

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7081	A	1217	1545	TRHLVLRASSSQGPWGGFRVRCWKGPPRAPQCLLLGPRAPSPSTDS PLLRRHVPLLQGERPEEGVAGGLNRNQLNRLMLAVRDMMANFHLNDL EAPHEDDAEGEGEWD
7082	A	2	1665	KKKKKQKNKKSSTGEASENGLEDIDRILERIEDSTGLNRPGPAPLSS RKHVLYVEHRHLNPDTELKRYFGARAILGEQRPRQRQVYPKCTWLT TPKSTWPRYSKPGLSMRLLESKKGLSFFAFEHSEYQQAQHKFLVAV ESMEPNINIVLLQTSPYHVDSLLQLSDACRFQEDQEMARDLVERALY SMECAFHPLFSLTSGACRLDYRRPENRSFYALALYKQMSFLEKRGCP TALEYCKLILSLEPDEDPLCMLLLIDHLALRARNYEYLIRLFQEWEA HRNLSQLPNFAPSVPLAYFLLSQQTDLPECEQSSARQKASLLIQAL TMFPGVLLPLLESCSVRPDASVSSHRRFFGNABEISQPPALSQVLNLY LGRSHFLWKEPATMSWLEENVHEVLQAVDAGDPAVEACENRRKVLYQ RAPRNIHRHVILSEIKEAVAALPPDVTTSQSVMGFDPLA\PSDTIY\S YVRPERLKSLSSH\GNT\IALFFRSLL\PNYTMGERP\EEGVAGGL NRNQLNRLM\LAVER\DMMANFHLN\DEAPHEDDAEGEGEWD
7083	A	420	627	IILWVLNAFLQPPGRHMAIRERQPGRTNSDYETADGVYMTLNPRAP TDDDKNIYLTLPNDHVNNSNN
7084	A	2	380	FRVDDFVQKLQAGSIAIVRQTFNKEIKTMKKFESPNIIRIFGIWIDE TVTPPQFSIVMEYCELGTLRELLDREKDLTLGKRMVLVLGAARGLYR LHHSEAPELHGKIRSSNLLVTQGYQVKIWPVG
7085	A	2	657	VKCRGIPNIRIFGICIDETVTPPQFSIVMEYCELGTLRELLDREKDL TLGKRMVLVLGAARGLYRLHHSEAPELHGKIRSSNLLVTQGYQVKL AGFELRKTQTSMSLGTREKTDVRKSTAYLSPOELEDVFYQYDVKSE IYSFGIVLWEIATGDIFFQGCNSEKIRKLVAVKRQOEPLGEDCPSEL REIIDECAHDPSPRPSVDEILKKLSTFSK
7086	A	2	842	MATSELSCEVSEENCERREAFWAEDLTLSTCQVQSCPRFAWAVH CVECCSPHCPDHPVYKPPASPPSLCAAFLLCALSEDTHGHQGHPLSLP LACESERRMDGASPCHLSPCTCYPCRGAAATFTLQKRVLGLREGIK WPEVTWRSKWPSLQPSGAALVEKATLTGTGEPVWSMSQTSLLPSHGP GLSVSARLCPWPTSPPPRLGPSGPAGGVNEPSCSSAALAWHVGSDW QVPGRQGRVRGQGLRRHCCLCVKTLGRPCPYPAPTGTGQRLQVG
7087	A	174	463	GSLKQGMFPGSLNRRLLPTESPLQILRATFL*KEVA*GLHQYHLPL\Q LLSGPVFGLTHLQSAVPFREKPDPPPELPSLRVLRRTLDSWGARTH YGI
7088	A	69	194	RALTRKTNSKAEPCLLPAQPTCNFPSPVARRRNINLARPRD
7089	A	1348	2204	TWRLDPQIISSPKPQPGGTYTLEVVKSSKSKKVLSPHP*WPPLRLWQ R\GGSPEGGTQAPDGLPPPPRPKSERVGSPLSGGKR/EGSHPGG PPHITHP/DGEEKAKSSWFGLREAKDPTQKPSHPVKPLSAAPVEGS PDRKQSRSSLSIALSSGLEKLTVTSGSIQPVTPAQAGQMVDTKRL KDSAVLDQSAKYHHLTHDELISLLLQRELERLSQRDEHVQELESYIDR LLVRIMETSPTLLQIPPGPPK
7090	A	2	762	RDPPSLSSASPPGSRESSIHSGPEELPTPPEPDFPPPPPLPPWASHHR GGSPPPCSPLSEAWPLTSSAPPGEALLPGPHEPSPPGGSPALLRE DLAAATPASPLVLLPLETRPAEPPQPSASHPVKPLSAAPVEGSPDR KQSRSSLSIALSSGLEKLTVTSGSIQPVTPAQAGQMVDTKRLKDS AVLDQSAKYHHLTHDELISLLLQRELERLSQRDEHVQELESYIDRLV RIMETSPTLLQIPPGPPK
7091	A	2	218	DFADDDLVLKELRGHSSFVNEATFTQDGHYIISASSDGTVKVKYLLS VYFGMSTPSLSFEFSVVMGMIVL
7092	A	7	78	WGRLCICEGRGYMGNLCFTCPILL
7093	A	553	954	SRSRRGQKRRRWSTVWRLSAGACALSMQTPSRTSWPTAPFRAIWRAE TVAAWCRLRRPVWRVWSWCLPTPITRATPLGARSWPGRMWPPPLQ AGSAVPTLR*RPLK\FPLPRVPGRRPSGAQSHREQCLOQT
7094	A	1	1215	MTLKEHAFAKHLFNKAHLAPPLIHLTLSGHSTCFREHWVGDIVHRDL KLENIMVKSSLIIDNNEINLNIKVTDFGLAVKKQSRSEAMLQATCGT PIYMDRGWNSLEGSEQDRKMWDSELELPRDLLNVFEQNADNDMDDEIQ

				AEVLSGDDEELLGNWSKGDSCYVLLKQLAAFCPCLRDLWNFKLERDD LGYLVEEISKQSQSIQEATWVLLKAFSFIREAHEKNLENLQPDNAIEK KIPFSEEFKFLAAEICISNQEANVNPQDNEKNVSRACQRSSSQPLPL PRVLGGKSGFVGWAQDSHAEIYTFGRILGKGSFGIVIEATDKETETK WAIKKVNKEK\LLMKSNFLQPVRTTICAVQVSHLANSFQLKSREK WRKPL*LKEHAAFKHLFNKAHLAPPLIHLTLSGHSTCFREHWGDIV HRDLKLENIMVKSSLIDDNNEINLNIKVTDGFLAVKKQSRSEAMLQA TCGTP IYMDRGWNSLEGSEQDRKMWDSELEPRDLLNVFEQNADNDMD DEIQAEVLSGDDEELLGNWSKGDSCYVLLKQLAAFCPCLRDLWNFKL ERDDLGYLVEEISKQSQSIQEATWVLLKAFSFIREAHEKNLENLQPDN AIEKKIPFSEEFKFLAAEICISNQEANVNPQDNEKNVSRACQRSSSQ PLPLPRVLGGKSGFVGWAQDSHAEIYTFGRILGKGSFGIVIEATDKE TETKWAIKKNKEKSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAEI KGEMEKTPVTPSQGTATKYPKSGALSRTKKKL
7095	A	1	770	MVSLIGELKSHQDLHTSHCAQCPCVPIHPQMVPQSWCSPWFLWSA SGVGFSQRFQTSKGNECPPIPSYHPISHRSRKILCEWHYASLGKEV AQTTETFSLTSHGLSRSSPEVISAHDYSSQCDIWSIGVVMYMLLRGE PPFLASLKKKLFELIRKLGELHFENAVWNSISDCAKSVLKQLMKVDP HRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTE EKNKPSTEEKLSYSTLGKCP
7096	A	7265	7684	IVSLFLFILLVFWWWCFFFFFFFETVLLFSPRLQCRDVTSAHCNFCF PGSSDSRASAFRVARITGAHHDWLIFCIFSRDRVLSCWSGWSRTSD LR*SALPKCWDYRCEPPCRA*FFFFLYPLTIPTSLPAPHYPPSLW
7097	A	1	344	MDKSLLELPILLCCFRALSGSLSMRNDVIEIVQCRMCHLQFPGEK CSRGIGICATTEEACMVGRMFKRDNPWLTFTMGCLKNCADVKGIRW SVYLVNFRCCRS HDLCNEDL
7098	A	3	285	YGPLNLLTFNVFYHNEHDLNIPGKSLPLVRKIAAEYYDNLPHYNS WIKVLYDFVMDDTISPYSRMKRRPPGRDGAGPNIIIALGILLQNR
7099	A	346	517	RGLVGSPSSAPSAAPSWSSEKQGCRGHCGLGGS LVPHGR IHHSSNFP SCSGDPSQDS
7100	A	3	173	LYSQSSFHSLNVFATKFFTVAFVKLETIKMSISRGLGTLIRTVGNSV PEGGMKRTY
7101	A	256	352	LLFKVTVEYRPIIDKTLNEADCATVPPAIHSY
7102	A	1	203	VPIHEFDHSMPPFRGHRKKPFGGHWGKHTLSYVDVSTGKVTVKCRPII DKTVNEADCAHCPPQPIHSY
7103	A	1	112	PVGQTGLELLTSGDLTASASLNAGIPGMSHHAWLKLF
7104	A	1	1213	MEAGEEPLLLAELKPGRPHQFDWKSSCETWSVAFSPDGSWFAWSQGH CVVKLVPPWPLEEQFI PKGF EAKSRSSKNDPKGRGSLKEKTLDCGQIV WGLAFSPWPSPSRKLRWHHPQAPDVSLILATGLNDGQIKIWEVQ TGLLLNLNSGHQDVVRDLSTP SGSLILVSASRDKTLRIWDLNKHGK QIQVLSGHLQWVYCCSISPDCSMLCSAAGEKS VFLWSMR SYTLIRKL EGHQSSVVS CDFSPDSALLVTASYDTSVIMWDPYTGERLRS LHHTQL EPTMDDSDVHMSSLRSVCFSPEGLYLATVADDRLLRIWALELKAPVA FAPMTNGLCCTFFPHGGIIATGTRDGHVQFWTAPRVLSSLKHLCKRA LRSFLT TYQVLALPIPKMKBEFLTYRTF
7105	A	3	413	FRHEQASKDRNVVFSYPYGVASVLAMLQLTTGGETQQQIQAMGFKID GEPRDTRGGGWHAETQYQKPRKGWLWLSRAKPHTAVLQGP PHLPTT LQVTGPLNLQGCLTSRFTAYSPPCDLNLVKFAHLQNE DYLLS
7106	A	45	537	GQERCQEDPHAPLQQTVIPSSVSRPPPERGANRQSQGTSENFQMMS PALTCVLGLALVFGESAVHHPPSYVAHLASHFGVRV FQVVAHASK DRSVGFSYPGEDSVLAMLQLTTGGETQQQIQAMGYKIDGEPDTRG DKGMAPALRHLYKELMGPWEEQ
7107	A	2	224	FFFESHVAQDGVQLCDLSLVQRPPPGFKQFSCLSLPSRWDRHTSP HPANFCIFSRDGVLPYWSGWSRTPDLR
7108	A	179	394	DKWRRLPWKRGVEVG TAGSLAKAFGFFAEAKTEPREGCSESGVRISY Q*VQQTNSKCLKY*MEPARPTFSP

7109	C	21	410	MCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXH GISGFHYLENQEPTSQPCCFYKTELKQSLAVVLAL
7110	A	3	178	PPQPRVAGTTGVSRAAPPVLI FVFVDRRSHHAQDGLELLGSSDLPT SASQSVHIVIS
7111	C	134	295	MNSVPGLAKSVGLLRTRYDSPKQPLLCEAVVLICKDL SRGWQKPGT QGIGG**
7112	A	3	864	LYPAKLSGGWIAMPKYWRAPNCSNTGGRLGANNRPGSFYKFPLKDGP RLQAWLQHMGCEHWVPSCHQHLCEHFTPSCFQWRWGVRYLRPDVAP SIFSRGPPAKSQRRTRSTQKPVSPPP LQKNTPLPQSPVFPVSGPER LEV LGPTSGSPKTVA TMLLTPLAPAPT PERSQPEVPAQQAQTGLGPV LGALQRRVQRLQWCQERHQALQALERLAQQ LHGESLLARARRGLQR LTTAQT LGPEESQTFTIICGGPD IAMVLAQDPAPATVD AKEPELLDTR IPSA
7113	A	3	155	HEGPLALGFHLAYITMRLFLALI ITTIYHCEYHLPFLT SPECHDYHH IKQ
7114	A	1	122	TRVDPRVRKKTTMKII PFNR LTIGEGQQHHLGGAQAGDV
7115	A	84	579	NWKAGMRPSTADYAMFKVVHEVD\ KYRFTYAY FAGGDAEDAFDGYD FGDDPSDKFFTS\ HNGMQFSTWDNDNDKFEGNCAEQDGSGWMNKCH AGHLNGVYY\ QGGTYSK\ ASTPNGYDN GIIWATWKTRWYS\ MKKTTM KI I PFNR LTIGEG\ QQH\ HLGGAQAGDV
7116	A	19	418	VEMGFCQADQAGLELLTSGDPPASVSQSTGITVLSLSFFFETESRSV AQAGVQWRDLGSLQRP PG\ SRHSPASASRVAGTTGARRHAWLIFY F/LVETGFHRVSQDGLDLLTS* SARLSLPKCWGYRREPSAR
7117	C	207	401	MGXXIXPLXKTPPFPGVGKNFS PGXPXPPPRGGPPPLFFPQK KGXXPPPPFPKVLGLQA*
7118	A	2	681	FFEMESRSVAQAGVQWRDLGSLQAPPPGFTPF SCLSLPRS WDYRRP TL LANFFVFLVETGFHCVSQDSL DLLTLRSARLFFFFFETESRSVAQ AGVQWRALGSLQAPPPG\ SRHSPASASQVAGTTGARHYARLIF\ VFL VETGFHRFRSDGLDLLTS* SARLGLPKCWDYRREP RPAPVRVYFN R SVFIEYVQFCKLLFTFKINVR SQNILGSPN ILKSLLKNLN
7119	A	3	265	FFFETESRSVAQAGVQWCHLGS LQPLPP\ GSSDSPASTSRVAGV\ TI TAT* VAGTTVVRHHAWLIFVFLVETGFHHVQAGLEHL DLR
7120	C	359	583	MLPRLVSNSWAQAILL PRPPEVLGMLS SYPNNSGLE MSTIWLIKVTL QNILIWGL SHPKEEKR FLFLRRSFACRP
7121	A	279	566	FRRRFPLISLFFFFLFFFCFFFETESRSVAQAGVQWRDLGSLQAPP PGFTP FALS PRLEC SGAILAHCKLLL PGSSHSPA\ SANRVAGTTGTR HH
7122	A	237	524	PQEFKTS PGNVARPQLYNFFFFFFFFETESRSVSQAGVQWCDLGSLQAP PPG\ SHHSPASAS* VAGTTGAHH HARLL\ FVFLVETGFHCVSQDGLD LLT
7123	A	1023	1459	KGTRKRGQGIKVHLP IPI LENLICFCTFGLFLVFLFLFPFFFFFFF EIESHSVAQDGVQWCNLGSLQPTPPG\ SSDSPASAS* VABITGTRHY AWLIFLFL/VEMRFHHVQAGLELTSGDPPASASQSAGIRVM SHRGL VFLYYK
7124	A	1794	4614	RFFSFFFFFFESH SVAQAGVQWCNLGSLQAPPPG\ SRHSPASASRV AGTTGAHH HARLIF\ VFLVETGFHRISQDGLDLLTS* SARLGIPKC W DYRCEPHLASI
7125	A	2	441	FFFFFFETESRSVAQAGVQWRALGSLQAPPPG\ SRHSPASASQVAGTT GARHYARLIF\ VFLVETGFHRFRSDGLDLLTS* SARLGLPKCWDYRR EP RPAPVRVYFNRS VFIEYVQFCKLLFTFKINVR SQNILGSPN ILK SLLKNLN
7126	A	3	226	CETESRSVTQAGVQWS DLGSLQAPPP\ GSRHSPASASQVAGTTGAHH HARLIF\ VLLVETGFHRVSQDGLDLLTS
7127	A	153	504	KHFFFFFFFETESRSVAQAGVQWRDLGSLQAPPPG\ SRHSPASASRV

				AGTTGTRHRAWLIF/VYFLVETVFHRVSQDDEL*KLYRENSIENILV QKCLKVYFSHCSRSEITVTGNLL
7128	A	3	313	FLFFETESCSVAQAGVQWHDLGSLQAPPP\GSCHSPASASQVARTTG TRHHPRLIFF\VFLVEMGFHHVSQDGLDLLTLGSGHLSLPCWCWYRC EPPHPSSPSY
7129	A	3	307	FFFFFETESRSVAQAGVQWRDLGSLQAPPPG\SRHSPASASQVAGTT GARHYARLIF/VVFLVETGFRHFRSDGLDLLTS*SARLGLPCWCWYR REPPRPAYF
7130	A	2	91	EMESRSVAQATVQWRDLGPLQAPPPRRKF
7131	B	3686	14131	MTNAFQYVQKNRGIDSEDAYPYVGQSYYNLVSSSQBESCMYNPTGKA AKCRGYREIPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSGKVY DESCNSDNLNHAFLAVGYGIQKGNKHWIKNSSQAQTGLTPDECLLL GYLDKGLKRRKDKAGSLQWAYMAIARLGGFMDSMPTGIAIWGALX*
7132	A	8044	8378	YIDVKTFFFFFLPETESHSAQAGVQWHDLSLQPLP\PGSSDSPAS ASRVAGITGTHHAWFIFVFLVGTRFHHLGQAGLELLTSSDPPASAP QSAGITGVNHHTQPKFI
7133	A	3	283	HERFRVCAIROGQDSLGHQDLGCPYSTGLFISQRTPEPTTTNRYTV ESTRTRRALSQKQSAAVILELGAFFYIMNAFIIQYFAFKRKYNSIL
7134	A	2	177	RQNSLRGSFHSAAVLKMDDFGAVPCTDLVVQSSISPHQSKQSQPVELD PFGAAPFLYRQ
7135	A	1	491	KOPESFFKVLMLKDLGLNFHVSVLGETFTDVPDIFSEAKKALGSSV LHWGYLPSKDDYFQVLCMADVISTAKHEFFGVAMLEAVYCGCYPLC PKDLVYPEIFPAEYLYSTPEQLSKRLQNFCKRPDIIRKHLYKGEIAP FSWAALHGKFRSLLTTEPREDL
7136	A	3	612	LQYQKVDKFLHLPKFDDWLLDNDIALLLKSPNLNSVNRIPICTSEI SDIQAWRNCWVTGWGITNTSEKGVQPTILQAVKVDLYRWDWCGYILS LLTKNMLCAGTQDPGKDACQDGGALVCNKKRNTAIWYQVGIVSWG MGCGKKNLPGVYTKVSHYVRWISKQTAKAGRPMYEQNSACPLVLSC RAILVLYFGMFLLT
7137	A	2	137	SALGGAPPVPSRPGASPDPLGPPQVPSGPNRAPPGVPRITISDP
7138	A	1	2631	MGNRGMEDLIPLVNLQDAFSAIGQNADLDLPQIAVVGQSAGKSSV LENFVGRDFLPRGSGIVTRRPLVLQLVNATTEYAEFLHCKGKKFTDF EEVRLEIEAETDRVTGTNGISPVPINLRVYSPHVLNLTLDVLPGMT KVPVGDQPPDIEFQIRDMLMQFVTKENCLILAVSPANSDLANSALK VAKEVDPQGGRTIGVITKLDLMDDEGTDARDVLENKLLPLRRGYIGVV NRSQKIDGKKDITAALAAERKFFLSHPSYRHLADRMGTPLYLQKVLN QQLTNHIRDTLPLRNLKLSQLLSIEKEVEEYKNFRPDDPARKTKAL LQMVQQFAVDFEKRIEGSGDQIDTYELSGGARINRIFFHERFPFELVK MEFDEKELRREISYAIKNIHGIRTGLFTPDMAFETIVKKQVKKIREP CLKCVDMVISLISTVRQCTKKLQQYPRLREEMERIVTTHIREREGR TKEQVMLLIDIELAYMNTNHEDFIGFANAQQRSNQMNKKKTSGNQDE ILVIRKGWLTINNIGIMKGGKEYWFVLTAENLSWYKDDDEEKEKKYM LSVDNLKLRDVEKGFMSKHFALFNTEQRNVYKDYRQLELACETQE EVDSWKASFLRAGVYPERVGDKEKASETEENGSDSFMHSMQPQLERQ VETIRNLVDSYMAIVNKTVRDLMPKTIHMLMINNTKEFI FSELLANL YSCGDQNTLMEESAQAQRDEMLRMYHALKEALSIIIGNINTTTVST PMPPPVDDSWLQVQSVAPAGRRSPTSSPTPQRRAPAVPPARPGRGPA PGPPPAGSALGGAPPVPSRPGASPDPLGPPQVPSRPNRAPPGVPRC SRRSTLLTANVSSDSSGYLAPRSMVRCEICD
7139	A	2	112	DIKAHTQPVTKAPGGETKIPVTLRSVQNVQPLLAT
7140	A	67	245	AYNLSDGQYGLVDPEFEYFWLCCWLPL*LGGKCLWVLPVSVSGDRN DNDQAERNGSHL
7141	A	356	2252	RSFLDEEFPHYDSLSCADAIQQPLQEKLKQCCHKLYGGQEARIHQTP LTLKHTCWYTPLLDALSLDSFTAVPTLESTPFSGVANQIHTLCERP YGEVKDGA LDVQRQHKCPGPTSGPSPGTNLSCGIRMNDPSMEENG ERVCPESLLQSRGYSSLPLPRHTSSTDGTITSSDPGLEILNMACDL

				DRNSLCKKEEDTRSASPTIEAQGTSPAHDNIAFQDSTSCKDTILNLE AKEEPETIEEHKKEHASGDSVVSPLPVTTVKS VNVRQSENTSANEKE VEAEFLRLSLGFKCDWFTLEKRVKLEERSRDWAEENLKKEITNSLKL LESLTPLCEDDNQAEI IKKLEKSIKFLSQCAARVASRAEMLGAINQ ESRVSKAVEVMIQHVENLKRMYPKEHAELEELKQVLLQNERSFNPLE DDDDCQIKKRSASLNSKPSSLRRVTMALLFLPR\NYLGNAG\MVAGM ENNDRF\SRSSSWRILGSKQSEHRPSLPRFISTYSWADAEKCEL KTKDDSEPSGEETVERTRKPSLSEKKNPSPKWDVSSVYDTIASWATN LKSSIRKANKALWLSIAFIVLFAALMSFLTQGLFQKSVDAAPTQQED SWTSLEHILWPFTRLRHNGPPPV
7142	A	1	835	MRYHFTPTRMAMVKEERKLSTISSVHIPTINLTEESRVSKAVEVMIQ HVENLKRMYPKEHAELEELKQVLLQNERSFNPLEDDVKMSTDTIDST LGSFEALGGETSKGVLEVS DLIAYVADLHFNKRKLEENNKFKLALE TLEETNSQLSEDC TELRLQVKS AHQAIMRTNLLKEELEELKLSMNAS EEQKSMIVAQSKQLE TENRALILKIRILQEENFKNIMDIDRLKKEIE DLSKTETEHQVSTS QILMQLHTYENTL NKDTS LQKKWD PVEC
7143	A	1	3735	MMCRGT V FQAGGTAGAKALS PYPDEDGGDGGGLGTGAAPGPRLRHSKS IDEGMFSAEPYLRLESAGSGAGYGGYGAGSRAYGGGGSSAFTSFLP PRPLALDPASPLGLALAAERALKESSEGGGAPQPPRPPSPRYEAP PPTPHHHS PHAHHEPVLRLWGASPPDPARRELGYRAGLGSQKSLPA SPPAARRSLLHRLPPTAPGVGPLLLQLGTEPPAPHGVS KPWRSAAP EPPERLPLHVRFLENCQPRAPVTSGRGPPSEDGPGVPPPPSPRREENG LPLLVLPPPAPSVDVEDGEFLFVEPLPPPLEFSNSFEKPESPLTPGP PHPLPDT PAPATPLPPVPPPAVAAAPPTLDSTASSLTSYDSEVATLT QGASAAPGD P HPPGPAPAAPAPAAPQPGDP PPGTDSGIEEVD SRS SSDHPLETISASTLSSLSAEGGGSAGGGGAGAGVASGPELIDTYV AYLDGQAFGGSSTPGPPYPQLMTPSKLRGRALGASGLRPGPSGGL RDPVTPTSPTVSVTGAGTDGLLALRACSGPPTAGVAGGPVAVEPEVP PVPLPTASSLPRKLLPWEEGPGPPPPPLPGPLAQ PQASALATVKASI ISELSSKLQFGGSSAAGGALPWARGGSGGGGDSHHGGASYVPERTS SLQRQRLSDDSQSSLLSKPVSSLFQNWPKPPLPPLPTGTGVSP TAAA APGATSPSASSSSTSTRHLQGVFEMRPPLLRAPSPSLLPASEHKV SPAPRPSSLPILP SGFLYPGLFDIRGSPTGGAGGSADPFAPVFPVPH PGISGGLGALSGASRSLSPTRLLSLPDPKPGFAGGLRPGFSDVAD WLEWLGLAEHRAQFLDHEIDGSHLPALTKEDYVDLGVTRVGHRMID RALKFFLERYPALPRPLTQQTLSQPDPSSEERPPALPLPLPGGEEK AKLIGQIKPELYQGTGPGGRRSGGGPGSGEAGTGAPCGRISFALRYL YGS DQLVVRILQALDLP AKDSNGFSDPYVKIYLLPDRKKKFQTKLAQ RKLHFSVYDFDRFSRHD LIGQVVDNLLELAEQPPDRPLWRDIVEGG SEKADLGELNFSLCYLP TAGRLTVTIIKASN LKAMDLTGFSDPYVKA SLISEGRRLLKRRKTSIKKNTLNPTYNEALVFDVAPESVENVGLSIAV VDYDCIGHNEVIGVCRVGPDAADPHGREHWAEMLANPRKPVEHWHQL VEEKT VTSFTKGSKGLSEKENSE
7144	A	2	1161	ECVRLKPTDIQPDIFS YLLHMYTGKMAPQLIDPVRLEQGIKFLHAY PLIQEASLASQGA FSHPDQVFPLASSLYGIQIADHQLRQATKIASAP EKLGRDPRPQTSRISQEQVPEASQLSQLTSNLAQVNRTNMTPSDPLQ TSLSPELVSTPVPPPPPGGEETNLEASSSYEQPASLTIAHVKPSIMKR NGSF PKYYACHLCGRRFTLRSSLREHLQIHTGV PFTSSQQGESRVPL TLC SNAADLGKDAMEVPEAGMISDSELQHISDSPIIDGQQQSETPPP SDIADIDNLEQADQEREVKRRKYECTICGRKFIQKSHWREHMYIHTG KPFKCSTCDKSF CRANQAARHVCLNQS IDTYTMVDKQTL ELCTFEEG SQMDNTAAAH
7145	A	126	572	NFSSNKWNTSQNFANMDNSAQKNERTGKHPRRASEVQK\NDIPGPGF YNVIHQSPVSNVSLSKKGT CMFPSM CARLDTIVSKYPAANAYTIPS DFISK RDFSNSCSSMFQLPSFMKALKFET/PLAPNYYNASVSCCKRR NNVCTRAGF

7146	A	1	1261	MDNSAQKNERTGKHPRRASEVQKALRICIHNTRVLLGSRPGVLEYLA PQCLLLPASLSMAVSSSSVHRGSFSPKAGISTPVVTSHGARNIDIPGP GFYNVHQSPVSNVSVLSKKGTCMPFSPMCARLDTIISKYPAANAYTI PSDFISKRDFSNSCSSMFQLPSFMKALKFETPAPNYYNASVSCCKQR NNVCTRAGFMSKTQRGSAFADKGPPPEVTSSSSHKTEEAALFPEHP LHGHDINESLVKQSPNTLMSCFKSKTNRGLKLTSTGPGPGYYNPSD CTKVPKKTLFPKNPILNFSQAQPSPLPPKPPFPGPQGYEIVDYLGRK HFISSASFVSNSTRWTAAPPQGLPGPDWWHPESVQPRSMEEFEWL PWLGA MGPKERILSSSTGGRNDQGKRQQAGGRLCGQLPVTHH
7147	A	107	227	KKDKIMFLAGTWMDLKAIILSKLMQEQKTKYCMFSLISGS
7148	A	3	407	GGGSAAGSRDSGVWSSGGESGGGSGGWSSGGSGGDSGGGSGGGSGGDS GGGSGGWGGGWNGGWSGGGSGGGSGGWSSGGSGGWSGGESGGWSGGD SGGWSGGWSGGGSGGWARQQHVLSVTVPMEGNSRSELTP
7149	A	3	608	GGGSAAGSRDSGVWSSGGESGGGSGGWSSGGSGGDSGGGSGGGSGGDS GGGSGGWGGGWNGGWSGGGSGGGSGGWSSGGSGGWSGGESGGWSGGD SGGWSGGWSGGGSGGWNVHQSPASPGPALQRCWTGTHPRQRQF WPLCSLRVAPSRPAAPAPQRPQAGACRAASLTGSKDVP GCPHHVAGG PASFPLSAGSSCR
7150	A	2	212	DTPACTRLFDAAYFGQKDSVCGVSECIIMGIPMNIGTGLFKLLHKAD RDPNPPKRPLIFDTNEFHIPLV
7151	A	3	91	HCGGTLELSDDDTSDKTSVNETQPPQSE
7152	A	1	115	PTRPGGSILASLSTFQQMVISRQEYDESGPSIVHRKCF
7153	A	1	1279	MGDTPRQFGGARPRSGGALRGCRSRGGNRRGLCLSRALANGDRRLT MDDDIAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGMVGM GQKDSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTFAMYVAIQAVLS LYASGRTTGIVMDSGDGVTHTVPIYEGYALPHAIRLDLAGRDLTDY LMKILTERGYSFTTAEIREIVRDIKEKLCYVALDFEQEMATAASSSS LEKSYELPDGQ\VITIGNE\RFRCEALFQPSFLGMESCG\IHETTF \NSIMK\CDVDIRKDLY\ANTVLSGRTPPCTLGIAADMQKEITALAP STMKIKIIAPPERKYSVWIGGSILASLSTF\QQMWISKQEYDE\SGP S\IVHRKCF
7154	A	1	111	RLLVSSNSPTSASRNAEITDISHHTQLFNILLSISFT
7155	A	143	295	PSCEVQPSRLLMEPSGPYLSIIMPLIARFDHVVIHSSAFKFAVMVEI LAC
7156	A	186	439	HRCFREEKEKALDPEAACPIAPASLTGVRPQRTALSQDGVEDRKP IPVPYLYFDMGAAVLCASFMSFGVKRRWFALGAALQL
7157	A	3	356	SFPSNLDAYKHHWLQMCWSPWWRYPITVFSPATSTFLLHQHIKIFTL HVEKALNDSSTELVLSDEFAHLRTIVLQNMALKMLTAPQGGACTL LQTECCVYISGNSHNMILLGKPC
7158	A	1	220	ETEHRFSFSQAGVQWCYLGLSLQPPPPGFKLFSCLSLPSSWDYRCLPPC SANFCIFSKDGVSPCWSGWPRTPDLR
7159	C	102	407	MDAGLEAMQKYGKAAPGDRTMLDSLWAAGQELQAWKSPGADLLQVLT KAVKSAEAAAATKNMEAGAGRASYISSARLEQPDGAXAAAAAILRA ILEVLQS*
7160	A	1	2302	RAEGIPVEMVIGDDSAFTVLKKAGRRGLCGTVLIHKVAGALAEAG VGLEEIAKQVNVVTKAMGSEDEAHEGCSRENLGRIQFSVGYNFQES TLTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKKHKLKLETKVDQASL EDEGVVEEHEENDDVEEDCNILDAVDIKKSTTNEGLCEDPRAVGTL IVKNYTGDRINFLAREQARAEGIPVEMVIGDDSAFTVLKKAGRRG LCGTVLIHKAPVEKADKMYEQMRNSSRVGNSKSKQMEMLKTNTVADM NGFNRPIMRFDIIKERISGRQWTTDQQLIQVIRSIGVYDVVELKFAE NRANGQSKGYAEVVVASENSVHKLELLPGKVLNGEKVDVRPATRON LSQFEAQARKLLPVPKGGTARGSWSNRRRTGCGEQRARNGVGLRA SSEDGTGAPPPPAHGRIRHIRRRRDFPETPKRALSSGSCGRWRKEARR CSGGGASFGWRPRASGVLOEASVALEYRRAAPSLDMSYNYVVTAQKP

				TAVNGCVTGHTSAVDVYLLIVTNTRLEIYVVTPSGFRRQVCLPSR AHVACGLGPSASPLGIPACHRCMCVVTAADVGLTVASAILSLPLWMS VGLMCMLPAGGKAVNTAPVPGQTPHDESDRRTEPRSSVSDLVNSLTS EMLMPTQCEDNKDEDFYDDPLPLNEYSQVSEGLDGLSFAFNRSGRYP ENIPKGLDQEGWTRGGIQPQMPGGYALSQPVSCGGHPQPHGEPAP ASPRGKGNTPAQLLS
7161	A	1	178	VCVCVCVCVCVCVCSVPTRICLGAHCIFLCYGVVYIKHDRTRDNTIS HRSPLGSALKEE
7162	A	60	413	SGGAVGTARSPALGMALLVLGLVSCFTFFLAVNGLYSSSDVIELTPS NFNREVIQSESHNRGFRPFSFLGSQWIFPAVKGHSLSHSDSTSGPFN QEVVLDWSFENTATVNFCSIRKH
7163	A	2	1420	NSGVGAGARRAARCRAEAAAAGVTARSPALGMALLVLGLVSCFTFFLA VNGLYSSSDVIELTPSNFNREVIQSDSLWLVEFYAPWCGHCQRLTP EWKKAATALKDVKVGAVDADKHSLGQYGVQGFPTIKIFGSNKNR PEDYQGGRTGEAIVDAALSALRQLVKDRLGGRSGGYSSGKQGRSDSS SKKDVIELTDDSFDKNVLDSEVVMVEFYAPWCGHCKNLEPEWAAAA SEVKEQTKGKVLAADVATVNQVLASRYGIRGFPTIKIFQKGESPVD YDGGRTSRDIVSRALDLFSDNAPPELLEIINEDIARTCEEHQLCV VAVLPHILDTGAAGRNSYLEVLLKLADKYKKMWGLWTEAGAQSEL ETALGIGGFGYPAMAAINARKMKFALLKGSFSEQGINEFLRELSFGR GSTAPVGGGGFP\TIVEREPWDGRDGLPVEDDIDLSDV\ELDDLGL\KDEL
7164	A	547	980	CPQGVSEECSAAREKKCLCINKVGRLLFLKFLILLHQQSIVNVCVCF GHFSLRELSFGRGSTAPVGGGAFPTIVEREPWDGRDGEVSAREDS CAQQILVYSLEPVHLCTWESSPSHQTSALGAPVGLFKRFFSEDPSSSL SQV
7165	A	3	1290	LYSSSDVIELTPSNFNREVIQSDSLWLVEFYAPWCGHCQRLTPPEWK KAATALKDVKVGAVDADKHSLGQYGVQGFPTIKIFGSNKNRPED YQGGRTGEAIVDAALSALRQLVKDRLGGRSGGYSSGKQGRSDSSSKK DVIELTDDSFDKNVLDSEVVMVEFYAPWCGHCKNLEPEWAAAASEV KEQTKGRVKL\AAVDATVNQVLASRYG\IRGFPTIKIFQKGESPV DYDGGRTSRDIVSRALDLFSDNAPPELLEIINEDIARTCEEHQLCV AVLPHILDTGAAGRNSYL\EVLLKLADKYKKMWGLWTEAGA\QSE LETALG\IGGFG\YPAMA\AINARKMKFALLK\GSFSEQGINEFLRE L\SFGGSGNGTL*GGGFSLPIVEREP\WDGQGCGRGFPWGDDH*PSV DAE\LDDLGLKDEL
7166	A	335	519	ILFPGSGQGLRSSDQKAAKLALL*FQKRSEMYKTK*FWGRKMSQFFF SVVRHTNPGSRLWA
7167	A	2	386	RQSLFSIIQAGMHWHLVSLQLLPPRFKRFSCLSLPSSWDCRCVPPC PANFGIFSRDGVSAAMLARLVLSWASCDLPTLASQSAGMTGVSHCTQ SEFFFIILIALTALIVLHQGKPYTNSVRHRLGNFC
7168	A	311	493	NIIITHKFMVKELICCLVLLLLTTVLYRIYHGLLTAEKGTVEFSHTK DYTGNRLLLLNVP
7169	A	2	82	WCDLGSLOPPPPRFKQFSCLSLPRHS
7170	A	51	347	LPRLDGVQWCDLGSLOPLPPRFKQFSCLSLPSSWDYRHAPPRPANFV FLVEMGFLHVGQAGLELLTSGDPPASASQSAGITSVSHRARPLHL NQPR
7171	B	188	353	XDVVVPVANCGVQEYNSNPKEHVTLRDYITYWKEYIQAGYSSPRGCL YLKDWHLCS*
7172	B	188	353	XDVVVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL YLKDWHLCS*
7173	A	753	1216	QVVEVGPPRGHPSAAGCPSPA*RRWKTRRAGWAARSPAQSRRRRRR PAPRRRLPGPEPGRRRGRHPPGLGSGCRRGRASRGPS SARVEGPSS SLPPERKR*GPASEPEDAGRVSAPPAPGA\RACHTARGSPRSSLR RRAEAARSALGLV
7174	A	1	1777	MPVLPVTATEIRQYLRGHGIPFQDGHSLCLRALSPFAESSQLKGQTV

				TTSFSLFIDKTTGHFLCMTSLAEGSWEDFQASVEGRGDGAREGFLLS KAPEFEDSEEVRRINRAIPLWELPDQEEVQLADTMFGLTKVTDLTL KRFSVRYLRPARSLVFPWFSPGSGSLRGLKLEAKCQGDVSYEETT IPRPSAYHNLFGPLISRRDAEVVLTSELDLALNQSTGLPTLTLP RGTTCLPPALLPLYEQFRRIVFWLGDDLRSEAAKLFARKLNPKRCF LVRPGDQQRPLEALNGGFNLSRILRTALPAWHKSIVSFRQLREEVL GELSNVEQAAGLRWSRFPDLNRILKGRKRGELTVFTGPTGSGKTTFI SEYALDLCQQVNTLWGSFEISNVRLARVMLTQFAEGRELDQLDKYD HWADRFEDELPLYFMTFHGQQ\NIRTVIGTM\NHAVYVYDICHVIDN LQFMMGHEQLSTDRIAAQDYIIGVFRKFATDNNCHVTLVHPRKEDD DKELQTASIFGSAKGGEWSAPHSTSSRPSAQPKSDSTVAEAAPLASD FTAYWIWFLTWGRGRASRDREFGYLAALN
7175	A	1	666	GTSDHWADRFEDELPLYFMTFHGQQSIRTVIDTMQHA\YVG\YDICHV IIDNLQFMMGHEQLSTDRIAAQDYIIGVFRKFATDNNCHVTLVHPR KEDDDKELQTASIFGLSQRQAR\EADNVLDPAQTGKLGNRGQKRYF AGVPKEPF*WEM*GVFPLEFNKNSLTFSIPPKNKARLKKIKDDTGPV AKKPSSGKKGATTQNSEICSGQAPTDPDQDTSKRSK
7176	A	27	285	VFFFFFFFFLRRSLALLPRLECSGTIVFLVETGF\TMLARMVISIS*PR DLPALASQSAGITGVSHRARPAFNFNLTINILPPLLLWTF
7177	A	12	336	SPVQL*F*LFLVFC*LWSWSAVVYLGLGTPSADAHT/AGLSKTPPH WAARARLDDVFSRLTFSSHSLNMELVQDLTASAPMYSSTSRDPP/CL GLPKCWDYKREPPRAH
7178	A	74	463	HISQHDRSYLQVLLASYKTASFLFFFLRQSL/DSVTQAGVQWRDLGS LQAPPPGFTPFSCPSPK*L/SSWDYRRPPPRPANFFCIFIVEKECF TLLARMVISISWPRDLPASASQSAGITGMSHRARPAQVS
7179	A	1	412	TRMGLPDASRRRTCRMDPEGWQEAMSSA*GRITLQRLSTG\PEGQGG REKVGPEGGSENPPQPKAAGVLSKHLPGAPAQPQRPPSSPPPLAGP LTERVEKVCDFLDAAGDYLN/GTPG*PSPGESPAAQDPPVPPWPP
7180	A	117	295	TFFPHHTPPPELPDPKRPNTFEKKGKHENKAPGCSLKEEKEGAERP AGALSPCGPNVV
7181	A	279	1066	IQHPRLSADDFRVNCETEPAM/*HAVENDIHGLCELQLETEIQAFKE ELL/FMKKNHEEEVKGLQAQIASSGLTVVVDAPISQDFAKIMADIWA QYDEVAQKNREELDNRSQQIEESTTVVTTQSTEVGAAMKAMTELTR TVQFLEINLDSMRNLKASLENSLREVVARYALQMEQLNGILLHLESE LAQTWAEGQCQAQEQYQALLNIKVKLEAAIATYRRLLEDGKDFNLGDT LDCSNSMQTIQKTTTR\R*TRQIVDGKVVS
7182	A	60	847	IQHPRLSADDFRVNCETEPAM/*HAVENDIHGLCELQLETEIQAFKE ELL/FMKKNHEEEVKGLQAQIASSGLTVVVDAPISQDFAKIMADIWA QYDEVAQKNREELDNRSQQIEESTTVVTTQSTEVGAAMKAMTELTR TVQFLEINLDSMRNLKASLENSLREVVARYALQMEQLNGILLHLESE LAQTWAEGQCQAQEQYQALLNIKVKLEAAIATYRRLLEDGKDFNLGDT LDCSNSMQTIQKTTTR\R*TRQIVDGKVVS
7183	A	645	861	KYYRKRGIHSAIDASQTPDVVFASILAAPS*ATCKDLVMFI*CWVQE GISFHPCEAMGGNDRTGKEKLPSG
7184	A	2	1327	RPQSLSPVLSLSPDSMSFTTRSTFSTNYRSLGSVQAPSYGARPVSSA ASVYAGAGGSGSRISVSRSTSFRGGMGSGGLATGIAGGLAGMGGIQN EKETMQSLNDRILASYLDRVRSLETENRRLESKIREHLEKKGPQVRDW SHYFKIIEDLRAQIFANTVDNARIVLQIDNARLAADDFRVKYETELA MRQSVENDIHGLRKVIDDTNITRLQLETEIEALKEELLFMKKNHHEE VKGLQAQIASSGLTVEVDAPKSQDLAKIMADIRAQYDELARKNREEL DKYWSQQIEESTTVVTTQSAEVGAAETTLTELRTVQ\SLBI\DLQ\ SMRNLKA\SLNSL\REVEA/RRTPQLQMEQL\NG\ILLHLESELAQT \RAEGQRQAQEQYAL\LNKVK\LEAEIATYRRLLEDGEDFNF\GDA LDSSNSMQTIQKTTTPPG*VGLGKVVS
7185	A	2	345	FFFFFFFFETESRSVAQAGVQWRDLSSLQAPPPG\SRHSLASAS*VAGT TGVCHHARLIF\VFLVETGFHHSVDGLNLLTS*SAGLGLPKCWDSE

7186	A	178	389	KLFFFFGDKSFRFCCPGWSTMV RREPLHPANLLLLFFFFFFFEMESPSVAQAGVQWRDLSSLQAPPP\GSC HSPTSL*VAGRLRNKNCLNPDW
7187	A	546	850	FSVLFFFESESCSVLQAGVQWRDLGSLQPPPP\GSSHSPTSAS*VA GTTGTCHHTQLIFIFLVETGFHHIGQASLKLLTS*FAHLGLPKFWDY RCEPPHPA
7188	A	4	412	PIERPHELKHRLPHVQKLVEDVGDGVIPAALLEGQAGWSHGFLVFLV EIKSAEGP/PGPADSRVRGVRPQRSQSAGPA*RAGRDQGVCRSLGQG RGGGRATSLVLHPPGYPGCWFSVGVPSLPQYTGIRSSSPRTRG
7189	A	148	268	LQPR*PLTCAPPPCPVQTQTHPISVSQTLGLLEFCCSLSL
7190	A	397	1449	RSHPSGTGRRTSRLESWFLGVSCCKSKVREGPLGPA**AG*RGVRPQ RSQSAGPA*RAGKRQDGG/SPEPRAGVGGEVGTQSP/GPSGASGYPG MLVSKPVGGSASWLPAGCPIPS*LS*QRSQSPSSCLIGHLLALWA AFGLGVTSLPQYTGIRSSSPTA*ATVQGDSCGHKGGTGGTGLGRGRNT QPDACGRGHRSSPTR/RPHGNPNGNTGCAEGGQARSLLPKLAPKLP GWPVSVPAVG\PGDFGWRQAQYQSSLWDLSSPRNTLGRSATSAGPA PPALLGAGSGRSSGTSPAAPGCSSRCHCWASAPAGVSGGPG\GRGAE APPSPTLAQRGSPPG\AAIFPPACGIPP
7191	A	47	1654	LHVPARPPGCGAFLAGGPCPGWGPRAQLWPQ/SAAPGPPHP\PAL PSPVFTWPRLLSH*S/RPA/VEQCPPEPHVYP\DPASSWPKSASP PRVACPCPAL*/PPFGDSCLLCTAGLRGPHDTELQVWVRP/HPG ASAEM*AHKPPPLAQKPPRPSISVPQPSAQLWYPAGWPVT*AGTWL GYGAI*SPQGLFSFYEMEHGVPASLNPPKWEPHDRV*LGGGR*GKSE VPRGTPSLTGLFRGVPQGPAPTGTQKHFPNDMVSLISFFCLFCF GFQLG*/PPGL*SIHIEPLTGLPGCQG*A*P*VLLSTAGSAHAV**G SELVHLQS*LHFPSFCPPPVLAALDLQVCRPALSAFLACGPPAIPGSW SPEGPVSLWMGVRGVVPLCGLSLYPAL*NLARRGPGQPFYTGK/IGEG TPTPHKPCNHQVRKLGVLPGGVKTKIEVGVGPTR/PKAGETRG*V GRVPQSLA*PQCVSPEMLP*LSGTPGRSWG/PVLSPTPAHSQALRLC GHSPPCWSLVIGLELYFDAMKTLFISNVYIF
7192	A	4	496	NRRTERLGRWCPCTGAWPAPVNLAKLAPS/HDSEQVSGSCVPLAQSM APPGPAWRAGHH\RRRSENPRPGPFFGSFFKRFGTNRGWSRRDDDPG GPGSGSRWPPAPRRGGQWRCPREPG*RRSSSAGRGSSPCALRHRATK ASSSCSSPCPPTPTKRERAAASC
7193	A	3	516	SVPKREELQGHHRVVRGGEHRVWTRQDVLQHRLPATSVWTHPVLPPTA RAPALGRASGAARRTAARAAPL\PAVPAAAAAPGRARPTTTWPASPP SPRSASPPTAPSSACWSPTP/GSPFALRPLRAGLGAVYTRSAHPRR PLPAHLCLVRHRATKASSSCSSPCPPTPTKR
7194	A	2	326	GGGFRPLFPPLWRPKPVGPVRVEIFGPACPPWENPFSKIPNLPYV GPSDYSRF\SEGLARKLPLTRKGRFR*PKFPPLPSFLGKKREIRFPK KTKKKIFINSSSSC
7195	A	3	345	ERQKLHYKYSKQFLTTFQDWNTN\VKAEPEEQKLATMFREQQKSCL *ARMVQRQRH*NKLN*NQQLRSLLEDLEENQSS\FTDEQSDLRKEMA RLQTKLMKETLQDDLALIHSC
7196	C	68	319	MWFPWACTLGGQGLSGVTPDHAWDLFRAWLSHLSRVVPSRGPLSASS PPPLLPGTLGCLRLRSCCHMGLEPPTASSLSRGPPLSP
7197	A	56	947	HRKLDNRYSRHMGCGSPGPEPRRAEPCPP\RCMPTKETGAFRSHTR SRLGPF*SLAEPF/PRVPVSRGPLSASSPPPLSSRDAGLQTSQLLP /SWGWS\PNSIPELDLGPLSPTGRLSAAFPCRSPPSTGNGKDATSQ VDSHPH\PSFRSPGLELSRCGDPVTATSPHEWTQQGKDWRPCSCPL VMQAPPTSHIFLPPSRSSLRPRAPSGCPWGCLG/RPPAGPWATPL AGLPSWS\GVRLPG*GVLPASRGSG*GPPRHRPDAGSERPAAAAAG FAGP*VCSNSSLALPSVYEGLL
7198	C	161	262	MLKGIPCLHPPPLASSSQSDNSQKCLQTLPSLPR*
7199	A	132	1007	NPQAPQATKKEGRKNARKGGSVCSGVWPWGPPrKVPVWRAESPGP GESHAGFESLRHGHAGAGPKGMPRRLPTENTVSAEGSTGGESGARVP

				DTGKGL*PATHPLPWGSLSGF*ETQRL*G/PCLEGG/YPGEAGQSLE TFLAVV*LGAAG*GWVEARDTFKHPTVCRAPTKEDESPPETQQSGAG IGEAAVWCQPHIGRRALQEACGEHGDGRGFGGNHAE/PDRGGNEAAP TMNNPHTPDGHTSL*G/VTGPSP/PGRWGN*GPESSEPGLDPGPPHP PTSWCGLFLRSFRLHS
7200	A	59	326	TGLSPGSEIGALPGNLV*APFFFNPKNLPNAVGP\PGVPPFWGG*AR GLGGPRSSEFPLVGLGPLAFRLGTLKGPVFKKNQESKKKTSV
7201	A	3	263	TLRKKFFQPGKTTRFSPHTP\FSSFFPQKKEKL*GGNPPKFPPPKKK PPPKKP/HHPSSSPPKSSSSQSHAPPKKGPPPEPLKKNPP
7202	A	1	348	RYRSGIPGRRTAGETPSLLKIQQPG/GDGARS*SRLRLRLRQENRL NPEGRGCSELRLCHCTPAWARE*DSLKKKKKKEFKPIYFLTLWDV FRTQYYSIPMCLLCGEMVTDI
7203	A	3	442	SSGSRSECRFLPLLNFVLEILAGAIRQ/QKE/IKGIHIGVKVSIK LTEVINKFIKVA*YKIN/S/NKSVVCLYTNNQLEKKFKISSSSSSS SSSSSSPNH*GKOLYNENLKTLLKEMKENKWINIPCSWIRRLNNVNI SILSKVTYKF
7204	A	3	310	TINCVDITDIYRLLHPSTADCTFCPSSNGIFTNIGHILG\KTHINKF ISIEFI*CLLSDHRIKLEINNKT\WKIPKYL*INTLIKEKCEEQF*N TVN*NPNTI
7205	A	3	90	AIFFLPDEGKLQHLENELTHDIIITKFLG
7206	A	2	1053	TMPSVSVWGILLLAGLCLVPVSLAEDPQGDAAQKTDTSHHQDQDHT FNKITPNLAEFASLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTK ADTHDEILEGLNFNLTETPEAQIHEGFQELLRTLNQPDSQLQLTGN GLFLSEGLKLVDKFLVDKLYHSEAFVNFQDTEEAKKQIN\DYLE KGTQQKIVDLVKEL\DRDVFALVNYIFFKKGWERPPFEVKOT\EEED FHVDQ\ATTV\KVPYELKR\LGFMN\IQHL\KKL\SSWGAA**KYL\ GNATHLLSCLDGGGNLQHLGKIELHPTIIHSPSFLGEIEGQ/DRSC PALHFTQIVPLLGTYGFLKSVLGFNWGIH
7207	A	2	334	RDPPGPGPAITARERKCAKH\PSLHQTIVTHLKL*VVLAQLTLEBPT HCHANPDLIFEDMEAMTDLELHELCOQDRHINNQLDMDLILDSGKF QVVGCI LSELKQKDSSN
7208	A	1	306	LRRS/LCSVAQAGVQWWDLSLQPLPPGPMFPRLSLPSSWDHRRPR PLPANFLYF**RRGFTVLARMVIS*PCDPPASASQSAGITGVRHRT QPPRYVFM
7209	A	156	331	QPLILRCLPPRSIYRFNSIPIKIQVTFF*EKEKSLKFIQNLKGP* ITKTILRKKKVD
7210	A	50	271	FRNIKHQORDYNEQ*YG/NKLDNPEDMNKF*ETRYT*/PNLHQEEIGM LNRPVTKNKL*LVIKIPLTKKSPEPDGFV
7211	A	584	1001	ILKLWGVGTG*TKVPPQVPPTPHSRA*GPPRRECLRRQ*PRP*SPGF GPLSFPTSVELMGVKTVLSQGASRERGSWG*KGSPLNGRQFWAQGGA /LSWVAVGGGGGWRGSNGKG*QPGEQGSSLOPLIPPPRTWRMGPGQ
7212	A	79	317	ERDFLFVPRVGFQGPNLG*LKFPLPGLPLFSGLTLP/RNWGLRGPFT TPG*FLDFLKRGFNIVAQVGLKFWTSGDPPPL
7213	A	247	828	KYLEIVLLLY*RNSESCVFILKCSFSLILLELTMKKKILCLIYI*L LTQVTVQWIFVCPKTF*S*AIFNKDV*IIILIVVKLLLVVWVQY ILSFLILLKINI*DVCVLLH*VLFLKNSLCVYELILDFLYSMIKD N*KECT\FLGPWKVFV*YFLRMSIYFVHNKLALYMKMGLNQIKKVML LSSKKK
7214	A	1	311	LNREKLKAPPLTSGT*QE/CPLSPLLNFNVREVLATAIRQEKEIRGI QIGKEEVTLSLFDVDDMILYLKKPKDCTKKPLEL/NTFSKVA*YIINI QISVAFLNAKSK
7215	A	6	375	ESLRSPSRFS*PSPAYRGHCSRPAETHNGDPCRAEALSDTPVPQS SGSGDHNEKGPSRSPFQLH*PGPWGPAGCRGRPAPTWR\ PAGPLR DSQEDPPSPPEPGSGGAAGQGGG*GLSCFP
7216	A	80	251	GKPHISKTL**NINILL/VQLSVVAIGINIYRTSNVEVLLQFLEDQN

				TFPNFEHLAYR
7217	A	161	334	GKFHISKTL**NINILL/VQLSVVAIDINIYRTSNVEVLLQFLEDQN \TFPNFEHLAYW
7218	A	3	299	PPFRTHQARRFAPTQDWQIGFTQH/RP/GVRKQKYLLV*VDTFTG*V KAFPTRSDKATAVITSLSDIIPRIGLPTCIQSSSTLALISQISHPS CQAATIO
7219	A	526	1108	TQTKNSKIYFN*LLF*ETGPHSLSPQAGVWWHSHISLQPQPPGLK\H PPHPSLLSSWDYRHTSLRPANF*KIFVETGSLHVAQDGLFGLSSSP PVSASQSARIAGMSLGARARPCLK
7220	A	181	272	IQSWFNILKSIHVIHHSNRLK/NVNHIVSSSSSSSSSSSSSPFLIKK Q*KG
7221	A	2	336	YDEEWRRTVHPDEVGNLK*EDR*ALQNRRLRVFLSLMDTGWLDNLLL DIDKADVIVKMLDA\SVIKMEGGTDNDLNILDQDVEDEHA*KPGEPS KNEEGRAVSGLDGERK
7222	A	1	324	VVSYLLVFESSK*KKIYQDCIGFVQDCLNI\IDPIDSLRGKNV I SLDTEKVVGKIQ*PFMTKIFSKLGIEGNFLKWLKYQSSSTVSLNV* ILKAFLSRTE*GCM
7223	A	2	692	ATYIVDFGFQYNI\REGQMLTAFCGMPYVAPERSLGQACQ*PARDI QSLSVILYFRNTVGRRTARTLFFYS/AEASKLQEKILTGRYHAPPLFA LQLDSL/IKLLMLNARKGPSL*LMKNPVWKRIQKMPILIPYEEPL/RG PPQTIQLMVMAGFQAKNISVAIERKFNYPMATYLIL*HTKQERKCS TIRELSLPPGVATSPSPSTELSTFPLSLMRAHREPAFNVQPPEESQ
7224	A	2	340	SSSYTPEYWQ*RSRSHSPMSNQRRHTGRRANPDNTCLRVFGLSLYT TDRDLREVCS*YGPLNGANVVYNQQTGRSQGFVHF*GIDDSKEAM VRANKELDDRR\IRVDYS
7225	A	604	842	RPGGQFCLMEASPSGFNPFLLNLPREWELRVPPPTRGNFF*FLKKN GFI/EVNPGGFDFLN/SNDPPAFASKGVGLTALTP
7226	A	3	343	HEPNGFYAEIECERCNSPELDEEGYSIIPDEPGSTNGKHFYSSSESE Y*E*SHKI\YIQIKPSLSTDILNNAAPVDELKASIGNIALSP*PEGA IKRNLRSREEVARPRRFTSP
7227	A	3	304	HEEKNEKIRNVGLCEAIVQFTR*YL*VCL*RSVNS*NCCWRIVPNIF F*PL*\TFSPSKPAKSLHTQKNRQFFNEPEENFWMVMVFTYTVYLSE IVWVELW
7228	A	1	167	SARGPDGFTAIFYQTKEELVQILLKQFORIKGE\SSLKSL*ETSIT LIPKTRKGT
7229	A	2	334	ARDRAALETVIRRARPELRRPGVQGI PRVHELKIEEYVQRGLQRVGL DPQLPLNLAALYAHVA*EKRVVSILSRILIVIL\VESLILLIIVLT YGYQLSILCTCSVGNIF
7230	A	1	792	FFYREVKPSLFVDCKILITEIPKES/NRVLOITRELSKMLAYKVSML KSILFILT\REYKKVKMPFNIVY/NNTKYSRINLMKDIYDLYTAIYP STAALKYRYMCNLQNIARRN*RPPLNKWW/REE*YSWIEGLVVKILV FPKQIYRFNAPNKKSPPLFNKLIPKFP*KYKGRRISQTNLGRI/TL QDLKIYYKTTLK\NIVWYWEVRQRLLPAPQSAPIPRTCWQLSPSD LQGLKGAEEGLTDWGGKQSGTEITSGHLPLSTFG
7231	A	1	2541	MKPPRPVRTCSKVLVLLSLLAIHQTTAEKNGIDIYSLTVDSRVSSR FAHTVVTSRVVNRANTVQEATFQMELPKKAFTNFMSIIDGMTYPGI IKEKAQAQYSAAVAKGSAGLVKATGRNMEQFQVSVSVAPNAKIT FELVYEELLKRRLLGVYELLKVRPQQLVKHLQMDIHI FEPQGISFLE TESTFMTNQLVDALTTWQNKTKAHIRFKPTLSQQQKSPEQQETVLDG NLIIRYDVDR AISGSIQIENGYFVHYFAPEGLTTPKNVVFVIDKS GSMGRKIQQTREALIKILDDLSPRDQFNLIVFSTEATQWRPSLVPA SAENVNKARSFAAGIQALGGTNINDAMLMVQLLDSSNQEERLPEGS VSLIILLTDGDPVTGETNPRS IQNNVREAVSGRYSFLCGLGFGFDVSY AFLEKLALDNGGLARRIHEDSDSALQLQDFYQEVANPLL TAVTFEYP SNAVEEVTQNNFRLLFKGSEM VVAGKLQDRGPDVLTATVSGKLPTQN ITFQTESSVAEQEAEFQSPKYIFHNFMERLWAYLTIQQLLEQTVSAS

				DADQQALRNQALNLSLAYSFVTPLTSMVVTKPDDQEQSQVAEKPMEG ESRNRNVHSETTMTTQTPACPSCSRSRAPAVPAPIQAPSAILPLPGQ SVERLCVDPHRHQGPVNLLSDPEQGVEVTGQYEREKAGFSWIEVTFK NPLVWVHASPEHVVTNRNRSSAYKWKETLFSVMPGLKMTMDKTGLL LLSDPDKVTIGLLFWDGRGEGRLRLRLDTRDFSSHVGGTLGQFYQEV LWGSPAASDDGRRTL RVQGNHDSATRERRLDYQEGPPGVEISCWSVE L
7232	A	560	901	GNPATPSHCSLPQPPTPQEGAA/YNPDDFFF*KQP*QPKPQVSSQPP WPLSTSLPPACPSCSRSRAPAVPAPIQAPSAILPLPGQSVERLCVDP RHRQGPVNLLSDPEQGVEVTG
7233	A	13	2931	EEGRQQSPAADVKTGLRAPLAASAWPHRCCVRRLLARITMKPPRPVR TCSKVLVLLSLLAIHQTTAEKNGIDIYSLTVDSRVSSRFAHTVVTS RVVNRANTVQEATFQMELPKKAFTNFMSIIDGMTYPGI I KEKAEAO AQYSAAVAKGKSAGLVKATGRNMEQFQVSVSVAPNAKITFELVYEEL LKRRLGVYELLKVRPQQLVKHLQMDIHIFEPQGISFLETESTFMTN QLVDALTWQNKTKAHIRFKPTLSQQQKSPEQQETVLDGNLI IRYDV DRAISGGSIIQIENGYFVHYFAPEGLTTPKNNVVFVIDKSGSMSGRKI QQTREALIKILDDLSPRDQFNLI VFSTEATQWRPSLVPASAENVNKA RFAAGIQALGGTNINDAMLMAVQLDSSNQERLPEGSVSLIILLT DGDPTVGETNPRSIOQNNVREAVSGRYSFLCLGFGFDVSYAFLEKLAL DNGGLARRIHEDSDSALQLQDFYQEVANPLLTAVTFEYPSNAVEEVT QNNFRLLFKGSEM VVAGKLQDRGPDVLTATVSGKLPTQNI TFQTESS VAEQEAEFQSPKYIFHNFMERLWAYLTIQQLLEQTVSASDADQQALR NQALNLSLAYSFVTPLTSMVVTKPDDQEQSQVAEKPMEGESRNRNVH SGSTFFKYLLQGA KIPKPEASFSPRRGWNROAGAAGSRMNF RPGVLS SRQLGLPGPPDPV DHAAYHPFRR LAILPASAPPATSNP\ DPAVSRVM NMKIEETTMTTQTPAPIQAPSAILPLPGQGVRLCVDPRHRQGVNL LSDPEQGVEVTGQYEREKAGFSWIEVNFKNPL\ VWV\ HASPE\ HVVV DSGTEESSAYKVGRET LFSVMPGLKMTMDKTGLLLSDPDKVTIGLL FWDGRGEGRLRLRLDTRDFSSHVGGTLGQFYQEV LWGSPAASDDGRR TLRVQGNHDSATRERRLDYQEGPPGVEISCWSVEL
7234	A	3	338	DAWVSVLCCNLSEAKRRINSLSYNCENIRRLPSF/RDVWNGENSRY VEKQASEQQVELLTNERYLMEESQLLLQYLHVYHMNYFLDLTCRPTF YCYLTEAPIG*PMCKGYLS
7235	A	147	380	ASCRFDFFCLLCYRVLFNSLTVFCFAYRYFNIYMSFCFTFFLYFWWL /FCYDFLL/DYVF*TLILVLCFFPVSVFMFLI
7236	A	1	257	PTRPDFFAQOQHLTPDKIYHVTVMPCYDKKLEASRPDFFNQEHQTRD VDCVLTTGEVFRLLLEEGVSLPDLEPAPLDSLCSGAYA*EPTSHR\G GGSGGYLDHVF RHASLQLFDS/DVV*VSSIHLR**DFFAQOQHLTPD KIYHVTVMPCYDKKLEASRPDFFNQEHQTRDVDCVLTTGEVFRLLLE EGVSLPDLEPAPLDSLCSGAYA
7237	A	2	502	PVWWNLQRRTSAGPGTAVPGLAVA*FRQTGLTRSPSSGRD GAGVRDL WNPPPPVPIPL\PLGFHLRGPDSTLAEQPSACLPGS/PPCRNGLGQP QQHGHLPWPG*IGIQFRLGFHGNQPPGPSNLPPYPPFLFAAPLHTRHV PC/LHHCCPLTWAALPTPLCLWRCSAIQD
7238	A	1	828	MGKDFMSKTPKAMATKAKIDKWDLIQLKSFCTAKETTIRVNRQPTW EKIFAIYSSDKGLISRIYNELQQIYKKKTNNPINKWAKDMNRHFSKE DIYAAKRHMKKCSSSLAIREMQIKTTMRYHLTPVRMAI I KKSNNRK KKNNIKLYVCRVFITDNCEELIPEYLNFI RVLVDSEDLPLNISHKML QQSKILKVIRKNLVKKCLELFTELAEDKENYKKFYEQFSKNIKLGIH EDSQNQKKLSELLRWLTKRREDGAAILNMIGTTDGIYVCLA
7239	A	2	775	NISREMLQOSKILKVIRKNLVKKCLELFTELAEDKENYKKFYEQFSK NIKVGNNH*FSNWPL*FFFFFFNSESLCKEHTL FQLGIHEDSQNRK KLSELLRYTSASGDEMVS LKDYCTRMKENQKHIIYIT\ GKRTL CYS HTRRSYNLVGSVGVFSTQVALLQLVLI*AR*LT*TRSF SVL GSA*VS G*QEKSELDETILNC*KV*K*LCNTSGETKDQVANS AFV\ERLRKHG

				LEVIYMIEPIDEDCAQGLEEF*GK
7240	A	1	2303	QLLQRPVAVPLVLCGHLAKMPEETQTQDQPMEEEEVETFAFQAEIA QLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDPSKLDGK ELHINLIPNKQDRTLTI VDTGIGMTKADLINNLTIAKSGTKAFMEA LQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGG SFTVRTDTGPEMGRGTVILHLKEDQTEYLEERRIKEIVKHSQFIG YPITLFVEKERDKEVSDDEAEKEDKEEKEKEEKESEDKPEIEDVG SDEEEKKDGDGKKKKKIKKEYIDQEELNKTTPWTRNPDDITNEEY GEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFVPRRAPFDLFENRK KKNNIKLYVRRVFIMDNCEELIPEYLNFIIRGVVDSDELPLNISREML QQK/SKILKVIRKNLVKKCLELFTL/AEDPANYQK\FYE\QFS\KN LKALEYHEDS\QNRKEAFPELLRY\YTSAS\SEMDTLKD\YCT\RM KENQKHIYYITGETK\QVA\NSSLCGTVFRKHGL\EVIYMIEPIDE YC\VQQLKEFEGKTLV\SVTKEGL\ELPED\EEKKKQEEKKTKFEN LCKIMKDIK\EKKVEKVVSNNRL\VTSP\CCI\VTSTY\GWTANM\B RIHGKLQALKETTSTMGFTWQPKHLEINPDHSI IETLRQKAEADKN DKSVGILVILLYETALLSSGFSLEDPQTHANRIYRMIKLGLGIDED DPTADDTSAVTEEMPPLLEGDDDTSRMEEVD
7241	A	158	405	RMNLDSDGMDIIISQESSLDMEGNYKKAQKNEREAIRLILAL*SFFD DGSRIYIS/CEQSGKQIFSPH**GINFQIGLSSTWSP
7242	A	3	442	TLLMFNNNVSLTLTFCMFLEFSLPCTEDVPTCGDSCDKVLECGIHR CSQRCHRG/CT*VIYFHAVFQAGPECLHCEEGCSKSRPLGCLHPCI LRCHPGCEPPCVQMLGTAESAVLPQACHCPQFCLQSPFLLFTHKEPQ SSWSSG
7243	A	2	324	SGWSLTEQDPYNNIVRTAIEAMAAVFGGTQSLHTNSFDEALGLS\TV KSSLIPFSLHFLFS*QFSLSYISIFLFIFFFYLSLLIHFFYIFY LISIFLFFFLFIY
7244	A	1	361	RELLAFWQNFKLRPQGPFFSP\GPGGEKKR*SLPKTPPKGGPPGP/S PNGRLPSGGQLPPPRGG/SPQSSSLPKGPQGWGPPFP*RSPPCPH RIGVPQVSSSPTPGLVFPGRPLNPGNLGG
7245	A	115	314	LVRSLTSLPHSPNPNTLSLPS*LPPYGPVYLSHYPPSPPTITSLTHPP PSPSPPTSLPPP\SPITPTS
7246	A	2	326	NEGECRKDVEMEPVLQAEKTNFQNHKGHEFIPTL\WHFPANCDAK PLWHVIKPPPALECRCHVKCHRDHLDYTDLLIFPCNIRYDVSSTLR YS*LLHFSDEITII
7247	A	1	364	EHTRAEDHMLEEREER*RAERAQREE*LPEYQERMTL*EADRNIRP RELEIEERER\RTTEERILGDSSLSRKDSRWGDRDSEGAWRTGPEAH SEWTIGSPQMEWRP*EWLYDDRSYTD
7248	A	86	512	RGRVEAAPGYGSHLCHNFLPCTYQKFGQPPGLQRTAASYSSDTMLG TKAETHPTFAFFPAQGPCKESWQSRDTSARSETLGTACS YNTGNNA GAAHGDTEDLQWLQKRE/RSERKTRTDLKGVRTSNGTARDDNCAY SP
7249	A	2	703	PDCPSRPT/YARGTSPGNKTENAHKGPKSVSSAPKMR*SLQDTG/RE DTREPVRFHDTGTKEQTVIFAD*KIAGRCKT*GQFPRQRPPHGGGS TPQLFSAAGTSFPAFPAVKVHGFKTSPTGRGGGHWANTR\SFSLW ATKKRESERKTRTDLKGVRTSNGTARDDNCAYS PHRRERGAPPPAHG LYRRSVCARKNHI VLSKTGGRSVRRHDHRRSRWRLPGVSHHMRRS QR
7250	A	148	359	LGIDLTKKVKLSKKNYKTLMKKIEDDSN*KDNSCL*IR/MTILPKA IYRFNTISVNIPMRFLPDADAW
7251	A	1	389	RGAQAI IIVF/NLNDVASLEHPSKWLADALKENDLPSVLLFLTRAQY ALMEKDALQVAQEMKAEYWAVSSLTGENVREFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
7252	A	1	144	YALMEKDALQVAQEMKAEYWAVSSLTGINSDDSNLYLTASKKKPTCC P
7253	A	174	810	DQGGNWAYECQWEGPCRLTHPLLSTSHGRQWLADALKENDPSSVLL

				FLVGSKKDLVSVPVGGPLPSLVRECPPLTLAFPQTPAQYALMEKDAL QVAQEMKAEYWAVSSLTG/EVGGFRALL*HSCALLSLLHLQLCPVS PDPALPLSTYLLSVSGENVREFFFRVAALTFEANVLAELEKSGARRI GDVVRINSDDSNLYLTASKKKPTCC
7254	A	1	524	MERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAI IIVFNLNDV ASLEHTKQGVAECLKEE*PSRVVLF\LLGFKKDLSTPAQ\YALMEKD AFPGGPRRLKAEYWAVSSLTGENVREFFFRVAALTFEANVLAELE KIGGLDVIGMFVRIN\SDDS\NLYLTASKEEAPHVCP
7255	A	1	258	FFFFLPEMTSTVYCRYTNEPSLWLGTVHGPADDEHGQPTFPPTPESCA VIHSRQKVAVSNTGHRFPWLGGASLIHRLAHLSEWPTSR
7256	A	2	564	RCFARYRPVHADPLYCQGHAAVPGYSTVSRTHAPGG/VQLPPPPPYT A/GRGAQVGRGCSPARSGAWPHRSGAVDHLPTQGDHTAPDHSSGLND HSHHGAGARHLPPQGHAAWPP*DLNPCRTQPS*PSHSPRPGSLAP VAPPWALGWNQYFYPKSDSLLLLAKLYLIQWVPCTVDFPNVINFI K
7257	C	30	323	MRLQLPSTSHLPVKRGXKEGEAVVLPEVEPGLTAREQEATPRPRETT QLPTTHQALGWNQYFYPKSDSLLLLAKLYLIQWVPCTVDFPNVINFI NIK*
7258	B	249	374	RLRWPLREVGQSVDQRC*TKPREPVSGIRYCDFLPGVYDCT*
7259	B	77	867	XAGALQDITLSQQTPTSTWKDTQLLTAIPTSTPEPTGLEATAASTSTLP AGEGPKKEGEAVVLPEVEPGLTAREQEATPRPRETTQLPTTHQASTTT ATTAQEPATSHPHRDMQPGHETSTPAGPSQADLHTPHTEDEGGPSAT ERAAEDGASSQLPAAEGSGEQDFTFETSGENTAVVAVEPDRRNQSPV DQGATGASQGLLDRKEVLGGVIAGGLVGLIFAVCLVGFMLYRMKKKD EGSYSLEEPKQANGGAYQKPTKQEEFYA*
7260	A	93	1050	TSGSHSGITQFLPCFSGAQPTGQSP*KRSPGPQHRAARCTHFPEG SPFFGSSCSRPRNRWVSAWWAGS*RPQWSQELTQTPKQAGGQWRG PAPSRTPMPRRLEPPQHPKEQERHGVLEQSR/PRTLPPALGHTCV* DQPSAFPVPAQPWGNPSMGSA/HERSWVCHVL*LSSHPLIQRRGSP CPPPVGLGISPSPCPGGQPRQPD\SSLLGA*ASGFSGTPKFKGPGT HHGPCQPLPSPAGLGSGLGEDLEAVGRTQPSNA/PLAPGQ*ATGSSA LQPPVHTASNAPGPVSPDAPPPLPDQAQRLQDQQAkakPCPR
7261	A	2	643	PRVRLNGIVDR*VLGCLPCYDLGIFTDRDLGVHADAHDLVENL\KDL IA**IPFLAEGIRIHGDKVTVALRPFHERMEACFKQLKEMVENEYGV RIMPSSLD*RGIRPRSMVRAFTMPSSSRPLSVASVSSLDSTPSR PGSDGFALEPLLPKKMLSRSHDKLYKDDLDTDKKDYMTYNWTCRQFQ ISRDKMKRTDVSLEYIMLVSPNPNLSY
7262	A	59	340	LLDSEIFATSSSPDSSSMIPPMWLTSMFMFCVGGWAQRKLGCGGTNT DDGDGRGCRFLSEGCWAQRKLGSGDPPASASQSAGITGMSHHARP
7263	A	2	519	ILFLFLFYFISFLRWSFTFVAQAGVQW*DLDSLQSPPPRFK*LACLS LLSSWDYRHMPRPANFLYF**RWGFTMLARLVLD*PQ/CDPPASA SQSVGITGMSHHAGPTMKLLNPQSEVIFSPRNSHSTLLTPLSRHLPH PISISTWCIHYAPLHTVSI SAEAPWLFACQPS
7264	A	19	658	VQPLGDAGMP*DGQRAAPRSPALGARALAQGSTGATAGASRKQEVAA GPAGHRLVSTAAAGGGPSLRQVCSA/GPPGRAVRSGGRGQVRETTPG CLGGAWHPREPNGHSAFRFRPAGPIGVLPQPGP\PGK*PCTKAFPP LPPNATAKAGPPPRCFPCQPCILGPPSPPGTLEGPIPLSETLPTPH SSALGAIFAQGGGDDGAGATEPAHLNL
7265	A	3	317	EESFTHMLRHRGVQPFPCGQCDKAYGTQRDLKEHQVHSGARPFAC DQCGKAFARRPSRLRHRMTHQ\GQLPMLALHALCGAAPGSQGFLLNH MRLHT*KKPFL
7266	A	285	673	PLCTREKSEYMCTSYSLARSRVGQTLCKGVQWRHLSSL*PPPPGFKQ F/SCLSLPSRWYRCPPPHLANFFYF*QRQGFILARLALNS*PRDP PASASQIAGITGVSHRDLIINFLDFEGYT*SATDS
7267	A	3	231	QIEQLHRRF*AA*/RGDQPTIRKENFNVPDLELNPISKIVRAFFD NRNLKRGPRGLADEINYEDFLTIFYFLSI

7268	A	88	362	KINMGILLKLVRFSIHPVKTGALF/TKNEQ**TEFDKRILKSIWK CKE/PYSTRTPFKKTEAKGLPS/P/DFKTYEATEFKTS*DQQKDRY KE
7269	A	2	355	RRLFFFFFLRRSL/DSVAQGVQVHWNIGSLQAPPPGFTPFSCSLSP SS*DHRPPPCPANFLYF**RQGLTMLAKLVSTS*PCDLPAPAHQSA GITDMSHRARLIVSLFKRQKTYGNN
7270	A	1	337	RGDTGRTLQARGARSSG/LPTV/LNPGRQLTSAG*PH*YGKARAAMP TPSLVRPVLKVGHSPEVSGSAAEIAPWTISSPLYNPSSLPGPASS PMPIPNSSPLASPVSYTVLV
7271	A	1	371	RSRPELNDYKDKKAATKNVQKK*MQRQKG/DIAIDATETQRIIRDY EHYNKMSS QSLPSKKNSSGSEGFTAIFYQRYKTPLILKLFKK
7272	A	2	406	ARAARVFLHRTSLNLSNGGTQC*KTMVVHDDSEYSEPCMTSPSKEGT LI VRQTQSASSTLQKHKSSSSSFTPFIDPRLQLISPSSGTTVTSVVGISC NWMRP*SI\KHYPTQKGSLSF*ISTH\TYPQSAFCVIFLHYC
7273	A	1	165	GSLPLLFNIIILEVLAKAIRQEKS IQNEKEKV*LSLLTDHMI/YM*N PTVKLLTT*KLTT
7274	A	110	409	PWYLAQAGYEVVGLDWTVA PKKARECVGKTVTTLQGNLDPALYASEE EIGQLVKQMLDDFGPHRYIANLGHGLYPMDPEHVGAFVDAVHKHSR LLRQN
7275	A	53	930	ARSYRQLTMEANGLGLQRIHTDTYPHPHLIARPQGFPELKNDTFLRA AWGEETDYTPVWCMRQAGRYLPEVRETRSAQDFFSTCRSPEACCELT LQALRRFPDLAAIIFSDILVVPQMFSPPP\ALGM\EVTMVPGKGSF PEPLREEQDLERL\DPEV\VASELG\YVQAITLTRQRLAGRVP\ LIG\FAGAPW\TLMTYMVEGGGSST\MAQAKRWLYQRPQASHQLLRI LTDALVPYLVGQVAVAGALQLFESHAGHLGPQFFNKFPALPYIRDVA KQVKARL\REAGLAPVPM
7276	A	86	552	KQPQPTAPLWQPLKLSKGLGLAPGHGPCCLHLLSALGSLPGLVPWLP SRVGC/SS*GLLLTKSPQPSADPGQRRVALHHVL*VEPFASQEAQPP PSLP/WW/PLRGDTESPGSPSLSARCTHPGCRSVRGRWGRARGWPA RCQGAGGPGGWRTTCPCR
7277	A	176	779	NSVSKGLGLAPGHGALLPAPAERSREASQIPRGRAPGVHYLCLKQPRP RGLLGPQGNRPLPSKPHLCAGLCGGPGPTSPLPFETIRNWARRPP EA*PQGACI/LLLSLGDPRGVG*PWV*TPGGLVFWMSLWHFGPQLKP PPLPRSLRPRPSLDLLGRKRHQGQDEKPGGAAPQMRAL*PVLPLPPH PGTAPQLVTATRP
7278	A	32	494	FALVGQAGTQ*CDLGSVQPPPLGFK*FSCLSLSS*DYRHVPPCWL IFVFLVE\QGFVILAKLVSNP*PQ/CDPPILASQ/SAGITGVSHCAW/ L*LSFSFFC*DRSVTQAGMQWHDLSSLQPLPLGFN*FSCLSLPSSW DYRCVPPHPANFFIFSR
7279	A	19	253	LENSFLKTLPLAIACRN IKYMNLT KCESCKLREI\KDLNKGSTPCS TIGKL RIVKMSFLPKLIYKSQKTFFLQTLIK
7280	A	3	1023	FLNWKSKILYSTDDMI IYIENAKESRKKLE*VN*SKLLDTRSMYKS NAFLYTSNNLGKPAF*KPYPLAIACRK\IKYMNLT KCESCKLREI\K DLNKGSTPCSTIGKL RIVKMSFLPKLIYKSQKTFFLADIDKSCFF* DSFTPLRPLEWPWPRSQA* KPSNLPSSNSPGLSPSSWDSTSAC HRRLANFFVFLVEMW*CMPTVPTTWEAKERAHLSPDVRGYISDCAT TLQPGQONEISASNKTTVINIVSYWCKVIHTR\KWCPEQTTSMSLRV FTNL*RLGHWESRVSTNRTEPTNHTDKKVNLDPYHIWYTKMNSKWIT DLNVKGKTIKVP
7281	A	1	408	DVCKPDLTVGLRYAPHQYKSVVATNLPEAKYWFLNWIADLSKAAPRN ND\ALGTSQAQYGYRKQEQILL*EEDALTGTNESLERQMREMEENF AVEAANYQDTIGRLQDEIHNMKEEMARHLREYQDLLNVKMGP
7282	A	1	3003	MNIDAKIHNNKILANRIQQHIKKLIHHDQVGFIPGMQGWFNSTKSINV IQHINRTNDKNHMIISINAECTFDKTOQPFMLKTLNKLIGIDGTYLKI IRAIYDKPTANII PNGQKLEAFPLKTGTROGCPLSSLLFNIVLEVLA

				RAIRQEKEIKIGIQLGKEEVKLSLFADDMIVYLEKPIISAQNLLKLT NFSKVSGYKINVQKSQAFLYTNKRQTESQIMSELPFTIASKRIKYL IQLTRDVKDLFKKIYQSLNDIKEDTNKWKNIPCSGIGRINIVKMAT LPKCLPTTCIHMIRPQFRVSSVRRDFNSEVAMEELKQTRKPIFLARE VRTLTSPFPIFQPYGFLILRGHRQEQTSTTVLRLITWTKGILVIQVNP WLTLEAGISKAPDKPWNPSQVAPALPQKPAQVLGLWLAFSVNRTWM QLETIILSKLMQEOKSKYCMLSLISGSESVSKRRIALGSAHVEGPT AHSKAMAQLSPRQRRSRAPTTHTRALVRLFSQSAPPFPPRPSPP SAAMSTRSVSSSSYRRMFGGPGTASRPSSSSRSYVTTSTRYSLGDAL RPSTSRSLYASSPGGVYATRSSAVRLRSSVPGVRLQDSVDFSLADA INTEFKNTRTNEKVELQELNDRFANYIDKVRFLQEQNKILLAELEQL KGQKGSRLGLDLYEEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRL REKLQEEMLQREEAENTLQSFQDQVDNASLARLDLERKVESLQEEIA FLKKLHEEEIQ\DLQAQIQEQHVQIDANVP*HDTT\ARDERQQT SVAA\KNLQEAEBEYKQVC*PLLRASNRN\N\DLRQAKAGVPLSY RRTGCSPLTCESGCP*KGTK*SPLERQ\MRE\MEENFCR*KLLNYPR PLLARL\QDEDSGIWKEEMARHLR\EYQ\DLL\NVKMGP*ALEIAT\ YR\KLEGEESRISLP\LPNFSSNLRET\NL\DSLPL\VDTHSKRT LLIKTVGTRRLDRLINETS\QHDDDL
7283	A	2	178	PRVRWN/RKVQKQIISIHYGQ*IVDKGSRTIQ*RKNSVFN**C*DK* IFTCKRMNLYLFVSSSSSSSSSSSSSSSSSSSSSL*EENTGINLHD LGFGNGFLDMPAKAQAATA*LYLYF
7284	A	699	2528	MQYNIQVLYILDELHGILGNLTINKFIHRSIVANNLDDDLDEKTHQL TKLAQKEIKNPNRPVTSKEIEPVIKNLP\TKESPGLNEFTGQ/YGQ TY*RKELTLILLELSQKMEEG/V/IPVTFYKADITLTPKPKDLTG \NYRPISLMNIDAKKL\KILAGQIQQLIKMITQHD\QVRFIKEMQGW F\HIQMSIDVIIYHINRMKGKK\HMITSIDKKHLLTKIQHPFMVKTL CKLGRKGNFLNLIKTSIKTHS*QHNSKTLKIFPLIS*KFLISPLLFN IILEGLARAIRQEKEIK*I\QIGRSKTTFAENMVLYIKNPKESTK*F RLI*KFSNVAGCKINTQKSKKNLRGN*/RQF/PFTIT*KRIKYLEI NLTKKVQDLDETEKYKTLLEKEIKEDLNKWK/NILCWQVGRNLIVKMAL LPKLVRFNFTIPIKIPVT/LFTETEKLTLEFIWGLQV/N*RYSSLFK TILNKNKVEGLTFSNFKIYCKATSIKTVLCWYKNI*SNRVEWKVQKQ ITPI\HLWSIDFWPRGSRTIQ*RKNSVFN**C*DK*IFTCKRMNLYL YFIPYIK\INS\R*IKDPKCKSVNPIKL*EENTGINLHDLGFGNGFL DMPAKAQAATAKKKKK
7285	A	2	577	KKIKNIKGS IQQEGTLTVNMYAPNDKPSTYMKQKLT*LKGE\DNSTL IVGVFNITISVVDRT/SQYLSKEI*DFHNTINQLDLTTIYRTLYPTM KYTFFSSIHRINSKIGHKLSLN*F*KTA\NIFPDHNGMNLV IIPKKK TGKFKNHRN*HTLNH*IKKETTRHWLKITPRLWPWQVRFGAQSLOG PQLTAR
7286	A	17	377	QRKACAPRAWSGDPSACRPSVRS*GSTT*G/KPVNFDDYGDIIYIPAV NLKTFRLRELAESLLTFQAYDQILGITCEYLPWRRSGGLSPHMLSLIY WPMVRLWGGRGDVYPSCYCHMALYGM
7287	A	1	893	SISSQQT*SSWAPCYRSLPASTWASSLCSSSSLISFSFSSVYSSPP GSSTPLASILSAFF*PLDFSSLASVSSLLPSLNLTFVSWLPASP SLAFPASTLVSGLPASSLMSSLPGPSACLSSPTSQHACSS/STLSQ SLPSTSCCLSLQTP*TLPDWGFERSQKGT*V\S*ALRKTSSPFSSSTS GLGPAESREQQLGAKTNCASSRDRSSRCGSTENSST*GPTPRSSSR* PIPGSSSPGEKAAPAASAWAASPSSAPTHSGYELLESSRKEKESCTS WDESSSRAGAKSSGPES
7288	A	827	1393	ARCQQAREDGRLVQRLCRRGHFVPLQHRRGAQERAPGIAHSSCAAEP RPLSLRTDISSALVWPRASCARSCPEMGPPNLKWASGA*TLEECPP\ LSGSPRKNLD*PPGLEEPSRLEGGTPSSALLKG/PAPTYLPPYALD LPKPTSA/VQHSPSTYPPHVLPIPPTPSSWRVAVGALCSRQDNLHD QPRL

7289	A	104	464	HLSVKLKLKFWHEHMLQGQKEWIIISIPLLLPHPLLQONPHQPPHNPS QGQPYLHGPKLTRLPPSPHPTSEQRHAWHTSGQTCGPGEPRPQQWL WCCSACTQLSVWPGLHQAPQWEAGS
7290	A	2	394	PRVRNHPIQKWAKKGL\DSHLSKEGPQ/AAISHMKRCPASPATRE/V QIRATGETHLRGCGNIGTLTRC*WGCK/LLQPLWKPVWWFLRSLSIG LRCD/PVATPLLSV/WPQACKPGTQRDLHTTVFTAALFTVAEQ
7291	A	2	344	DTRTHVAEEDKLAIIVEPEKRGKYVWFDPLDGSSNIDCLVSVATIF GFYITNSS\D*PSFNHA\LST*RNLYLVSLPFHLAFLSTPHLSFLFF FLSFLSLFSYLFFLFSSFFSS
7292	A	1	348	RYRSGIPGRRTRAGETPSLLKIQPG/GDGARS*SRLRLRLQENRL NPEGRGCSELRLCHCTPAWARE*DSLKSKKKKEFKIPIYFTLLWDV FRTOYTYSHIPMCLLCGEMVTDI
7293	A	10	436	EYYRFLEAKENRTATY*NL/MDHAAKAELRGKFIISIYAIKKLEKFQ IKNLTMQSKKLEKF*IKKSSNVFQARKEQTKPQISQRK*ISEKE*T KLRLNQCHKKSLKQPLLS*TKKDQNK*MRKEKGDIKLSGRVGRPEYL QT
7294	A	2	404	CPTSTSTSWTMWGPACREHL*PLPTFP\PGQQPNTLP/RPTLRP/SP *TPTSACS/RP*/PAVPSRPSHPSHLPSPCPPQFTFNPHL**GGPH PTHNLPPNCPALLQLPGFSTLPRLS*TPPPTPICHCVSRLAP
7295	A	27	88	CREEDDLVESEDS*QWGESLKRVSFTLLDDEATEDAGDLNVKKNSD EVKS\FEKROEKESA*VGRKMMTWLKVKTVNNGEKA
7296	A	109	411	KFKNMWKLNDTL/LNNHWVKEEIKKEIRKYLKRNNENKNTTYQNL*DS AKPVLREFVVINAYIKIEEGSYISNLTLYLKDLEKEIKAKVNRKDI RITEIN
7297	A	13	811	VCRRWSGGLARRFGSGCCSSCPQRRARRSQVQNGKYL/FDQINRS LENYEPCSSQNCSCYHGVIEEDLTPFRGGISRKMAEVRRLGTHY QITKNRLYRENDCMFSPRCSGVEHFILEVIGRLPDMEMVINRDYPO VP*MDGACHPS/PSPSVRHQS/DHIMYPAWTFWE/WGTCCLANLSY RSWTEGPLQRRSGKVS\TQWPWKKNSTAYFRGSRTSPERDPLILLS RKNPKLVDAEYTKNQAWKSMKDTLGKPAKDVHLVDH
7298	A	22	427	IFSHYFFQKFLRLPFIMFIMHLLGCKVDLFIQCFHFLVFYFGLFY LKLFCYTFKFTNCFLYSFSTVHLI*YIFPSDIMFLYVEV*FKSFF* RYLPLCHVHAFISFLNIL\ISLFSS***LTIFYCPYLLFYH
7299	A	131	353	IFLPEKKLYKLEKWDRAFDNT*NF*T*K/IHTGEKS*KCKKWDRAFK GWPHFIIGKIVHTEKNFYKGEQCGKTFN
7300	A	131	418	IILTEKKLYKLEK/CGQGF*QHLKLLNIKNHTGEKS*KCKKWDRAFK GWPHFIIGKIVHTEKNFYKGEQGGKTFNEGSHLIAQESIYT*KKLSK YKD
7301	A	305	326	KTFRSQKKK*IHW/DYIKILNFCARKNTISKVKRQPT*EKIFANHI SA*G
7302	A	3	416	FLR*IGSHSVTQAGVLWRDFGSLQPLPPGLKFLSCLSFLSS*DYRRV PPCLAKFCIFS/VRRGFAMLARLVLS*L*VVCPP\CHVDLYN*SAS QSAGIKGVSHHTWPHKYHLKNLNVFSYQSKSTVNNQLSSQILLN
7303	A	3	476	PESIKRAKEMDLVGLGLHPLFSSRFEEEEELQRLRLVDSIKNYRSRAD IFSEVGRKRQRSGPNRGAKRRREARQDQEFYIPYRPKDFDSEGR LSISGEGGAFEQQAAGAVLDLMGDEAQNLTGRQQLKWDKRRFVG QSGQEDKKIKTESGR
7304	A	2	1050	REDTKAAVLLHLLHNVRPQDQTVVFVATKHHAEYLTELLTTQRVSC AHIYSALDPTARKINLAKFTLGKCTLIVTDLAARGLDIPLLDNVIN YSFPAKGKFLHRVGRVARAGRSCTAYSLVAPDEIPYMQDLHLFLGP LPHPRPTPQGALRVWAGVDGHAGVGVPQSVVDEEDSGLQSTLEASLE LRGLARVADNAQQQYVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSR FEEEEELQLLD\LVNSIKNYRSRATIFEINASSRDLCSQVMRAKRQKD RKAIARFQQGQGRQEQEGPVGPPSRPALQEKQPEKEEEEEAGEBK CEDIFSEVGGRRKRQRSGPNR
7305	A	3	872	PKSWNGPPHPGHRHSRSHSNFSGCSVDEERSRTSKDSSSPVNDHRG

				RQ*MR*KNPFAASSRSTSSSSSSSSPPLWSTAGRTPTTRSGPSPA LDKVQIYMEHLATAST/EPAGSAHVPGHLFRAE*VLPAL*GRALLG TPVTNNLLGEIAKPSLSQSKRLKAAS/AAKYPHDVVNHLSCEARNH YGRRGQPHPPHPT\K*KNGSPTPRSCRARCCST*VSPRTRRAPGD PLVLP RP*GPSGPLNTSVDSSQKPASNPGDVQNHGGLLVGNCNSE PGAPSAESFAV
7306	A	99	433	KLKVKGGKRYRMLTLIKRK*H*IKIQNSCVFLYTSN*ELENK/IFGR YVSFMIA*KIKS/LGIILMKDV*NLHSEDIYERLLTKIKDDSNKWTDM QFTRIR*YHKMLILK*PIIY
7307	A	18	146	LHDSNTRSPQFQKSLGFSTGRHRCPV*EGL/RSVTQAGVQWPIHSSL QPRPPGLQSDPPASACQAARTLCRWY
7308	A	1	240	LVCLSKSECLQPLFYHHLTLKNCQFHLCRILLHPQC*KQALRHGKAC PLCHCCSHAALYMICLAKED*KTFDPQELMYSL
7309	A	2	1790	ANQLQEGEVRFFVVD CRPAEQYGAGHLSTAFHLDSDLMLQNPSEF/D TAIL*SLLEAQKQSIESGSIAGGEHLFCFMGSGREEEDMYMNMVLAHF LQKNTYVSIASGGFMALQHHLADINVDGPENGYGHWIASTSRSS INSVDGESP/KWLCKLRWILKHQV
7310	A	1	1426	ARILLDNDHYAMEKLKRVLEYLAVRQLKNNLKGPILCFVGPPGVGK TSVGRSVAKTLGREFHRIALGGVCDQSDIRGHRRTYV\ SMPG\RII NGLKTVGVNNPVFLLE\VDKLGKSLQGDPAALL*/EVLDPQEQNH FTDHYLNVAFDLSQVLFATANT\LATIPAALLDRMEIIQVPGYTQE EKIEIAHRHLIPKQLEQHGLTPQQIQIPQVTTF*\IITRYTREAGVR SLDR\NLGPLCRAVAVKVA*QORTE\PIWTVLM*LREKVAENTS*KM KNLNL/ RDTTDLALPPEMPILIDFHAKDILGPPMYEMEVSQRLSQ PGVAIGLAWTPLGGEIIFVEASRLDGEQQLTLTGPPSGTVMKESAHL AISWLRKQRKESTKLTNAFGSFDLLDNTDIHLHFPAGAVTKDGPSCW EVTISNLSRPQLFSGRLVRSDVAMTGEITLRLGLALPVGGIKDKVLAA HRAGLKQVPIPR
7311	B	169	379	VSQRLSQPGVAIGLAWTPLGGEIMFVEASRMDGEGQLTLTGQLGDVM KESAHLAIQLGSAATQRTSTQLTNX*
7312	A	3	413	HHFLTCKRIKNKINYTIATKTIKYLRLNRNF*SLTKPKLLKDIKVDL NKWKNISSWLR*FKLTNISVLPILY\NKIPI*KINTFFIKLDKLM PKFI*KNKHVKIGRK/ITKKKSYKGILTSLDIKTYKVSIIKTV
7313	A	2	423	SFPLPFPPLPCSSPQGPQLLRKAITRPWPGTCYPASTQVGEFTLRT RPQLSVGV*EEGCPYSPADSPMSDEPGAAPPHPRSP*\RNR/C/S SKGKTAVFAWPASHLASPLQPTGLPGKRNNMLSVPNNTQPDWVAP E
7314	A	2	417	ILSTLFQICHCLWSSQLLLTSHCQYHYCCSSKNKNLAWLLKFLY NLEA*FIHLAVIFLYLSCLGFTALYEFVVCFLLLVLRYSVLLFLSF /LFWNFS\THILELLCPICLLNFVLLFMYFSFVLQFGYFLFLCLQ
7315	A	2	411	RQGLTLSHGPEVQWHDLS\ LQPLPPGLKKIFPPSASRVAGNTDVHH HAWLVFFPFFV\RRGFAIVAQAVLQNPGLQAICPPMASPKCWDYRRG PPHPAQE*EHFLRSLPSTGESYFGEL*HISTRIKILVHFEETN
7316	A	2	333	TEPALSPRLECSGTISAHCKLR/LPGFMLFSCSLP\SSWDYRRPPP HPAGFFVFLSRRTGFHC/RLARDGLDLLTS*SARLGFPKCW\DYRRD DPMPGPVSFNRMENLMEVD
7317	A	3	232	AASTPRPLRFLPSPTRGLVPN*RPRIIRRTSSAA\ITPAPEPAPTSAR PTRSNTHRRLSPWSSRPVTEEMQSAAKHNG
7318	A	1	386	IPWSRVG*NHPVKNAHLPKAVSKFKTISIKKPPLFFPRMEKTIKFL WDSSSSSSSLPV*SSSSSSSSSSSS\FSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSPTHKIKPNTYRQLIFDKANKN
7319	A	2	411	DRKEERLRSRSGAAATMSSGGKGVAEWDPLPCLDPELWDQFDNLEN \HSLEKFIISAKERTEIELSYTKQLRNLLKTCQPKRNWKEKEYIT*N SPSLPVNKMSDHARQH*VIFFEVLNFQITVELQGHVQNKQKE
7320	A	58	502	DPRVRPGTRGPRSGTAGGETTWEGPFGVIVRVLMLFSYELRAAELGE VGAGGPRGARPSQTETAA*PASRFVRGLGPQTLRPTSPGPRRSRPL

				LGDEPPRRRVGGASFPPTRNGSGAW\ALWRRPCWECSSRSFLRTTKL FLFFGFG
7321	A	381	2378	AASMEHIQGAWKTI SNFGFGKDAVFDGSSCISPTIVQQFGYQRRASD DGKLTDPF*TSNTIRVFLPNKQRTVVNVRNGMSLHDCMKALKVRGL QPECCAVFRLLEHHKGGKARLDWNTDAASLIGEELQVDFLDHVPLTT HNFARKTFLKLAFCDICQKFLNGFRCQTCGYKFHEHCSTKVPTMCV DWSNIRQLLLFPNSTIGDSGPALPSLTMRMRRESVSRMPVSSQHRY STPHAFTFNTSSPSSEGLSQRQRSTSTPNVHMVSTTLPVDSRMIED AIRSHSESASPSALSSSPNNLSPTGWSQPKTPVPAQRERAPVSGTQE KNKI\RPRGQRDSSYYW\BIEASEVML\STRIGSGS\FGTVYKGGWH V\NVAVKILKVVDPTPEQFQAFRNEVAVLRKTRHVNILLFMGYMTKD NLAIVTQWCEGSSLYKHLHVQETKFQMFQL\IDIAQTAQGM DYLHA KNI IHRDMKSNNI FLHEGLTS*KFGDF\GFATVK\SRWSGSQQVEQP T\GSVL\WMAPEVIR\MQDNPFPSFQSDV\YSYGHRCMELDGRGEL PYSSH\INNRGFRSIFHGWGRGY\ASPDLSKLYK\NCPK\AMKRLVA DCVKKV\BERPLF\PQILA\SIELLQHS LPKINRSASEPSI\HRAA HTEDIN\ACTLT\SSPRLAGLPS
7322	A	3	419	EPQWIQALMPEKEPARQSRGGALRTDSSEPSRNEVKKTISFIILAKR TYLEIYATQDA*NLCTEKYKIFLKGKEYRTKWKDILQSWITRHNVK MAKLP/KFIYSFTICIKMP\LSFYKLILIFMRKYKGCRIANTI* RER
7323	A	3	222	DAWVTSTNADKEFEKIQHPLMIKLSK*VY\NMSYIYPLFKI IKGIY DKSLVNIILNVEKLAFF\LRTGTRER
7324	A	2	395	GRQPRWRLWGQLLSSGRRPLEPGWHRPSRGERGHHASFPEPGPCPGP QQRPPQG*VPVPEP\PPKGGPEPRSSGRKASGSAQPPPA GDGARER RQSQQLPEEDCMQLNPSFKGI AFNSLLAIDICMSKRL
7325	A	63	452	KNQEQUESEETLPNLFYKASITLIPKLD TQK*KKRKEKKRKKK\EN* KPITHRNIYAKILNKILAHQIQYIGKIIHHDQVGCIP/GAFDKIQY RCMIR/TLOKMGIEGTHLNI IKA IYIRPTDSI IENREKP
7326	A	2	137	SKAKINGWDYI*LKCWYTAKKAISGVKROPT EW/EKIFAN*SSDRR
7327	A	755	1287	GGWDFAPAEGRERLAPCQIWDPSCLPTHW*PLSGLLSRPPPGTQSPQ LSPYSCAKSWCPCPSLSPGSPMN*PSVPRTTGPSHPEPSAHGSHTSP IVATTERAPERISGGDSLGLSPSGLEGVNREPLFT\PPSSSGSSVSL MSTP\PPAGHSA*SPQPGRCSGPAQGOATRSVRGP
7328	A	1	2240	MEERKGHEIHLRRLKVRILSVRMSAIKESPRLLIGNQEP LKQLKQE SKMNRVYFNTDYSGCIRLIQSRLSHFPESGQONPKPYMRKFKTPLM IAEEKYRQKKEIEKQKQESSYYNIVKTQSQNQHITEVEKEMPLQKT NEEVSLSGIDSECTVVQSPSGSQSNARILGVCS DNQLSTTSPETVAA KRLHHVLAASEDKDKMKKEVLQSSRDIMQSKSACEIKQSHQECSTQQ TQKKYLEQLHLPQSKPISP NFKQSEIDVQTFTKKQYLKTKKTEAST ECSHKQSLAERHYQLPKKEKRVTVQLPTESI QKNQEDKLMVPRKQR EFGSGDRGKLPGSEEKNQGSPSMIGRKEERLITERKHEHLKNKSAPKV VKQKVIDAHLDSQTQNFQQTQ\NQTAE SKAEHKKLPQPYNSLQBEKC LEVKG IQEKQVFSNTKDSKQEITQNKSFSSVKESQRDDGKGALNIV EFLRKREELQQLSRVKQFEAEPNKSGLKTFQTLNTIPGWLISEDK REYAVHIAMENNLEKVKEEITHIKTQAE DMLVSYENIIQTAMSSKT GKPANGA/ALVSTKTS PKVSNVHVSNNENSEQKEN*IAKEKTVQH QV AAHDEATVRSHVKTHQEIKLDDSNIP\LPL*KHSPPSPFTITIESTA RRTENPTKNELSQSPKKDSYVEPPRRPMSQKSEIHRANTSPPSPRS RSEQVLRLKDTTAKLSKGAIPCPAATPVPIVEKRSEIIMSPATL
7329	C	110	298	MPWISEGRATRPLRVPSARRGDEGLHQRATANSVYKSRNTWLCWIC KPPQSSSPKISEKRF*
7330	A	127	744	LVRVFPWREDKVWWHCQE/CRPKR*KSKPGLSGPV/APGHSWDSTET TEATGLLLIPGPTRRPPTLYHTPCCLSVPRWCRPSSPLLAEGTRRQG LVALPSLIHGIQPMGLEWGLASPPR\PGRKWHR*KDKMATOALSVC RA*TCILPPSTKTSRPRPHSTPRGPAPTTVQRNSRRVNKGSPESPLP RPLGPVSEPHVAGTRTARDG

7331	A	2	433	FEDIK*VIGKVKKMMSKQRCNINKGKIIKRNQKEIVELKSTVTKIKN LLGGFKNRL*QTDK*ISYF/EDTTVEISQSGKQSSSRLEGREQSLKN LWNTIKLTRVYTVGVSEKEKKEQIV*KISAGNFSNLIKNMNINIQEA QRTF
7332	A	1	281	PR/PDRDSEAPGADGAGPRGALPVPVGGHGQDPAEDGPGVHAGGARDG GPDARGAYPPMPSTRGCRKGSANLP/PVGFQYVHPPF*FPGVTAK IQRRMDQVFTLAVRETEALIPPEVPTRQCPAHEAVGVHVLICHSWF SICPSLFLISRAQYFYP
7333	A	33	428	GSPAPGLPKGWGFRGGPPGPGKFVFFKLPKGGFPGAEIFLGEFFQRG KKGLGPFIFFPVFLKTEEGGTL/NSFFKGRVFLVFKPKAGSSSSSSSS PNYKPIYLNNTDTKFFNNMLANRI*QCIKEVMQYDRTRG
7334	A	491	731	DRGLCLPTLEVQWAPILGSLQPPPPGFKQFSCSLSPNSWDYRCMPTC PANFFVFFCIF**\SRFHQVGQAGV\QLLTSSDL
7335	A	2	575	AGQVQQLGFPWAGGEGRRPPLL*LSLPGRQLPREEGLTSVSGHPC WP/DSFPGLPGVEKPQGNL\AGGALLPKLQRQSGPGNHKTLPI SRGP ADPGAVPVCHSTVGPGR*HSLALHTVPPEKFNIYFFTCPENSSFNSL PLPFRSSLEGIQAGVSSAWGHSAGPGTLGLSGDGRQRQARRFSLHSC LPCSP
7336	A	19	422	GEKTDKIQHPLMIKTLTNLGIEKAYISIIKVIHNRPMACIINGAKV KAPFVRSEQRCSPLLENIGLKVPVRAIEKEKEMKGI*IGKKEIK LCLSGND\MTLYLKHPKNSTKTIRTDTFSKAGYKNTDAWV
7337	A	33	193	GNLGETLMDIGLGKEFMTKTSKAQATKPKI/DWDLN*KSFCTDTNIM HMVLIYL
7338	A	87	713	DIYYNCFGFASRKTDCLSTRIPCFERTSSNS*TQNLTALE*IKYDCA TVQACRSRNKWEVRDALNKFSGTNSIFYIIKRFYIYIYIFFFFFFFE TESHSVAQAGMQWRNLGSLPAPPPGFTPFPCP\SLLKWLGPTRRP/ RQTLANFFVLLVETGF\TMLA\RMVLIS*PRDPP/ASASQSAEITGV SHCTRLKKIRFAKHVEFFESHVE
7339	A	2	105	ENGWCWIATYG\KRKLD SYLSLHARVNSR/WDLDLGTETMEILEENL GEVLLDIGLG/KEFMTKTPKADSTEIKINR*DSYIWKNNENWIPI SHY MQELTQEGLGSRN
7340	A	2	362	STHETFSKIDHM\MSTSLSKIKETIVLSIPSSSSSSSSSSSHSKSNLQ NYTNTWK/LNLLQND*VNNEIKMET*KFFEMNDNDTSYQSLWDTAK AVLR*NRKDHKLTT*HLKELQKHEQTQS
7341	A	58	341	IKKFRWGPKPPLKEPPGV/SPDFPII/NFGNPGVPVPGKDFKFPNFSS SSPWGGRAPPVVPPTPGG*MGRFP*PPAFGVPRGGDGSPPPGAPKEG PLS
7342	A	2	428	FLRRVSLYCOAGVQWPTSVTEPPPPGFK*F/SCLTLPSWDYRRAPP RPAKFCIF/M*RLYFTILARMVIS*PCEPPASASQSAGI\TGVSHR AGLVFLFNKPVTLGLGFDSSHHPYHSQISEKDPPPISSIFNKKSIHTNL LIPN
7343	A	2	688	PGPPPEVRQHIRVPGTRTGRAAIWPGSFVPVGFPLHRAQGRGQSPFPF PQGTKGLGLEWKGCCHAGAQETGSPPLPIMVHFGSGSWEMVSRGKPS* QLEA*GRGRAPGLGSKAGPRLHQDTPASQCMWVCLNTPSRQVRGPD TQGYVCVPLPPQPHAPRMNQGLPPGAPPPPPPSLVPKYFPPSQSS WDRKIPRLQAPPCPRH/GPPS/AVTNALPNGPRLSAEAPWLG
7344	A	1	603	SGCSRRCPGPWACWTPQKGFRGGRKRRSGLWGLCCWC\RPHSHRRAG CHHQDGECDRWGLLPRDHSRLWIFLRYWHQLGGE*KANAGGSDRVY QFWG/AGPPSAAPSGAAYLQHSTLNRGPSREDASFTPVGWGTCTMS TRQSPVTPWTASAS*R*EATPVTAVTSMPPAGAQSPPPTMSSASA AARTGCTWNGFWAL
7345	A	32	773	FWSGPALGPSPLSGE/GDMVATDETVCVCSGCEGAPDPGS*PQAPD QRLGQCPV/WLPVT*PTSTRGTWTASWP*LTDSSTVTGPTS*SL*CSG REKRRQWAPWTMATSDSSRTGGLPAAPST\ADASRARDVPGAEEAP GVHGLAATAGCLCQGEVPVGPVAVPVQESGADPPQDEEGPQPAQG PGCEGA/EGKFPSSSSSATSVAAPSGSASCPALATGS*PAASTARPR

				PGPSSTRRTAGTWPS
7346	A	19	1562	GRYWRVVDHGRESRVSGPRFRP\SFLAALPPGRHPWPWDAAAGGSPA S*GGAA*SALGLSQPRPPGASDAAPDSTPAGV*TASSALI PSRAR* KSGGTLEETKSRPPHSHRSGPVDLSRSSHSDSTPVHGPYFRSAPD P\GAPPRPSAGQSQLGGGSSGSPGNSIPCAVQ*LERARSHS/SP GSEHRRAS*SGGLRQGVQGIEVFGLGHPPGGYSCGPQPQEKSPPPAHP LGVEIWCGRGLYIGWKSHSPHPALAEWDQVPVPPAAMAVGAPGLRRIQR TSRRWGQCNEAGHAADPRDSGPPGNYQPVSLHILHMDPGTC*PE*Q QHPRPPL*MAGKQWPCT*LDKGQSLGLAGSHQHQCQWW*QQLQSHT SLCRSPPPR*RASASPC*ASWGRSSAGAAGFRALGR*HLGTSPLGSA GSLPPCTAEPPADASP*LSPTVLAELGSEGASEECHSCPHGSPQSL GSHRPAESQYHVER/WKQDMGPISVKSPTPRRGPTSGSGLRLARSS L
7347	A	473	792	MLARALDARFLRWCRRDQPLVYHSP*PPGASDAAPDSTPAGV*TASS SAPAGEKDANQMEWARR/VPRAPPPGSPGPSLIPSRAR*KSGGTLEE NKSRRPTQSPFGAG
7348	A	3	411	LCAAVNRALDEGIPLTSALYYATVTLQVRNLRSDTDVSMPLVEER HRMLYDTGKILLEKFGGCFNLNCRENSAQKLMHWS\AESCPYSYRD VTLVEGKRASFYKRTQILVSYTCIVLEGK*DACLQDILSITML
7349	A	2	331	AGGPGLPCVPHLPAGARAWRCQPPGAACCPGRRRLPLP/GKPSPGSS RSSRQRGQSCRTVSVLPPSSPGC/RGSQVRPDLGPPKAEGCSPWGLR AESCGATGARVRCHRCV
7350	A	1	1062	EAGPGGQAARSQRGSSGLVLPPLRLQRCGAPEGHASPTPAGPGAPN QLAAPWLLWPCA*PPPGLCYPAPPPPPQKHP/GLLPAPRALPSPRE LPGEEPSAHPVHQG/PSCRATRPASAFKSHSGEFGRLISAHIQ ELPGPAG\ENFQKVFNGAAGPAARHGPSSRSSC/PCTHGTSGNREKP LSTKSKKNKSAWQATTQAGGPGLPCVPHPAKQVLAHGDASKPPGAA CCPGRRRLPLP/GKPSPGSSRSSRQRGQSCRTVSVLPPSSPGLPGTKV RPW*GHLASLVWPGPPGKSPGQSTRPVGTILKRGVHPLPQVVGQSRFA ILVLFGRQCQEGRAGMLGTCCLLAKPEVTVA
7351	A	423	826	QKVCAHT/CLRGITC*IFTHLCVLRGLCWLLGCEMCM*MKYVCMC EK\CCTFVGRC/M*VCVCAGDREHLAECVRGCVRHWCTRA*VRMCI/ CVCTC/LCV/CV*VSGVICCKSPCVLCKSIVN/CV*A*THTWFCVHV CV
7352	A	310	863	STHLSLPKCGWGLQA*ATLAQPNSRSLKFKIYMSKGYSVKVE\KQ PTEWGRKIFWQTMVSG*GGLESRIYKELLQLSNKKTNA*LKSGAKAQ HRHFSREHTHMGQHQ\QQRCLIASLIREMQIMT/LRGYFTLIRMI TRKSDNN*CWQECAEIGTLL/HYWECEMVHGRGKIVWQFLKNIQLP
7353	A	3	358	SISNENFPTKESQGPETFTGFEFYQTFI/DLSPILLKLFQITD*AGTL PSSFYEISITIIIPKPE*KSQENYSAMYLNMNIDTKIF\HKILATQI*P YINVIIHYDQVG\FIPG\MQSSFNVIN
7354	A	2	207	GRVDHTHPGLRPLCPHSPDP/PQRM*SHSAVGASGLADPYERIVVS *DGNSSSPNHQGDGASQTSGEQI
7355	A	1	803	QPRDPSSGTHHPDGRGGQPAPICPRQGSCSHSPLEHAPCPILGPGS WPRWHL/DLLSLLGDPKVGPIACPPGSPPHAWTG\PVACPLGQPC SCTPILIPHPICQHPKAPGGHPLCSKLLTCLPATPAVPSQPGHHHP LFIMSGLMGAWPSPEAGPGVLPWSWTAE*GTRHWTHEEEAALGATDA VTSP\PGFGRQVPAPRMPAWKCPICIRGLLHSL\PSEKPLQVHRECQV PCEGLGPLAQTGAPQAQAWGPTDLSPLPHRKLK
7356	A	3	927	SSGTRHPDGRGGQPAPICPRQGSCSHSPLEHAPCPNLGPGSWPRWH L/DLLSLLGDPKVGPIACPPGSPPHAWTG/PLWPVRALASPAAPP ILIPHPICQHPKAPGGHPLCSKLLTCLPATPAVPSQP\AIITPCSL CQASWEPGLLQKLAPA\PPKLDHVGPRSQPGPDVGVVCTPKSRPS TCDTTPPLPLGLNEERATGHMRKLPWELLM/PVTSPLWLWAGPCT *DACLEMSLHWPSPQPPPREKPLRSAQGVCAAL*RAGTTLPRLGEL RHKAWGPTDLSPLPPQKASKINTRGMESVK

7357	B	73	255	XGSSEQDTCNSNPGPCSSPTGNPEWGLRDTALLEDLGKASGLLLERM VDMPPANNKCLIFRKN*
7358	A	1	710	PIEITSQCGGIPRFAPITVGVVSSLPHHSRGEGLQPPPSQSG*GSP AS/HHSRGEGLQPPPSQSG*GS\QPPPSQSG*GSPASGPGFCWGQ/ RP/PLPSCSYSPGALQSSRTPAQTQGPAAHHLRG\SGPVHGGPPAPSP SCCLLP/SLRVLPGLPAPPPATSTVCPPLPVCTPPWVICQPPYPLA HQAGLG*LPLGDREGVPFHSPNPSLQVCPR\PLR\KPRPWSSGLGPH AHNPMPMSMGRSPPRATWTLT
7359	A	3	750	GRGAEQGSHLARAAVPGSGPAWRPRPRGGLGLRPARSALRAGLPFG RVAAVGRGPALPGQG/HLQSSRTPA/PNPGPCSSPTGEGVPFHSPNP S/H/GKSVPGSSGKYPDLPVGLCPHAHSPMPSMGRSPPR/GKRGL* PDAQMQEP/SKWGLSGHSPPGGPGKQWPAPGEDGGHASQQQMPDLP EKLSPSFTPAHLHSLPEA/PVRHEPCLPR/HGPCGRQPHFVCAHRR ARRAQPAQNKACPAAGKKKKKPVPN
7360	A	102	380	GKKIPMLYFAEIEQCILKFV\KRS*KAK*ILPKNNKAGGLKFPDFKT YYKAAASKHQVGGWLKELRSTLQAQQTWVPREELRSTSPSYQTQVQ
7361	A	190	375	VIYRVSIIISIKIPTFFTEIEKTYNLG/WNDNRP*IPKAILSL*NKV GDIPLPDYEHLMNM
7362	A	102	345	GKKIPMLYFAEIEKCILKFV\KRS*KAK*ILPKNNRAGGLKFPDFKT YYKAAASKHQVGGWLKELRSTLQAQQTWVPREELR
7363	A	12	380	DPTVCCLQE\HLTFKDTHRLKVK\WKKILHANRNQKKAGIAKLISD KIDFKSKTVKRDII*MIRASIHPRRLINSYI/WAPNIGNT*IHKILK DLKGGINCNTIIVGDFNT\HR*SRQKINKHWA
7364	A	3	298	RRSI/NSVAQAGVQWRDLSSLQAPPPGFTPPS*LSLPSSRDYRCLPP CLANFLYF**RLGFTVLARMVLIS*PSDPPTSASESAGITGVSHCAW PISFS
7365	A	82	526	NHSELQLKLRA*KKMCTADLSLLEKDT*IKLEENR*QERIMLRAEV NEIENKIENINKTGGSSSEKYYKIDNPLTRSIRRK*\T*ITSFRNEK GSVTTNPTEIKRTVKEY/YEKLKYANKFNNDDEMCKFLKHNLPKLTQ KINRKSECS
7366	A	146	589	LPQVMAEFRNPNPEVEGRKAKSMKGQTTGKNQDNVPVIDEIDFLEAFK NIQPSS/LFEASLGLMGIKPVDWEBIGGLEVDKPEVKTAAH/WSLRQK SGHCPV/GARLPTGLLATLGSGLSGSGRATEAVSGPAG*KRASIGGSS QRPRRFPTVP
7367	A	2	1041	CREAMHALLHSEKDNVPVIDEIDFLEAFKNIQPSSFRSVIGLMDIKP VDWEEIGGLEVDKLLKQSI\ESPLTFPWEFVRMGLTQPKGVLLYGP PGCAKTTLVRLATSCHCSFVSVSGADLFSPVVGDSKVLQSIFRQA RASTPAILFLDEIDSILGAS/RQPSKTGCDVQERVLSVLLNELYGVG LKTIERGSGKSSQQEFQEVFNRSVMIIAATNRPDVLDTALLRPGRLD KIIYIPPPDHK\ARLSIYKRLYKPCPIGPDVSLLENLAAETCFFSGA DLRNLCTEAALLALQENWTRPQLTVKQEHVF*NHLRL*NRSVKVART WLYMKTYLRKKDFTVEGI
7368	A	1	2046	MAANRKDFIHRRCGPESLQSEAVPQGLCRAERSSALAMLSGSPVPRRT QLRPACKGTQRRRCRRGGEADSGGEAVGGGAAERRSAAARRRGRRRG GEAVGGGAAERRSAAARRRRGRRRRRGGEAGGGGAAEARRAAARR AAAAARRAAARRAAARRAAARRIAESGGEAHSRGEAHSGEAHS GAGAERRRRLHSPALKTHPGQSSEGHVEYKLNHVEFEDQDDEARVQ YEGFRPGMYVRVEIENVPCFVQNFDPYPIILGGLGNSSEGNVGHVQ MRLKKHLWYKKILKSQDPIIFSVGWRRFQTIILYYIEDHNGRQRLK YTPQHIHCGAAFWDIVFMRTWYPVSIPAFYNPVTSLLKPVGKDTWS GMWTTGQLRLAHGVRLKTNKDSLYKWWDTAASQSLKGQAQHQGPON GGALLWLEPSGAGTSTATTSPLGEADISFSTIVLKALQMSNCKSYKK SVSKLLNRRRTQRAPNVHLQILQKECLNLLNQKKCSTRPQSEQNVRLQ ILQKECFQTAQPKGRSVCFFPAKAEAGPTETVPAAYSDGVYEVQAD EADISSASRMEVENLGLGPRTVDHAGLPWTVTDSCHQDPQNRPLKK MLPSGQVALADIILINKTDLVPEEDVKKLRTTIRSRSSAGRGSRRMP

				FSVSPLQPYTKCAPCISNSIVESL
7369	A	1	4340	MSAFESVPDDEEVDVDAVPENKLTFDNLAEGFRLFKTACDFLYHMDL SMNEDIEKEVKKEIDPDEEESPKKKHLDKKRKLKEMFDAEYDEGEST YFDDLKGEMQKQAQCLGGRSSVSMQAHRRPVVHGGDSCSDPAAMLTT VKAFTTGGVLQRGGLQQSWQAPIFMDVGEWEQRNWRNLNCRKLLWGF AAERSREMKPLLVEEVESKGFEIRERTEGRAVGIKSRKSGWCLGCP RTENQPACLQSDLNSDPRALVIRTSTKVKETLSLEEGTVKNTDYSEL GHMGREQWSSEQPLEQTLQDYTKRYTQQHYTEIDQDGGTQDLTKKH HIPVVDRTPLEPPPIVVVMGPPKVGKSTLIQCLIRNFTRQKLTEIR GPVTIVSGKKRRLTIECGCDINMMIDLAKVADLVMLIDASFGEFEM ETFEFLNICQVHGFPKIMGVLTHLDSFKHNKQLKKTCKRKLKHFTE VYPGAKLFYLSGMVHGEYQNEIHNLRGITVMKFRPLTWQTSHPYI LADRMEDLTNPEDIRTNIKCDRKVSLYGYLRGAHLKNKSQIHMPCVG DFAVSDISFLPDPCALPEQOKKRCLEKEKLVYAPLSVGGVLYDKD AVYVDLGGSHVFQVSDEVGPTHELVSLSISTHSTIDAKMASSRVTLF SDSKPLGSEDIDNQGLMMPKEEKQMDLNTGRMRRAIFGDEDESGDS DDEEDDEMSEDDGLENGSSDEEAEEENAEMTDQYMAVKGIKRRKLE LEEDSEMDLPAPADSDDDLERSSSAEEGEAEEADESSEEDCTAGEKG ISGSKAAGEGSKAGLSPANCQSDRVNLEKSLLMKKAALPTFDSGHCT AEEVFASEDESESSSLSAEEEDSENEAIRKKLSKPSQVSSGQKLG PQNFIDETSDIENLLKEEEDYKEENNDKETSGALKWKEDLSRKA AFLRQQQAAPNLRKLIYGTVTEDNEEEDDDTLEELGGLFRVNQPDRE CKHKADSLDCSRFLVEAPHDWDLEEVMSIRDCFVTGWEDDKDAK VLADEELYGDFEDLETGDVHKGKSGPNTQNEIDIEKEVKKEIDPDEE ESAKKKHLDKKRKLKEMFDAEYDEGESTYF\DDLKGEMQKQAQLSRA EFEHQDDEARVQYEGCRPGMYVRIEINVPCEVFQNFDPHYPIILGG LGNSEGNVGYVQMRLLKHRWYKILKSRDPIIFSGMFNSALEVAKFE GAVIRTVSGIRGQIKKALRAPEGAFRASFEKLLMSDIVFMRTWYPV SIPAFYNPVTSLLKPVGKEDTWSGMRTTGQLRLAHGVRLKANKDSL KPILRQKKHFNLSLHIPKALQKALPFKNPKPTQAKAGKVPKDRRRPAV IREPHERKILALLDALSTVHSQKMKKAKEQRHLHNKEHFRAKQKEE EKLRQKQDLRKCLFRIQGGQKERRNQKSSSLKGAEGQLQ
7370	A	18	731	KEELYGDFENLQTDGVH*GKFGPDSLNEVDQ\IQEEIDPD\EEESAK KKHLDKKRKLKEMFDAEYDEGESTYFDDLKGEMQKRSTGKQHTRFPP RAPRHVQLNHAEFEDQDDEARVQYEGFRPGMYVCVEIENVPCEVF*N \FDPRYPIILGGLGNSEG\NVEHVQMRLLKHRWYKKI\LKSQDPFIS SVGGRRFQTIP\LYYIEDHNGRQRLKYTPQMHMGCA\FWGKI*LQ *LAYCRD
7371	A	97	373	TYSEYFLLLLFLFFRRQSLALLPRLECSVKIIAHS*\NVKLLDSSD LPDSASRVAGIAGACHQAQLIFIFIFVEMGSCLSFSLVGLNQLF
7372	A	1	466	LVFFSWCLFVCLFVLKTESHSIAQAGVQ*RDLSLQPPPPGFNRFS LSLLSSWDYRRA/PTMPN*FYCWPAGLKLLTSGDPPASASPSVGITG VSHCAQPRIVSFTSNILKFKNLSLKGCLIEAYFDKTVKATVLEYLA LRNPKPEEHIWGLY
7373	A	181	654	QNRDVHPAASPNSAAQGS*RAKTHS\EGPLSVPGPSPAA/PARSL* EQNPK\PKHSLP*LSSQLGSPLEDVGNDTLLSRHKPQSPPSRGRPR PEGTRLHF\TEPQRLRSSRQPTITAHVVLPMPLPTPPAAHACPLP THARGTSSKQAEPSPSACS
7374	A	56	482	TRPTEHLKLSSAVSPGFCRWPPSAPKAELSPAVPRS\PAAGAATIAV VRSRWSPGEPRLQTTASVRCAPMHRPVDGACSPPVV*ACRAAAR LGPREGPPWDPQSPQSRAEQKMLPVFGRASDAPFIDKKGFFCLISCC G
7375	A	265	2253	LSILSHCKRGVGCWLFVALGWDHEQPCAPSTHGRAQPE/GPRVLP RSRRP/GTQTLAAPQPEPGECTSQARSGGPVSPHKAGSEAES*EGS EDPDQ*ELQQERTAKNILGKRLPQ*IILYCHSHLGEQPOT*NPGER V*PPEFGLGCG*D/STLLLAEGSGWRGP/PWPAGASTPLEAQAPV*

				AGGCGPPAELPPQPGGAGHPGR\PGGGSLGHQAGG*GQ**PHPSGPA *PSA*GPRSR\PSGGRSQPAVSGPGWAWHCPASGPPGTSSFEPQLW LWPLPGLPGQQRPPRLSAARGPQAHGPPRGPFSSPGDRHGPAGGPAV HPARHQR*PAVPAGVTQPGAVQLLLPPHRAGPLQGGPGLGSLAWASCE GPPSLLLALPRASWLQTENWCQWLPPPSQVVSCLGNRQ*RPDFAQGI PLRGAPLGPRLPWRGLARAPAPGPGWAGPSQCQLPWGRHPSGHLASCP GLP/GGSVSGPPSGGPAGSPPTGPS\GAPGSAG*GPGMAQGGPQEL* GQGPKAGEADSPSPWPCLQGPPGLWAPLPRALDAPPPAWVYPPRPP ASAGGSPCAAPRSPPAAS PAGPASGF/SAAPACSLITLKQDGGGPSI SGPASFLQLAWPPGFHPPARLHGPSAREARAGSPGPGAGFSAGRGGF PWSLSSAGCPVSPAA
7376	A	58	414	RPAGCGSTRGTCEWARPSAAPCQTAAGGACSPWTPAPRSPAGRSWAS SSWPG*CWAPPSGHGAQQPSPSSGQWVWMRWAPAS/WLPSGATPGPR FLALGTIGVPAGPRSPSPSFTQRF
7377	A	1	1548	DKDNSGPTVLHLTARFGHPKVNVNLLHHGGDPTAATDMGALPIHYA AAKGDFPSLRLLVRHYEGVNAQTNGATPLYLACQEGHLEVTQYLV QECGADPHARAHDGMTPLHAAQMGHSPVIVWLVSCTDVSLSEQDKD GATATHFAASRGHSKVLSWLLHGGEISADLWGGTALYDAAENGELE CCQILVNGAELEVRDRDGYAAADLSDFNHSHC*THCLRTVENLSME HCVLSRDPSPVELEAKQPDSSMSSPNTTVSVQPLNFDLSSPTSTLSNY DSCSSSHSSI KGQHPGRGLS/KH*SCRHTELHGHAEPRAAGPALGHDW EAHTPTTPTQLPPATPAPRHPTAPTPT*LPISQASCGTTGS*HLHAD QEQTTPRGRDRGPQEGAE/PPATATTGYGGRTPAASPALSASSPARGT TTGSWAAAPARRWSHARAWRTARRRNSLGTTCLTAAPRTPRRPGSSS CRRRRRRRCPRRPRVRRRRSRLCPSRALALAAGSAAPRPPAAPSLS T
7378	A	2601	4760	LTAASSCCYPREGWRYPREGWRYREHNAILWPFGLMTEADILRIE QQSSPCSI TAPPTSCAHWTRRPRAVRAASPRSPAPRSASPSCRRTT WRPALASPAPPPPTARWPTGSPWTPWARLRHRIARRRYSPPSSWRAG RPSARNCAASRTTSTCARSAFTSSWSTGASGPSSDRAFRGPGAPRQ TAPWRDGRPCWPELEATDAPRLPVSKGEAHSNERLRQLLRQRAVG KLLHHWRS LR RHVPPSPGLAHGVYWPQHFLSPLDGGAPPRYESITLD LFMLGYFQLPEMGLSREDRKFRLLCYEMFHRDLSHPWERIRLFHRV VLEEVEAGRRGWSGDFEDLRHRFFGNGLAEPAPEEQAKKKEEKKE QERTEEAAPVQKGDPPKQGREALAPVPQPPPPPARPPARRASPPRLP GSLVFQEEEEARLASMPAWRWDLLRKKLSAFSPPGSTQHLSRQSLQC KQRYQDLQEKLLSEATVFAQANELEKYSSHAGEPLLKQDSKQVQVD LQDLGYETCGQSKNEAEQEETWPPAPTWSRALPRVAPRSPSSRRGRY PERSQRRREVAATAMPKNKGKGGKNRRRGKNENESSEKRELVFKEGQ EYAQVIKMLGNRLEAMCFDGVKRLCHIRGKLRKKVWINTSDIILVG LRDYQDNKADVILKYNADEARSLQAYGELPEHAKINETDTFGPGDDDD EIQFDDIGDDDEDI
7379	A	1	741	MSEGWEI EEDKEKGKV VETVVAKEGLSEPLLKQDSKQVQVDLQDLG YETCGQSKNEAEQEETTS PAPTWSRALPRVAPRSPSSRRGRYPERSQ RRREVAATAMPKNKGKGGKNRRRGKNENESSEKRELVFKEGQEYAVQ IKMLGNRLEAMCFDGVKRLCHIRGKLRKKVWINTSDIILVGLRDYQ DNKADVILKYNADEARSLQAYGELPEHAKINETDTFGPGDDDEIQFD DIGDDDEDIDDI
7380	A	3	5650	LLEKLRQRIHDKAVALERAIDEKFSALEEKEKELRQLRLAVRERDHD LERLRDVLSSNEATMQSMESLLRAKGLEVEQLSTTCQNLQWLKEEME TKFSRWQKEQESI IQQLQTS LHDRNKEVEDLSATLLCKLGPQGSEIA EELCQRLQRKERMLQDLLSDRNKQVLEHEMIEQGLLQSVSTREQESQ AAAEKLVQALMERNSELQALRQYLGGRDLSMSQAPISNQAEVPTG RLGKQTDQGSMPISRDSTSLTAKEDVSI PRSTLGDLDTVAGLEKE LSNAKEELEMAKKERESQMELSALQSMMAVQEEELQVQAADMESLT RNIQIKEDLIKDLQMLVDPEDIPAMERLTQEVLLLEKVASVESQG

				<p>QEISGNRRQQLLLMLEGLVDRSRLNEALQAERQLYSSLVKFHAHPE SSERDRTLQVELEGAQVLRSLRLEEVLGRSLERLNRLETAAIGGAAA GDDTDTSTEFDTDSIEEEAAHSHQQLVKVALEKSLATVETQNPSPS PPSPMGGSNRCLQEEMHLRAEFHQHLEEKRAEEELKELKQIEE AGFSSVSHIRNTMLSLCLENAELKEQMGEAMSDGWEIEEDKEKGEVM VETVVTKEGLSESSLQAEFRKLQGLKNAHNIINLLKEQLVLSSKEG NSKLTPELLVHLTSTIERINTELVGSPGKHQHQEEGNVTVRPFPRPQ SLDLGATFTVDAHQLDNQSQPRDPGPQSFAFSLPGSTQHLRSQLSQCK QRYQDLQEKLLSEATVFAQANELEKYRVMLTGESLVKQDSKQIQVD LQDLGYETCGRSENEAEREETTSPECEEHNSLKEMVLMGELCSEQGR RGSTLASSSERKPLENQLGKQEEFRVYGKSENILVLRKDIKDLKAQL QNANKVIQNLKSRVRSLSVTSYSSSLERPRKLRAVGTLEGSSPHSV PDEDEGLWSDGTGAFYSPGLQAKKDLES LIQRVSQLEAQLPKNGLEE KLAEELRSASWPGKYDSLQDQARELSYLQKIREGRGICYLITRHA KDTVKSFEDELLRSNDIDYYLGQSFREQLAQQSGLTERLTSLKSTKH KSEKDQAGLEPLALRLSRELQEKEKVEVLQAKLDARSLTPSSSHAL SDSHRSPSSTSFLSDELEACSDMDIVSEYTHYEEKKASPSHSDSIHH SSHAVLSSKPSSTSASQGAESNSNPISLPTPQNTPKKANQAHSG FHFHSIPKLASLPQAPLPSAPSSFLPFSPTGPLLLGCCETPVVSLAE AQQELQMLQKQLGESASTVPPASTATLLSNDLEADSSYYLNSAQPHS PPRGTIELGRILEPGYLGSSGKWDVMPQKGSVSGDLSSGSSVYQLN SKPTGADLLEEHLGEIRNLQRLEESICINDRLEQLEHRLTSTARG RGSTSNFYSSQGLSIPQLCNENRVLRREDNRRLQAQLSHVSREHSQET ESLREALSSRSHLQELEKELEHQKVERQQLEDLREKQQEVLFHRE ERLSLQENDSSGPCLSLVRLQHKLVLLQQQCEEKQQLFESLQSELQI YEALYGNSKKGLKAYSLDACHQIPLSSDLSHLVAEVRALRGQLEQSI QGNCLRLQLQQQLESGAGKASLSPSSINQNFPASTDPGNKQLLLQD SAVSPVVRDVGMPALVFPSSASSTPGSETPIINRANGLGLDTPV MKTPPKLEGDATDGSFANKHGRHVIGHIDDYSALRQQIAEGLLVK IVSLVRSACSPGLEAQGTEVLGSKGIHELRSSTSAHHHALESASL LTMFWRAALPSTHIPVLPGKVGESTERELLELRTKVSKQERLLQSTT EHLKNANQKESMEQFIVSQLTRTHDVLKARTNLEVKSRLALPCTP AL</p>
7381	A	1	1131	<p>MKVTFANKPEGGGRLAKQRPGRGARPRPKHEGGQSVLGTRRPALLQ VSCDVSLSSEQDKGATATHFAASRGHSKVLSWLLHGGGEISADLWG GTALYDAENGELGCCQILVNGAELEVRDRDGYAAADLSDFNGHSH CTHCLRTVENLHRGMVLALGAAEHSKAQRPEAAGGPEGELPPEKESL EENEWPSRGQGLVPSAPTAVAQSMHECVLSRDPVSLEAKQPDGMS SPNTTVSVQPLNFDLSSPTSTLSNYDSCSSSHSSIKGQHPRAPNPQ ILQYKKRFSELEQLLERSGELEQQQLRDAEHSQDLESALIWLEEEQQ GGPGLAAWPPGRAPTDPLCPIQECQPGPGGECHALRTAGPGRFGQPGS E</p>
7382	A	421	582	<p>LPGAQGMPRPGVQ*PSGLHIPQGGSTRTSGLKAMRSPPKNHQVPDSR AGPWAYC</p>
7383	A	3795	5290	<p>WNWTVHGDGSAGQGPWLHLFCHKRQHGGISWPLVQREGRDEHFRNQR EIAPPAGREQTAVQKQREMFCNSTGRLPGQPTEEIQV*RV*RPHKI YABE\ERQFKEEKLAELKQAEELRQYKVLVHSQERELTQLREKLRE GRDASRSLNQHLQALLTPDKPKDSQGQDLQEQLAEGCRLAQQLFQKL SPENDEDEDEDVQVEEAELVLESSAPREVQKAEESKVPEDSLEECAI TCSNSHSPCDSNQPHKNINITFEEDKVNSTLVVDRESSHDECQDAVN ILPVPGPTSSATNVSMVVSAGPLSSEKAEMNILEINEKLHPQLAEKK QQFRNLKEKCFVTQLACFLANQONKYKYBECKDLIKSMLRNERQFKE EKLAELKQAEELRMGSGKYLNEHFVFTENDEDEDEDVQVEEAELV ESSAPREVQKAEESKVPEDSLEECAITCSNSHGPCDSNQPHKNINIT FEEDKVNSTLVVDRESSHDECQDAVNILP</p>
7384	A	125	605	<p>EAEALNQSQPCDTG/PQSAFSPPGSTQHPRSQLSQCKQRYQDLQEK</p>

				LLLSEATVFAQANELEK*RVILSEPLLKQDSKQVQVDLQDLGHETCG QSKNEAEQEETWPPAPYLVPAPRSCRPSQ\SRGRRYPERSQRRPR GRPPPPCPRIKVKDGKNKTQG
7385	A	310	329	TVKLL*HVGNISLFPSPSP*MLNTQWGKKS\FNEWWENWISTCRRI KLDPYLLPYIKTN*KSIKDLNCKTTK
7386	A	310	329	TVKLL*HVGNISLFPSPSP*MLNTQWGKKS\FNEWWENWISTCRRI KLDPYLLPYIKTN*KSIKDLNCKTTK
7387	A	3	642	GKGLFDDDEDEESDLFMEAPQDRQAGASVKEESSSSKPGKKIPAGAVS VFLGDTDFGAASVPSLKEPQKPEQPTPRKSPYGPPTGLFFFSAPH SKPSKTRKVQSTADIFGDEEGDLFKEKAVASPEATVSQTDENKARAE KKVTLSSYSKNLKPSETK\TQKGLFSDEEDSEDLFSSQSASNLKGAS LLPGKLPTSVSWFDDDEDEEDNLLGVQ
7388	A	1	3096	MVTHQQPAARKPNMTSKKPKPMGPKAHGIFSGTRKNNLEIYMDQTRT GIAKTKLSKNNKSGGMTLPDFKLYYKAIVAKIACGGSMYNSDTEDE ETEPSSSSGQQIIENSITMNMKLLKAKMKNMNLKHHITQVSDEEED DDGCDLFADSEKEEKDIEDIEENTRPKRSRPTSFADELAARIKGDV GRVDEEPTTVSYEDDRGKNQDAYTEGGLSTIKTVNCSSSL\PSGEA KLKRTL/KEKKERRTPSDDEEDNLFAPPKLTDEDFSPFGSGGGLFSG GKGLFDDDEDEEDIEESSNPLWSGYSLRWAREPPQOPETHTVVSTNEK PEQWLKGENWGSVSTPLQKRSRPTSFADELAARIKGDAMGRVDEEPT NEEDNLFAPPKLTDEDFSPFGSGGGLFSGGKGLFDDDEDEESDLFTEA PQDRQAGASVKEGKLGSGCVSVCRVPKLSFSLGDGTLRRHGCAASV PSLKEPQKPEQPTPRKSPYGPPTGLFDDDDGDDNDFFSTPHSKPS KTGTEKPFKIGMDCDLGDTSSYHTKVSTVHITKNRNGGSLNNYSS SIPSTPSTSQEDPQFSVPPTANTPTPVCKRSMRWSNLTSEKGSDDP KERKAPENHADTIGSGRAIPIKQGMMLKRSKWLKTWKKKYVTLCSN GVLTYSSSLGDMKNHKKIEIDLQSTIKVPGKWPSLATSACAPISS SKSNDLSKMDTGLGDSICFSPSISSTGPKLNPPSPHANKKHLK KKSTNFMIVSATGQTHFEATTYEERDAWVQAIQSQILASQCES SKSKSQLTSQSEAMALQSIQNMGRNAHCVDCEONPKWASNLGVLM CIECSGIHRSGLTRLSRVRSLLEDDWPVELRKVMSSIGNDLANSIWE GSSQGQTKPSEKSTREEKERWILSKYEKLFAPLPLCTDLSLGQQLL RATADEDLQTAILLLAHGSREEVNETCGEGDGCTALHLACRKGNNVL AQLLIWYGVDMARDAHGNTALTYARQASSQECINVLLQYGCPCDECV
7389	A	1	238	SDLFTEASQDRQAGASVKEGDTDFGAASVPSLKEPQKPEQPTPRKS PYGPPTGLFDDDDGDDDDFFSAPHSKSKT
7390	A	1	1374	DDIFATEAIKPSQKTREKEKTLESNLFDDNIDIFADLTVKPKESKK KVEAKSIFDDDMDDIFSTGIQAKTTKPKRSRAQAAPRFEHKVSN FDDPLNAFGGQLRSPSRCCQADCCPPDSGLWVGALVGLGGARAAQ ITQVSDEEEDDDGCDLFADSEKEEKDIEDIEENTRPKRSRPTSFADE LAARIKGDVGRVDEEPTTVSYEDDRGKNQDAYTEGGLSTIKTVNC SSSL\PSGEAKLRTL/KEKKERRTPSDDEEDNLFAPPKLTDEDFSP FGSGGGLFSGGKGLFDDDEDEESDLFTEAPQDRQAGASVKEGKLG CVSVCRVPKLSFSLGDGTLRRHGCAASVPSLKEPQKPEQPTPRKSPY GPPTGLFDDDDGDDNDFFSTPHSKPSKTGKVQSTADIFGDEEGDL FKEKAVASPEATVSQTDENKARAEKKVTLSSYSQNVK
7391	A	1	419	MDSSRSVGNFTYQDKLSSSKLTSVLEAVAGEYALVINGHSL/ARHR YP*LGQYLSSEHFCPGLLYLVLIISPDRFREDWSQRGLGGAETPRCLLE RLALSGLSVLQAHLEADMELEFLETACACKAVICCRVTPLQKAQV
7392	A	3	701	LVKSYLAQFAARAIISELVSISELAQPLERGTFFPLFLCLQQLAKL QDREWLTFLFQOSKVMQKMLPGKRKLTCLFCFFNIISRDFRYLEWI YVGQTV*LSCSDNDKHYHRSHL*REIYNLTTFI*SRC*VFFICWGS LLCYKDLKYLGDIIICEALLSGQDHLVK*TIR*CRWLCLF\ESDQNKD RMLEILEGKGLSFLFPTQLEKDLFEQ\IKLDPSPQTIYKWKDNI
7393	A	83	3064	GRPRLLPPPSLPLFFVFRSPFPLPYPRRPDPPEAAVAAAEFLGEG ISFLLSPPLPTPSINIILLKILRCQAAKVESAIAGGASRFSASSGG

				GGSRGAPQHYPKTAGNSEFLGKTPGQNAQKWIPARSTRRDDNSAANN SANEKERHDAIFRKVRGILNKLTPKFKDKLCLELLNVGVESKILKG VILLIVDKALEEPKYSSLYAQLCLRLAEDAPNFDGPAAEQPGQKQS TTFRRLLIPKLQDEFENRTRNVDVYDKRENPLLPEEEEQRAIAKIM LGNIKFIGELGKLDLIHESIHKCIQTLLEKKKRVQLQDMGEDLECL CQIMRTVGPRLDHERAKSLMDQYFARMCSLMSKELPARIRFLLQDT VELREHHWVPRKAFLDNGPKTINQIRQDAVKDLGVFIPAPMAQGMRS DFLEGGPFMPPRMKMDRDLGGLADMFGQMPGSGIGTGPGVIQDRFS PTMGRHRSNQLFNHGGHIMPPTQSQFGEMGGKFMKSQGLSOLYHNQ SQGLLSQLQGQSKDMPFRFSKKGQLNADEISLRPAQSFLMNKNQVPK LQPQITMIPPSAQPPRTQTPPLGQTPQLGLKTNPLIQEKPGKTSKK PPPSKEELLKLTETVVTEYLNsgNANEAVNGVREMR\AHKHFLREML SKVILSLDRSDEDKEKASSL\ISLLKQEGIATSDNFMQAFNLVLDQ CPKLEVDIPLGEIPILAQAARAIISELVSISQNLAAQ\LESGETH P/LSFLL\CLQQAKF\QDREWNQELFSTKPRSNMQMLPEIDQNK DRMLEIL\EGKGLSFLFPLLKLE\KELFEANKSWDPSPTIYKWIQD NISPKLHVDKGFVEHL*MTSF\LQLHF*WS*TPPADETSSSAPPQR NS*EQEKQLLLSFKPVMQKFLHDHVDLQVSALYALQVHCYNSNFPKG MLLRFFVHFYDMEIEEEAFLAWKEDITQEFPGKGKALFQVNWQLTW LETAESESESEAD
7394	A	259	1159	EARWQDVGRQLTKTV*PWGRGWSR\ASDPRHLHAYFSYTAATGKAEP RARTPAPCK\ARERLGSCLD*SPPPPPGWRPLRYPTPRRAGPAQFG KK\RSASARSTWP*/VMQRLAPKTRKEQSANDHPIGGPEGRLFTSQ LQLKFRALSERISWLEVSRAVTP TSAAVTSTPSTSKPRQKRPTNSQS RSAAKPTPGRRCQPGGRCPTCTRSP*LR*ARGRRHGEARRLPLREAR RLPLREARRLPLRAPRSFRKVPSPGQGRSAPQAGVGAGTGRRRRSMD AWGRARSLAGSAGVISLGG
7395	A	3	433	HIKRVKKNHMIISVGTEKAFDKIQHSFIIFFKFRKK*EWGHFFNLIK SFS*KVRANITLSDAFSLILVIRQGCLLLPLLFDKVLKVLDSAVKQ EKEIRDI*VGKEEIKLSLFEDDMIVYIGNNK*/SYRKLPEFINEFSK VAG
7396	A	3	504	AASGGGWSEFESVAPGSPDTTAAPTCPQRTPRSLE/LPHFQS*TG PCLNISPERSVSEPQNRGKPRPHYPGPQNPQWGPAG/GGCWSKPGST PALSDDQANTQVDRN/DLQVASEGEA*PAELFPKMKKRLGDLGPG FEGKNGLSTEDKNLIPQAWVPALCGYHVL
7397	A	376	419	VRKYSLCFYIL*NLFQNIKAEGILPNSFNARITLILKQTRHSKENK PYRPIS\MDRHABILNKISAN*IR*RMKRIIHHGQVRFS*G/MWGWF NIRKQINV/IHHTSLKKKNHMIISINAEKEFDKIRKLPKLRNIYKQ NI*LTS*VMVRNS
7398	A	205	1464	VYKKVEASRNEKGWVCGTHAGAFPDEGEGPEEAFLGAETAAGAP/G ARDHPPFNHGYAGLLEGPDQLQVGSHPSPGRRQA*VCG*RAPQSDCPG GSGRGSMEAGMPPR/QGPGGLQPPQEGSVFAVMYSIGGQGAARRIP VRPQP\GREGVQGSLLQPMKPDGEAASIP TAGSRSGRCGPAGRRRA LVGRSLRP*PPC*PSPR*SPPPSS\GASSPGHPRPALAHNG*SGWAT RGS**DTAPS*HLLVPKQLAGTCLLCRCPKST**AKLEEIVPGSFHS PRGSYSRGLGAQHQLPSPASVAHPRCQAPSAASH/G*RRRPRACLS LHGQLGMIW*S*APSGVQAQGHTHPPGPDISAERAPAGS*LSQLQGP G*DSGGLGSGGCAVPPVAAGHPGSGLAWQLPPPR*SPAPGSGSPAGR P
7399	A	2	681	EAALTDLRVQARSQPGTMSIGTENRGSGLSAVAVQEVISDVVEVRLA NRPGGLEVLLNQEVLSFTEQSWMDLKGMLSVAAAGDRVCIMLASWAV LFVSLLGPFLLSVSVLLPEKFLTHTHGLLGTNLNDPTDDFTLHSGRVL PPGTSPQELFLFGANWTVHNASSLLTYDSWFLVHNFLYQPKHDPTFE PLFPSETTLNPSLAQEAALCGDDHFCNFDVAATGSL
7400	A	658	1657	PGILSLRNALLTGVDCKVVVPVPPGHTHPQLRFLHFHFKPTCSGWGEW GDHGVVWAGPAPA\YHLHRDVQALWTNDHALAW\ P*AMTSERTLWPG

				HEL SARPGRSWRISCPTGL\ PQGGDDRTGRHWVTATCCSADGLRLCR YGD\ GVRGGLPTVAWP* LTGSCSLRYGSGQQCCYTADGTQLLTADSS GGSTPDRGHDWGAPPFRTPPRVPSMSHWLYDVL SFYYCCLWAAPDPG KDRAGLGCTPT* PSTLTLASAFGDPHFVTFDGTNFTFNGRGEYVGMG *NQGGRLEPSGSRSAPTTAGTETRGTGLTAVAVQEGNSDVVEURLAN RTGPER
7401	A	1	423	RPKPKNSF* LGGEKANKI PHPLMIKTLTKLGIEKTYVNI IKVIPNRP MACII ING TKVKAFFVRFERQRCSPSPLLFNIGLKVPARAIEKEKEM KGI* IGKKEIKLCLSGND\ MTLYLKQPKNSPKTIRTDTF SKVAGYKN
7402	A	247	660	NWSGRRRLRMWPSAALS PAVSSPALALTSPPKPLVKGRDGKPPAGRPP GREGPGAWR* GPSPPTTLGPAKAGSGQRRGRCQP* GPGWRPAASQPL SGCPWCPCGITELLLES PSETAEQDRGPGSGEDS* TPDFYTPTRP
7403	A	229	1047	HSVQKAKADKTGVDGSGECGPPLLSLLQSHPRP* P* PLPQKPPEREE VWPKDGKLLASRAGGLVCI SLL* EPRVHSCTGPGLPVKAELGLLRAQ GLPHPASPARLGNTG/ VGLATE* TGISEHKLGPLGN* GVMGDAVR* G LCSEGLCPPSRPWGPMGVCGLAAKARPH* QG* VCAPGTHLEGSSVW SLPSPQLFPTPGPPAVCSALAPAPTPTARTDGTIQNHLVPVTRKSALP VQEWGDSWGTGQAQEEGPSVGYPGCP* LPGEGRIPPL
7404	A	595	626	CPMPLVPPDISLINEQTEKEAGDLVCPS/ AGVPVDSFPLGSEPSSHG VSELKTRAKRQRERHKKGGTEKDRKAERGT/ PPGPLLPLFLVH* SG* CQVAQGALDI ISWLKII VPKSVFPGCPLKSWAAAATPCSPCHPSSH SPVGVPGRASKFCACPLECP* SPPSPLPSLQGPPLCPFFHASPPDG NPGGQGVPLCPLRGSPGHL CAMSRCPLRWNP
7405	A	1	603	EMESRSVT* AGVQ* QDLSSLQ/ PLPLHPGFKQFSLPPVSPSKLGITR HTAYLNFFVFLVGDDFAMLARLVNSSSQ/ CDPSSASQSVGITGV SHCACLTCSLCCQTMCFVLVASRYF* FWDGNLFCYNLQIGDVYFIFI YLF\ MRPSYSITQARMQWCD\ LGSLPSPPPRFK* FCSLSLPSSWDYT QHAPPCLANFFVFLAEM
7406	A	211	389	PNLG* LNPPPPGLKNFSCGLP/ SKWE* KGQCLPPGPVNFGLTKLG VFPCGPGWLEIYN
7407	A	3	326	LSGVMSPGFPGYYLFST* CIMDNKATHRYCVYISS* IFLQK/ HIH DYLEVRRGSSETSTGIGRLNGPQIPCFLLSTTHETSLYFHSQYQNK QGFHIEYQGERSNKK
7408	A	1	555	SDPRTEESHKMLTD* RSSYLSLTALPF/ PLPKSEAITNRASRAAS LVRLTPSKKDVGFLQKPRLRSCSPSSRCPPGSAARST* AAGTACGCC GTSRQR* APGALGLRRPPQS* GRRSSPRPSLTHPSSALPPPPPTS PRTRYRG* SRAAPLLSLRLPSGKLFQPTCRPRVSLR* RPSQRVE
7409	A	3	379	KLSPSKPILASTLMGPIYHSHKVF/ IPGMKGQFNIQKSI IMTYHINI TKNKNDMVISSSSSSSSSSSSSSSSSSSSSPIEGNYFPITKE/ YE KSIANIILDS* KLKAFFS/ LRSGKRQGYLLSLLLFN
7410	A	1	411	NKVFNHNNKRSIHQENKTI LNVPVNNKDPK* LK/ QLTCLTEDTSS IIVKDFNNPLS/ TL/ DRISTQNIS* DLENLKNMTMNQLDQINIYRT/ L MPSNTKIEHMMGHKISFIKFQRIKIIQNTFSENGVT KSNRYLENPKL
7411	A	3	414	KGQDLYGEV* KVLKVIKQVLNWKDMSCSN* HTNFISN* NCIKVF F* LDEI/ CSFV* *NKC* RIAKEVLSSSQ* CLGGHL/ TSPHIRRSYNT TFSQSIWCCYRTKQID* WTRTQNPEDLRI* GDLIYDLRCCSSRA
7412	A	3	333	LIKEGQIQKLSAKNGTPQDRHLFLFNSMILYCVPKLR LMGQKFSVRE KMDISGLQVQDIVKPNTAHTFIITGRKRS\ ELQTRSSRATIEKHQ NSETF\ KAFGGRL LARD
7413	A	3	392	EEDIVNPANDLIKEGQIQKRSKNGTPQDRHLFLFNSMILYCGPKLR LMGQKFSVRENMDISRLQGQDIVKPNTVHTFIITGTRSL ELQTRTE EEKD\ WIIQIIPATIGKHQ\ GETFKAFGGPLNQGW
7414	A	3	1811	RYIDVLGRRYTAPGLG* LWRHPAQSAVPTAHCGDPVSLAAAGDGS IGPTGELSGSLKIPNRD SGIDSPSSSVAGENFPCEEGLEAGSPPTVL GAHAEMALDSQVPKVTPQEEADSDVGEEDSENTPQKADKDAGLAQH SGPQKLLHIAQGFLAP\ EETY\ VKRLHL\ LDQ\ VFCTRG* RMRGIPP

				ERSSWGHNSLNI FLPPQ PASHGQFLLP ELKTRITEEWD TNPR LGDIL QKLAPFLKMYGEYVKNF DRAVLVSTW TQRSPLFKDVVHS IQKQEV GNLT LQH HMLEPVQ RVPRYELLLK DY LKRLPQDAPDRKDAERSLELI STAAHNSNAAIRKVEKMHKLLEVYEQ LGGEEDIVNPAHEL IKEGQIQ KLSAKNGTPQDRHLFLFNSMILYCVPKLRLMGQKFSVREKMDISGLQ VQDIVKPNTAHTFIITGRKRSLELQTRTEEEKKEWIIQATIEKHK QNSETFKAFGGAFSQDEDP SLSPDMPITSTSPVEFVVTEGSSGAAG LEPRKLSSKTRRDKEKQSKSCGETFNSITKRRHHCKLCGAVSPGRG GQGQEATLSSALTEQLSPHQHTSHAHQPCTEGLPDGGSWI
7415	A	189	392	KQKWEKKQLKKS PGP GAAHTCN PSTLGG*GGRITRSGNRDYPG\QH SETPSLT*NGKNLGRGMVGG
7416	A	2	325	SHAGCLIRFWRKSMTPTHSLPLTPTFLGTCEASFLEPRASPVPPQCS MALRRYRLDMGQSFWGGLPSSHPPDPSRPGFV/PGVGHVPGQEGPGG KPAPDSS*H*DPTGG
7417	A	9	1431	NDNASFGEVYHYPPVPGSQC HDESGAGFP PGPSPCGTWP TPALKPG REGSGGWLLGQASPVTTAPCPACIF*VPCCTGEGQGWLGAPGKDASH /GA*KM*GVKGRLCVGAPEGAG/PSQGI*SFFTEP**AHPQNGLYED EHKNSRWGHPHP*QWNWDRTS*CNIPSRP*VPHPWVRCAGLEPAG PGPHRTRTPSQVG VILFLQKRIKQPACEPYALFTPLSPHSS\PASAR PGSPSD*MCRAPEDESCPEMALLPGMGPPGSGERC SRAPSPGAQVTGG VPGPFTWGSGESRCFRAPSPGASGEEAKCSRSPFTGGSGESRC SGAP SPGAQVRAGVPRPITWGSGESRC SRPPSPGAQVRTGV\PGPFTWGS ESRCSGPLHLRPGS\YPVFLAPERKGP PQRSQEKGHKRGGSQAAPKP SSR/PQESPSPLTPSGGPGS\GRNGA*GVSEG*SAPGSGGEEEDVFG C*GPPALGPEG
7418	A	1	390	HLTFCHHYDDRVRGLYKGOKECPGI PRVYRIRHIGEGRHLYVLQFK DHPGIHQPLEPQVKYVGNMHSNKA FGR*LMLQLSEFLCEEIRKNKNQR IVQLIQDTRIHLPSMNPDCYQGG\VAKGPNKPWLC
7419	A	31	394	KHNRA SPPPS*KKSSSPVTTKGR\YTKTPHTDVPQG*QPPYKQRGGT SSSSPFSFIFSYSIVLSSSR\PPHPGPTSPRLHPSRSHLSEVPPLT QVPPLQGPVPHPDPTSPWLYLSPSSYLY
7420	A	2	704	TDSKCPFLVHQAHAA*KERHFLTANGSCIKFHQDINRLSSVFLP* ELVVRHCRGHQKRVDEIAKGNRLADQRAKS AVRRPQGP KTL EAPLIW EGYIREIKPQYSP/DRDRMGHLSRYTFQPSGWLQSEDCKVRLPASSQ WKILKILH*AFHLGKHKTSVHPKIVLRRKSTKNGQIGC*YS*NPLKN NPFNR*LLPHHNQRMGSYSGEDWQIDFTHMPKINGIQCLLEWVHTFI
7421	A	2	707	FSRDEVSPSWPGWSQTPD/LRDTP/CLGLPKC*DYRCGP PHLAESKF YFPII*KLYHSM LCL*ADSKS*KPMSLFLFLFLFLLTQNFALVAQA GVQWHGFGSLQPLPPGFKRFSCLSLLSSWDYRCLPPRLA*/FFVFLV QMGF\TMLVRLVSNS*AQ/CDPHALASQSVGTIGISHCSWP NVIIYI ITTM*IFFSIPPSPLLIRH\LFFLFFF FETESRSVA*AGVQWHNLGS LQPPRL
7422	A	33	777	VMGPAPAGEQLRGATGEPEVMEPALEGTGKEGKKASSRKRTLAEP KGLLQPVKLSRAELYKEPTNEELNRLRETEILFHS\SLRLQVEELL KEVRLSEKKKDRIDAFLREVNQRVVRVPSVPETELTDQAWLPAGVRV PL\PKCPMP*RACFR\FLAPKPRITVCEASYLSGQPSIRPDINVDVA LTMPREILQDKDGLNQRYFRKRALYLAHLAHLA QDPLFGSVCFST NGCHLKPSLLLRPQ
7423	A	74	576	LCWQPIRWWSP TLRANGHQ*/SGVAILISDKTNFKATAVERDKEGH YIMLKGLVQQENITILNIYAPNTGTLTFIKRLIDLRNEIDSNTIIV GDFSTPLTALDRPPRQKVNKETMDLNYTLEQMDLIDIYRTFHPTTAE YTFYSTAHGTFSKIDHRIGHKISLNTFK
7424	B	158	346	XLSQGEVVPQIPVKS GPGHAGVLGLHLEGPFISREKRGAPHAHLR SFEADAFQDLLATQGQX*
7425	A	1	1770	FFFVTFVMYFTTIFKKQTKTNLKSASPTPQNHP/GSSSLAQ/PLSHP DPGPLSHNPGLALWDQPSLPAPPRPSSQGGGALCGEWQ\PGPKAGP

				GLTSS/GDWGVPSEVGDDQHASSGF*/P*GWGTFKH*QPASLGTGRC STSNTSAENLTCLSLPGSPGKTAPLPGPAQAGAQPLPKGCAAVKAE VGIPAP\PP\PGGQDPHPSPAFLG\SPGACGLRSTPCALPQALPQAR PCPGRWFFPWLFPPQTGGAPDHPISLDPGDISFNWALQQEGKRTSAR A/RGAYLLCPRTAP/GKQGGREPPTPELKWRESQDNHP*RGAAPIPD V*PHCGCPQSQEGSRSPASKLFQGESRPVFATWVCSRAKGTQKMAG *H*WGEQGTLPVRHTALQHQAQSPQPASTGPGDV*RDVIEKRKQNA GHPWHSGLGSPGS\KNRGPGPSLPPGGQSGAPGNCALAQEPGCGF/T RCTPQTQEQKANP*LSTLPVTGPLPAGSSPPAHGGFTPWAPAT*LPA PPSH**HFPGVCRSPVP/PSCRQALSPTGAQGP*TTAQPSHPRP*M PSPGGQP\GWCHM*AQAKPGAKASPAGCTF\SQPPPPGRR
7426	A	36	620	QHLKLLNIKNHTGEKS*KCKECDKAFKWLSHFIIGKIVHTEENFYKC EQCGKTFNECSHLIAQESIYT*KKMYKYKDHEKAINIYSHL/NHWRV HT**KEYKCNYCQKIFQ/ININL*SEEGIYFEDEHYKCEEGCSTFIC ITDFIVHILY*KKTLK\CCSNFVQHQGIYIEBKLCFNF*KTLFQK VQLRRHQSSY
7427	A	3	276	PKKSTEKLLEVISNNSKFTRQKANVQKSITFLQYNSNEQVKFKM*NT LP/YKMKYLGISVTKHMQDPYEEKYKTLMKDNKEEQNK*RDIPCL
7428	A	125	456	LADWAHRAPASPQRNGADYAVYINTAQEFDGSDSGARPDEAVSWGKI RVDAQPVK/VKRWLGGA*GLWDDECGSHGLPRFPPTQVYAAASLVFP LLEAETFAQKMDAFTEK
7429	A	1	571	LSGKEVRENGIHR\IGNLL\VPN\ENYCKFEDWLMPILDQMVMQNK RGGFGLKK\WTPSKMIARLGKEINNPESVYWAQKNHIVFSPALTD GSLGDMIFHFSYKNPGLVLDIVEAERG/ADYAVYINTAQEFDGSDS\ GARPDEA/VPPWGKIRVDAQPVKYANASLVFP\LLVAETFAQ\KMD AFMHEKNED
7430	A	1	311	RRVSSSESRRWSLESRGRSLEIQGRMERPRCQRFRENSCVAPRHCKGP GGKGLQALF*VPVAQLGEPGAQLGDPGAHGEATVPEVQGE/PAALLP GTAK\PGGEGSPGFIPPRHCRGTGEEGSPGFTQGRETSKAQORTGCL LSCRGCLCLSVSGDS
7431	A	250	504	DDEKSKSIEE\VVVGSDEEEDNGKDKKKKTNKIKEK/YIDWHEELNKI KNIWIRNSDDI\TQEEYREFYKSFTSD*EDHLAVKHFSVE
7432	A	3	542	KRRGSFKMAELYQLPDESSAKALVSLKEGSLSNWNEKYSSLQKTP VWKGRTSSAVEMPFRNSKRSRLFSDDDRQINTRSPKRNQRVAMVP QKFTATMSTPDKKASQKIGFRLRNLLKLS*RH*WGIL/AKWFSYNI\ DKPLFEGDNDFCVCLKESFPNLKTRKLTRVEWGKIRRLMG
7433	A	3	322	FFLRWTL/DTVTRGGIQWCNLGSPQPP/PPRFKRFSCLSLSSSWDYR RPPPCPANFLYF**RRGFTMLARLVLP*PRDPPASASQSAGITGVG HRAWPMPIFENRFDL
7434	A	22	475	PRMISCRPTRPPTRP*SHSAPFRHFLLVHPVKAKYFLSAVMTTHHLA SASHFPFFAA*SATFPAAPQPMWTSDLPPQPPSTCLPLGTSPLPSRPL LPVSSCS/SFPDPTQMPPLPST\FPGLPFL*PHSSALSLPLL*LPHG FALSPSSVPFPT
7435	A	14	362	LFYQTFSNVN*KT/RHKMNK*TEDFNNTIEQLDLTVTFISLHSTVEY AILLITHATIFQIDHLLS*KTHLSK/CSADGITQIIPNYDTIKQEVK NTNMSKNK*KLNNKFSNTLLFKRL
7436	A	1	442	SPFPPKNFYPSLRPLIFLRGVGPKLPPPKRVFSKNPPEVFKSPPLK KKNFSFPPPVNLGPPKDLLKG/PPSSSSSSSSSSSSSSSSSSSSSSSS SSSPDRERPPTI *N*PTRP
7437	A	8	488	DEVSLVAQAGVQWHNLGSLQPLLPGFKRSSYSLLSSWDYRCPPPCL ANF\FIFSRDGGFTML\ARLVLS*PQ/CDLPASASQSVVITGVSHC AR\RAPS*MSASGVTCVWELFGMHPVAEANDHLSGALVPFSAL F\SHFMPGLLPTMFCPLRGCE
7438	A	1	445	IDCWHKCQDNSMGKDNLFN*SYWDYWISI*KKRTSNLISPIHKIES/ RWIINLVNSKALFRRKQKTLHDCGLGNSFVEETQKALTN/WDIK

				LQ/SFCSSKYTTKKLKR*ATDWGKIPTLFAKNNDKICEHTHNKRRY MFGQMHVKKWA
7439	A	131	763	PGISADSRGQKLS*WGPSHQPPPGPLKGSAPGG\LCGLVGPGAACH ALRPSFHSGAPSAAGNLGCFAAWASSLNSNOGSPSSKGHIPPDRGEP RGTVP SLRKATATGRKAERLSDEGRSSVHG*AGIPGHEGNAKENRDR HPWQLPGIASAAVVIASGRGALPPGGQAGPQKLAPPFSSLSVPGGAR WG*AEGAPSKQRGKVTGEPGRQC
7440	A	47	265	VHTVCARHTAPHPRAPAASPGGHGDCPQPNPPTPQGGAPARSMQGWA SPRPSPEVAFTTGGGRREENSFEL
7441	A	1	330	HHHLAPFSSLPFNIVL/EEVLARPINKEAK*KAP*LERKEVKLPLFA EEIQEMIWIYIDNSKESTKE\LLELINKFIKATRYRFHIQ*LVFLYTC NNLK*KLIKYLSINLTKV
7442	A	3	423	NNALLNNPWVKGAIKPEVRPYLD/TRENKVTA*QNLWDALKK*/CSG KLIALKE*CQINNLSFPLKIPEK*EQIKSPVNIKNVIFKKLKIKKG LKV*KK*RKISETKSWFLEKVIKIY*SQGRHARKKNEKSGITRDSRT RG
7443	A	1	689	YIYIYSYINIQFVFL*EHLLINKFLSFVYQMLKH*KKRTTNTLFT LIRTM*AFLFYQIICISYVIAAVLFCI*IFFP*HLCCLLVLFMYFF NILRFIPLLRSDITSFHYMPLFGRFLSC*SKQEHLLNCQPGIYFINL LVWKHFFLDVIFTLVYFVG/FALILYDFLMSVC*TFYLSLFSIR/ ACLLFYPHI*LIFIWAYISRLEIISFHTF*GIYTFASEIVFIIF
7444	A	3	545	TMLLFTLQNRCTSSHCMPAPALCPGKLTVGTGSMGPR\SPWPPPS SANA*PVDKPSGQEG*GQCTAAAPPCRVAVSLSKVRAPGDGLSCGSS CPPG/RQGRGVPCPAAGERREGREDLKPRE*IGSCIKNKLGISPAK* D*KNSQDKSKKNPIGD\RTSLAVGTVPQSTRPRVPLGYHYCY
7445	A	243	768	NLPNK*QDEGRGGGAEP PPPWPG/SLPPRDVEAPSPRLGAPAWPPA GRGWPPREGAWLG*VLCFRKRSPLPVLGVAGA*ASVGGGCVGRCPLS GAWPPPGVGDKPSYCSERPAASFP/PRTCVFPNAEGGGERAPRDSR GEGSLPCCRGEERGQGLKTTRINRFVYQEQARDFTS
7446	A	596	1335	LEQITFSVATAMDSRFPDFQDLDEPERACHDAAGTLEVDFFLFLNF GTVDLAGRKETTTEQALPPALLLGIRRPEFLSRPSVQTEDAPSKVNY VLCLLIAECSPGPSDYLP CAIPSAJR/RWYLDFCPR*FLPPYY*RRH PFQWTTVTQEAFFSHHDVAFTSTPVLFPDQAQPFIVKSESSSQIACA ALSQQRPSLIYERALLHFFS*SLQRHTIDLDQGIF*ILMLSEERQHLE ESSIGHPHTISKD
7447	A	199	451	ERSFSKMP*NPPGGGEPP*PTLGIPSSPPPHLLGPKFLEKIFGLPG LPGGKIFP/P/GFAFGPNLGSGBEIPGGINPRSLPLGER
7448	A	154	695	GLLSNLLISIFFIPPKKSAPKYQHMKMSQSFFHYCFNTHFNQNLKP /FNELO/K*HELKLE*SKIIYNQNKPSVTYREIMQLRAQLKKIIDS VKHKRTWQGLKQGV/YWGFYVNVIGKSFFYFWDKYFIFIDWAKNTLR INMGPERPTVFLPNFIYSQSTKLALNWINIMGQFIPSYSVSA
7449	A	203	443	FFVKGPKNTHW/RKDSIVNKWC*KN*ISTCRRMRIDTCLSLYTKIK* KLRPIEESGTEPR
7450	A	8	312	QTLALSPGLGVQWRDLGSPQALPPGFMPFLLP*ASQISRDYRRPAN/ LMPGPNFFIFQAETGFSTVLAPGWC\DLPLDVIHSASASPSAGITGV SHRCPARTF
7451	A	1	2554	MKVWLLLGLLLVHEALEDVTGQHLPKNKRPKEPGENRIKPTNKKVKP KIPKMKDRDSANSAPKTQSIMMQVLDKGRFQKPAATLSLLAGQTVEL RCKGSRIGWSYPAYLDTFKDSRLSLYNSRGLLREGQAGPMGSQPKVN PPTMARVPQVEPPVGETWESSTLLADGAVDKRSSFALCSSFISTWKL ATLNDPVHLLSLVCTWTLRTAGRSRTARHVAVAAASRCGHLTFAWQNO YISLERLSVYMCRFVTWVNCMSRGFGVDYFIIQVLKLIQVLPDPSVH PRSHKHLRLRSEIAKTTSYCPKHSSLSIPLRNQMRSGVSVTLEQR SESTSSPFPVTALLFVNLTSLWLGKGPILPKYVAVSVQLSRAGACFSD VTHREVLMSFCYMVVGGDFLLGGSLVCQVWFVVSRYTLLIFSES REYLKEEEELFLCKGPGYAGQRVKKNDPSSVKQNERYGQLTLVNST

				SADTGEFSCWVQLCSGYICRKDEAKTGSTYIFFTESGGRIISVLVNLV LTAQELLAHEPFDVSRNSAPNLKHHLTVTQRRQVGKKAKKNYLFQE HCGENTRKHVIRIGVSLALKISLCKYCNIPSONDPEKQRIQCTMPKK KSHQHQQKYPQKPSPEFLACPKDRIEKGELFVPSPSYFDVVYLNPD QAVVPC/PGDRAVGQSHAPQGIQPSQGDPSQWNGHCL*HEAGLCVSAT SFRAPGCGLLQGGGRGQISDLRQVPAALRGGPNNSSKPAFCSSCHMQ APW*V/LAALSRRPQFPPLPSPPLPSLLGHQVTGIPSGPPSTTILAS SNKVKSGDDISVLCTVLGEPDVEVEFTWIFPGQKPPSRVTGLWAGTW WCLYRVL
7452	B	1	2586	MKVWLLGLLLVHEALEDVTGQHLPKNKRPKPEGENRIKPTNKKVKP KIPKMKDRDSANSAPKTQSIMMQVLDKGWFQKPAATLSLLAGQTVEL RCKGSRIGWSYPAYLDTFKDSRLSLYNSRGLLREGQAGPMGSPKVN PPTMARVPQVEPPVGETWESSTLLADGAVDKRSSFALCSSFISTWKL ATLNDPVHLLSLVCTWTLRTAGRSRTARHVAVAASRCGHILFAWQNO YISLERLSVYMCRFVTWVNCMSRGFGVDYFI IQVLKLIQVLPDVS PRSHKHLISRSEIAKTTSYCPKHSSLSIPLRNQMRSGVSVTLEQR SESTSSPFPVTALLFVNLTLSWLKESREYLKEEBELFLCKGPGYAGQ RVKKNDPSSSVKQNERYGQTLVNSTADTGEFSCWVQLCSGYICRK DEAKTGSTYIFFTESGGRIISVLVNLVLTAEQELLAHEPFDVSRNFAP NLKHHLTVTQRRQVGKKAKKNYLFQEHCGENTRKHVIRIGVSLALKI SLCKYCNIPSONDPEKQRIQCTMPKKKSHQHQQKYPQKPSPEFLAC KDRIEKGELFVPSPSYFDVVYLNPDQAVVPCRVTVLSAKVTLHREF PAKEIPANGTDIVYDMKRGFVYLQPHSEHQGVVYCRAEAGGRSQISV KYQLLYVAGWMFSLVMTLTENPSSPFPQNPISIVHSGAASVLDQSSQ QFIQACFLFLSHAGSMVSAALSRRPQFPPLPSPPLPSLLGHQVRG IPSGPPSTTILASNKVKSGDDISVLCTVLGEPDVEVEFTWIFPGQK DERPVTIQDTWRLIHRGLGHTTRISQSVITVEDFETIDAGYYICTAQ NLQGQTTVATTVEFS*
7453	B	520	600	MIDCVFGAELAESLSFILGILGFTFL*
7454	A	78	624	TNKSQGSQGLCVAGPRACPQSSPVQQRNVPPLSILSAPFSGS*GL* PCGGVLGATGGAELMGLLRWCPPGVCTVSLGQQVGSLSLESEPPAS SLNNSRGLLREGQAASVGGQPKVTSPTMARVL*VEPPVCETW\GPHP SWQMGPPLRG/VWAGPPQTPPCGVTLAANGKQPVKPGSYP
7455	A	3	369	ISQPPKNLGPPKETYKRPSSSSSSKKEFPFFFPGESKGGVLSPRKGS SSRVKPFSAPTPPKGGPRSSSSSRGKSSSRNFKKKGFP*PRRF FFPGPGKPPRPPKAG/H/YRGKPPGPGPK
7456	A	2	650	QTLPFKGRLPQEDGLGIRRPSPKRPALPWLCPQGAACPLPASLQVVP HQMDPIQLVPPFLSPARPLEL*EGRQKGRWGRPSQAGGQEKQ\LSS SSASPTAERARPPRAGTYG*CLALP*VTGGVGPMASLTLP\VTGGMGQ DSRGNR*EGPGVR*/DWGCSPRER*EGGTGVALEERGLLQRQREKTS GVGVSEPGFVFQRPALPGPWVCPLHKLRLA
7457	C	89	376	MFCVSEVQKLXXXXXXXXXXXXXXXXXXXXXSLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXSSVVARLSLGVSEFDIQVPEFTDFTFS PF
7458	A	3	866	MNFSPLFPSNFGDFSQNIISTPSEQQPLAQNSSGKTEYMAFPKPFES SSSIGAEKPRNKKLPREEVESSRTPWLYEQEVEKEPFIKTGFSVSV EKSTSSNRKNQLDTNGRRRQFDEESLESFSSMPDPVDPTTVTKTKT RKASQAASLAS\KDCTPKSKSKRNSYSSWKS RV\KNIRYESASM\S STCEPCKSRNRHSAQTEEPVQAKVFSRKNHEQLEKI ICKNRSTEISS ETGSDFSMFALRDTIYSEVATLISQNESRPHFLIELFHQLQLLNTD YLRQAL
7459	A	2	743	KASAQASLASKDKTPKSKSKRNSTQLKSRVKNIRYESASMSSTCEP CKSRNRHSAQTEEPVQAKVFSRKNHEQLEKI ICKNRSTEISSAHARR ILQQSNRNACNEAPETGSDFSMFALRDTIYSEVATLISQNESRPHF LMEL\FHELQL\LNTDYLQRALYALQDIVSRHISESHEKGENVKS NSGTWIASNSELTPSESLATTDVFIQEK*KYASQKHLHINVHSIFS

				HDSLKLKHQEING
7460	A	1	336	IYFPTPEKFGPPKETLKKGAPSSSSSKQKFPFFGPGGKQKGGFGSLQ TLPPS/RSSPFPQPQKGFQGRSSSSG*ICIFKKKGFPGWAGGV QNPNPKGFGPPGPKPWG
7461	A	1	3010	YRIPGGGTWQSARPRVGSRRRAVDGEGARRGLCSPSSRRWRPQPQH CPGPRAPALSCAAAAPARRPRGHAESRRDGGGLGSAEEEEESWYDQDL EQDLHLAAELGKTLLELNKELEGLSQMYSTNEEQVQEI EYLTQQLD TLRHVNEQHAKVYEQLDLTARDLELTNHLVLESKAAQKIHGLTET IERLQAQVEELQAQVEQLRGLEQLRVLEKRERRRTIHTFPCLKELC TSPRCKDAFRLHSSSELELPAAPGAGERAAADPGGGAALPGEPGAAAQ GAGGARVHRGAAGVLGAGAPAVRDGGLSPACAGAGGRAAGAADEAG QDLPTGSGTTTWPRPCSHPSRRPLRPTIPSPAAGTTWAPRTGSPHRQ PLQATWCARAAATLRSTPSWPKTQPAQTRATSHCTPTALRKR/EHVH PAGGGRAVPRAAGEVRGAEEQVPAARGRSARRRRADLAPHLPGQLVE GPARG*GGPG*GQGRREEPEPARGGRGQAAGTEPARVQALQRDLLQ DPED/ARLTSTPPKSRRTAASDPSPACSLPQGGSRGPQAWAVQLPE SERPLAACHHSTRPPDP\KHAACSLLSGGSPVLPSPRSPWPPRASPK AQL*VQSQMS/PTPGIPQLPQPLAS*PCASPSDS*PGF*KPFWISW LFFFFWLSLFFLRDLQCKVSLTPC/RQLETLEGRGPQQLFQGFPGPP TASPQP*CADIPLAPAVPPPGVLTRSEMS PAMQSRKASAGPGVSLQ PCQGVSPWILLAHRRSVASQRRRRRSPSAEWC SFAQSLSPWLPTPE MTCWALSFPAGAVGSPHSL\PPPPTKPKLGL*LPSLCLPPSQGP*C LSHSTLPTGQPWHRSCLOPPESSGHAPP\PVVPMSTPASPSLGTGVF APCCIVVLGWG*GTCSLPPSHKMPALHLPPLWGAFEDPAASGVLLQ DVRKSSSAKRHPGQALALSSP\$GLLVPSAALPETLETRRAIQSVEGG GAPGLLHRDPKWEFMPYFLNG
7462	A	2	190	SSNKKKPPNKNHPEPDSFKTEFYQTF/INTP*IPILKLFQKTELQEI LPNSFCEVSITNSSTR
7463	A	1	395	QYGLYNGGGAIMAALHESFTSCLNYGGPQKFSPEGDLCSPPDKICY VCKKSFKSSYSVKLHYRNVHLKEMHVCTVAGCNAAFPSRRSRD\RKD *KADLIVTRHSANINLHRKLLTKELDDMGLDSSQPSLS
7464	A	359	1095	PKGGENLWCGASLLNARMRAGNKSPPPLRPPGATKSLPQALQFQ PLLAEPDSAAGLGTGGTPRLTEVGGAL/S**RSGSGFPENQKGPPDP ASGYLDLMHTPPFSQ\DPISPASHMPIPSWSTLFSVEDRRSRQKTP GRWGSRCGLPHTCSILVGGVTREGVEMLPMGTGCKCAPFAPHLAAS SNSVLTAGDPAPGAGRLGSAAQEAALGQGGGRRSQAPPRRALQRPHA WVETTSQWRSAG
7465	A	16	405	VGAIQRAPPAPPSCARCLHTPDIRATLTQTPGGLTPQQEKDHEHGH GRAHSGAVSVWVLDPGTC\$RRRR\WFSPLYLELLRSSGECRG*SPAS PSLSHHTAHVTPKAFIEHLLCARCKEDSGITGQAF
7466	A	16	255	ARPCPCSWSFSCCGVSPGA/LVTEAAIFYETQPSLWAESESLKPL AKLMTYFKNSTYLIRLFMIYRCKPVKSKKKRN
7467	B	1	1026	MRARRLPWALTVAELGWDQGGDQTSPPGNDRMSMEAECESTTVSP LSCSIPTGCGQTREEVSARATPPPSLGASLLQTLTPDTHCTGVSATI MSMLVVFLLLWPFSSHSTLAKHKRIHTGEKPYKCEECGKAFSRSTL AKHKRIHTGEKPYKCEECGKAFRQSSTLTGHIKIHTEEKPYKKECD KAFKRLSTLAKHKI IHAGEKLYKCEECGKAFNRSSNLTIHKFIHTGE KPYKCEECGKAFNWSSSLTKHKRIHTREKPFKCEECGKAFIWSSTLT RHKRIHTGEKPYKCEECGKAFSRSTLTGHIKIHTGEKPYKKECGK LLSTPQPLLNK*
7468	A	1255	2710	ARPCPCSWSFSCCGVSPGA/LVTEAAIFYETQPSLWAESESLKPL ANVTLTQCARLETPDFQLLKNGVAQEPVHLDSPAIAKHQFLLTGDTQG PLPLPLGLVHRMDPAEQAPWS*QGPKALFNSTPPTESLPAPWLSMAP VSWITPGPETTS\RRCGVLRGVTFLLRREGDHEFLEVPEAQEDVEAT FPVHQPGNYSCSYRTDGEALSEPSATVTIEELAAPPPV\STMES PPRSTLGNKVTLT\CVAPLSGSGISSLRGGERAAGNPGGSTSPDR

				IPFHLNAVALGDGGHYTCRYRLHDNQNQWSGDSAPVELILSDETLPA PEFSPEPESGRALRLCLAPLEGARFALVREDRGRRVHRFQSPAGT EALFELHNI SVADSANYSCVYVDLKPPFGGSAPSERLELHVDGELAG HQRGRARVQCPSPGPPVFLFPWASDGGALGLGSAPIAYPGGEQAIGG RSGDAWNFLFPTDASP
7469	A	3	1312	GEAGRGSGSTGLGAGQGCATSQGLAARSSWGHRSVGHQLGSRGPTRSS AQ*GAAAADLQAGRHSDHNPPPT*AA*G*NLPAAE*GGPRAGAPAH ASCPTDPSAGEPGTGAGAARRWHQPGLCSPSGV*PQASPGSSPRAQT QSPGAAQEHHEPRE*AAQAGERPAGGSEVGAGASGGPAAGTGDACGN PGPAAAGSPRGGQGSRAATGHTGCGAVQLPRPAPSGRG*KCPAAAAA QETEG*VRPTAATLRLLAGSGARRWCRRPSASHHGPPDIPGGDSGGHPG SAPQP*AAAGPGCPQLPQEAGGSEPQA*RATGCLQGPGRCILGPDPP EAPGLLPQHPRAGTGAGTAAGPGHDG*RATF*ATGVRGPAP/EAGT STKS*G*GSWQVQGTGPKWGLCLQPSPSIQGPAATRPSPK\GRAEQS SSASTEPSHPAPRKT
7470	A	1	1988	MWEPGCSQGD/GVFGCRDR*GG*GAAGCAGRPSPGDRGQWPHACGG GGRGHPSTSTGAPAGHGEEAASEQRLLSGGPLRPPGPH*AHRHVGP AGRGLC*LGRREPQHRVPSRSAPAAPGRLPALPFLDEDKG*AEPREA APRRPRAAGHSPGHVSHCGEAPGGDLHLHLPO/SPAGMGSEHDGRSG QC*PSRHTSP\PTRLQPSPPDTHPGGSSLPAPRPALSCWARVFASLG DQPAFLGGHTGPPDASGEPQHKH*PS/GPLSSSSFPGAPIQGRQR\T ESLPGTC*GMEWPTAALG*RGPRPVTATPGTPGGAPTS\GFP\GCQA QKPEAGLVVANGTMCCPAKHTWRS GPKIPTLISILPLLLHGGAVSL GSPPQGSALRPAPASLGPCVTDKSIPLAQN TKYSPDLP*ET**HLP ECSRGWGSPLLVLHPLLGHILVSAHIPLPGYKACPRPLNLLGRFGA\ QGPRGSLSRSSRG*/PGPAPSALGVSGSPSSHPPN/GLYAEAHRMG FLPDSKSKN\GLISKCLTFHPQTSKPPAPISP*SKTSGGRKNRLPG LHSQQSFGRMPPGMP*APSVYLLPLL SHPLPLRTAGKPSSLPQPRSP SLVSSHTRAQQLSLSV*GQPCVPGHTSTRQGLPPLHSILPAELPQS SFANRGIKASLRIRK
7471	A	2	353	DRKEERLRSRSGAAATRSSGGKVAEWDPLPCLDPELWDQFDNLKN \HSLEKFIISAKERTEIELSYTKQLRNLKTCQPKRNWKEKEYIT*N SPSLPVNKMDSHARQH*VITLGSIKLSSLR
7472	A	2	390	PLDPQVRKIEDKVNKSRSS*KN/LGLEDLGTYSVIVTDADEDISASH TLTEEELEKLKKLSHEIKNPVIKLISGWNIDILERGEVRLWLEVQKL SPAAELHLIFNNKEIFSSPNRKINFREKGLVEVIIH
7473	A	3	223	DAWVTSTNADKEFEKIQHPLMIKLSSK*VY\NMSYIYPLFKI IKGIY DKSLVNIILNVEKLKAFF\LRTGTRER
7474	A	3	1033	CPLPFSL*YSTCGEKQPMQSWRASAASPGQSA PSSSAVGCWKASCKQ YVWGTPSYSYTNRFPRTPHSPGVWKACISRAG*PARKNSLICGLAG KTGALKDT\SGKAPVFPLCHRHSDPGGGFHCAELGTGNSPLGRRLK GLP*PAAVPCPPGAPH\LPQRRPAGRPT*FPPAQSSPPQSVWSR SRC TRMPGPTGPRWGPAAGSWPATSLASGCPSEVCGATNP*APRLSTA LGSCCPSPPGKRRPNT\PATRPPCV PAG*APPPGHSRGNGGLEKKS SF\PASCGR*QSGAGPSRLDFPSSPSRLHSVPPGPFRTSHPQVQAS SVSEKGEKPLRSYDPRR
7475	A	63	389	KNQEQESEETLPNLFYKASITLIPKLD TSSSSSSS\FSSSSSSSSP* KPITHRNIPSSSSSSSSSHQIQYIGKIIHHDQVGCIP EHLIKFNIA A**EPSKNGDRRNT
7476	A	3	335	HASGKDRHTDQRNRIKNPETDT*IYSTF*QKC/RLI*WRKDSL VNKW C*SNWA\SPMKKIKLSSSSSSSSSSSSSSSV*NVKLLGN NVGGN LQYRGLRVHTVDVKAQHI
7477	A	50	379	LEAWAGLSQVQTPSKFLENPSQSYRLTVPLRKHVPRPKQHEIRRLA* VGNLSDFTG*/HPGCIRGLRPG\HLSRLMDLGLGLMVKS MERDQRL VERAQR LDQELLQALEK
7478	A	62	389	KRDPRKTFITPPPVS GERQIRRGPTCKWGFGLVGRGGPPEGEKSNL

				LLWNP GPPLGPN I K K G P R L T T P S S S S S N F Q R E K F H P G G G A P P * N P T / I L G R P G G P N K L G W G V P
7479	A	18	374	RGEPPSPAPIGIFKSPKRGFPKPTFPGGFLPKGKKKPGPIFPPGFL ETKEGGTPPNPFKK/ARVFLVFKPKAGSSSSSSSPNYKPIYLNNTDT KFFNNMLANRI*QCIKEVMQYDRTRG
7480	A	2	1289	FFFFFSCYAVNAAGNEGNDTALSFPERSQSRLCGFSQNTLCLLPAPT RSNFPGSCRPRQPPGSLPALALAAGDSPGEAGPPGEGSRGIQHTFP* IPRPRRVQGSQSSPSPTSHPQQFINGEQTS**QNLGLRTQEFECNP RLISRL*VVRFRSLFAFFPLFAFHSPSPFF*GNV*ARLQGGKMESL GAEGLHRRRPRQGWRTKQKAPSAYVGKNGNPAP/PWFPPKVFTGA AKP*GFPNPISPKP*RHSLDLAKGRGPDPCARTGTQLQSCLAFLWPSR ELITPGCHVLIGLSRLRGALFGG*GTAKRLSHKGRQSGP*N*P\GR HTAPLIPSAASGRVRVGLQRNEPL\QONPTLRLSSPLLPGGIKVET VGI**GVGMR/DLGS*NEVSAFIGN*ESRSGSSSRMVFLPLPNARE SPPSRFETVN
7481	A	3	352	QFSIE*KKRKIFPTQA*DKQRLNVQKYKILLVTRKEGPNKGRGKPCS *IRKLNIVKTSIFPKLIDSYNKFPNY/LSASLLELTSCILKLIWE/ QNPFMKQARARTVKTLSKKKNKVEK
7482	A	2	253	SMKKVERSKISILSFHIRKLEN/QLNPK*/RRRREIKIGABINEIEN RK*IEKINETKSYF\WKISKPLAKLIKEKTQITNTRNRAY
7483	A	2	1114	WSHRDWICPASGFQMLNVGSGVQILRKQLMTYAL*LLQLTVWRDSRL LCREGAPK*SL/SSLPESRRQSSEFEKAKTCQLFINAAVDSPAIDYH ISLAQSALQICLTHPELQNEICCLIKQTRRRQPONQPGPLQGWQLL ALCVGLFLPHHPFLWLLRLHLKRNADSRTEFGKYAIYCQRCVERTQQ NGDREARPSRMEILSTLLRNPHYHSLPFSIPVHFMMNGIYQVVGFDAS TTVEEFLNTLNQDTGMRKPAQSGFALFTDDPSGRDLEHCLQGNIVK PSPFQEPSPPTNSKEATLYKSKLCKKFNBSGVQNFNQSNLHDKKKKM QDFVKPIEFLIHNLYIYTFHIKERKGVSNNGNDTLSIRIIRVDM
7484	A	4	254	GDVEY*SIYSLAPIRHWRNGPRASTLWLFLLLLLLLLL/ETQSCSVT \RLDCNGMISAHCHLRLPGSSDCPAS
7485	A	95	671	FLEGGWAHFFPPPKKGSFPKIPKEGFKTPPKRKKIFPSPHPLNLGPP RDLLKGPP/HSSSSSSSPEVINIYCSPFREHGRR*SKVSSWSTEVN KPV*DKFPHTPSY/ATPCPLPQGYRTAVFSYSPPK/HMQSLPTFQKA CSFPYSFHHSDQSPTLVAPFFFFPCLMRSSDKLMNDVPAPVFLPSFK GNHACSSR
7486	A	2	340	ENGWCWIATYGRTKTGFLSLTTCKS*LKRDLDLGTETMEILEENLGE VLLDIGLGK/NFMTKTPKADSTEIKINR*DLIKLS*CTAKKS*T*/ SNRQSTEWKKIFGNYSDRTS
7487	A	117	334	LYAHKFNNLDEMDQFLQRHNTPKLIQEE/HRLTVIK*IKSIVINLPK QKA*GPDGFSGEMYQLLKEEIIYNVF
7488	A	325	354	CILKDRCR*LYAHKFNNLDEMDQFLQRHNTPKLIQEEEDLL/SIK*I KSIVINLPKQKA*GPDGFSGEMYQLLKEEIIYNVF*RTDVEG
7489	A	3	458	KSREITTLANNQCMATESVDHELGRCTNSVV\KYLMRPSNKAPLL LCEDHRGRMVKHQCCPGCYFCTAGNFMECQPESSISHRFHKDCAS\ QFN\NASYCPHCGE\ESSKAKEVTISLKQTPPRPWTPVPGQE*GSSL VGRADTTPGSGAR
7490	A	49	457	MHNPDGSASPTADPGSELQTLGQAARRPPPP/PRGTRRPQDTPISP ETP\GCFSSRRPMPREPPKTRGSRGHLHTHPPGPGPPLQGLAPRGLK T/RRPPSPVPAPAGTPQGGKQEDCV*G*VALPGPPGRQEAYWHP
7491	A	1	816	MDEAQPQEALGASDWQTCSTQCLQRCKARSQSDHFKGELGVSSPRV HPQAARRPPPP/PRGTRRP/PGPAHQPGNP*AAAPGGRCPPGSPQR LAAP/EGHLHTHPPGPGPP/PPAGTPQGGKQEDCV*G*VALPGPPGR QEAYWHP*GA*A*APPSARL*A*VPASEQ*EGTEPLCRSVPGPVRR VLGAPARGGVCTGKAQAAGGPAELPAPTPKPEGGPPSCSPGLEGV*DE ANGSWLPQGAGSLPLPEG*TEASQSDPEIR*PRRTRPSARKPLSCF SRRPMPREPPKTRGSRGHLHTHPPGPGPPPPQPGPHKAKTKKIVFED

				ELLSQALLGAKKPIGAIPKGHKPRPHVPDYELKYPPVSSERERSRY VAVFQDQYGEFLELQHEVGCAQAKLRQLEALLSSLPPPPQSQKEAQA ARVWREFEMKRMDPGFLDKQARCHYLKGLRHLKTQIQKFDDQGDSE GSVYF
7492	A	27	447	MHNPDGSASPTADPGSELQTLGQAARRPPPP/PRGTRRPPQDPPISP ET\LSCFSRRPMPPTREPPKTRGSRGHLHTHPPGPGPPVSLDREGVPR PGL*AKDLAPAV*GTPVFPTPRFNSRPRFPVAAAGTGAPRPQNRPP
7493	A	1	368	FQQNLTLISAHCNLCRKF*FSCLSWDDRHVPTCLDNFLYFW*RWGG FYHVDQAGLKLLDSSTPSAS/SFPKCW\DYRHEPCTWP*KYSFLTEH *LLPVY*K*IAKPFPGKQIVKTF*GCKNI
7494	A	10	505	EGDKGTPVLRGFSSVSGSWSRMPPFLLLTCLFITGTSVSPVALDPC SAYISLNEPWEGTIDHQLDESQGPPLCDNHVNGG\WYHFGHGRGDA MPYLSFFTRKPLWEPTAPVWLNHSHPL*GDGIVQRQACASFNGNCCL WNTTVEVKACPGGYVYRLTKPSV
7495	A	84	250	NRIENPEIKLNTDSQLILPR*FNWER/DSLFNKCWWNWIFCKTKMKL DPFPIPDKN
7496	A	63	743	SSCLLAAFRGPAHASHC\P*SPAHSSKRPIHAQLFPLVASPGPEIPQ FGFAR*SCCLPVSPGPVLPSPWVYSPIS*LKTTYFGSAPAQHLAAF VGLKLPQVKRSRPRSCCPGAFGTGPATA*RWLPAQALPSPSLPRPSP CLTVAFPVHVTACYPTALTDQTLPSHWT*DKLIRLPASPGQSSCLT LASIGPGAESAMVCLGPSHAFLKTLQATIWPDTFCFCGPM
7497	A	340	368	VPTICQVMS*HFHPSSSSSSSSSVINY*/FGLLLC/QVAHFYNSI DQQMIQSQRPMMLQSALAFEQIIKVNGLLI
7498	A	2	826	LVKKTCEVPLQAGRLYLDHHQSKPFLKLHSKTHV*RCPLGIQTTGPV TLRR/AFNLRPVLSPOQRPVPEARPRKCETHTESFKNSEILKPHRAK PYACNECGKAFSYCSSLSQHQSHT\GEKPYECSECGKAFSQAESSL IQHORIHTGEKPYKCECGKSLSARNANLTKHQANPHREEEALTGCS ECEKAFS*LLS\LVQHORIHTGEKPYECSDCGKAFRHSANLTHQRT HTGEKPYKCECGKAFSYCAAFIQHORIHTGEKPYRCAACGKA
7499	A	64	372	KLSFFHRESVNEIKKKTIDWENICNTYE*KPVTYK*FLQIN*KEIN/ DQIEKWTATNRQIAEEIEQIVNKHIKRYCSASFRKKQIKTKKRCHF SITGKNYKE
7500	A	2	414	RQGL/DSVTQARVQWSDQ/GSLQPRSPGLERSSHLSLLSSW*FEISF RTLQQLVITGNILGHQKITGTNHR*FMLYSS\FCLFFEMESHSSVQA GVQWHDLLSSLQPPPLGFKRFSCLSLWSSWDYRHPSSCLAYFCIFGST
7501	A	18	73	SYPGAASVAPWSPGASPLRSSPELHLRLSSSASSLALAKNALSRAS PSPAAQ/ALPSPSPLWPLTSSPGRQASPVAPPASNGT*WGTC*PE AILGLQSAQPPGAPGPPH
7502	A	3	365	KTASPVQVKFCAGVALPNLKQRPLREKAQQCI*PLMAF\RNTGRIP CFSCNIPVLPQGKHGTEDYWFVQDLRATRQIFKAIYLVIPDAYTLM TLTSELYW/WSVLNLKDAFICIPLSPES
7503	A	47	231	NCSSVFCFPGSQRVGSILGKSW*GWVVATGVWLLNPLKAVGQEEYSL KMEGPRPEVTCRHL
7504	A	1	3099	MGSCSGGERLGTSPKYSMGKWEFVAKEQCGVPCPVQLGTLRNDSE QLHEYVKQGYVVKKILKKGSPHSPRVHSLFTEGLDPQAPDCL MARETONQDAPCPAPFMAEEASSPSTGQPSLCSEINEIYSGCLILE DDIEEPPGAASSLEADGPNQVDELKSMEEELDKMEREACCFGSEDES SSKAETEYSFDDWDWQNGSLSSLSLPESTREAKSNLNMSTTEEYLI SKCVLDLKMOTIMHENDRLRNIEQILDEVEMKQKEQEERMSLWAT SREFTNAYKLPLAVGPPSLNYIPPVLQLSGGQKPDTSNGYPTLPRFP RMVRDFQGGHFGKRSRKRNGCGWKPFTQVSKVNTGDQSEISHQLPTL CDPGKQNTDEQFQCTQGAKDSLETSRIQNTSRSLTDIQDLSSISYEP DSSFKEASCKTPKINHAPTSVSTPLSPELLKQQGSSSTVLHE\TQV MEEALQMIKGT*KNKKLTVKKKIVVCFCKPKLKILERTQRE/PHSTL DEDLERWLQPPEES\GSYKTFPRALKVAVRAAVPVLDLTMQYPLL GDPRLDQEQNHFAIP/PPHLKSQKTQTLASHASSRQWKVSPPRESS

				TEEAVRASQGAEVGSSCFINPRCQIYSSVEFSRPEE*LTITNLRR*P TIQGEPEPPRSQSSP*DFVLPKG*SSTN*AHPKNYDY**DQISKESLS PRARKQLCLLQTIQRPQRRVPVEESETGPYGPISPKPKALYRNMNLD SLLKLSVLKSDSGVHRVSARVDPESLHKYSAYPETKPSAKVLVSSQV ESNVRTPIRGNSEVGRRTISPGV/PVSRANSPCDSSISV*GLPQVI HVCYSRAHL*T\QTQKPPEITYMSQGPTRYPPELSQKPSIHAELELT PRPLPPRSLPRYGPDDSSWWPLLNEVETPQSQSLTTPDFEPKCSPLD LLLSGFKIDSSPFCEDLKQREKASLSPSPPKFPPSWAPLSEVPQT PKHTCKQPIQRFTAFFLAWGIPERGRFFGLHTIWLNLKLEKLVDSAV SSPVS
7505	A	2	708	LTTH*IIHAGEKPYKCEKCGKAFNQFSNLTKHKIHTHGEKSYKCEEC GKAFIQSSTPSK\QINDGEKPYNCEECGKAFNQASNL*/HKIHTG EKPYKCEECDAFNQSSI FTKHKKIHTGEKPYDCEKYGKGFN*SSVL NTHTIILTAELKYKPVRCDSASDNISNFSNHKRNHIGEKS*KCGECN KVFKWLSHLIIGNIHIGKISYK*EQCGKVFN*YTLHRKSFIFEKNC RN
7506	A	1	683	IVTADQLLGMQGWAAIRNQTMLNDEVIEQLWKCCLDWDKIQDDDKL CPCF*QPSDGAQT*NRI PHFNCP I FKDAAEKSY* IARANDLL*NL AYEQVNPR/LCQVAICPIKGKIPPGDVLTSYIKVCEGVRGTLRTAM VMAQAMVSI RMPGQFP GKCF L CSQSGH SKRNC PWHTDRCSFQHQQPK FFQQQAPLSTICPRCQKGNHWVAQCHSKFDIDGNPLRSLP
7507	A	2	342	STVKGPCSMCRTIIHVP HIMGFI FG VQGWHD M/C/KSINVNHSVNRM KNKNHMI I /SND A E K A F D K T * S V S I K T / L / N K L E V K G M Y L I I K V A YDRLPARI I A D D * R A E S F P L R L G K R
7508	A	1	359	VFQSF FKH R N Q K V P E P P L S K T / A K N L F A Q L A E N I A S C L D D S S C Y G Y K K A N I R D Q W P * E A K E L M P Q D N F N * L F P Q T D A T R S S I W / L L K T S I I K K Y H V T H Y E K A L K T H E K E L T C L R H D R V G T C
7509	A	2	681	WEALCQQAEEAAPPTQEAQGETEPTEQAPDALEQAADTSRRNAETP EATTQOETD T D L P E A P P P P L E P A V I A R P G C V N L S L H G I V E D R R P K E R I S F E V M V L A E L F L E M L Q R D F G Y R V Y K M L L S L P E K V V S P P E P E K E E A A K E E A T K E E E A I K E E V V K E P K D E A Q N E G P A T E S K A P L K E D G L L P K P L S S G E E E E K P R G E A S E D L C E M A L D P E L L L R D D G E E E F A
7510	A	670	1466	KKIRPFFQIFDGFISNVLVFAQSGFPCCLPVAPSVTS**LKA AVTAG LEVP SD V S D R A F E \ W L S A F P L \ D S P Y S I H H P R R I Q V \ F L K R E G S S R R W V L E P I T A D S D P A Y S S K V L L L S S P G L E E L Y R C C M L F V D D M A E P R E T P E H P L K Q I K F L L G R K E E E A V L V G G E W S P S L D G L D P Q A D P A G / S W V R T A I R L C A G P E L G I D L S \ A V T K W W R F A E V S V P A A G D P P G G L Q T V V V Y L P G C L D H H A Y F G R K W E G P G A K Q K A A R G S S P N P G R H K G
7511	A	155	361	VNSSHRDQWNRIGGP/ETNAYIYGQLVFGKEAKFI*WRKNSLFNKWC WET/WISLQKRMELDSYLTAYVKI
7512	A	2	495	RKDILYSWARRFNIVKMLMLLPKAIYRFTVPIPIFLLQND*TAFFAEM EKPVLKFI*SYRRP*IAKQS*SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SPVNSSHRDQWNRIGGP/ETNAYIYGQLVFDKEAKFI*WRKNSLFNK WCWETGFPYKKE*SVDSYLTAYVKI
7513	A	155	361	VNSSHRDQWNRIGGP/ETNAYIYGQLVFGKEAKFI*WRKNSLFNKWC WET/WISLQKRMELDSYLTAYVKI
7514	A	2	495	RKDILYSWARRFNIVKMLMLLPKAIYRFTVPIPIFLLQND*TAFFAEM EKPVLKFI*SYRRP*IAKQS*SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SPVNSSHRDQWNRIGGP/ETNAYIYGQLVFDKEAKFI*WRKNSLFNK WCWETGFPYKKE*SVDSYLTAYVKI
7515	A	1	401	NVLIWEDCIAGQAEVLHDSYGI IIDWSPKGMFSMNCTSSQS\CPWPHY VQLV*TERSDSRNDK KYG K S S Y L E T W Q Y S G \ P Q P Q M I W P A V G A K H K D L W K L L I A F D K I K I W E G K Y T M P S Q Y N P N Y I L E L V E N N T I W
7516	A	10	225	YCNTIIVGDFNTPLSGMDRSSR*KT/NKETSELNYTVDRSLTDIYR TFHPNNLMIHLEKELEKQQT K S N I N
7517	A	37	350	WKMGLPGRPQLPQLSQEKILSLNSPNVFSSSPLK***NILPKKKRP

				DCFTHKFYQTFKEEII PFLKTH\QEFEKKEILLKSF\YEGSVV*AAK LNADINKKTTTH
7518	A	3	353	CRLGGLKGRSREQGAVIDEGEDTLG/SETEAGRPAGSLRQQRRGR WLNVPVPGKHGVPTEGEEHWAGEPAGWGGSVSGQAG*AESRLSSSGHSG QKGGAVMLLAADRRRGQRRRGSSG
7519	A	54	284	NHKTPEENIGEKLVDIGL/NNDFLDMTPKAQAMKAKVDRWYGIKL*N LCTSKETINRI/NNRQPMELKKLMANHISDKR
7520	A	29	261	NHKTPEENIGEKLVDIGL/NNDFLDMTPKAQAMKAKVDRWYGIKL*N LCTSKETINRI/NNRQPMELKKLMANHISDKR
7521	A	5	2089	LSSPSQGRGADSA/PGEFSGTQLPPQGGELVPQHLAQPHAVPAA/EV GPAWWPGAGP*TSPPSGRGRPRLCPPAPGPPLPLPAAGPG\SHGQPPF MLLDGL\PGPPGGSGAS\GLPGSSALP\RPRGEGVTPGIRGEGLRHT GA/GAPSHSHSTCPSRRWQAGCPTLTAPPPPGWATSPPPPPESRCRV SCTSR*A*NPGHAAASSGRWDRGPGAAAGPRPG*AHFA*GSGASGSS PGPEGGRARGT*PCSTEPSPGH*STGPSPCPAGGPRGRLLPLPGPD QGRWAPTSGIPLRTG/PKLQTPPTSCPGR/KLAEGEAGPLMGVQVRQC EAQHTQRVPLVVLQEGQDAVCVELEPVVRVPAGPRGAADGRGCHRRQ A/P*RAGPGRRLPLCSCTAGAAGSFPPAPRSGQGQGLLGLAPGTAAEQ AAHRAEPPRCKMPA*/PGPCVSTTCPCVSASELGTGSEPLAGRWRE AGSSQAVGLAA\GGGGC*DQRTFAGFGS*GAGKGLRGPPGLVTSLSA VGRCASEPGGASGAAGRRGRSGSPREPRVSGSASRSPCG*AGCRRAS SAGCRPRPGRA/GSAGEKADTYSCCRAAS\GRPERPSRPGARS*TPV RVYTA/GMVGQGLATPGSPCCCP\GPPGGRPRSRPE/SFPRADPSG YRGLPADRHWSKGP*GPALPGPGRSQAWALLGPQHPRSPAPAGARG RAGHRAR
7522	A	45	301	AGHHHWRKGPEAPRHEMCPGSSKNQGLVQGLAGWGTKGKILKGS\S TSPGEPGSGQIHLKKAGTCCGSSSKDRGVNYSGRLLRR
7523	A	453	704	AGHHHWRKGPEAPRHEMCPGSRSGSEGATCFARGR*RPPGNSLNVSR MGTSSSYSCRRHSPAFLSWGKGRCHLCNKAHLLAGA
7524	A	3	543	TCCIQAAAGTGGSGAPGLASVVGGAAPLWSSF*NSLP*QIRFALVPLP GCRAPGTFFPA\PLYSQWPPPGPQWRARSLARGEVGVLAPHPQPPT WPGRRHQESPRRHGVBHHHGHVMAAGADMRRGLAAVAALVAS*AGR VLGWCGRPARRAAQLGQEGAQGTVLALNGLFFPSRRHGC
7525	A	218	533	AARRAGRPHHPKTRPAQLATSAATAASPRR*GRPWRGLGPAWRP RGAALGAQRCGHGVRAPVARAELGAAGFGGAAGPGAARGQCPALLP GRVEPRAARGVRTTTPRPGQLSSQQAQPPRRARAAYPRREP*HADDD LLHGADRSSRFGEVEHPVQGHNTANPSDGGPVQHQHGLPHRYHLHL V*HSRPSGPPGATG
7526	A	3	1185	GP RR*GRPWRGLGPAWRPGGRGAALGAQRCGHGVRAPVARAELGA AGFGGAAGPGAARGQCPALLPGRVEPRAARGVRTTTPRPGQLSSQQAQ PQRRARAAYPRREP*HADDDLLHGAGGVSVPRGAPARWAAGVG RRRPLLPWPGCERSFSSSL*I*HSQICFF*SSLEQCGEWEGVY\DP SDGGPVQHQGH/PASQPLPEWKVAEVTGDARSTEDTSWGKGAGGSS *EGGPGSGPPPGAGGLPGHNGLDGQPGPQGPKEKGANGKRGKMG TG*L*RYGWHLGASFALL*AGHHHWRKGPEAPRHEMCPGSKGSFRE NGHTPSKPAQSSEQ*LPSPYQSGRWQKLLMGQGVQORTHGAREQV AVPRKVDLLDHQDLREPAGCQDTTDWMDSLVLRAQKEKKEQMEKEE WGLQDNIEDMAGISEELPLPCYEQAITTGEKAQKHQGTCAQGARAA SEKTGTHRPSQLNPQKASNYHWNITAAMD RSYRIIIIIHEHRCRIM MPIGLSWEVLQKCD SVLRPRQWA
7527	C	35	217	MXDSRGRXPGARTYRESGPXXRMXGRSREIARWPRRRPLAPLLHRL LPSRPGICGGA*
7528	A	2	342	RALPPPKDPSLLSSIGSYRVPAPESVEGPL/SPWERKQPGERPLSCM S/GLPQLRVGGVGR*EPQGLPDGDPAHTRCGAEP SLLDSL PQDGV QDAASFLHTPSQTPCVQRE
7529	A	2	441	PRVRPRVRQSSHL SWRCRVPPPPPTMCLSAHPAGPDPGTSCESHV

				IPMTSIAQWGN*V*RGEITCLKSQE\GKS*GHGASCPMTGELKCPHC WG*TGPHQLPG/MSHMFVCILRGLAGSPARTAARGFLEVAFFKGTI PERKPLM
7530	A	3	471	RALAAAERPLAPLLHRLLPSPRPGICGAA*PWERKQGPGERP\FPVS QYLPSAC/GASPPG/PLGTGRGHGADDAPRRTS*ISEVGSVSVRDPG *IEQGS DGRLPIGHSRWDERGLRGLGFVTGK/PWIKGGAILPVGPSK VVGLGYTGRGAGLARSLOQY
7531	A	2	1022	FFFFFSCETTIENTLIFFSGEVSNLILPIPVGHK\GL*GGVKEEGCGC VLGLRPAVGSPAGMAQPSAPGVQAGSSILEEGLEVLSQPRAPSRGSQ GPVSPPSWKVLQQPVRRTPTPHASWGKPTHASSFVGGLGAQGGKRM LGGPGCRPAPGLGAHLYVVCPEFSAPIRGLRSGMVPLKKAATS*DT GSSPGLGEPASQQLHLFN*SLRGASSVPLSTAS\PEPGGLRTQALG RY*ETGKWPF TGLLPLRLSGPSTDSGAGTR*EPMEERSEGLG/ER PARDPGGSVPTCGWRGRGSPGTGCG/LPGQRPLGRALRAAKTRPGTCR ATDRGVPPGLPRLCR
7532	A	40	405	QWHRLAACSNLASAVSFRIFLYYGERRPSGGARPMLTSPSLTAWIIN PLSQQLL*YLAAEQQLHRGPPTPAPVSGAE*RWTFI/IARTHCLR RGQGRQPPPVSGATGAPSFPLQQPMRR
7533	C	182	289	MRARRVILNLRAVHAVPSTKGALSSHHVNANVWI
7534	C	50	223	MEQLCTKVRPFKITTLALILXXXXXXXXXXXXXXXXXXXXXLF LYEWYPCHLK*
7535	A	3	399	SNLASAVSFRIFLYYGERRPSGGARPLLTSPSPATAWIINPLSQQLL* YLAAEQQLHRGPPTPAPVSGAE*RWTFI/IAHCHLRRGQGRQPP PVSGATGAPSFPLQQPMRRFTPGASSSHQEQATKSSTREF
7536	A	287	568	CLRDGSPPEPSCGLHCHCPACQ*PTPHPHYKHPAGESIPGNTPMSAS RKRPASTSRRLRAPPALILSFLLCCKMGTLPHASRGCKWERSEIVLK
7537	A	574	1268	SIPCPSSSFSTWLQSSRNFTEDILASVLISASTQSAQSRSPQNQNL KGGQAAPPASSHPISSHGWGLCLDDPPAKDIIDFPLVLPGIPYAVS HQCRLOYGAYSAFCEMDGDSSLI SPWAKYPKQRPQGVFIRVPKKH MQKGSACPLWPVRGKSLPVKMHNPGLAGRWKSS*STWT/IQS/RSC GLHCHCPACQ*PTPGPHHKHPAGESIPGTTNFCFEKEACVPYFM
7538	A	1	785	NRQLSCGTALSTTGGIYIGERSVRVWGHFRHCLGNESLLDNCQMTVL GAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICL EDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVQC CGVAFNATVSAHFEGSGPIWLDDLCTGMESHLWQCPSRGWGQHD RHKEDAGVICSKFTAFRLYSETETESCAGRIEVFYNGTWGSGVRRNI TTAIA\GLCCR\HLGCGGRNGC*PPCIHGNTVSVICTGSLTQPLFP LANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFW GTICDDGWDLSDAHVVQCGLGCGVAFNATVSAHFEGSGPIWLDDL CTGMESHLWQCPSRGWGQHDCHKEDAGVICSKFTAFRLYSETETES CAGRIEVFYNGTWGSGVRRNITTAIARIVLQATLAVGEEMDANPSPL
7539	A	1	1113	GLVFSWGDGDFGKLGRGGSEGCNIPQNIERLNGQGVQCIECGAQFLL ALTKSGVVTWVGKGDYFRLGHRSDVHVRKPQVVEGLRGKKIVHVA AQHCLAVMDSGQVYAWGDNDHGGQNGTTTVNRKPMVLVQGLEQKIM CVACGSSHSVAWTMDVATPSVHEPVLFQTARDPLGASYLGRVYSH KFSPTQSFQEWVYNLNSLMDQALTPQCGSGEDLYILTGTVP VSDYKVKDKSFTGSALAALVKGLPEALQRFQYEDPIVRGGKQLLHSPFFKV LVALACDLELDLPCCAETHKWAWFRRRPDDWNLSAGSGTIGWGH DHRGQLGGIEGAKVKIPSPCEALTTLRPMQLIGGEQTLCCDS
7540	A	1	216	VAFFKSAGASVQEQQAQLQEQVKEQVRVCCQRLAHPVASAQKEPEAAR GPGAP/WAWGRV*QLYGPPEGEGRP
7541	A	3	143	GGGRDGTARDMPPECHQCPRTGPPMGPGYQGPLLLPADVPLVSSVV
7542	A	39	212	EWAEPVPPPHCPDVLHRSAADRRPPAADRWPRTAAGDPGNGLAAAA DSEPLGSSAP
7543	A	72	353	QRCPPGGHIYSHKFSFNDSVLPGTVVCESPQPNPGFDPFTVWQGRPI YPHRHSALRLQS*QSGSGP*VCLAGSLCCPWRRLGHGLCQAHPGQ

7544	A	5	728	AAILYSGRLLSSQPVVVEISHPYTYDTSTSGTVKIPGAEGLRVEFDRQ C\NTERRHDLPTVMDGVNRIVSVRSGREWSWSELRI PGDELKWK ISDGSVNGWGWRF TVYPIMPAAGPKELLSDRCVLSCPSMDLVTCLLD FRLNLASNRSIVPRLAASLAACAQLSALAASHRMWALQRLRLKLTTE FGQSININRLLGENDGETRALSF TGSALAALVKGLPEALQRQFEYED PIVKGA
7545	A	441	1009	GLSHGRNTGPLTTSQASTSPRGNNPRACVARTRVGVPATELLWMEEM RCVQLFCYSKARSQC SHQG*DV*VFYQ PACWVSDTWHYLOPLTDSG* YA*KLS/D*VMSGPILATGPCTSHLA*LLDSEPLERSVSSFCWKDVR LLGKTSLLCCVGLAALSSSEIFNCLLG VFWNLASCLGSSACCRVFLR DT
7546	A	59	378	KFLEQLFDDGDVYLLLLGSQAQQNNGTQQLLPKPGCSWWSC TIGCAV GLSRRGSSSLASSWAEVRLTSRRSPCLSAAPSSWGAGAPGPGSSAGL WAAARNFLCPLL
7547	A	31	302	KGRRVLWWGDKNHERSWHKGVMGQRVQDRQKRKLCQLMGKRSQRA* ILSGTEHLHVHSHLL\CQQQVSTGRALHLLP*RIWRARAKNEQ
7548	A	1171	1731	SPRWSAPRSPSGAPSDASCDGLVPMNGRKMCAWPVDIPKTDWSPNPW QEKREIVSSEDAVTPSAVTPSAPSASARPFIPVTDDLGAASIIAETM TKTKEDVESQNKAAAGPEPQALDEFTSLLIADDRVVVDLLKLSVCSR AGDRGRDVL SAVLSGMTAYPQVADMLLELCVTEL*NPRSRTP*CFS CRACDEEVSLALECWEPEELPRTQSPALTTQRAQNTMNKLNHNRVM QDRRSVCIFLPNDESINI/DKCLVFSWGDGDFGKLGRGGSEGCNIP QNIERLNGQGVCQIECGAQFSLALTKSGVVWWTWGKGDYFRLGHGSDV HVRKPQVVEGLRGKKIVHVAVGALHCLAVTDSGQVYAWGDNHGGQQG NGTTTVNRKPTLVQGL*GQKITRVACGSSHSVAWTTVDVATPSVHEP VLFQTARDPLGASVYLGVPDADSSAASNKISGASNSKPNRPSLAKIL LSLDGNLAKQQALSHILTALQIMYATDAAVGALMPAAMIAPVECPSPF S\SGAPSDAS\AMG*SP*MGEK\CLLAC*YSENRL\SPNPWQEKREI VSSEDAVTPSAVTPSAPSASARPFIPVTDDLGAASIIAETMTKTKED VESQNKAAAGPEPQALDEFTSLLIADDRVVVDLLKLSVCSRAGDRGR DVL SAVLSGMTAYPQVADMLLELCVTELEDVATDSQSGR
7549	A	2249	5398	KCHLRAGRCRDVTAIFWLQSSFMDQLEEKADLRKSITFYQNQGCRAK DAALGGGHHQAGAQQGDEGEAAGAAADGVAAYSNNNGHHRKFLATAQ NPADEPGPGAPAPQELGAAGKHGGLPNLRLSFKLALIRDMAILPFQW NLLISFNAVLGLVFSWGDGDFGKLGRGGSEGCNIPQNIERLNGQGVC QIECGAQFLALTKSGVVWWTWGKGDYFRLGHRSDVHVRKPQVVEGLR GKKIVHVAVGAQHCLAVMDSGQVYAWGDNHGGQQNGTTTVNRKPM VQGLEGQKIMCVACGSSHSVAWTTMDVATPSVHEPVLFQTARDPLGA SYLGVPDVSNSAASNKISGASNSKPYHPSLAKILLSLDGNLAKQQA LSHILTALQIMYARDAVVGALMPAAMIAPVECPSAASDAFAMASPM NGEECM LAVDIEDRLSPNPWQEKREIV\SSEDVTPSAVTPSALSAS AGPFITVTDDPGAASIFAETMTKTEEVKRHSFFALYCEITKWQVEPQ IDDPNSNLEEVINEAEAITSENSLGLISRWPRLFSQIQPDDSVLPG/ DGGT*ISTA*WTRL*PHSVAVADMLLELCVTELEDVAT\DLQSGRLS SQPVVVBESSHPYTDSTSGTVKIPVPSSARSSSLKENS CASARTPL TPDVRVLHTKRFS SLDTP EVEVLLTSNAHSPGAEGLRVEFDRQCS SEWHHDPLTIMDGVNRIVS VWSGPVEAWNRTQRTVPAVQLSGSHSS PGVEGVVAGVILRLLVYSGSVSVKSAHRLAVACVGTPAVAFWWVGL GGATLVCWLLMGWSLACETQGCLQCSFTGPKELLSDCCVLSCPSTDL VTCLLDFRLNLASNRSVVPCLVALLAACAQLSGLATSHRMWALQKLR KLLTTEFGQSININRLLGENDGEARALSFTGSALAALVKGLPEALQR QFEYEDPIVRGGKQLLHSPFFKVLVALACDLELDTLPCCAETHKAW FRRRPDDWNLSAGSGTIYGWGHDH RGQLGGIEGAKVKIPSPCEALT TLRPMQLIGEQTLCCDS
7550	A	1	609	AAATTTTKLAAARQPLPGGGGESAVGAGAGREVFIYLFATASAKRG GRAKRTPGAQSSGR/AVLPSLGPPGRFLAGVC*GSGGSPFSSPPPN

				HSG/Q/PGAGGEPGNRGPKMGVLAYSLHL*VPCGVSRLTLPAGDGNP VP*SPFLSFTWSP/VP*PWG/ANGPWWADPPPSTHTVP*PSGPPGAS GAGPPPSWPRPAKFAPPRGL
7551	B	222	360	XAVLALRPWDVEAEQFLEVSFLLFFFLFSDPRPRDRLRLRLERLREPT *
7552	A	1	603	RDTSRNCASASTSQCRKASTAPGAEG/DGPQASGRGGAVTTGRSSASS GRGRSVMPLCSRA*DVRARRRRSQARGSSGKLHLCGSKPLRKRSPCS RSVPAPGQSRGRRFTSSPPGFASPSPCITERSRQKARRRTRSSSSSS SSSSSSSSSSSSSSSSSSSDGRKKRGKYKDKRRKKKKKKRKLKKG KEKAHSRQSIIR
7553	A	42	384	LKSAALSHGGAKQAGDPNLHPLPLRRDWAGPETNPRGKGHQHPSGFP LAP*NLPLRGRQSSSTGLGQRGPSGKQPSSHLEGQAVPSGRLAGEES TQDGRGTSQTDAGGWMAGM
7554	A	1	713	AKGAGLEARGAMAHVGSRKRSRRSRGRGSEKRKKKSRKDTSRNC SASTSQGRKASTAPGAEASPSPCITERSKQKARRRTRSSSSSSSSSS SSSSSSSSSSSSSSSDGRKKRGKYKDKRRKKKKKEEESLKEEGQRKK AEAQ/RGRASSASVDP*DGHAQAY*REM/DEGPKRKS*PKNDTERS TSQATQRGTDAGHCQMSDGYASREGPPHGQGPDRQLAAQPGQVSG CQWEA
7555	A	2	643	HALTTAFNIVLEVLSAVRQEKEIKS\IVIGKKEIKLSLFTDDMIV\ YVEYPKIDKNA/LLEIISNFT\RVVGYKVNTQNSVTFRVYHQ*AS/E YLKLLKILFALEPPKVEYLGSNLTKHAQDLYEKNCKTLIKEIKELNK WREILCG*KYSVFKMSVLLNFVYRFNAVPIQIPVSCFVGI/EQT/SL KFIW\KAKRPRIANSILIENNKVTGLTLPPFFKA
7556	A	3	578	TSNECGKTFRHNSVLVIHKT\IHTGEKPYKNECGKVFNRAKLARHH RIHTGKKH*KYECDKVY\IVNQVLKDRRIHTGEKAYKCKS\CDKNL GRDSHLAQQTRSHTEGKPYKCTECGKAFSGQSTLIHQAIHGIGKLY *CNDYHKVFSNTTTVSNHWR\IHNERF*KCNKCGKFFRHCSYLAVHR* THAGE
7557	A	286	336	GL**NTTS/PKISTEYISP*AKPPVMRGQDSVLYHSDYDEEEWNRVW ANVGKSLSCSIAMVDKLIERDGGSEASGGINDGEEKERSLTDAIPSLP REDWYEQLYPFILTLKECV
7558	A	2	246	RPLKHTLVTCDKGGL*FEPSEVSG/PPRCA*GDGTPKEVPFIGTATF YHYLPATAYGCMILTST*RKVEETELDDFYDGNSRRGR
7559	A	3	349	GWRLVRPLFMGHRQPVISGLQPEQPLHLKL*FLCSGVSDCASFPV/Q SPEPKVVFQAEQLARRKLQAEAGASATLSCEVAQAQTEVTWYKDGKK LSSSSKVCMEATGCTRLVVOQ
7560	A	16	221	HREMKTGNDLKILQKVNKLWHLYTTAY*KRAIKKSKLLVHTK\TWN LKGVLSE*SQSQRVKYWSTRP
7561	A	204	870	KGNQVSHEYSWKFRTLSLS*KQF*VLKR\YYRRAVKLVNMSNIAEHP GFMKTGECLRCMFNNLGC\HFAMSKHNLGIFYFKALQEE*QCLCT APVQVALIQVKNFQGRPMCTLLNPIRGYE\LLYNGGIS\LLHIGRPL AAFECLIEAVHVVHANPRLWRLAECCIAANKGTSEQETKGLPSKKG IVQSIGQGYHRKIVLASQSIQNTVYNDGQSSAIP
7562	A	1	1047	MVSISWPRDLPASASQSAGITGLIGALVLSVGIYAEVER/HEI*NP* KCLPGSSSHHPHPPGRRHVHGLLHWCAGVPP*QPPELLASRLSRGYG LVLSWLEPRYEKMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKT RGIFETKFLSQIESDRLALLQVRAILQQLGLNSTCDDSLVKTVCV VSRRAAQLCGAGMAAVVDKIRENRGLDRNLVTVGVDTGLYKLHPHS RIMHQTVKELSPKCNVSFLLSEDSGSGKAALITAVGVRLRTEASS
7563	A	77	2246	DKTSRGTTIRQQHSRFTKIRCSAATAADTQANRVWSGPLANRPAAE GPRDPPASASQSAGITGVSHRLRFYFDHQDVAPECGAYFFHELAKK RKGVERLLKMQNRGGPAVFQDILKPGQDEWGKTEAMEAAMAPGN LNQSLDLHALGSAPTDPHLCDFLESHFRDEEVTFMPRKSADLHAAG EAASLGGVSLNVMKGASLHALCLRLNSFGPGVATLCGERVVHKNR ASALRKCIFWPVSLNSSRARPRQRTTAGGAVPTAALQRVIPASSQCL

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				FPAPMGTTEATLRMENVDVKEEWQDEDLPRPLPEETGVELLGSPVED TSSPPNTLNFNGAHRKRKTLVAPBINISLDQSEGSLLSDDFLDTPDD LDINVDDIETPDETDSLEFLGNGNELEWEDDTPVATAKNMPGDSADL FGDGTTEDEGSAANGRLWRTVIIGEQEHRIDLHMIRPYMKVVTHTGGYY GEGLNAIIVFAACFLPDSSLPDYHYIMENLFLPPGQQTTPGPVGLTQ PAAGVEAGRVGTAGVLTLDPSMLGPCLLCPVSRVVISSLELLVAEDY MIVYLNATPRRRMPGIGWLKKCYQMIDRRRLRKNLSLIVHPSWFI RTVLAISRPFISVKFINKIQYVHSLEDLEQLIPMEHVQIPDCVLHDR QIILTTLCAYGEGEALASHLFHVILPFHIHSCFPSSTETSDPPCPG LDLAYTTPFSTHFAQRGK
7564	A	1	475	HIKNMTFIYFSSFIFCFPPRWSL/DSVAQAGVQWRDLGSLQAPPPGF TPFSCSL/LQSSWDLQAPRHRARLIFYFLVEMGF\TTLARMVSI S*PRDPPALASQSAGITGVSHRARPETYNFCSFIISSLPVEPEARK MTKNSDIGEIWINLGTCLIV
7565	A	3	364	SAIIV*DINT\PIMGGTTRQMINKEIEDVNSAINQEDLLVIYRTLHT AAAEFTFFSSLHEVSSSI\DMMLGH*TSLNKF*SIETIQNI\SDHKG IKFEINNKEI*KIHKYVEISSSTLLSKQG
7566	A	188	1057	VIKAAEGDSGSAAVLDEADPTGGPGLGCRGTYLLRSGAGGLSD/GG PCGPGTDLALSPKPPGLHGPSPGALAG*D\LSRLLPRAHSENWPGA AGGGSHRA*VGS/ADQADNDTEGNNKOPGRPQAQPSGRSLGPATGR SGWPYCGSP*PTWGQGPVSTPREGPAGVRIEAKGKS/NVGGTGGMAPS PSRTCNNLSLPKLSGVV*EAWNPGRADVHIMHAVGLIKTSHEWLDPP ADSQAGSCGASGQEPQPAASGSAAWRRCSQGGLGRLRHQQQEFGPS QHVGVCCVPCGG
7567	A	2	380	AR*LFSRVNHMVGHKLSLNR*F*KIDIIQSIFYDHNSMKLENNKRKT GKFINLW/RII*IIYL*TTHK*KKKITREIEKYLEMTENRNKTYRNL WDAKVVPKG\EFIAIGA\SL*KGGKSPIQVS
7568	A	1	371	GTSAPVQYKLDNDK*PENGTFEFSILQVLDNSCHKMGKWEVDPVQ AFF\SHWSLPSLCSQC/GLIPNLSSFSFWSFG/PPPQVPSF/TESF FSMDSSDLPPSPQAAPRQAEPGPNSHLASAPPPY
7569	A	3	369	HEVKTMLILEENLGEYLLDLVGKDFINRT/PETIS*NKIYKFNFIKI KNFCSLKDILKEIN/RIDWEKIVTKHSDKGLVSRIKKPHDSV/YKMR TQFFPPKDKDLGRYFTNKET*MVASGHLKMC
7570	A	1	2722	MGSAPVPSQACLEALLIVPWGACGVSQEEEESPAEGSKDEPGEQVEL KEEAEAPVEDGSQPPPEPKGDATPEGEKATEKENGDKSEAQKPSK AEAGPEGVAPAPEGEKKQKPKARKRMVEEIGVELVVLDPDLPEDKL AQSVQKLQDLTLRDLEKQEREKAANSLEAFIFETQDKLYQPEYQEV TEEQREEISGKLSAASTWLEDEGVGATTVMLEKELARLKLQGLFF RVEERKKWPERLSALDNLNHSMLKGLARLIPEDQIFTEVEMTTL EKVINETWAWKNATLAEQAKLPATEKPVLLSKDIEAKMMALDREVQY LLNKAKFTKPRPRPKDKNGTRAEPPLNASANRAFPSPPLTPWADQNV STVSPYPKILGKGETMVVPRVFGRMVGKSREAVAQAMVLEMFREEDY YNDVLDQMGASILGVEGPRRHPDEPPPEDEVFELFPMFMGGLLSAHN RAVLAQLGCPKIKNLDALENAQAIKKLGLGRQVLPSPSELLDHLFFH YEFQNRQFSAEVLSSLRQLNLAVRMTVPVCTVVAVLGSGRHALDE VNLASCQLDPAGLRTLLPVFLRARKLGLQLNSLGPEACKDLRDLH DQCQITTLRLSNPLTAAGVAVLMEGLAGNTSVTHLSLLHTGLGDEG LELLAAQLDRNRQLQELNVAYNGAGDTAALALARAAREHPSLELLHE VQRNLNSWDRARVQRHLE/HP/SCGIWKIAGVPLILGARPSCEWR ARAPSKSPLRRCPNSHPEPASVM*PA*TNLSIPWCCVASSLLRRCGS QSL*PSS/HPAAVSMETYHVTLLPPTQRGEEQVELSTIEELIK\VP *SAPSQP*WSTGLALPQEAWPVRSH*CPRLSQSPDLTGYSYGS FGHLTWEMSWKAPRNCV
7571	A	2	395	LSNNQLTAAGVAVLMEGLAGNTSVTHLSLLHTGLGDEGLELLAAQLD RNRQLQELNVAYNGAGDTAALALARAAREHPSLELLHEVQRNLNSW RARVQRHLELLLRDLEDSRGATLNPWRKAQLLRVEGE

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7572	A	1776	3257	TNLSIPWCCVASSLLRRCGSQSL*PSSPPLPSPWRPTTSL*HCHQHR EVKNKWSSPQLRN*SRMP*SAPSQP*WSTSGLALPQEAWYP/REKPP MMPQAQPAIPRPNRLFRLQLRASH/CGK/WSWKAPRNCV*LNSTTP CSRSGPSPRGLDPRWSGQKTWHLLGSQA*ATTPGPLMEL*/ELFNPD ACGRRVQTVVLYGTGTGKSTLVRKMVLDCYGRLPFAPELLIPFSSS LCQLVAQRYTPLKEVLPLMAAAGSHLLFVLHGLEHLNLDLFRAGTGL CSDPEEPQEPAAIIVNLLRKYMLPQASILVTTTPSAIGRIPSKYVGR YGEICGFSDTNLQKLYFQLRLNQPYCGYAVGGSGVSATPAQRDLVQ MLSRNLEGGHHQIAAACFLPSYCWLVLCATLHFLHAPTAPAGQTLTSIYT SFLRLNFSGETLDS TDPSNLSLMAYAARTMGKLAYEGVSSRKTYFSE EDVCGCLGGWASGRRRSFSWLHIFRSGWP
7573	A	201	1436	PCDPREYP**ATSPTRRSWPWSISHPRPGS/HPLALSQLFNPDACGR RVQTVVLYGTGTGKSTLVRKMVLDCYGRLPFAPELLIPFSCEDVSS VGRAPASMCQLVAQRYTPLKEVLPLMAAAGSHLLFVLHGLEHLNLDL RLAGTGLCSDPEEPQEPAAIIVNLLRKYMLPQASILVTTTPSAIGRI PSKYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYAVGGSRVSATPA QRDLVQMLSRNLEGGHHQIAAACFLPSYCWLVLCATLHFLHAPTAPAGQ TLTSIYTSFRLNFSGETLDS TDPSNLSLMAYAARTMGKLAYEGVSS RKTYFSEEDVCGCLEAGIRTEEEFQLLHIFRDLRFFLAPCPEPGR AGTFVFHRRARHAGIPRCPLHCAGFAQDDPAKGQGS
7574	A	1	377	PFLPPYMKINSR*SKDINVNFKSGSSSSSSSSSSSSSSSSSSSSSSSS SS SSSSSSSSSSSSSPL*KKNTPIKKWVKMDMRPRA
7575	A	288	468	KAEAGGWLEPRSSRPAPWRREAGAGQSPGPQ\GRGCSEL*LCHCAPAW TTE*DLASKKKKQK
7576	A	1	378	YRKP/TADNIINGERLDAFPLRPGTRQG/TPFLLLLFNIVPEVLVRA IKQDL\ETIIIVI*IRKEEGKLSLCTDDMIFYVENPKEFIKILLEQI SS\QVAEYKINIQSVVFLYTWNEQSKYEIKIISRA
7577	A	840	1093	QHKNLVL*SGRR*LLSQEES/GIFFTLVITTFCWER*NRRILSQI* RMTGARIHFQEPVIPAPWEAKAGGSLEIRSSRPAPWPTW
7578	A	254	701	KTGKEGPVRWLMPVILAPWEAKAGGSLEVRSSRPAPWT**NPIS/K NSKNIKISLAWWCTPVVLATEEAET*ESLEPGGRGCSEPRSCHSTPA WVIGAPSQKKKKKEQARRSWLAGHSGHLHYASYAGRCGRVGGLLPEP RNSRAAWAT
7579	A	12	154	CLCMSTCMCACVCSVCMHICVCDVCV/CVCVCACAYI*LRVCVLVC VFLMVFIVSVIVCMCVCVRIYLAPPHKSLLLK
7580	A	139	351	AIMAPNFPS*VKT*SQEDGQTPNRIKLKSTSRHII/IIAEN*/LAK *NILKAVREKWLITCRRTVISMTMDF
7581	A	17	245	GG*GCSCSEL*SCHCSPAWVT\SKTLTQKKNPQF*QVV*NI*IPCLL IDFSEFGLFLPKSYCYQCKVTLQCSKSL
7582	C	82	300	MLGIFEGQLQINQLVETGLKRWLRLRNSFLKRFCYLLKSLSRSSRTTT TTAFVCDGRWIMQIPGSVLPFPQCW*
7583	A	1	772	KENLITFPRIQIPISKDDFRYRGAIARKRIRLGRKYVISHKEEVPLC IHWDISKQASLSDSNVEALKKLAARGWEVSTSTVEKIKIYTLEHDV LSVWVEKHV/VEVQHI*LIRLLSDFTKRPLW\DPHFVSL*SHRLG*V KDDQLY\HITCPILNDDKPKDLVVLRIHEGKPLKDGNTYHS/VAVKS VILPSVPPSPQYIRSEIICAGFLIHAI*QQFMHSYLTLTICLLGILP YFGWEILGGLGPKSIGRKQQLVYSS
7584	A	3	307	RFTEHHRTLTGKPYECKECGKRLSSNTALTQHQRHTGENPFCKE *GKAFNQKITLIQHQRVHTGKPYECKASGK/AFSWCGRFILHQILH TQKTPVQA
7585	A	1	375	TGVTPTAATQASWTPPPIDGPTTQEKLS*ANTAPGTEGEQQVHGEKKE DPAVPSAPP*YEESTSGEGRKAWAFPAPTGEFPHPNWAYVDPNSNS RYDNGVP\TGDHEL*TTFSWDDQKVRVVFVR
7586	A	1	512	AAPESAPRLPGRFRGGRGKRRRQAAVTQAATRASGTPSPRDGMTQ GKLSVANKAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAG

				AFPPAPTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTFSWDDQK VRRVFVRKVYTILLIQLLVTLAVVALFTF
7587	A	1	401	FFFFNYITRYNKHYRYKMSKKRCHKI FQMIDMLNAASCAALGRHSR WVLGGAHPTPP/GSAQAPAPWSHAMGARTLPPRPFRS\FGHSSATPK VSPSAAMPTEAQR/LPGCGPGSDFAGHPQC*PPQVQIPTSC
7588	A	49	430	KWWKVDVCVGDMLECASIGRSEAFKTSSQFSLATSEVCGHSSATPKV SPSAAMPTEAQ/QTPPGCGPGS\ALLGIRSADHPKCRSPLRVPPFR STSKVLAPFLASSDHLEHTCSSQVRLPAAVRGAST
7589	A	467	1518	LANCRCVPGGHWMQEMVRELWMWNVEEEEHEVGICTWGGQHCPCPAK SLPGPHPGVSAPOSASQLMVKLLVWQKSVHKLKVSATSSIAVYPC PGQSSGGAESPAPGPGLAGWSHLGGAALAEVQAAPVSQAASDASLG PEWSQEGCRPGLTSGQHGGRDGR*RGSRQGDQ\QSPSPGIPASSAA L*VGLVLVKWRPVHKAYDPVPEASPLSANFRNPGPAEAPGPMGKTKG RGSAGGA\GAGSAGLAPPPRSSQGAAGIGQ*PGLPEEAVHPCKGSCP ASSLSAGTPRAPPPHPCPLGPRRQGPCSHGVTPGCRSLG*AGGVG*A PPRTQREWRPRAAQEAFAFNMSII
7590	A	296	423	MVI*KL/PYKKSQGLGTFTDEFYQILKEELISILLTLFQKIQKE*VT YKKSQGLGTFTDEFYQILKEELISILLTLFQKIQKE
7591	A	3	168	VYTKILRADRDMLTGYPCCSTGLLTADD***DNTLEV/IALRRGPFY LEGLDLSPK
7592	A	19	406	PLQELGGQSLSLHYVGGRAPGPPAPGHPPVQSLQRPCVPTQQLLTPE WFCPAL/RQQQ*GHRQGTG/PVPTPGPPLKGWQQGPPQKEWQMRPK AFGHHPGGLCQSLGGAPRRWNRDITYAGPRQCGGALM
7593	A	2	3532	SGSGVRCALLGATCLFACVPLSSVALESRRRAAPSLDMSYNYVVTAAQK PTAVNGCVTGHTSAEDLNLLIAKNTRLEIYVVTAELRPVKEVGM GKIAVMELFRPKGESKDLLFILTAKYNACILEYKQSGESIDIITRAH GNVQDRIGRPSETGIIGIIDPECRMIGRLRYDGLFKVIPLDRDNKEL KAFNIRLEELHVIDVKFLYGCAQPTICFVYQDPQGRHVKTIEVSLRE KEFNKGPWKQENVEAEASMVIAVPEPFGGAIIGQESITYHNGDKYL AIAPPIIKQSTIVCHNRVDPNGSRYLLGDMEGRLFMLLLEKEEQMDG TVTLKDLRVELLGETSIAECLTYLDNGVVFVGSRLGDSQLVKNVDS NEQGSYVAMETFTNLGPIVDMCVVDLERQGGQGLVTCGAFKEGSL RIIRNGIGIHEHASIDLPGIKGLWPLRSDPNRETYDTLVLSFVGQTR VLMLNGEEVEETELMGFVDDQQTFFCGNVAHQQLIQITSASVRLVSQ EPKALVSEWKEPQAKNISVASCNSSQVVAVGRALYYLQIHPQELRQ ISHTEMEHEVACLDITPLGDSNGLSPLCAIGLWTDISARILKLPSFE LLHKEMLGGBIIPRSILMTTFESSHYLLCALGDGALFYGLNIETGL LSDRKKVTLGTQPTVLRTRSLSTTNVFACSDRPTVIYSSNHKLVS NVNLKEVNYMCPLNSDGYPDLSALANNSTLTIGTIDEIQKLHIRTVP LYESPRKICYQEVSCFCVGLSSRIEVQDTSGGTTALRPSASTQALSS SVSSSKLFSSSTAPHETSFGEVEVHNLLIIDQHTFEVLHAHQFLQN EYALSLVSKLKGDPNTYFIVGTAMVYPEEAEPKQGRIVVFQYSDGK LQTVAEKEVKGAVYSMEFNGKLLASINSTVRLYEWTTEKDVRTECN HYNNIMALYKTKGDFILVGDLMRSVLLLAYKPMEGNFEEIARDFNP NWMSAVEILDNDNFLGAENAFNLVFCQKDSAAATDEERQHLQEVGLF HLGEFVNVFCHGSLVMQNLGETSTPTQGSVLFGTVNGMIGLVTSLSE SWYNLLLDQMQRNLNKVIKSVGKIEHSFWSFHTERKTEPATGFIDGD LIESFLDISRPMQEVVANLQYDDGSGMKREATADDLIKVVBEELTRI H
7594	A	3	300	KGPWKQENVEAEASMVIAVPEPFGGAIIGQESITYHNGDKYLAIA PIIKQSTIVCHN\RVDP*WPQDTLLGDMEGRLFTALQKNPTEKKIPQ ALQQAN
7595	B	1	819	MARGSAGLVLRGRRLHDWQLGSGHSAPGMLGQVALAGRTTELAVPSLD TPGGGEQRASDLSTLSSSHESDHTVRAAHSPLPAEALTRSLPCLQN VAHVRLYIKCQLDFGGDSIAVGTPWYPMVWIPVWVWIPVWVWME HTVLIHLPVGGHVGS SHLSAPVNNVCGNVAEPPALCGTKASKPPLT

				PPPIRSKAKFLGGSVCLGRHNKLSQTRWLKQQTTFISHDPGGWKSNIK LTRPAQDLLMSVCMNCNTHGSEDMDVISHLIKIRLKP*
7596	A	2	3235	SPASPAGRSAAHGSASPSGSPHPSWCTVGRSSCWSSPSP*ASSGSGT PPTQPGRCSLG*MRRRPAGGAQAFQLKGKKWRRFGGW*PRWEAGCFQ GEW*GATDSRTASNQLGPPHLQHLHINPPARQPPAFNRVVKQAPWRP QARAGAPG\KPDQDAHQRVLQNGHLGAQTQEEVAVTLGWVPLVV GLRLLCGTAPCAGSARSP\RGELADGGDHSVEPPDGIPLDG/EQSGS GMSGALPGSSFLLCPRRCRPPSPAL*CPASWTRPGRR*CAPRSAPAG AARGLYPEGTPGSPTPHPRGRGTGS*TPSPGTAAPCAPA*APGRRPG S*SRAWA**SP*LGPRGPQVVVLVGQ/QGPGAPWPGTWAPALSCA AVRYRGPACCSGSGRWRAH*RSPT*WWCPGCPCARSAAP*CTA*SG* GGPWA*GGS*SGVR*TSMSEPC\GCSSCRRTSAGPGPAGSAWGSAA TSPASAPPAAPPYSRRWR*GAAGGSWRRCRWAGAGSAGPAACPGHT PPRSPRALRTWA*AGPP/GIGAQLLLRDQQLRLGCPPLREGCGLL PAPRSPATRP/GLPLQQHAPGGHSGVE/GPSGCCPQTSYSEGCPPRS APPGSPRCTP*QRSRASSRPPRRRP*GGYRPAQTPGCSWPW*S*WRR PAAGGYTEPQ*RPQWRRCA*SWPGT*GSGRGCCQAWRG*PSAASRP RTARPRSCHRCPPA/PAASISSSTVGSTSIGTTDGLIDGEMARFS ATAASAR/PPQGTQCGGEFGAFGETGEGRGTRGRRIPLA\PEG RPEGAGFSRVDVFDLSA*PFEPRAMKSPGGGCP/GGFRGAGPAHR GGLGPVHPAPSLAAPGGCGVTSGPSRPERRRRHPTPESETDLTALE DPTSGTTGRKTVRREAGPEGGARGP/PAPA*CLQRPMAAGGGLAGAA RMWSGPGGSAARGR\PGL\PFTGGAGLPGKSSDPLAS/NERGPVPVP PPGRNSLLPEAGGCPGSMHQALAGWCPPAQAVALWRRGSQRLFTIAGC SCWARAPPGSEPPNMQTPASKQKLRGS*VGEQ/PSGWRLGSAFQQLS GGFCPAGADDTAGAGA
7597	A	2	1066	HMILCVENSKDSTKKNLLDLINFEFSKVAGYRINIQKSMALFTNNNL AEKSRKQCPF/TDNIKHLRIHLTKMKVHQYSLHTENHKTLMKYIEE DTNK*NDIPCS*IGRINVVKVSILPKAIYRFNAIPIKISSAFFTEIE K\IIQFLWIHKRSQITKAILRKKNPGGIILPNLNLKYKTRVIKTIQY WHKRYTGQ/WK*PEINPNMYG**IFDKSTKTK\WEKGSLEFNK\WCW DF\TCRMLKG\PYITPYTKINPKWIKDLNVRT*SHKSRKENIRGKA PWTLGFGQCFLGYHTKTSYKSNK*MKLYQSKKLLHRTKTINKMKR QCTDKEKIFANHISGKVLIFRI*EELIQLNS
7598	A	3	333	TLLPEIQAYTQEQWLGSPEEATALAERLQESAGPGLQMNGLVLGA WVCLPP/SSRPPAEPSTGAQSWVGG*EGPGGCGKVMVTGGSVLVLAW TAESEISSHTCVLRIVS
7599	A	252	686	HLFRQLFLEVLMSLQSPCLVAHSASRWCTAPVTADAPSLWRALALWL WLAHQGGPGTGWPVLSLRRRSASRLAASPSENPPSRNIH*SPQRPVC SRGPSGPATCPLGLPRTSPGATRPGPVSPSPSRGIAAAPGLAPAS TPP
7600	A	156	889	FRSSVSPGSGPPFSVSVTSGGCPS**HSGRPGVLVLKLPQGS*ASLP PAFPGGSDVAAGRGLSSAADCFSLTGLGTLATPVLFLTSNLKLLQES VPK*LNSASS/PGVPRP*LQMHRLCGG\PRSLAVGTRPGARNWLAS AFS/VGGGQLLGLQHPLQKIPPSRNIH*SPQRPVCWKAGRRKTKPRV DLQALETCPGLPRTSPGATRPGPVSPSPSRGIAAAPGLAPASTP PLSPGPTPLPP
7601	A	231	457	QWLSLLPLGLGEDTKSLRANTSNELEHSQATIWEEGPTSSSLWRPF NFPGSPTNRPKLPAPVQPPHPSG*TPSVT\WLHISWRWSP*GQSKA SLPLPLPWNSTCYPQTNKETKTQSALSTPSTNCNQPERRPVCLPWV PPTSCSSTDREPPAWAHSTDPSCDGTAKVPSSAGSKLGRKHHPRAA VGS LGASSHNLKAMGEEPTL/VTALRGSKVTTV/SETTRPRKKLSTD QYT*APPTGSHPKASTPKIRCCVSPFSRCYEEIPETG*LIKERGLID SQFHMAGEPSGNLQPWRKAKEKQAPSSQSGRTE*VPAGEMLDITYKTI RSHETHSLREQHGENHPYDPITSTWSHP*HVGIMGITIQGEIWVGT QSQTISLTYPSP*NQTKVEVSNK*RPYGRREDQPLPPCGGLSTSLVP

				QQTGTPSSCQCSRPIVPAEHPQ
7602	A	2	289	LACYSPFFGGP/PSSPPFRAGGSNPPGPPGLTPFPKK/AKKL/RP SSSPPLFPPLGRVPGDSFYPGGEGFP*PRVPIT*NWGFPPPRGTK KKLPP
7603	A	3	805	DRVSLLLPRLECNGAISPHCNFRPPGSSSHSLASASRVAGITGVCHHA *LIFVFLVEMEFHHAGQAGLELLTSGDPSPWPSPKV/YRITRHGATA TWPYIFKNFYPTSPS*NSLSLKRTS*IQMPAL*MERLQFVCPS/LAE DLTKF*EKQDSKFTSQNREN*AFSRRS*GMLEKD*KWTTSDIV*VFV LFKSHVEMLSPVLEVGSRRFLGHGGRSLMNGWVLSLW**VSSYSIS SCESWF*KESSVFLTFLLLPFWPCDMPAPPLRLPP
7604	A	75	485	EIQLVLSLKTSLNKFKKIEI ISSILSDHSGIKLEINSKGLQNHANT WKLNNLLNEHWVKNKIKMEIKTF/FELNDNNGTAYQNLWDTAKAVL RGKFTALNAYIKKYERAQTDNLRSHLKELEKQOTKPKSSRRKKK
7605	A	3	1105	HQNLSTCACFSSTCTGIRMMQRRRLAWSLHKDDAQIREVFIKTKKKK KQLQQNPPKETLSSDTPSPAPTQWSYPTHPVHGTFSKTDHMIQYKAS LNKFKENEI ISSTLSDHSGIKLEINCKRKLQNYANTSKLNNLFLNDH WLKNEIKMEIKKFFELNDNSDTAYQNLWDSAKAVLRGKFIALKAYIT KSERAQTDNLRINKNHNMI ISIDAFAFDKIQHPPMIKTLKIGIQR TYLNVIKAIYDEPTANI ILNGEKHAVGI VVNKEAKGKILAKRINVRI EYIKHKSQDSFLKRMRENDQKKEAKRGRTWVQLKQQAAPPREVFV RTNGKESGLLEPIPYEFKHNRCNKIKDLWTVKMFLEIK
7606	A	802	1204	VLEVLTRAVRQEKEIKGIQIGKEEVKLLLPADDMMYLENPKDSSKK LLGLMNEFSRVSGYKINVHKSVALLYTNSDQAEQIKNSAPFTVV/S KKK*LND*IKYLGIIHLTKEVKDLYKENYKTLKESIDDISK
7607	A	3	421	RVECVVGLEYDRSAAASNTITQVVVTHIQALSHEQ/SAAYTSFSNKH ESFSRIHLLGLHKLGLNHF*NVGIM/PN/IFSNPNRITLBNTRSKT EKSTNLWKLNNNTLLNSQQSREEIPREKENT*NENENAAAQHLQDAK AA
7608	A	1	341	RMGTCVNPRSLKGFGRPGGKKKPKSSPLKS/SPKALMGGNPGGAP PFFRFLFFNFRFGPKKSSSPAPIFFFLKKGL*INFGPPREPFGFNQK PQFPSAPGFEPWNPPQGPKP
7609	A	1	409	VWCNSLRHLTNTMETIDWKDFESWMLHWLLYEMSRHSLEQKPTDAPP KVLTKCQEEVIHRAVHPGSFKPKRDENGNYLPLQCYGSIRYCWRVL PNGTEVPNTRSRGHHCSETLELEDPSGLGGTKHDLGPVPM
7610	A	3	644	GDQRDLISNNEQLPMLG/ERPAPESQRPAPQSRDTRPPLPSPKIAS PMCSLKKG*KAITPMPLLPQSPKTPKP/VSKMRMATPLLMQALPM/D ALPQGPQNATKY/GNMTEDHVMHLL/TVLTKC/QEEVSHIPAVHPG SFRP/KCDENGNYLPLQCYGS/TGYCWCVPNGTEVPNT/KSRGHHN CSAPSPSPISHLYLIP*DPGAWLFRHPGQDKPSRNSR
7611	A	1	1032	MHRRRSRSCREDQKPVMDQQRDLISNNEQLPMLGRRPGAPESKCSRG ALYTGFSLVTLTLAGQATTAYFLYQQQGRDLKLTVTSQNLQLENLR MKLPQAS\KPVSKMRMATPLLMQALPMGALPQGPQNATKYGNMTED HVMHLLQNAD\PLKVYPPLKGSFPENLRHL\KNTMETID\WKVFE\S WMHH\WL\LFEMSQPLPCSKSPLDAPP\KVLTKCQ\EEVSHIPAVHP GSF/RGPKCGRGTGNYLAIPVAYWGASATC\WCCLFPNG/TREVPNT RSRGGHN\CSESLGTWKDPSFLGLGVLTQ\QDLGPVPIVRASRGGLQ HPASPTQLQLSCSLQPPAPPPSPTL
7612	A	59	321	LSGSPLVTATSQVPLSRGKTGGPDAL/SALPAPTSPISPPPSR SSLRRPRAPSGCPWGCPSLQQAPGPHWQDYRPGVRVRLPG
7613	A	1	465	DEEDGENAHPYRNSDPVIGTHTEKVSLSKASDSMSLYSGQSSSSGIT SCSDGTSNRDSFRLDDGPYSG\PYCDQATLHTDFTSPYDTSLSKI *KGDIIIDICKTPMRMWTGMVNNKVGNFQFIYVDVISDEEAAPMTIK ANRRSISILSKTLQ
7614	A	1	2119	LSLFLDLNENDFLSNNIHTYQKTLQGTSYQAIKSGSDPVESMGTLK RLQKLVTKKARVQNLDEVKPTLINLQDEDDTLISCLKLTKSREKKV NSVSTRRKEEMEIRLDTLSASLGRSSTLNNCLEDKLAWYEGEAYMW

				HHWKPFPENPLWTCLDFQIAQVGPWDHCSSCIRHTRLKSSCSDMDLL HSWVTLCRQESSNITCWTKLREKRGDLFCILFVCFIDRKTPrKFSDQ QALEILKIGRKQKVHSLGVVRIQNAQEKAIQCFREGETSKTKEYESV IKFYPKQRSSSGFNDRFRNNSLSKPDDSTEAEHGDPTNGSGEQSKT SN\KEAVWGKKMRAISWTM\RKKWGKKYIKALSEEKDEEDGENAHPY RNSDPVIGTHTEKVSLSKASDSMDSLYSGQSSSSGITSCSDGTSNRDS FRLDDGPGYSGPFCGRARVHTDFTPSPYDTSCLKIKVIGEQGCLVTW KGDIIIDIICKTPMGMTGMLNNKVGNFKFYVDVISEEEAAPPKIKI NRRSNSKKSKTLQEFLEIRIHLQEYTSLLLNGYETLEDLKDIKESHL IELNIENPDDRRRLLSAAENFLEEEIIQEQENEPEPLSLSSDISLNK SQLDDCPRDSGCYISSGNSDNGKEDLESENLSMDLLTDPLQLSPQLP QRGAGNINRRKTGFSLGHGKLNKEQRKDKKRLIQGWEVAEELGPSAA FG
7615	A	3	452	QTQREPTMVLSPADKTNVKAANGKVGAGHAGEYGAELERMFLSPFTT KTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDL HAHKLVRDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
7616	A	1	475	PDSSGPHRLRENPPMVAVSCPTKTNVKGPPGGKVGAGA\AQYG\SEA LGR\IFLSFPT\TKTYFPHFDL\SHG\SAQV*GATGKKVADALTNV AHVDDMPNAVVRP*SDLHAHKLVRDPVNFKLLSH\CLLG*PWAHL RPSFTPCGGTPSLEQSSWASC
7617	A	26	461	WESCGPHQRTG*AGSSRCGWRRRAAGPGCHQPRAGVPGRTRCAGRSP AADAAGRCWLGGPPPPGCGPRCLR*CAGHPPAGSARVWSVAGASTG LGRLWGRRWSPSCHRCQSPGCQAGRRGTARLSWPLSRRTSCRIPAAR VYPR
7618	A	3	420	LLDPSDGKSCGPTSKDCRRRIQYSVEALPRPALPHTTRGSGRKEAR GEGQSGAGAPADPDKLEAAVAVGEDVQQAPGCHQPRAGVPGRTRCAG RSPATRGTRDGT/QGRAGPATVPIPPGPWGGPTCRRRCRTLLARRS
7619	A	2	227	AGVFCDAGLTFTSSSGQQAQRAELLCPPAALRRRSEPFVHLLDI S\GEYLLGTFFYCVENLRDGPVADAV
7620	A	11	394	SEFCDWVADLDVQKYEQPS/HEALTSMSGSTEARDVDMGSSILMGIFS NADLKLQDEWKVNLYNTLDSSITDKSEIFVHGDLKWDIFQVMISRST TPDLIKIGMKLQEFFTQQFDTSTRALSTWGPVPYL
7621	A	3	185	FFFFFER/CPTLAQARVLWCLHSSPQPQSPW/VSSNPAS/ASQAAGT AGMCHRAWLLKTEVGLD
7622	A	1543	1745	FVKSKALAFFLSFFFFFFFLKQSLSVTQAGVQW\PVDSLQPLPPRFKR FSCLSLPSSWDYRCVPQCPAN
7623	A	1	259	SENQEQUEEVI TVRVYDPRVQNEGSWNSYVD\YKIFLHTNSKAFTAKT SCVRRRYREFVWLRLKQLQRYAGLVPVSELPGMPTLYGLY
7624	A	3	265	CCHPRLACSG\MIL\AYCQS\RLPGSKRFPCLSLPSSWDYKQPCHHT RIILVFLVET\GFHVGQTGLE/MLRNSGDPPTLASQKCWDYKA
7625	A	2	376	RAALTPTYKGAAPSPK/GAPHST\GVTSASPKEAPTPPAVTPPSPEK GPATPAPKGTPTSPVTPSSLKDSPTSPASVTCKMGATVPQASKGLP AKKGPTALKEVLVAPAPESTPIITAPTRKGPQ
7626	A	2	427	IFPPPKRGFFSKKKGVFNPPASSSRFFARPPPGVGPPPPQVSSSSSS PFYFYASSSSSYSSSSNFPS/HSSSSSSSSSSSPRQQHPLYPHCRIG WAERAW/PPGTPLYHYKTQRKQGTSASPGRGTTCHTPQSPLPGHHR CPW
7627	A	3	255	TFIRTVGWAGQTRLAPGTPLYHYKTQRKQGTSASPGRGTLRREVT IKTLLGRTLQPLGATKPAPPRSKRFMGDTASLDDW
7628	A	48	557	AGLGKARLAPGTPLYHYKTQRKQGTSASPGRGTTVTQRGHYQNAAPG RTLQPPPCGQQTSGH*GPGWPYESQRLWKTPQRS*Q*FLHPPPR/HC HTPACGAASASPCVGRYCPRCSCAPARSASLAALTRETAPLLPSPSW APGDPTLEGWPGNGSPLPPRGM*PHLYPHCRIGWAKRAWPRGHHCIT IKPRGNKEQVQVRGEGPLSRKEVTVIKTLVVHFSHHLAASKPAAIE GLDGLMSLRGYGLHKDLNDNFCILLALPHSCLRSSFCITMCRA

				PEMLMCSCSLISGRSDSGNSSSSSSFSFLGSRPHVGGGLAREWFTTP TEGDVTGIEDGL
7629	B	122	1028	MENGQSTAAGLGLPLTPEQQEALQKAKKYAMEQSIKSVLVKQTIAH QQQQLTNLQMAAVTMGFGDPLSPLQSMQAQRQALAIMCRVYVGSII YELGEDTIRQAFAPFGPIKSIDMSWDSVTMKHKGFVFEYEVPEAAQ LALQMNNSVMLGGRNIKVGRPSNIGQAQPIIDQLAEARAFNRIYVA SVHQDLSDDDIKSVFEAFGKIKSCTLARDPTTGKHKGYGFIYEKAQ SSQDAVSSMNLFDLGGQYLRVGKAVTPPMPLLTPATPGGLPPAAAVA AAAATAKITAQEAAGAAVLX*
7630	A	3	408	KSMTEAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGI/WIETL FKSKDYEFMWNPHLGYILTCPSNLGTGLRAGVHIKHEKFSEVLKRLR LQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVVDGVN
7631	A	1	170	KFSEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMV VDGVPTMHP
7632	A	1	412	SYEVFKELFDPIISDRHGGYKPTDKHKTDLN\PNLKGGDDLDPNYVL SSRVRTGRSIRKGYTLPPHCSRGERRAVEKLSVEALNSLTGEFKGKYY PLKSMTEKEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGI
7633	A	2	1250	LPTDGAPPPPPGRPPAAAMPFSNSHNALKLRFAEDEFFDLSAHNNH MAKVLTPELYAELRAKSTPSGFTLDDVIQTGVNDNPGHPYIMTVGCVA GDEESYEVFKDLFDPIIEDRDGGYKPSDEHKTDLDPDNLQGGDDLDP NY\VLSSRVRTGRSIRGFCPLPHCSRGEGR\IEKLAVE\ALSSL\D GDLAGRYALKSMTEAEQQQLIDDHFLFDKPV\SPLLLGLGHGRRNW PDARGIWHNDNKTFLVWVNE\EDHLRV\ISMQKGG\NMKEV\TRFC TGLTQIETLFKSK\DYEFMWNPFHWATSLP\CHCNLG\TGLRA\GLH I\KLPNLGQGMRFSEV\LKPAAELSKSRPPGGVEHGLRWAGVFDV FQTLNRPGPSQSVEL\QMV\VDGVK\LL\IEMEQLRLEQQQAIDDL HAWPKK
7634	A	1	175	EQLPYFVTFISMPATT/EGRRGFSLSVESACSNYATTVQVKVVRMH ISPRALGTLHHN
7635	A	1	83	SVTLFSPMATMKGRGFVSVESACSN
7636	A	61	2028	GELLCPPPPPHFRAPGTMSALAGEDVWRCPGCGDHIAPSQIWRVTV NETWHGSCFRCEQDSLNTWYIEKDGKLYCPKDYWGKFGEFCHGCS LLMTGPFMVAGEFKYHPECFACMSCKVIEDGDAYALVQHATLYCGK CHNEVVLAPMFERLSTESVQEQLPYSVTLSMPATTEGRRGFVSVE SACSNYATTVQVKEVNRMHISPNNRNAIHPGDRILEINGTPVRTLRV EEVEDAISQTSQTLQLLIEHDPVSQRDLQRLRLAPLPHMQNAGHPH ALSTLDTKENLEGTLRRSLRRSNSISKSPGPSSPKEPLLFSDISR SESLRCSSSSQIFRPCDLIHGEVLGKGFGQAIVTHKATGKVMV MKELIRCDEETQKTFLTEVKMRSLDHPNVLKFIGVLYKDKKLNLLT EYIEGGTLKDFLRMDPFPWQKVRFAKGIASGMAYLHSMCIHRDL NSHNCILKDKTVVADPGLSRLIVEERKRAPMEKATTKKRTLKND RKKRYTVVGNPYWMAPEMLNGKSYDETVDIFSFGIVLCEIIGQVYAD PDCLPRTLDLGLNVKLFWEKFVPTDCPPAFFPLAACCRLEPESRPA FSKLEDSFEALSILYLGELGIPLPAELEELDHTVSMQYGLTRDSPP
7637	A	3	295	LWPSRPTTDPQPRPADPGLRRLPPD/SPSPSRPARPTLCPFSAPAAR FPVAPSSALASSEDLQPPSPSSSGSLPGQAPPCYAPTYPFGGEPP PYAP
7638	A	517	1038	NKRIYNCMMISSRRVISLSPIVLLQIFDCPRLKFSEIPQRLTALLP PDPIVINHVI\SEVAPACFSDQGMISFLPSLPLPLPLPSLLPPCWI CPSPGALGPVWGHGHEGLDFPGSVDPDQKKTACYDIDVEVEEPLK GQMSSFLLSTANQQEISALDSKVGPKPRAGVGH
7639	A	154	1594	LSRCRTLPSMTPLGQHPPTTVQRPMPSGARMHQGRPWAPRAPRTW AAPPCDPAWPPRDGARQASSAPARQSQASQGGQPEPTAPARSRAK RRKMADKILPQRIRELVPESQAYMDLLAFERKLDQTIMRKGVDIQEA LKRPMKQKRKLRLYISNTFNPASDAEDSDGSIASWELRVEGKLLDD PSKQKRKFSSFFKSLVIELDKDLYGPDN\HLVEWHRTPTTQETDGFQ

				VK\RPGDLSVRC\TLLMLDYQPPQFKLDPRLARLLGLHTQSRSAIV QALW\QYVKTNRQLQSDSHDKE\YTMGDKYFPQNF\DC\PRLKFT*IPQ RVTAVL\MPDPPIVINHVIS\VDPSD\QKKT\ACYDIDVEVEEPIK/ GGQMSSFLSTA/NNQOEISALDSKIHETIESIN\QLKIQ\RDF\ML SFLRRPHKLCARTWLRSEQEPGTSR*LTDVAGNPPEERRA\EFYHQ\P WSQEAVSRYFY\CKIQASAGKEAW
7640	A	256	427	HPICPQTTKAFLPRMELQNGHIVCLNSVLALSAIPGA\IDYCTSEA ADFGFMESLT
7641	A	1	985	RIARPGEFRPLPGSAARRMAWKRLGALVMFPLQMIYLVVKAAGVLVL PAKLRLDSRENVLTGGGRGIGRQLAREFAERGARKIVL\WGRTEKC LKETTEIRQMGTECHY\FICDVGNRD\EVYQTAKAAREKVGDIITIL VK\NAAVV/HMGKSLMD\SDDDAFLKAQ\NINTLG\QFVNHQGPFSG KLCWKQONGPH/LVCLQLPLLGIVLAI/LPGAIDY\CTSASAFAM ESLDPG/VLAGTCPGV\SATTVLALSTSTEMFQGH*EFRF\PNLFP PLK\PETVARK/TQVEAVQLNQALLLPWTMHALVILKSILPQAAL EIHKILKETYNLE
7642	A	1	376	KQAASNQLDSLMLGLG/DSHPVEERGIIICEFCGVQLFYDVLVHYDQ WDLRPGTAFFRVTEGIPRLHSQ\AQETWPEL/PLRRVRQENLSSGY LDDTLLETANGPTFCLPARPF\NNMTATYNQLSRS
7643	A	1	2753	MKEFSSTAQGNTEVIHTGTQLRHERHHIGDFCFQEMEKDIDHFEFQW KEDERNESHEAPMTEIKQLTGSTNRHDQRHAGNPKIKDQLGSSSFHSHL PELHMFQTEGKIGNQVEKSINSASLVSTSQRISCRPKTHISKVYGN FLNSSLLTQKQEVHMRKESFQCNESGKAFNYSSVLKHKQI IHLGAKQ YKCDVCGKVFNQKRYLACHRRCHTGKPKYCNDGKTFQSQELTLTCH HRLHTGEKHYKCSECGKTFSRNSALVIHKA IHTGEKSYKCNECGKTF SQTSYLVYHRLHTGEKPYKCEECDKAFSFKSNLERHRKIHTGEKPY KCNECSRFTSRKSSLTRHRLHTGEKPYKCNDGKTFQSSSLVYHR RLHTGEKPYKCEECDKAFSFKSNLERHRRIHTGEKPYKCNDG\GKAF TSHSHLIRHQRIHTGQKSYKCEECDKAFSFKSNLERHRRIHTGEKLY KCNECGKTFSRKSSLTRHRLHTGEKPYQCNECGKAFRGQSALIYHQ AIHGIGKLYKCNDCHQVFSNATTIANHWRIHNEERSYKCNRCGKFFR HRSYLAVHWRTHSGEKPYKCEECDKAFSFKSNLQRHRR IHTGEKPYR CNECGKTFSRKSYLTCHRLHTGEKPYKCNECGKTFGRNSALI IHKA IHTGEKPYKCNECGKAFSFKSSLTCHRLHTGEKPYKCEECDKVFSR KSSLEKHRR IHTW/REKPYKCKVCDKAFGRDLSHGLT\HTRIHTGEK YKCNECGKNFRHNSALVIHKA IHSGEKPYKCNECGKTFRHNALBIH KA IHTGEKPYKSECGKVFNRKANLSRHHRLHTGEKPYKCNKCGKVF NQQAHLACHHRIHTGEKPYKCNECGKTFRHNLSVLVIHKT IHTGEKPY KCNECGKVFNRKAKLARHHR IHTGKKH
7644	A	1	150	DSFGASRFLRIHAE\TYFTLRAYFAESRCIEALDELASLQVTMHQAQ KHT
7645	A	81	331	KGARFLLLILYLLDAFLF\NLDLFFLEYPSYFLLCFCSLLFFFC FSLYFFVCRPSSSLFSSSILLILLFFLVRLFLCLFL
7646	A	701	1116	ATRHSMLSCTIYTYIYIKHTHTHVFIYIYTYIYIHTHIYTYIYI THIHIYIYIYIHTHFFFFFETESRSVTQAGVQWHDGSLQAASW GHA/DSASTSQAAGTTGAHHHAQ/LIFFFVLVETGPHRASQDS
7647	A	1	207	RSVFRERGKLSAG/SLVERLYRVRFRDRFERILKMARKAVETHVLR PHLVSDYRDSIIPSESLALPC
7648	C	244	432	MFFTNIKMIAYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXILFSAWLR
7649	A	898	1145	IFQLLLMEGPANIIGNTGSSNTGRSNTGPSNQSSYLISFLFLFCFFE TESRSGRPGLGVQAWISGSL\QALPPGSTPFSCLS
7650	A	1	476	ATRELVTSSGLRRKTGLWARPREKPTAWHLASLRPDELVRNPQEPQ PGPREEGSLGHVARTPAPGGGQRHLSRAGHSRPGRRFKATLWL\SE EHPLSLGDQVTPIIDLMAISNAHFAKLRFITLRLPPG\FPVKIEIP LFHVLNARIHLSGNLCGC

7651	A	1	1071	MTSAKTEIVLGKRDILLEVIDILPAPVQAFLYETACQERFCABLCDA LRERHDSGEILSYLQAHQVFLVPVTPALIFAITVATIGSFQFGYNTG VINAPETIIKEFINKTLTDKANAPPSEVLLTNLWSLSVAIFSVGGMI GSFSVGLFVNRFRGRNSMLIVNLLAATGGCLMGLCKIAESVEMLILG RLVIGLFCGLCTGFVPMYIGEISPTALRGAFGTNLQGLGIVIGILVAQ IPGLELILGSEELWPVLLGFTILPAILQSAALPCCPESPRFLLINRK KEENATRILQRLWGTQDVSQDIQEMKDESARMSQEKQVTVLELFRVS SYRQPIIISIVLQLSQQLSGINAVSVIL
7652	A	2	240	SCSIGSFQFG/YYPGVINAPETIIKKFINK/SLTAKANAPPSEVLLT NLWSLSVAIFSRRGYESASLFPSSGLFVN\RFGQVLT
7653	A	2	391	QTGRGMWCSSLVFLLLPATPRKQSEPKTDDAAAPGTADTAGPGTMD TAVPRKAETAVPGKRNTAVPGTADPASPGTADTAEPMTTPTVTLAS WPSLTQST\KAPSPRLLPAPSPGSCSATSTSCSRSP
7654	A	1	200	SSGHAEPGSGGPGFLSPHCYEEVCGFFPSLSSFSPPSPPECSQQLVPA GARVDALDRAGRTPHLAK
7655	A	3	416	CLFPVQLLLLDHGADPNQRDGLGNTPLHLAACTNHVPVITTLRGG\S GFFPSLSFSPPSPPECSQQLVPAGARVDALDRAGRTPHLAESKLN LLEGHAQCLEAVRLEEKHIHMLKEHLELLGRHYQLINAWMTLD
7656	A	1	397	KVQSRCSSK\ENILRASHSAVDITKVARRP\RMASFALTSMDKAFIT VLEMTPLVGTETINRYRYGMARGLVQYVVSDDIVFSFLSLLYEYFIR SFHFSLSLFIYLSLRSFFKLRESFFCFSSIFLSSTFALS
7657	A	210	441	LNPILYSPGRDHRVQNPHLPRLCIQKLFK\SKCFIYELPAHRKKLV QLEPLTDDLEPDFVRQVTEMSYIPSHSMI
7658	A	8	399	RVGVAGPAPWWLRVSLGGR\DFHTPIS\VTKVAERGAEDADLRPGD IIVAINGESAEGLHAEQAQSKIRQSPSPRLRLQDRSQATSPGQTNGD SSLEVLATRFQGSVRTYTESQSSLRSSYSPTSLSRA
7659	A	2	260	WEPPWPGPVLGLPLPPLPPPSSPSLPPIPPPRGCSLGASSA/WTAW VSSPKEPVRPQEPPEGGEGSNENHRRKWHPPFSVMLKSCY
7660	A	2	442	PRVRVYFROGHEAYVEMARKNKIYSINPKKQPHWKMBELREQELMKI VGIKYEVLPTLCCCLKLAFDPDTGKLTGGSFTMKYHMDPVIDFLV LRQQFDDAKYRRWNIGKE/CSDRFRSVIDDWWFGTIESQEPLQLE YPDSLQ
7661	A	965	1232	TGVQWPDGSLQPLPPEFKQFSCLSLLRGWDCRRPLPQLADFCIFSR DGGYCYVGQAGLKLLTSN/DLPASASQSAGITGVSCTQPKSS
7662	B	111	374	MVAAATGSEILLWALQAEGGGSEIGDSGNWIEIAYGTSLGGVRVIVQ HPETVGSGPQLLQFTTVHRSPTVKIMLWEKHLISVCADNNH*
7663	A	387	545	RQDGQGSVPSEAAEPAQPSGASAAARTASPCPTEQHDAPQPWQCRAA GPNAG
7664	B	181	4716	MGRPAPAVPRPARPATPPAWTAALPAGRPRGDPGFRAFLCPLICHNG GVCVKPDRCLCPPDFAGKFCQLHSSGARPPAPAIPLGTRSVYTMPLA NHRDDEHGVAASMVSVHVEHPQEASVVVHQVERVSGPWEEADAEAVAR AEAAARAEAAAPYTVLAQSAPREDGYSDASGFGYCFRELRGGECASP LPGLRTQEVCCRGAGLAWGVHDCQLCSERLGNSESVAPDGPCTGF ERVNGSCEDVDECATGGRCQHGEACANTRGGYTCCVCPDGFLDSSRSS CISQHVISEAKGPCFRVLRDGGCSLPILRNITKQICCSRVGKAWGR GCQLCPPFGSEGFEICPAGPGYHYASDLRYNTRPLGQEPFRVLS QPRTLPATSRPSAGFLPTHRLEPRPEPRPDPRGPEFPLPSIPAWTG PEIPESGPSSGMCQRNPQVCGPGRCISRPSGYTCACDSGFRLSPQGT RCIDVDECRRVPPPCAPGRCENSPGSFRCVCGPGFRAGPRAAECLDV DECHRVPPPCDLGRCENTPGSFLCVCAGYQAAPHGASCQDVDECTQ SPGLCGRGACKNLPGSFRCVCPAGFRGSACEEDVDECAQEPPECGPG RCDNTAGSFHCACPAFRSRGPGAPCQDVDECARSPPPCITYGRCENT EGSFQCVCPMGFQPNAAAGSECEDEVDECENHLACPGQECVNSPGSFQC RACPSGHHLHRGRCTDVDECSSGAPPCGPHGHCTNTEGSRFCSCAPG YRAPSGRPGCADVNECLEGDFCFPHGECLNTDGSFACTCAPGYRPG PRGASCLDVDECSEEDLCQSGICTNTDGSFECICPPGHRAGPDLASC

				LDVDECRERGPALCGSQRCEINSGSYRCVRDCDPGYHAGPEGTCDDV DECQEYGPBICGAQRCEINSGSYRCVTPACDPGYQPTPGGGCQDVDEC RNRSFCGAHAVCQNLPGSFQCLCDQGYEGARDGRHCVDVNECETLQG VCGAALCENVEGSFLCVCNPSPEEFDPMGTGRVPPRTSAGMFPGPSQ QAPASVPLPARPPPPPLPRPSTPRQGPVSGRRECYFDTAAPDADC NILARNVTWQECCTVGEWGSQCRIOQCPGTETAQYQSLCPHGRGY LAPSGDLSLRDQVDECQLFRDQVCKSGVCVNTAPGYSYCSNGYHYH TQRLECIDNDECADEEPACEGGRCVNTVGSYHCTCEPPLVLDGSQRR CVSNESQSLDDNLGVCWQEVGADLVCSHPRLDQATYTECCCLYGEA WGMDCALCPAQSDDFEALCNVLRPPAYSPRRPGGFLPYEYGPDLG PPYQGLPYGPELYPPPALPYDPYPPPPPGPFARREAPYGAAPRFDMPDF EDDGGPYGESEAPAPPGPGTRWPYRSRDTRRSFPEPEEPPEGGSYAG SLAEPYEELEAECEGILDGCTNGRCVRVPEGFTCRCFDGYRLDMTRM ACVDINECDEAEASPLCVNARCLNTDGSFRICRPGFAPTHQPHHC APARPRA*
7665	A	209	1288	EEKNERRDRDTERKGEARTSKTSQKRETKETGGKTKQKRKKEKTTD KKTTRKKRTSKTEENKKRKQEKEDRERDESTKRRKEGERERRGNARR RKKGGEHKKRGERRNNSKGEGEERGRKTKAKTRRTRQATNTDSK NEKGRKKGQTRARRPAETGRRRRKRRQRKAGETTPGETGRWCASV RSVDGSPPTAFTVLECEGSRRLLGS\RPRRYLLNCQANGSLAMWDLTT A\MDGFGQAPAGGLTEQELMEQLEHCELAPP/R/CASSSLNGAVSPS PSPRISLT/NASTQASSNTSFVWPTVGSPPKPPARLKARRRGWGEALW KAARNWCGVGQTSBGHPHQAPWPSKRSRHSPTTFQE
7666	A	3	1704	GGRRAAALGVAIGAAGAAAWTGPARRASPRALHPGRVRPALRPW ADRLPLYPDLRAPQRHQQRSSRRGGPGGTRLPLRVPSAAEPAQP SGASAAARTAQPLSDGATRCPTLAMHGCWAECWMRKPLPHPQVRFY LVEGQPEEPMVRLVCGHHNWIAYVAYTQFLVCYRLKEASGWQLVFSS PRLDWPIERLALH\ARVHGGALGEHDKMVAATGSEILLWALQAEQG GSEIGVFHGLVPVEALFFVGNQLIATSHTGRIGVNNAVTKHWQVEV QPITSYDAAGSFLLLGCNNGSIYYVDVQKFLRMKDNLDLLVSELYRD PAEDGVTALSVELTPKTSDSGNWIEIAYGTSSGGVRVIVQHPETVGS GPQLFQTFVHR\SPVTKIMLSEKHLISVCADNNHVRTWSVTRFR\G MISTQPGSTPLASFKILALESADGHGGCSAGNDIGPYGERDDQQVFI QKVVPSASQLFVRLSSTGQVRCSVRSVDGSPPTAFTVLECEGSRRLLG SRPRRYLLTGQANGSLAMWDLTTAMDGLGR/SPAGGLTEQELMEQLE HCELAP
7667	A	8	567	TLVTVGNSQGREGLAFLVSCPEGRADCASESACSSDSLDEARSSGSE GTPADTGDLSPGHGASAPSVSREARQTVPPLTVRLHTQSVSECITED GRTVAVGDIVWGHRR*GRTCWPGASDLCSGTL*AFWPAACRAHWARW SAWCEVPRGPAVCSGRGT*AQRLPLSVFVPTTQMAALAHEAV
7668	A	2	610	SPEILVDPRLRPRVRLAFLVSCLVGRADCASESACSSDSLDEARSSG SEGTPADTGDLSPGHGASAPSVSREARQTVPPLTVRLHTQSVSECIT EDGRTVAVGDIVWKGIFPWWPARVLDISL/WPEGGRRAVLAR\RK VSWIGSPTTSFLSISKLSPFSEFFKLRFNRKKKGMRYKAITEAANAA RHVAPEIRELLTQFET
7669	A	3	392	ADAAVPTRCVTSGHSLPISGHAAESELFHR/P/AGIILPSRRNVLP RGASSTRRARPLERPATVPVPAPSSRAARSRHIDPLQSSSPTPPGP TGSAAYVAVPTPNSSSPGPAGRPAGAMLYHSWVSEITE
7670	A	5	395	GFRNPPRDSHHPHSTRRRRAFLRRWEKDPGRGKGRAPEPAQQRDASP PTRRPLEGP/PREHLRQWERLFPKSPWKEVFAFVSANKACALS VAPVETAAEPSPPS/PRVGRSGPRTKGARPRNRCCDD
7671	A	2	399	ARTNTGGRPYCFIRM\SNLIHRTQQGYNNRPLSTNIIISDIQTETK LRPPYQISMCELGSAKGVTSAFSADCKGAEKISSGHORLEPATLSGI A\GFILSLLWALNLIPIGFHAIQRLLOREGDDFNSFIALP
7672	C	151	339	MSTFPIHISPKLRGDDVRGRXLXWRWPLRGFCATVRWCPPGAAGWCA XPVRAESAFXRPAKS*

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7673	A	19	444	SVRWNSCRAEAPQWPAPAAAPAAHSPHLSLGSGLGKILINSLFLT DLYSPEYPGPSQRIKKPVQVYILVFLIDDKLE*Y*YTQSTCCNFHYA S\QSWQPAINYIDSKFEDYLNESRVNRCQMPGNRVQGCCLYFIAPSG H
7674	A	152	532	QALRANRPAPVAEGATDRTVAQKLLNGQORQLOPRPPTRLI*AWVEQS KVLIK\DCGVQQLLTIVDTPRFGDAVDNSNCWQPVINYIDIKFEDYL NAESRVNRCQMPGNRVQ**LYFIAPSGHGPLHN
7675	A	1	628	GSARSAAEERSVNSSTMVAQQKNLEGYVGFANLPNQVYRKSVKRGF EFTLMVVGESGLGKSTLINSFLTDLYSPEYPGPSHRIKKTQVQEQC GV\LIKEGVHLLLTIVDTPGF\GDAVDN\SNC\WQPV\IDYIDSKF EDYLNESRVTRRQMPD\NRVQCCLYFIAPSGHGL\KPLDIEFMKRL HEKVNIIPLIAKADTLTPEECQFK
7676	A	2	373	VLELEERALLREARLGRARSSGMOATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHLHRPWKCGLCSEFGSSQEEELLHH\TCQVC GQSFTQSWFLKGHMRKHKASFDHACPVCGR
7677	A	44	985	RGSMEGSRPRAPSGHLAPSPPAFDGELDLQRYSNPVAVSAGSLGMA VSWSES RAGERRFPCPVCGKRFNFNSILALHLRAHPGAQAFQCPHCG HRAAQRAILLRSHLRTHQPERPRSPAARLLLELEERALLREAPTGES KLRGHAGHPLPLMVW\PRPQAPSSSAFRCPYCKGKFRT\RLERERHL HILHRPWKCGLCSEFGSSQEEELLHHS\TAHGAPERPLAATSVAPPPQ PQPQPPQPEPRSPQPEPEPEPEPEPEATPTPAPAAPEEPPAPPEFRC QVCGQSFTQSWFLKG\HMRKHKASFDHACPVCGR
7678	A	1	583	GNAGLSSLTEGVLDFAVKAVYMGHPGIDHTVCVQNKLGSMFLSET GVTLLYGLQTT\DNRLHFPVAPKHTAKMLFSGLLELTRAVRKMRKFP DQRQWLKQYVSLYQEDGRYEGPTLAHAVELFGGRRWSARNPSGT SAKNAEKPNNMQRNNTLGISTTKKKKKILMRGESGEVTDDEMATRKAK MHKECR
7679	A	2	429	SVGSESDSSKE\GPSMTRSGPLRRSRAPVG/PEESQGNLTIVIRVVIH DLQQTCKIRFNPDATVWVAKQRI\LTCTLSLKDVLNLYGLFQPASNGR DGKFLDEERLLREYPQPVGEGVPSLEFRYKKRVYKQASLDEKQLAKL HTK
7680	A	1	248	VIFLVNSGSEANELAMLARAHSNNIDIISF/RTMCPDVFGRGPWGG HCRDSPVQTIKRCSCAPGPTGQGGCQWSVGSKWGHE
7681	A	1	501	MTLIWRHLLRPLCLVTSAPRILEMHPFLSRKWKPGGRGSVEDQREEH AWDRGDLHREGCERSCPERMIPNSNGEGPQQRADCGPMCEEKTTTL ESPSWQLQHRAEAEKNFSTDQTLSLRRPNPNTASAGLHGRQCLKRTS RTSVTKLSLHTKPRMPPCDFMPERYQ
7682	C	60	380	MELPGGTGCQPTMCPDVFGRGPWGGSHCRDSPVQTIKRCSCAPDCCQA KDQYIEQFKDTLSTSVAKSIAGFFRRTYSRCEWSCPVKGVFKGSL SLVRARGRPCALQ
7683	A	3	649	LSPSYFHSISFPHSLFLPLEGTVTRNRELWGLLQAMGVHHSRIPLLA PPPHNLKVVQDSEQLEPGLQASMGVGFSLGRNDSNLETFAETLVP GSIPLPGILEMHPFLSLGTSRTSVTKLSLHIKPRMPPCDFMPERYQV IFLVNSGSEA\NE\LAMLARAHSNNIDI\ISFRGAY\HGCSPTYLG LTNVGTYKM\KLPGGTGCQPVSLIIFLLFL
7684	A	27	211	FHIVQYFNFFVCLFVCLFETESTLSRLEGSGVISAHCNL\TLPPGF NNSCASASRVAGTTQ
7685	A	1	312	RPRRRGDHREVKGGRGGKGGEGRPQGGQRWAVGKGGEGRPQGGQWA VGKGGEGRPQGGQRWAEKGGEGRPQGGQR\QWVGKGGEGRPQGGER \GPGGKGGE
7686	A	2	320	KYVFTDISYSIPHRERFIVREPSGTLRKASWEERDRMIQVYFPKEG RKILTPIIFKEENLRFEPDSTEYIKVHHKTYEDIGKRGK\YDLLRST RYFGWEWVWVFC
7687	A	22	1071	GVLRAWNGSVSGLESSPGTVACSNRYLALSRWGCHSRRINSYGAESG SPETKKPTFMDEEVQ\RVLTMTGLNLQKTFKPAIQELKPPTYKLMT QAQLEEATRQAVEAAKVRCLKMPPVLEERVINDVLADKDFWKGTET

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				TKYVFT\DISYCIPIHRERFI\VVREPSGTLRKASL\EDRDRMIQVYF PKEGRKILPPIIFKEENLRMTYSQDRHVDVLNLCFAQFEPDSTBYIK VHHKTYEDIDKRGKYDLLRSTRYFG\EMVWYFVNNKKIDGLLDQIQ RDLIDDATNLVQLYHVLHPDGQSAQGAQDQAAEGINLIKVFATEAQ KGAYIELTLQTYQEALSRHSAAS
7688	A	2	383	FSAPAASEPLPFGSGPPSEPLPFGSGPPSDPLAFAAPPPSEPLTFSG PPPPSEPLTFSGPPSDPLCFTAPPPSEPVPFSGPAPSDRLPFFGPT TSEPPNR/PGMPTQPHPICLSKNTPLPEPTRLHP
7689	A	3	2485	PAIKIRRRRVRDLQDPPQMAPEIQPPSHHFSPEQRALLYEDTLYTV LHRLGHPEPNHVTEASELLRYLQEAHFVEPEEHQQTQVRVRELEKPI FCLKATVKQAKGILGKDVSGFSDPYCLLGIEQGVGPGSGPSRHRQ KAVVRHTIPEEETHRTQVITQTLNPVWDETFIEFEDITNASFHLDM WDLDTVESVRQKLGEITDLHGLRRIFKEARKDKGQDDFLGNVVLRLQ DLRCREDQWYPLEPRT\ESYPDRGQGHQGLVHKRRATSASR\SQP SYTVHLHLQLVSHVETQHEAGSTS/WGRVAES\QAATVLFHATQ KDLSDFHQSMQWVAYSRLYQSLEFPSSCLLHPITSIEYQWIQGRK AEQQEELAASFSSLLTYGLSLIRFRSVFPLSVSDSPARLQSLRLVL VQMCKMKAFGELCPNTAPLPQLVTEALQTGTTEWFHLKQHHQPMVQ GIPEAGKALLGLVQDVGDLHQCQRTWDKIFH\NELISSTLKIHLS MAFREQLVLAKRVQDHTTVGDVVSPEMGESLFQLYISLKEQLR MSSSERDGLALDNFHRWFQPAIPSWLQKTYNEALARVQRAVQMDL VP\LGELTKHSTSADVLSTGFAQISHTARQLDWPDPPEAFMITVKFV EDTCRLALVY\CSLIK\ARARELFFRARRTKARAANMLCVVNDMEQ LRLVI\GKLPAQLAWEALEQRVGAVLEQQQLQNTLHAQLS\GALAGL GHEI\RTG\VRTLAE\QLEVGIAKHQKLVGVRESVLPEDAILPLMK FLEVELCYMNTNLVQENFSSLLTLLWTHTLTVLVEAA
7690	A	31	511	GDHASDKETITIVNIYAPNIRACSKYIKQTLTELKGEVDSNVITAIS ILRFQQLPTLIKTESLRNRNSSSSSSSSSS/PSSSSSSSLKSLPTK ESIGPDGFTDEFYQTFKEELK/PKSSSSSSSSSSSSSSSSSSSS SSSSSPEKDATREENYRPISL
7691	A	2	189	TYHIDRIKDKSHMIISIATEKAFDKIEHPFMIKALSQLEVVG\MTNV IKAIYKKSANITQQ
7692	A	3	411	NTANRAARVSASIEDSPDNSETLPPDESFRNGENAKRFAIDIGGTLT KLAYYSTVQHKVAKGRAFDHSGKDTER\DTSRPMRVQFKKRALLDGT SLRRRKPTPKPAWTSSKTISSTQRP/EVIQATGGGAYKVKDLI
7693	A	88	482	KEELYGDFEDLET/G/DVHKGKSGPDTQNEIDIEK\QDEIDPDEKSA KKKHLKDKRKLKEMLDAEYDEGESTYFDDLKGEMQKEAQMRLKNHRW YKKILKSQDPIIFSVGWRRVHTILLYYIEDHNGRQRLKY
7694	A	1	1068	MAANRKDFIHRRCGPESQSEAVPQGLCRAERSSALAMLSGVSPPRT QLRCPCKGTQRRRCRGGEADSGGEAVGGGAAERRSAAARRRGRRRG GEAVGGGAAERRSAAARRRRGRRRRRGGEAGGGGAAEARRAAARR AAAARRAAARRAAARRAAARRIAESGGEAHSRGEAHSRGEAHS GAGAERRRRLHSPALKTHPGQSSEGHVEYKLNHVEFEDQDDEARVQ YEGFRPGMYVRVEIENVPCFVQNFDPYPIILGGLGNSGPNVGHVQ MRLKKHLWYKKI\LKSQDPFISSVGRRFQTIPLCYIEDHNGRQRL LKYTPQHMHCGAA\FWGKI*LQ*LAYCRD
7695	A	66	844	KEELYGDFEDLETGDVHKGKSGPDTQNEIDVEK\KEEIDPDEESAKK KHLDKRKLKEMFDVEYDEGESTYFDDLKGEMQKQAQITAYRFSPT PSC\LNHAEFEDQDDEARVQYEGFRPGMYVCVEIENVPCFV*NFD PRYPILGGLGNSGPNVGYVQVGPFAAYLVPEALWISPPSIILPSHP PQMRLKKHRWYKKILKSRDPIIFSVGWRRFQTIPLCYIEDHNGRQRL LKYTPQHVRHG/AAFWDKICLQ*LAYC
7696	A	1	1177	LRLMLGTRSALWACRGWGQHMHWLQPLGVLFPEELYGDFEDLE TGDVHKGKSGPDTQNEIDIEKVEEIDPD\EEESAKKKHLDKRKLK EMFDAEYDEGESTYFDDLKGEMQK\KAQLN\HVEFEDQDDEARVQYE GFRPGMYVRVEIENVPCFV\QNFDPHYPIILGGLGNSGPNVGYVQ

				RLKKHRWYKKILKSRDPIIFSVGWRRFHTIPLYIEDHNGRQRLKLY TPQHMHCGAAPWGPITPQGTGFLAIQSV\SGIMPDFRVAATGVVLDL DKSIKIVKKLKTGFPYKIFKNTSFIKGMFNSALEVAKFEGAVIRT SGIRG\QIKKALRAPEGVFRASFEDKLMSDIVLMRLSTCSIPA/FY /NPVTSC*TIGEKHLVRMRPRP
7697	A	163	371	KGTTKLVLVLSDFKSYFKAIVIKTVRN/WHKYK\HIDQWNRIQNPEI NPHIYQGMIFKKRAKNKQWKKDGL
7698	A	270	1479	PGCAFSSSGTSRQLAPVLGYLGSQRKHSLPDLPHYDGALEPHINAQI MQLHHSKHHAAAYVNNLNVTEEKYQEALAKGRFQAEREKNVCTFNF* GDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGEKPGWIYCAPL STTCTVGIDVISWAL*QKIF*IHVI*HFTVIIGNLFICGWFWDFPF NR\ELLEAIKRDGFSFDKFKELTAASVGVQSGWGLGFWNKQRGHL QIAACPNQDPLQGTGTYI*IGLSVVPVWKTSPLLKNVDSKVKGKRTV YQGDGHYVNHHPNQVFWGRGAVKALNRNLKGAPDLELDGESRANCGE KGREESERSGR*AWQLCSVTGAPFFLTGLIPLLIDVWEHAYYLQYK NVRPDYKAIWNVINWENVTERYMACKK
7699	A	94	330	KRSYKMKCLHFNFSGDVTAQIALQPALKFNGGGH\INHSIFWTNLS PNGGGEKPGWYILVHPYLHFVHSRNLRLIYWR
7700	A	33	807	GPRAAQERHSLWLLRQRLQOIGGISGSTSTSSMLSRVCGTSRQLA PVLGYLGSQRKHSL\PDLPYDGALEPHINAHIMHLHHSKHHAAAYV NLNVTEEKYHEALA\RGDVTQIALQPAL\KFNGGGHINHSIFWTNL SPNGGGEKPG/EELLEAIK\R\DFGSFDKFK\EKLTAAASVGVQSGW GWLGF\NKERHGLQIAACPNQDPLQGTG\LIPLLIDVWEHAYYLQ YKNVRPDYKAIWNVINWENVTERYMACKK
7701	A	2	436	SGRGASLRPGVRPPSVSWEPYSGPGSTPPPPSSRSKDVGKPAQSWVR CGSTQPN TGQLPK EGLSTPHVPVPRAGIPSSRQALLSSGNPGTRAPSA PALRPEAQASPAEFPGAP/SPELGGERLGGARFQEPFPQPAASFPGA AATQA
7702	A	1	389	PGSSRQRCWHQPCFACQACQALINLIYFYHDGQLYCGRHHAELLRP RCPACDQLIFSWRCTEAEQQRWHENHFCCQDCAGPLGGGRYALPGGS PCCPSCFENRYS DAGSSWAGALEGDAFLGE/HWKVTHSLGRLDSTN
7703	A	1	1217	MGGHLANVPTGTSLQQTGLMEKHFTSGKQLLKTQNNIPQTTERTHN GWHQAWLLVFSVRSFYVAALFAVGLGCGIHWFC LAVFSVCAGHSTA VVS LPSQOHL SANMFVALHSYSAHGPDEL DLQKGE GVRVLGKCDG WLRGVS LVTGRVGI FPN NYV IPIFSTPSQLSGCREVGPTLVKPVVHK MGVYGE EGSISEGD\HGKAVPSNPS/VVPTAIVNPVRSTAGPGTLG QGS LRKGRSSMRKNGSLQRPLQSGIPTLVVGS LRRSPT/MGPSASAV PILPATGDPLPLSRGGGDGVQA/SPSRGSPPSRASAGAVRPGSTPR PAPSLWTKKSPSRVS/LLPKPPASAPPSILVKPENSRNGIEKQ/DQ NREISEIQALLPPNITLPYPTSGKPEQPSLPQCVPA
7704	A	27	211	FHIVQYFNFFVCLFVCLFETESTLSPRLEGSGVISAHCNL\TLPPGF NNSCASASRVAGTTQ
7705	A	27	211	FHIVQYFNFFVCLFVCLFETESTLSPRLEGSGVISAHCNL\TLPPGF NNSCASASRVAGTTQ
7706	A	1	514	LSQSEKNYYSSRFSPDSQYIDNRSVNSDRASQ/ARERAPRLNHPPE QIDSHSRLP HSAHPSGKPPSAPASAPQNVFSTTVSSGYNTKKIGKRL NIQLKKGTEGLGFSITSRDVTIGGSAPIYVKNILPRGAAIQDGR LKA GDR LIEVNGV\DLVGKSQEEVVSLLRSTKMEG
7707	A	65	517	DPRVRAAGILYEFTWNQFCDWYLELTGPVMNGGTEAKLRGTRHTLVT VLEGLLR LAHP IIPFITETI WQRVKVLCGITADTIMLQPPQYDASQ VDEAALADTEWLKQAI VAVRNIRAEMNIAPGKPLELLVAG\CTRNPN TSVNENRGFL
7708	A	2	507	EPVKKIFNYIIHVFNRIMDFKLFLV FVAGVFLFFYARTLSQSPTFY SSGTVLGVLM TLV FVLLLVKRFIPKYSTFRALMVGCFASVYIVCQL MEDLKWLR YDNRIYVLGYVLIVGFFSF\VVCYKHGPLADDRSRSLM WMLRLLSLVLVYAGVAVPQFAYAAIIL

7709	A	2	419	EPVKKIFNYMIHVNRMIMDFKLFLVVFVAGVFLFFYARTLSQSPTFYF SSGTVLGVMLTLVFLVLLLVKRFIPKYSTFWALMVGCFASVYIVCQL MEDLKWLWYENRIYVLSYVLIVGFFS\FVVGTSMSGPLADDKSRNL
7710	A	14	428	RPIRMAVKQKISMLCHVNPEQVICIHDVSSTYRVPVLLEEQSIVKYF KERLHLPIGDSASNLLFKWRNMADRYERLQKICSIAL\VGKYTKLRD CYASVFKALEHSALAINHKLNLMYIDSIDLEKITETEDPVKFHE
7711	A	61	204	GRYAYVWHCPQGPGLTPL\VADTSGAYFRREGLGSNYLGGRSPTEV S
7712	C	537	710	MCHHTQPIFVVFVEMRFYFVGQAGLEVLTSGDPPVSAAQSTGITGLS HRAQPSSVRF*
7713	A	788	896	KHG\WLGTVAHTCNPSTLGGQGGWIMRSGVQDQPGQ
7714	A	1	453	SPVPQLIVPTVLSVVLLEPFLGAPLPANRLWTHLWAPRAWKQSPWQA P\GLGRLPSSLGIGSCGAPGAYTRPDIRLHDKACPAEHGGGRGPGEA ASRPLTAPSPGGCPEGLGTTSPSPQSRTASSGGSYRSFTDPPPPPI CHHRRFFLTL
7715	A	48	421	DLQSSQGGQQRVQSWSPPRGIPQLPCAALYNYEGKEPGDLKFSK GDIIILRTQVDENWYHGEVNGIHGFFP\TNFVQI IKPLPQPPQCKA LYDFEGDKKADKCLPFAKDDVLTVIRRD
7716	A	2	494	LTLNITITPSLARNFYPLEGGRVLLDGKPI SAYDHKYLHRVISLVS QEPVLFARSITDNISYGLPTVPFEMVVEAAQKANAHGFIMELQDGYS TETGEKGAQLSGGQKQRVAMARALVRNPPVLILDEATNALDADSRDL IQHALS\GNLRKHRDFLSPPVWP
7717	A	2	721	EGKVEEPENPAAKEKCEGKEEEETDGS GKESKQCEAEASSVKNEL KGVEVGANTGSKSISEKGSSE\VKRKSWMNTNKSEESSQPEAGAVSR GKNFDEESNASMSTARDETRDGFYMEDGDP SVAQLLHERTFAFSWP KDRVMINRLDNICEAV\LKGKW\PNRRQMFDFQGLIPGYTPPTVDS PLQKRSFAELSMVGQASISGSEDITTSPQLSKEDALNLSVPRQRRR RRKIGN
7718	A	111	383	DRGLASFAQGLEVQWHNLSSLQPS\PPVLRRF/SPCLGLPRGCDYRP VPPHQANFCIVSRDGFYHVGQAGLELLTSSDPPTSQSQSAGITGV
7719	A	1	190	ENKEEGQLPSSFYEASII LTLKPKDKDSTKKS/SYRPT/SLMNFDAK\ IFNKMFTNRIQQYIERIIH
7720	A	1	2499	MAAAVAAPLAAGGEEAAATTSVPGSPGLPGRRSAERALED VATGT NLNRRLLKHFPRGAARSYDLS DITQADLSRNFPEVPEAACQLVSL GLSLYHNCLRLNLPALGNLTALTYLNLNLSRNQLSLLPPYICQLPLRV IVSNKLGALPPDIGITLGLSLRQLDVSSNELQSLPSELCLSSLRDLN VRRNQLSTLPEELGDLPLVRLDFSCNRVSRIPVSFCRLRHLQVILL SNPLQSPPAQVCLKGKLHIFKYLSTEAGQRGSA LGDLAPSRPPSFSP CPAEDLFPGHRYDGGLD SGFHSVDSGSKRWSGNESTDEFSELSFRIS ELAREPRGPRERKEDGSADGDPVQIDFIDSHVPGEDEERGTVEEQRP PELSPGAGDRERAPNSRREEPAGEERRRPTDLQLWQERERRQQQSG AWGAPRKDSLKPLRAVVGGA AVSTQAMHNGSPKSSASQAGGCSG AGSP\APAPASQEPLPIAGPATEPAPRPLGSIQRPNSFLFRSSSQSG SGPSSPDSVLRPRRYPOVPDEKDLMTQLRQVLESRLQRPLPEDLAEA LASGVILCQLANQLRPRSVFPIHVPSPAVPKLSALKARKNVESFLEA CRKMGVPEADLCSPDLLQGTARGLRTALEAVKRVGGKALPPLWPPS GLGGFVVYFVVLMLLLYVTYTRLLDPRSPQVAWEVAPSRMTPLAPWD PKYEAKAGPRPVVWSWGQTCGTGWGAQGA VRWPEAPVLCPPHPRGPT VAQEPRSQAGRCVTPHSGRCMKQPRAGVSGPWPLPQGTGMDSRRPQM QGSRWCAVKMSSRTLCCPGGSVFPCTCPRPPSR
7721	A	1	647	RPPVPVQVPDKDLMTQLRRVLESRLQR\PLPEDLAEALASGVILCQ LANQLRPR\SVFPIHVPSPAVPKLSALKARKNVESFLEACRKMGVPE ESLCQPHHILEEGAPGRG\LRLLIAAVVQRPAGPALGVKVGAAQGP RPGPREQKTRLGSALEKHVVVRVAVAWARLGLPRLAASGVEGLGGRT CGCRRCRVSRNKQKPEALWKRGC KIKKKL
7722	A	3	451	SRSLVQRGGIPLGGWRMGVRRRTGQVGPTMHPPPVSGASP/PPPPPPP

[illegible]

				QSLTPSPGWQSLGSSGAKPVYGFQCMTSDHAPTCQVDEPGNDDKVKL GPLTQRIKFRNLNGMKKQQVEVFENTDSEIRLDSSPSFVTCQPCDFGH DLNSQSHHSPCKDPEVSFRMTESGTSPPQPPQLDPLDAFPQKGLEPG DIAVLVLYFLFVLAVGLWSTVKTTRDTVKGYFLAGGDMVWVPGASL FASNVGSGHFIFLAGSGAATGISVSAYELNAHALKLPVRHAKKFGF QIPIVAFKDTFVQEVTPFVGAISTCKLVHGTVPQORQLPEGINVLKD SVKYAVFVNDLTALAVTQTGLGHHVSRTGTHAHWTQHIQPIPRLQER IQDPEEQPRRIDGHRCKVTCRMIPVLALRTGSSGGTSSLPCKEQCPT EKTRTQTLIVLRDPPVSAIKSPRGVRTPVPRQNADPPRAKQKQKA TMGLMCLPYLLPAECRAVTAHFTRPFLRFSRPLFSLHTSAGPGREV NPHSATPSGSTTPTGPQDGGPSNWTRRLGSLSVPPQFAGVLWHNGRTS RNHIGPTQQVDRTRDTPVCQIAPSGHSHRQKRNELIDPLCDMRKAI
7734	A	1	662	SLFASNVGSGHFIFLAGSGAATGISVSAYELNGLFVLMALAWVFLPI YIAGQVTTMPEYLRKRFGGIRIPILAVLYLFYIFTKISVDMYAGA IFIQQSLHLDLYLAIVGLLTAITAVYTVAGGLAAVIYTDALQTLIMLI GALTLMCYSFAAVGGMEGLKEYFLALASNRSENSSCGLPREDAFHI FR\NPLTSDLPWPGVLFGMSIPSLWYWCTDQGG
7735	A	3	315	PPATPAPGFGPGGPPRSPPTGLPRQPQGSLLQPAAPPAPLKSSGRPR HGGAGQPSQPGPGAGHRRGRTRAVPQAGPGPQRSSGHGSPWRRGGRA APGLCPPPP
7736	B	107	388	SKKLLFAGSRSQVLQPLVADCIKYRSCADCVLARDPYCAWSVNTSRC VAVGGHFGSLLIQHVMSTDTSGICNLRGSKKVRPTPKNITVVAGTDL *
7737	A	98	473	IRGDTISYTVRSPPPRAGREYA\MSTAGPPSPFSPLTQPPFALYREE GKYKIPLNPGAK/YVRAPPNPSQTHSRHLFPSPHPENIHRPWSRTR PTSPALPLKGHSTLSTPPPYVHRCPTFGGSGG
7738	A	2	433	GDTGHRERSLGLLREKHTWGPHPQATPQAAPVSSRYTQPGPQ\GWV TVQGGPPSRGEHPRPAAGLSQLLHLGVPDILGLQSGLDCEVTPKPSY SFPGTSGAGPPGTMGSSSLPGNGNWDEEAHTLPQGGEGMNEGGVPWRL IFR
7739	A	328	497	HNTDLFIY/CIYEMESCSVTQAGVQWRDLGSLQPPPLGCKQCSCLSL PSSWGLQVPATT
7740	A	1	374	MEKEEPGVERKKENRVKEVIHKNRKAEGPPAGAALPLGGRGEGP/S PEPPGGAAPRAGERCGQLAGASPEPAETGTREPRPRGASAARKLAA AAPVGLLRPGCPRAGRRAWPWPGKRLSEPRV
7741	A	34	367	ERPGPVGTLTTPQTQGPHPAGP/S/GRPGSLGFTWPYPGPCTWRPAW FPARPPAPGSIPTPGFCTHTLVSLDPGRDCPSPTGDCDSLCPHPD ASPGIKAFCAQGGKKKKKKK
7742	A	2	464	IRARNYKLRKVMVDGDIIPRV\KKDAHELILDFIRSRPLKQVSERR LRRLLPPKQRLHEKILEEIKQERRLRPVGE/ELGCPRVWLS/SPAS STPAPEMPSPPPASTCQSQMLGAAPSAR/VPRVLLKAPTLAEMEEMN TSEIRAQGRNVTAHNQ
7743	A	2	1004	TGPGVPMCQVGEDYGEPAPEEPPAPRPSREQKCVKCKEAQPVVIR AGDAFCRDCFKAFYVHKFRAMLGKNRLIFSCEKVLLAWSGGPSSSM VWQDLEGLSQDFAKRLRFVAGVIFFDEGAACGQSLEERSKTLAEVKP ILQATGFPWHVVALEELVGSEGAYKAAVDSF/RPAAACAGGPGVVL ARLKGRNSHPSP/SLDPQNLARPPAPAQTEALSOLFCSVRTLTAKKE LLQTLRTHLILHVARAHGYSKVMTGDSCTRLAIKLMTNLALGRGAFL AWDTGFSDERHGDVVVVRPMDHTLKEVAFYNRLFSVPSVFTPAVD KAPEKAS
7744	A	2	397	APDTPDSSKFQRSK/NYKGPLDPORGKIEDKVNKSKVILKEPGLEDL GTYSIDIVTDADEDISASHTLTEEELEKLLKSHEIRNPGIKLISGWN IDILERGEARLWLELEKLCPAELHLIVHNKEIFRLPNR
7745	A	1	850	QKKELGHVNLVDKSGKRTTSPSSDLDLDRSASKTELKAIHAHARIL ERRASRPGTPTSSASTETPTFEQNDVDEDI IDVDEPVAEPPDYVQP QLRRPFELLIAAAMERNPTQFQLPNELTCTPALPGSSKRRRKEETT

				KNVKKTQ\RELDHNGLVPLPVKVCFTCNRRRCRVAPLIQRDYCPLLFH MDCLEPPLTAMPLGRWMCNSNHIEHVVLNHNMTLSYRCQVDFRQDT VSQHVVKVDFLNRHKKHPPNRRVLQSVKRRSLKVPAIKSQNQVST P
7746	A	1	201	MKKKKEE/EEEEKEE EEEEEEEEEEEEEEEEEEEEKKKKKKHNIFKILSNLYIFIIIFYCSKK
7747	A	3	112	KRTRLGMMHAH/CNLSTLGGQGGRVTRSGVRDQPDLK
7748	A	1	1478	LTVIRRVDENWAEGLADKIGIFPISYVEFNAAKQLIEWDKPPVPG VDAGECSSAAAQSSSTAPKHSDDTKNTRKRHSFTSLTMANKSSQASQN RHSMEISPPVLISSSNPTAAARISELSGLSCSAPSQVHISTTGLIVT PPSSPVTTGPSFTFPSDDPYQAALGTLNPPPLPPPLLAATVLASTP PGATAAAAAAGMGPRPMAGSTDQIAHLRPQTRPSVYVAIYPYTPRKE DELELRKGEMFLVFERCQDGWFKGTSM\HTSK\IGGFPGN\YVAVPT RAVTNASQAKVPMSTAGQTSRGVTMVSPSTAGG\PAQKA\QGNVAG SP\SVVPAAVVSAAHQITSPQAKVLLHMTGQMTVNQARNVART\VA HNQ\ERP\TAAVTPIQVQNAAGLSPASVGLSHHSLASQPAPLMPG\ PATHTAASISIRASAPL\ACAAAAPLTSPTSITSASLEAEPGRIVTV LPGLPTSPDSASSACGSSATKPKDKSKK
7749	A	139	6503	LSGITKMTLHATRGAAALLSWVNSLHVADPVEAVLQLODCSIFIKIID RIHGTEEGQOILKQPVSERLDFVCSFLQKNRKHPSPECLVSAQKVL EGSELELAKMTMLLYHSTMSSKSPRDWEQFEYKIQAEALAVILKFVL DHEDGLNLNEDLENFLQKAPVPSTCSSTFPPEELSPSSHQAKREIRFL ELQKVASSSSGNNFLSGSPASPMGDILQTPQFQMRRLKKQLADERSN RDELELELAENRKLLEKDAQIAMMQORIDRLALLNEKQAASPLEPK ELEELRDKNESLTMRLHETLQKQCDLKTESQMDRKNINQLSEENGDL SFKLREFASHLQQLQDALNELTEHSHKATQEWLEKQAQLEKELSAAL QDKKCLEEKNEILQKLSQLEEHLSQLQDNPPQEKGEVLGDVLQLET LKQEAATLAANNTQLQARVEMLETERGQOEAKLLAERGHFEEEEKQQL SSLITDLQSSISNLSQAKEELEEQAQSAHGARLTAQVASLTSELTTLN ATIQQQDQELAGLKQQAQEKQAQLAQTLOQQEQASQGLRHQVEQLSS SLKQKEQQLKEVAEKQEAATRODHAQQLATAAEEREASLRERDAALKQ LEALEKEKAALKLEILQQQLOQVANEARDSAQTSVTQAQREKAELSRKV EELQACVETARQEQHEAQAQVAEELQLRSEQQKATEKERVQAEKDQ LQEQQLQALKESLKVTKGSLEEEKRRAADALEEQQRCISELKAETRSL VEQHKRERKELEERAGRGLEARLQQLGEAHQAETEVLRRRELAEM AAQHTAESECEQLVKEVAAWRERYEDSQQEEAQYGAMFQEQMLTKE ECEKARQELQEAKEKVAGIESHSELQISROQNELAELHANLALALQ VQEKEVRAQKLADDLSTLQEKMAATSKEVARLETLVKAGEREQATAS RELVKEPARAGDRQPEWLEEQQGRQFCSTQAALQAMEREAEQMGNEL ERLRAALMESQGGQEQEERGQEREVARLTQERGRAQADLALKAARA ELEMRLQNALNEQRFVATLQEALAHALTEKEGKDQELAKLRGLEAA QIKELEELRQTVKQLKEQLAKKEKEHASGSAQSEAAGRTEPTGPKL EALRAEVSKLEQQCQKQEQEQADSLERSLEAERASRAERDSALETQ QLEEKQELGHSQSALASAQRELAARFTKVQDHASKAEDWKAAQVARG RQEAERKNSLISSLEEEVSILNRQVLEKEGESKELKRLVMAESEKSQ KLEE\SCACCRQRQPATVPPELQNAALLCGRRRCRASG/REAQKQV ENLRQELTSQAERAELGQELKAWQEKFFQKEQALSTLQLEHTSTQA LVSELLPAXHLCQQLQAEQAAAQKRHREELEQSKQAAGGLRAELLRA QRELGELIPLRQKVAEQERTAQQLRAEKASYAEQLSMLKKAHGLLAE ENRGLGERANLGRQFLEVELDQAREKYVQELAAVRADAETRLAEVQR EAQSTARELEVMTAKYEGAKVKVLEERQRFQERQKLTAEVQEQLEVF QREQTKQVEELSCKLADSQASKVQQQKLKAVQAQGGESQQAQRLQ AQLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQONQELQEQRLS LEQLQKENKELRAEAERLGHELQAGLKTKEAETCRHLTAQVRSLE AQVAHADQQLRDLGKPVATDALKSREPQAKPQLDLSIDSLDLSCEE GTPLSITSKLPRTQPDGTSVPGEPASPISQRLPPKVESLESLYFTPI

				PARSQAPLESSLDSLGDFVQDSGRKTRSAARRRTTQIINITMTKKLDV EEPDSANSSFYSTRSAPASQASLRATSSSTQSLARLGSPDYNSALLS LPGYRPTTRSSARRSQAGVSSGAPPGRNSPFYMGTCQDEPEQLDDWNR IAELQQRNRVCPPHLKTCYPLESRPSLSLGTITDEEMKTGDPQETLR RASMQPIQIAEGTGITTRQQRKRVSLPHQGPPTPESKKATSCFPRP MTPRDRHEGRKQSTTEAQKKAAPASTKQADRRQSMAFSILNTPKKLG NSLLRRGASKKALSASPNTSRGTRRSPIATTTASAATAAAIGATP RAKGKAKH
7750	A	1	5290	MTLHATRGAAALLSWVNSLHVADPVEAVLQLQDCSIFIKIIDRIHGTE EGQQILKQPVSERLDFVCSFLQKNRKHPSSECLVSAQKVLGSELE LAKMTMLLLYHSTMSKSPRDWEQFEYKIQAEALAVILKFVLDHEDGL NLNEDLENFLQKAPVPSTCSSTFPEELSPSHQAKREIRFLELQKVA SSSSGNNFLSGSPASPMGDILQTPQFQMRRLKKQLADERSNRDELEL ELAENRKLLEKDAQIAMMQQRIDRLALLNEKQAASPLEPKLEELR DKNESLTMRLHETLKCQDLKTEKSQMDRKINQLSEENGDLSEFKLRE FASHLQQLQDALNELTEHSHKATQEWLEKQAQLEKELSAALQDKKCL EEKNEILQKLSQLEEHLSQLQDNPPQEKGEVLGDLVLETLKQEA TLAANNTQLQARVEMLETERGQOEAKLLAERGHFEEEEKQQLSSSLITD LQSSISNLSQAKEEELQASQAHGARLTAQVASITSELTTLNATIQQQ DQELAGLKQQAQKQQAQLAQLTQQQEQASQGLRHQVEQLSSSLKQKE QQLKEVAEKQEAQRDHAQQLATAAEEREASLREKDAALQLEALEK EKAALKLEILQQQLQVANEARDSAQTSVTQAQREKAELSRKVEELQAC VETARQEQHEAQVAEELQLRSEQQKATEKERVAKEDQLQEQQLQ ALKESLKVTKGSLEEEKRRAADALEEQQRCSSELKAETRSLVEQHKR ERKELEERAGRKGLERLQQLGEAHQAETEVLRLAEAMAAQHTA ESECEQLVKEVAAWRERYEDSQQEEAQYGAMFQEQMLTLKEECEKAR QELQEAKEKVAGIESHSELQISRQONELAEHLANLARALQQVQKEV RAQKLADDLSTLQEKMAATSKEVARLETVRKAGEQQEQLVKE PARAGDRQPEWLEEQQGRQFCSTQAALQAMEREAEQMGNELELRRAA LMESQGGQEEERGQQEREVARLTQERGRAQADLALEKAAARAELEMRL QNALNEQRVEFATLQEAALAHALTEKEGKDQELAKLRGLEAAQIKELE ELRQTVKQLKEQLAKKEKEHASGSGAQSEAAGRTPTGPKLEALRAE VSKLEQQCQKQEQADSLEERSLEAERASRAERDSALETLQGGQLEKA QELGHSQSALASAQRELAAPRTKVQDHSKAEDEWKAQVARGRQEAER KNSLISSLEEEVSILNRQVLEKEGESKELKRLVMAESEKSKLEE\S CACCRQRQPATVPQLQNAALLCGRRCRASG/REAEKQRVASENLQRE LTSQAERAEELGQELKAWQEKFFQKEQALSTLQLEHTSTQALVSELL PAKHLCCQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQRELGE LIPLRQKVAEQERTAAQLRAEKASYAEQLSMLKKAHGLLAENRGLG ERANLGRQFLEVELDQAREKYVQELAAVRADAETRLAEVQREAQSTA RELEVMTAKYEGAKVKVLEERQRFQEEERQKLTAQVEQLEVFQREQTK QVEELSKKLADSDQASKVQQQKLKAVQAQGGESQBEAQRLLQALNEL QAQLSQKEQAAEHYKLQMEKAKTHYDAKKQONQELQELRSLEQLQK ENKELRAEAERLGHLELQAGLKTKEAEQTCRHLTAQVRSLEAQVAHA DQQLRDLGKFQVATDALKSREPQAKPQLDLSIDSLDLSCEEGTPLSI TRSGGSLPPYVCLWSACCLSGCILVR
7751	A	241	6574	LSGITKMTLHATRGAAALLSWVNSLHVADPVEAVLQLQDCSIFIKIID RIHGTEEGQQILKQPVSERLDFVCSFLQKNRKHPSSECLVSAQKVL EGSELELAKMTMLLLYHSTMSKSPRDWEQFEYKIQAEALAVILKFVL DHEDGLNLNEDLENFLQKAPVPSTCSSTFPEELSPSHQAKREIRFL ELQKVASSSSGNNFLSGSPASPMGDILQTPQFQMRRLKKQLADERSN RDELELELAENRKLLEKDAQIAMMQQRIDRLALLNEKQAASPLEPK ELEELRDKNESLTMRLHETLKCQDLKTEKSQMDRKINQLSEENGDL SFKLREFASHLQQLQDALNELTEHSHKATQEWLEKQAQLEKELSAAL QDKKCLEEKNEILQKLSQLEEHLSQLQDNPPQEKGEVLGDLVLETL LKQEAATLAANNTQLQARVEMLETERGQOEAKLLAERGHFEEEEKQQL

				SSLITDLQSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLN ATIQQQDQELAGLKQQAQKQQAQLAQTLOQQEQASQGLRHQVEQLSS SLKQKEQQLKEVAEKQEATRODHAQQLATAAEEREASLRERDAALKQ LEALEKEKAAKLEILQQQLQVANEARDSAQTSVTQAQREKAELSRKV EELQACVETARQEQHEAQAQVAEELQLRSEQQKATEKERVQAEKDQ LQEQLQALKESLKVTKGSLEEEKRRAADALEEQQRCISELKAETRSL VEQHKRERKELEERAGRKGLEARLLQLGEAHQAETEVLRRLEAEM AAQHTAESECEQLVKEVAAWRDGYEDSQEEAQAQYAMFQEQMLTKE ECEKARQELQEAKEKVAGIESHSELQISRQONKLAELHANLALALQQ VQEKEVRAQKLADDLSTLQEKMAATSKEVARLETLVRKAGEQQETAS RELVKEPARAGDRQPEWLEEQQGRQFCSTQAALQAMEREAEQMGNEL ERLRAALMESQGGQQEERGQQEREVARLTQERGRAQADLALKAARA ELEMRLQNALNEQORVEFATLQEALAHALTEKEGKDQELAKLRGLEAA QIKELEELRQTVKQLKEQLAKKEKEHASGSAQSEAAGRTEPTGPKL EALRAEVSQLEQQCQKQEQADSLERSLEAERASRAERDAETLQGG QLEEKQELGHSQSALASAQRELAAFRTKVQDHKAEDEWKAQVARG RQEAERKNSLISSLEEEVSILNRQVLEKEGESKELKRLVMAESEKSQ KLEESCACCRQRPATVPELQNAALLCGRRCRASGREAEKQRVASEN LRQELTSQAERAELQELKAWQEKFFQKEQALSTLQLEHTSTQALV SELLPAKHLCCQLQAEQAAAQKREHRELEQSKQAAGGLRAELLRAQR ELGELIPLRQKVAEQERTAQQLRAEKASYAEQLSMLKKAHGLLAEEN RGLGERANLGRQFLEVELDQAREKYVQELAAVRDAETRLAEVQREA QSTARELEVMTAKYEGAKVKVLEERQRFQBERQKLTAQVEELSCKLA DSDQASKVQQQKLKAVQAQGGESQQAQRFQAQLNELQAQLSQKEQA AEHYKLQMEKAKTHYDAKKQONQELQELRSLEQLQKENKELRAEAE RLGHQLQQAGLKTKEAEQTCRHLTAQVRSLEAQVAHADQQLRDLGKF QVATDALKSREPQAKPQLDLSIDSLDLSCEEGLTSLITSKLPRTQPD GTSVPGEASPISQRLPPKVESLESLYFTPIPARSQAP/LESSLDSL GDVFL\DSGRKTRSAARRTTQIINI\TMTKK\LDV\EEPDP\SAPNLS FYS\TRSAPASQASLRAT\SST*SLTRLG\SPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFYMGTCDQDEPEQLDDWNRIAELOQ RNRVCPPHLKTCYPLESRPSLSLGTITDEEMKTGDPQETLRRASMOP IQIAEGTGITTRQQRKVSLEPHQGPPTPESKKATSCFPRPMTPRDR HEGRKQSTTEAQKKAAPASTKQADRRQSMFAFSLNTPKKLGNSLLRR GASKKALSKASPNTSRGTRRSPRIATTTASAATAAAIGATPRAKGKA KH
7752	A	775	1128	REGLYLSRFPFHSLKLPRT\QPDGTSVPGEASPISQRLPPKVESLES LYFTPIPARSQAPLESSLDSLGDVFLDSGRKTRSAARRTTQIINITM TKVRLGQGLQGSNSHFLSRASLQ
7753	A	331	531	LKIFFFFPSGGDMSKNVSQSQMAKLNQQMAKMMDPRLV\HHMGGMAG LQSMMRQFQQAAGNMKGMM
7754	A	1	1517	MVLADLGRKITSALRSLSNATIINEEVLNAMLKEVCTALLEADVNIK LVKQLRENVKSAIDLEEMASGLNKRKMIQHAFVKELVKLVDPGVKAW TPTKGKQNVIMFVGLQGGSGKTTTCSKLAYYYQRKGWKTCLICADTFR AGAFDQLKQONATKARIPFYGSYTEM DPV I IASEGVEKFKNENFEI I I VDTSGRHKQEDSLFEEMLQVANAIQPDNIVYVMDASIGQACEAQAKA FKDKVDVASVIVTKLDGHAKGGGALSAVAATKSP I I F IGTGEHIDDF EPFKTQPFISKLLGMDIEGLIDKVNELKLDNEALIEKLKHGQFTL RDMYEQFQNMKMGPFQSILGMI PGFGTDFMSKGNQESMARLKKLM TIMDSMNDQELDSTDGAKVFSNNSGRIQRLARPSCVSTSDVQELLTQ YTKFAQMVK*MGGIKGLF\KGGDMSKNGARSQIAK\LNQQMAKMMDP R\VLHHMGGMARLQSMMRQ\FKQGAAGNMKGMMGFNNM
7755	A	42	451	FGLFNRLPYPPQHPKPHYSRIPGA/HAPPGQNPST\FLSPLYCWGP SSKSPGAPKRCPSISITPPPSATPPRTLTGSWPGQRCQKDGAEQSYQ VRQDPTASPPAQQSRLPSWSGNQTYLQGLHGRGPRARTLQLPG
7756	A	3	359	LLIHSSTHPPTYPPPIHPPGHFFLPLFFPFFFSFSPSFHPSTHPLIH

				LSTYPPIHPSVYPPVPLSLSVYSSIHLPTEYFLQPVAH/RRSHGR ISSMPGEQSPIPRLWKSPSSKPPFPW
7757	A	1	1668	MLVHTQPPEVHQYNHSSAATRSRFQRLQLQLIWGWSQVLPMSAFYQI IIQASGLRLHACVTPGAGTHSLPFLPSVGNLPSNKGNSRVYCFFAAD LFDILLPMLNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPA CEGRMLETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSK LEELSRMIVEGCDILLDTSQTFIRQGTMKNSNTIIVKHEWGRQLHSD WTLLLSGPDILCSSKEDRSAWPTAVAVPSADDTQAKAQEKAL\SKP FHIRLGTMSQEQS*SLHQRTQE\GKLPCSGHHRFTTLQIPLNSSAPP LSTAWRTDGGQCPLLCFTGFCFCNSHSCSRWE\PEEEDDCLPTS QARCNEYVGLRKSIMLVQKKDKKNITCRSLTPSEEGLTIVKLVFS EIMFNLDKFIVVEPPDAAFTVLLAPSRQEKAAMSDISQVDNIR CNGLMTIVFEENSKVTVPHMIKAKVNGCTMSHLDNSLTLPTDTEQG RSSSWTAGHVKAPCPLHAQLPLLASLFLQELQAFARMSPPY
7758	A	1	2247	MTILPKAIYKFNAIPIKIPPSFFTELDKIIILKLIWNQGAHIKARL SKKNKSGDITLPDFKLYYKATVTKTAWYWKQRHVDQWNRNENPEIN PNTYSQLIFNKRKNVRCREGTAVQRMSSKVSEAGYICNQALPTMT GVRRLALETASLGDSPLAHAKATDFELNNELKMNVLRRARRSLARPR PSSPRKESRREYPQAVYFSSVHVFASSPLMQQHMLVCDVLATGLAL SQDDQDDIHLKLEDIIQMKHSLRVSANPPQQQGSAAALAVLEVDIIPK AGCVYVCLSSCLIWGSQVLPMSAFYQIIIIQASGLRLHACVTPGAG THSLPFLPSVGNLPSNKGNSRVYCFFAADLFDILLPMLNIYQEFVRN HQYSLQVLANCKQNRDFDKLLKQYEANPACEGRMLETFLTYPMFQIP RYIITLHELLAHTPHEHVERKSLEFAKSKLEELSRVMHDEVSDTENI RKNLAIERMIVEGCDILLDTSQTFIRQGTMKNSNTIIVKHEWGRQYI LTGRSSSAARTFSAAPRRTTEEDDCLPTSQARCNEYVGLRKSIMLV QKKDKKNITCRSLTPSEESDPRERLTMKMGAKLNSSAPALNRNFP VGSKPLPMSNLVASQIMNYADVSSRANAIEKWAVADICRCLHNYN GVLEITSALNRSIYSAAAA VVWAGWRGVKLPLHFPDSLAAAMVLDV NSVPLIDALGKTQKAEVGAIFLWLKVSHGDVSALGQCQHPALGF
7759	A	1	3711	MQKSVRYNEGHALYLAFLARKEGTRGFLSKKTAEASRWHEKWFAFY QNVLFYFEGEQSCRAGMYLLEGCSERTPAPPRAGAGQGGVRDALD KQYYFTVLFGHEGQKPLELRCEEEQDGKEWMEAIHQASYADILIERE VLMQKYIHLVQIVETEKIAANQLRHQLEDQDTEIERLKSEIIALNKT KERM RPYSNQEDDEPDIIKKIKKQVSFMRGWLCCRKWKTIQDYICS PHAESMRKRNIQVFTMVEAESEYVHQLYILVNGLRPLRMAASSKPK PISHDDVSSIIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDIL LPMLNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLEELS RVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQGS LIQVP SVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRSSGGKLHLK TGGVLSLIDCTLIEEPDASDDDSKSGSQVFGHLDFKIVVEPPDRAAF TVLLAPSRQEKAAMSDISQVDNIRCNGLMTIVFEENSKVTVPHM IKSDARLHKDDTDICFSKTLNSCKVPQIRYASVERLLERLTDLRFLS IDFLNTFLHTYRIFTTAAVVLGKLSDIYKRPFSTIPVRSLELFFATS QNNRGEHLVDGKSPRLCRKFSSPPPLAVSRTSSPVRARKLSLTSPLN SKIGALDLTTSSSPTTTTQSPAASPPPHGTGQIPLDLRGLSSPEQSP GTVEENVDNPRVDLCNKLKRSIQKAVLESAPADRAGVESSPAADTTE LSPCRSPSTPHRLRYRQPGGQTADNAHCSVSPASAFIATAAAGHGS PPGFNNTERTCDKEFIIRRTATNRVLNVLRHWSKHAQDFELNNELK MNVNLNLEEVLDPDLLPQERKAAANILRLASQDDQDDIHLKLEDII QMTDCMKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLQGWMKL DKNERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWAVA DICRCLHNYNGVLEITSALNRSIYRLKKTWAKVSKQTALMDKLQK TVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGTPNFTEEG LVNFSKMRMISHIIREIRQFQOTSIRIDHQPKVAQYLLDKDLIDED

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				TLIELSLKIEPRLPA
7760	A	1	226	SLEFSQSKLQYLSRVKH\DEVSDTENIRINLAIERMIVEGCDILLDT SQTFFIRQWDHENQQHNHASKARVGQAVTF
7761	A	41	1065	GRLGPHWSPQREGEAQAWQAAGPEPCPAGRQLRPGEKSSTAAPGPGA KLPPTARGQRGRPAALSAGPTEPAEPTPTRNSGWPASAPPV/PRWGQ PLLGVPGEAGRYSA\APSLSALRFPWWPQDVPVAVQSATDDAYEA LSPSSCAFAM\PSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPS GEPGREKKSNSPKHVYSIASKGSKFELVTHGDASTENDVLNPISE ETTTFTTGGFTPEIGKKKHTSTPFWSIKPNVSVIVLHAEOPYIENE EPEPEPEPAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDKSTGI GDLYRIRRCSSALR
7762	A	3	344	KERSREKTGGGDLQREVAREDRRWRRS\QREDAREDRRWRRSSERG RLRRQAVABIFRERDAREDRRWRRSSERGRPRRQ/RGGGDLQREDAR EDRRWRRSSEREMPEKTGGGG
7763	A	205	340	NPYIYSQLFFDKGTNIHWG\RDSL FNKCCSENLSII\RKIKLDP
7764	A	1	668	GDPGAGPGDHNRFDCGPQPPPPPKCELLHVAIVCAGHNSSRDVITLV KSM LFYRKNPLHLHMTGAVARNIMETLFHTWMVPAVRVSFYHADQL KPQVSWIPNKHYSGLYGLMKLVLPALPAELARVIVLDTDTFASDI SELWALFAHFSGVILLRLDRLRQAGWEQMWRLTARRELL/GLPATSL ADQDIFNAVIKEHSGLVQRLPCVWNVQLSNHTLAE
7765	A	3	1289	INFPTTSGLDGDPGAGPGDHNRS DCCPQPPPPRCCELLHVAIVCAGH NSSRDVITLVKSM LFYRKNPLHLHVTDAVARNILETLFHTWMVPAV RVSFYHADQLKPQVSWIPNKHYSGLYGLMKLVLPALPAELARVIVL D TDVTFASDI SELWALFAHFSDTQAIGLVENQSDW\YLG NLWKNHMP WPALGRGFNTGVILLRLDRFR\KAGWEQMWRLTARREL\LSLPATSL ADQDIFNAVIKEHSGLVQRLPCVWNVQLSDHTLAERCYSEASDLKVI HWN SPKVL\VKNNHVEFFRKIYLILLENQGNLLLEEVFLCPSQPPT \GADQLQ\RPLPQLDEEDPCFEFRQQQLTVHRGH\LLFLPHEPPPPR PHDVT LVAQLSMDRLQMLEALCRHCPGPVSLALYLTDAEAQQFLHFV EANGVGIDRV
7766	A	530	820	RVSRGRKWFFIALKRMPAMKKAMNLFGLGSNVRTVHPEGFTVYISTH ISFPSLSGYRTGLRSFGLVKQKKSPIRMPVCVYNPCVSI VSRMAQAS SL
7767	B	1	954	MATAATIPSVATATAAALGEVEDEGLLASLFRDRFP EAQWRERPDVG RYLRELSGSGLERLRREPERLAEERAQLLQOTRD LAFANYKTFIRGA ECTERIHLRFGDVEASLGRLDRLPSFQQSCRS PRAARNAVS IMAAG AGTAGPASGPGVVRDPAASQPRKRP GREGGEGARRSDTMAGGGSSD GSGRAAGRRASRSSGRARRGRHEPGLGGPAERGAGEARLEEAVNRWV LKFYFHEALRAFRGSRYGDFRQIRDIMQALTFFRGTLDSKQELSL DLSSSEIKNIQVNITYSLRSRDCANFDILYDIKPF*
7768	C	97	408	MKTKVQPRLTVRVARNCSPKNKAHDNKQNSWEEDSQITEPSAGLNS SQEAVSAPPSKPTVFNQPLPGEKNPKYEDLLCRNFGAGWWSWLGLVL LPGIKETFS*
7769	A	1694	1868	PLIACSFFLFLFFFFLQSLG SVHPGLGV\QWRDLGSLRPPFPGLTQ FSCLSLPRSWN
7770	A	106	317	CSAETEREIGRRK*CIQESSSPSPLSIKKCPICKAD*YL*SHLGATA DAAPLFQLSSL*QDLPSYREADL
7771	A	321	451	KIMLCFQLTTCPRMMSITSSAMWMMRVSV EQVFLSNSVQKMR
7772	A	2516	2719	FVKSKALAFFLSFFFFFLKQSLSVTQAGVQW\ PVDLSQLP LPPRFKR FSCLSLPSSWDYRCVPQCPAN
7773	A	3	282	LVLRLRNSRKELNVFLFEFTPGRDTADGVSQELFSAGLVDGHDVFIV AANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFAQVSVS
7774	A	1	1126	MRPGSLTDVTL EPRSEGGKEKSI PERRNGPCKDPGAAACKLCLTSVL FATNRHMYLHNL LRLRQVSRASRSALTQSSGTPAMYQCSKTYIFIQ GIQVDYQEVHTGPLSIEGSM LDIIKYI\ VNRGEHKNGVLEEAIAT ILKEV\LEGLDYLHRNGQIHRNSRKELNDIRFEFTPGRG PKGNDGEC

				DEKHTTVLMRVEQQWDHTERKTQTQMSTEAKVNDTADGVSQELFSAG LVDGHDVVIACPSRNLRLFIGIISTFPGAQAKTLGIVLDFSHTSH PTHNLNVPRIPLLTISHPITFQAPLNSQLSSCIHPFAAIPASVLASL QPVLISTARDPGTSHYSSALGFIGQIPAYMELSPVIGELCLSKVTE
7775	A	2	1622	AATGKQALHCIRMSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSH WMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLT KTEFEDIKQLVKRWAEPLKDTFWSYFSQVQEIMWTFNDILRKFCCKD IVSNKKLMKKLQESRFDVVLADAVFPFGELLAELLKIPFVYRPRFSP GYAIEKHSGGLLPPSYVPVVMSELSDQMTFIERVKNMIVLYFEFW FQIFDMKKWDQFYSEVLGRPTTLSETMAKADIWLIRNYWDFQFPHP LPNVEFVGGLHCKPAKPLPKEME EFVQSSGENGVVVFSLGSMVSN TS EERANVIASALAKIPQKVLWRF DGNKPD TLGLNTRLYKWIPQNDLLG HPKTRAFITHGGANGIYKAISPRIPMVGVP L FADQPDNIAHMAKAGA AVSLDFHTMSSTDLLNALKTVINDPLYKENAMKLSRIHHDQPVKPLD RAVFWIEFVMRHKGAKHLRVA AHDLTW FQYHSLDVTGFL LACVATVI FIITKCLFCVWK FVRTGKKGKRD
7776	A	1	698	MAAKLVGIEFDPCWVKMLMEKGHQKTREHNP SMEQSEKAGVTDN IQ GKTKALAGSRQSVANGKNSHCKENV TWLLIIHYVQPMKPYEVFWIEF VTHQKATKYL CQLPTTSPDAVFPFGELLAELLKIPFVYSLRFS PGYA IEKHSGGLLPPSYVPVVMSELSDQMTFIE/RGRPTTLSETMAKADI WLIRNYWDFQFPHP L L P N V E F V G G L H C K P A K P L P K T L G H G W D R A P
7777	A	1	1584	MSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSHWMNIKTILDELV QRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLTKTEFEDIKQLV KRWAEPLKDTFWSYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQ ESRFDVVLADAVFPFGELLAELLKIPFVYRPRFSPGYAIEKHSGGLL PPSYVPVVMSELSDQMTFIERVKNMIVLYFEFWFQIFDMKKWDQF YSEVLGRPTTLSETMAKADIWLIRNYWDFQFPHP L L P N V E F V G G L H C K P A K P L P K E M E E F V Q S S G E N G V V V F S L G S M V S N T S E E R A N V I A S A L A K I P Q K V L W R F D G N K P D T L G L N T R L Y K W I P Q N D L L G H P K T R A F I T H G G A N G I Y K A I S P R I P M V G V P L F A D Q P D N I A H M K A K A G A A V S L D F H T M S S T D L L N A L K T V I N D P L Y K E N A M K L S R I H H D Q P V K P L D R A V F W I E F V M R H K G A K H L R V A A H D L T W F Q Y H S L D V T G F L L A C V A T V I F I I T K C L F C V W K F V R T G K K G K R D
7778	A	2	1627	AATGKQALHCIRMSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSH WMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLT KTEFEDIKQLVKRWAEPLKDTFWSYFSQVQEIMWTFNDILRKFCCKD IVSNKKLMKKLQESRFDVVLADAVFPFGELLA\ELLKIPFVYRPRFS PGYAIEKHSGGLLPPSYVPVVMSELSDQMTFIERVKNMIVLYFEF WFQIFDMKKWDQFYSEVLGRPTTL\SETMAKADIWLIRNYWDFQFP P L L P N V E F V G G L H C K P A K P L P K E M E \ E F V Q S S G E N G V V V F S L G S M V S N T S E E R A N V I A S A L A K I P Q K V L W R F D G N K P D T L G L N T R L Y K W I P Q N D L L G H P K T R A F I T H G G A N G I Y E A I Y H G I P M V G V P L L A D Q P D N I A H M K A K G A A V S L D F H T M S S T D L L N A L K T V I N D P L Y K E N A M K L S R I H H D Q P V K P L D R A V F W I E F V M R H K G A K H L R V A A H D L T W F Q Y H S L D V T G F L L A C V A T V I F I I T K C L F C V W K F V R T G K K G K R D
7779	A	1	187	SGRPFFFFGLPFLFFFFF*DRVSLLLPRLQCNGTISAHCNLCPLG SSDSPASASRVAELP
7780	B	436	711	DVYKIGGIGTVPVGRVETGVLPKPMVVT FAPVNVTTVEKSVEMHHEA LSEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAAGFTAQ*
7781	B	26	384	MHHEALSEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAAGF TAQV I I L N H P G Q I S A G Y A L Y W I A I V D M V P G K P M C V E S F S D Y P L G R F A V R D M R Q T V A V G V I K A V D K K A A G L A S *
7782	A	3	523	FAPVNVTTVEKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GD/SKNDPPMEAAAGFTAQV I I L N H P G Q I S A G Y A P V L D C H T A H I A C K F A E L K E I D R R S G K K L E D G P K F M V P G K P M C \ V E S F S \ D Y P L G R F A V R D M R Q T V A V G V I K A V D K K A A G A G K V T K S A R K L Q K A K

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7783	B	32	188	MVVTFAPVNVTTTEVKSVMHHEALSEALPGDNVGFNVKNVSVKCIW FLASPX*
7784	B	60	209	MHHEALSEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGF TAQ*
7785	A	3	313	RYEEVVKEVSTYIKKIGYNPDVAFVPI SGWNGDNMLEPSANMPWFK GWKVKTRKDGNASGTTLEALDCILPPTRPDKPLRLPLQDVYKIGGI GTVPVQKAK
7786	A	13	555	INPPPPTVPVGRVETGVLKPGMVVTFAPVNVTTTEVKSVMHHEALSE ALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFTAQVILN HPGQISAGYAPVLDCHTAHIACKFGRVETGVLKPGMVVTFAPVNVTT EVKSVMHHEALSEALPGDNVGFQCEVCVQCQCSSWQRCW
7787	A	3	366	IGY/NPDTVACV/PILGWNGDNMLEQSANMPWFKGWKVKTRKDGNASG TTLEALDCILPPTRPDKPLRLPLQDVYKIGGIGTVPVGRVETGVL KPGMVVTFAPVNVTTTEVKSVMHHEAQKAK
7788	A	1	513	EAGISKNGQTREHALLAYTLGVKQLIVGVNKM DSTEPPYSQKRYEEI VKEVSTYIKKIGYNPDVAFVPI SGWNIACKFAELKEKIDRRSG\KK LEDGPKFLKSG\DAIVDMVPG\KPMCVESFS\DYPLGRFAV\ RDM RQTVAVGVKAIDKKAAGAGKVTSAQ\KAQKAK
7789	A	1	1099	MQSERGITIDISLWKFETSKYVITI IDAPGHRDFIQNMITGTSQADC AVLIVAAGVGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKM DST EPPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPI SGWNGDNMLEPS ANMPWFKGWKVKTRKDGNASGTTLEALDCILPPTRPDKPLGLPLQD VYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTTTEVKSVMHHEAL GEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFPAQVIL LNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKF LKSGDAIVDMVPGKPMCVESFSDWQGHQVCESG
7790	A	1253	2560	SLVMLPLFDMVPGQAHVLLRASQDYPPFGSLCWFVIMRTDSCGWVSI KSSGQKRLELIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVKQLIVGVNKM DSTEPPYSQKRYEEIVK EVSTYIKKIGYNPDVAFVPI SGWNGDNMLEPSANMPWFKGWKVKTRK DGNASGTTLEAVDCILPPTRPDKPLRLPLQDVYKIGGIGTVPVGR VETGVLKPGMVVTFAPVNVTTTEVKSVMHHEALSEALPGDNVGFNVK NVSVKDVRRGNVAGDSKNDPPME\AAGFTAQVIL\LNHPGQISA\GY AP\VLDCHTAHIACKFAELKEKIDRRSGKKLEDGP\KFLKSGDA/AP LVDMPV\GKPHVCLRSFS\DYPLGRFAVRDMRQTVAVGVIKSS\VD KKAAGAGKVTSAQKAQKAK
7791	A	39	362	AEKWARNMPFFPDLMQTDQVSLRLTWSELFGLNAAQCSMPLNEA\ P LLAAAGLQAYPMSADRRVAFMDHIRIFQEQA EKFRALHVGSP EKQCL KAIVLFTSNTWGRG
7792	A	19	386	FISSIKFIMSFNFTSLFHHFISLGQFISSHYISSK/SHFISFHVISS VHLIFSSHFMGSSQQLFSSDHFIIISCHRFMSYLLRSVQFHFNISFH YFRSSHLITSCHHIISSCNQNSSSSQHFI S
7793	A	16	451	TQGS HQSPPPGS\PHAAHTCCPGRGGEAGGTGSLCCLLGQHTREPAA LKDWPGGRPEGHKVRSDPPGRPASSTVQLKGLSGERDGCPLRRGPG PHRAEGSPSRALRPPGTRGNTATRTPVSSGMRAASCQAWRNEVRSLM VQAP
7794	A	1	427	VSCAPGYVLKGQASIKCVLGHPSHWS DPPPICRAASLDGFYNSRSLD VAKAPAASSTLDAHTAAAI FLPLVAMVLLVGGVYFYFSRRREN MKS PSRWGQSREVNSDLHHS PAARLLASCCPSTSCIYHLGGDAKPVLRP L
7795	A	1	330	FFFFFFQKHFNKETTEIKDCSLAGAQTPYNTLHVQSGFQAPAGRLP GALLPPVPCQIPGSLDYWLLSRNMPTSPYPITQWVKRESLTSGLGI GRRGLLGVKDVCNSLN
7796	A	3	1229	SPPSPL\ PGLASQDSRPVFPSPTPMAAVPTQPQSKEGPWSPES SP MLRITAPLPPGSPMAVPTLGPGEIASTTPPSRAWTPTEGPGDMGRP WVAEVVSQGAGIGIQGTITSSTASGDDEETTTTTTIITTTITTVQTP

				GPCSWNFSGPEGLSDSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVO NISLREGETVTVEGLGGPDPLPLANQSFLLRQVIRSPTHQAALRFQ SLPPPAGPGTFHFHYQAYLLSCHFPRRPAYGDTVTVTSLHPGGSARFH CATGYQLKGARHLTCLNATQPF/WDLKEPVCIAACGGVIRNATTG\ RIVSPGFPNGYSNNLTCHWLLEAPEGQRLHLHFKEVSLAEDDDRLII RNGDNVEAPPVYDSYEVEYPPPPPLQPHYHRVSV
7797	A	110	343	FVLFPPTKVYEGERAMTKDNLLGKFELTGIPAP*GVPQIEVTFDID ANGILNVSAVDKSTGKENKITITNDKGKEA
7798	A	1	335	NPCTREDHQYAPLDPKHGHLPPRMPPSERLMAAEAFYSPPYHDPRT NSEGWEHTGLYESFRAKLRSRRKGPEKRNSGPSRSRNRSKSRGRSS SRNSRS*SSGSYSRS
7799	A	110	409	PWYLAQAGYEVVGLDWTVPAPKKARECVGKTVTLQGNLDPICALYASEE BIGQLVKQMLDDFGPHRYIANLGHGLYPMDPEHVGA FVDAVHKHSR LLRQN
7800	A	40	621	HTDTPHPHLIARPQGFPELKNDTFLRAAWGEETDYTPVWCMRQAGR YLPEFRETRAAQDFSTCRSPEACCELTLQPLRRFPLDAAIIFSDIL VVPQALGMEVTMPGKGPSFPEPLREEQDLERLRDPEVVASELGYVF QAITLTRQRLAGRVPLIGFAGAPVMWDRAGRGAGRSLWKVWGRQKE GSVWLL
7801	A	1	338	GTSFYLYRKGYLSLSKGVPM SHYAGTLLLLLAGVACLRGIVRWTPH YRKMTIP*ASHRNQSSKYPRHVANYNCDFRSWPDDFHCDEPITRNE SQGGPIRRSVHTASPKPM
7802	A	1	390	ILDCHTDDSGTYRAVCTNYKGEASDYATLDVTGGDYTTYASQRIDEE VPRSDFPPELTRTEAYAVSSFKKTSEMEASSSVREVKSQMTETRESLS SYEHSASA*MKSAAL*EKSLEEKSTRKIKTTLAAR
7803	A	3	235	VNSABEAEQANTNLSKFRKVOHELDE/AVALPHPDLLIQLVLHLAD EAEERADIAESQVKNLRAKSRDIGTGGLNEE
7804	A	2	561	MRPHRLDEAEQIALKGFFKQLQKLEARGRELENELEAEQKRNAESVK GMRKSERTPSKELTYQTEEDRKNLAAACRTLVDKLQKA\KAYKROA EEAEQSPPTNL\SKFRKV\QARAGLRAEERADIAESQVKNLRAK\ RDIGTKGLEMKELAFATSLNLAPPLGRCPANAPCWSLCSNLFGREAE
7805	A	3	303	GRRPPALIDSRSPSPASPTQ*CRPPSFPGPAPPPRLWLAPPFCPPP PPHGYGPPFARKRRGAALGLTRVLPSPGSAVRRSPGPGPGSACDKVF RTTSR
7806	A	190	389	RRTYTSHLLACLRLQGLAFSPRLECGGKIRAHCSLQLYGSSDPPT*AP QTAGTKQHNQRIACNADN
7807	A	3	271	FFLRQSHSVT\RLCTGAI*AHCNLCPLGSSDSPASAS*VAGITGMC HHARLIFVLVETGFHHVGQAVLELL/NLMICPPQPPKVLGLQA
7808	A	610	923	FYLSEAEFFFFFETES/HLLSPRLECSGMMSAHCNLRPLGSSDSP ASAS*VAGITGGHHPAQLIFVAF/MYQPGFCHVGQAGQQLLA*VIC LPQPPKVLGITGA
7809	A	487	796	LSIFFFFFEGRGAIVANVSLNFPKSKPPPSLSKEPGTTGAAPPRE IFFPPKTRLGFALHPGSPPPGPWAPLWSKGEKVGILKKHKVGRGR GFSPVSPPF*KPPPSLSKEPGTTGAAPPREIFFPPKTRLGFALHPG SPPPGPWAPLWSKGEKVGILKKHKVGRGRGFSPVSPPF
7810	A	1	340	GTSQVLTLTIAEV**NLG*VGCK*CKHTEAKRMPCAEDYLSVVHEQI CVAHENTPVSDRVPIRCPESLAIRLPCFSALEVDETYGD*EYNAEAF TLHADICTLSEKERPIKKQ
7811	A	3	337	IESSLHQVESMHGAGNAKKNWQ/RIQEHFFFATFHPLKDYCL/EGTN LVEADNQAETDQVKKIIPWNSRVSDL\DL\ELLFQDRAARLGK\SI SR\LIRCGPSLHSDKPTNFREG
7812	A	3	927	YGEENLKTICTFLAVLSHLDIITQNIPEKKLILKQALIVVLQWCFN HNFSVRLYALVALKKLWTVCKVLSVEEFDALTPVIESSLHQVESMHG AGNAKKNWQRIQEHFFFATFHPLKDYCLETFYILPRLSGLIEDEWI TIDKFTRFTDPLAAGFQWYLSQTQLSKLPGDWSQQDIGNLVEAD NQAET\DVQKKIIPWNSRVSDLDLELLFQDRAARL\GKSISRILIVV

				ASLIDKPTNLGGLCRTCEVFGASVLVVGSLQCSISKQFQHLVSVAEQ WLPLVEVKPPQLIDYLQKKTEGYTII
7813	A	3	362	ATCSDQSVKVDKSESGDWHCTASWKTHSGSVWRVTWAHPEFGQVL AFCTFDRSSAVWDEILSESRDNL*GHTHWVKRTTLEDSIVSATCV*S FLSHVGIMLLSCGTFPPACICGVFP
7814	A	9	307	SHLLRSRLQENRLNPRGGGCNQPRSGHCTPAWATRAKLHLKKQTNKM LANLIQOHKIKKVIHHYQVGFTPGMQG*FNICKSVSVIYHINRTTHKN VAAAA
7815	A	3	219	AASTMPMSFEWQRQ*RFPPFYTLQPNVNTRQKQLTA*CSLVLSLCRL HKQSSMTLIKTRLTSDSITVMLDC
7816	A	15	335	QHPWERFHVTKDRINTVERQETDWKIFATYLMKKV*ISRKCYNKYKL VRKKQLNRKWAKEKNKQSQKKQSGQ*TKTVQPQ*NKRAN*RYYLS PISLAKSNKLN
7817	A	1	331	GLIEILVIYVSDTPVK*DV*SDIFEQ*AYGKIDGGNDVCDLQSSEGT NTKMKNNNEEMMIGEAMDETGHGDETENEGISTKTSKPDEAETNMLIA EMDTFVCDTVE MSTEG
7818	C	51	200	MSTPXXX XS*
7819	A	3	219	MLAGCSRTPELR*STHCSLPKCWDYRRAHNAQPFLTLN*RSETRRSL *F*IMWLPLEFLGFPLESQQGCTA
7820	A	1	358	VHCLVPDLLQSNNPCYWGVMKYAAEALLEGKPEGTFLLRDSAQED YLFVSFRYSRSLHARIEQRNHNFSFDAHDP*VFHSPDITGLEHY KDPSA*MIPELLSTPLIRTFPFCL
7821	A	260	482	LILKFV*NHKIPQIAKTILSKENKAGGITLPDAKISCKAVVTKTALY WHTNRHIEQWNRIANTEINPNICNQLI
7822	A	1	306	VKAKAKKLQIQPIQLELLYCSYDMQEEDFAHRAMDYFPKIENNLSTR MDHMVSSFCIENWHQLESLSLLILHNMPHYEEDFEGLRLDMVQ*R LTSCSDAG
7823	A	3	396	SSLSLSSSVSVTFGFGTFPSAVSSSIDPGLALAFSSSGLSTSFS SP*SHSSSSPPVPLSSDTRRSTSPADMAAPSAT*TRRSTAPSNPF PSLAAPREKGGNPPTNERRKLETPIPGRRRQRQR
7824	A	3	346	HEHECYAKVLYELKPVGEEPNVSKQNCDFEQLGQYEF*NALLVRY TKNVPPQGTTPALGQVLRNLKRVSSKCKHPEAKTMPCAEDYLSVILN QLCALHDSAVSDRVSRCWT
7825	A	1	413	RAGYRQKWGSLATVIGQLGLPSGEGLVWPQRRREGHRNAHCSELVLD DLHVITQNRANHRPRCGSLLSELKFAPLALQPGRQSKTLSQKQKQ TTTTKNTKKQPGSVAHACNPSTLGG*GRQITLPSGVRDQPGQH
7826	A	37	363	ASDWNQDRARGRGQGCETRDSSEQSQGTNGQPAPAEASKDSWSSGGK MAR*APSPQRQKAGYPGSPSPQPAPASMRSLGPPQFQEPQALFPLE VPIPSPHTRNKMAR
7827	A	3	356	HERAFLNNSCFL*AFDPYQCDRYLFKIVTDVYYTPYVLIYYI*APL PLLLQLTHTHFLSLFFL*VLNIYALVYLSTALPLSLFISISSPRYSL CLFFHFLSLMLFLSSLSMYCSHY
7828	A	2	269	ARVAPLKGVEQEVREHEGEVTKPEKEKBETRIENGKLI VVSDSCGR VYVSGKIYYP*AYNDGLILERYQIMPIDIIVSYVFIMICLD
7829	A	2	351	KDIRVGHRQNRALPPQASPTVAPGQPTALPPTGHSGPTMGWPSRLS QLSLITAPTSASPTVVKLPSGACWPLSSTFASSPLSLVQ*P*NSDSD HATSAMAPSSSRECLSPWPAR
7830	A	2	377	SHCLEPKDIRVGHRQNRALPPQASPTVAPGQPTALPPTGHSGPTMG WPSRLYQLSLITAPTSASPTVVKLPSGACWPLSSTFASSPLSLVQ*P *NSDSDHATSAMAPSSSRECLSPWPARPRA
7831	A	176	379	SVTDHPIYCNLSPSPNPGSPDPSPVLPFVMTDYLLP*CVICCCF LSDPPHCSHPVGGSF FGIN
7832	A	1	344	NSGRVSGNLI SPLPPGPPRPLEEATPVLLSQGIPEREDSFRNLR TDLYIHQLKS*DSPEISSLCQGEATPRHSDKHNS*NAASEGKGC GF

				PSPTMEVEIASHDEEDVIHS
7833	A	355	535	PNRPITGEVTTKNLTKSLRPDGFTEFC*TFKEGFIPITLLKTVKEG LHPTFLYEASITL
7834	A	61	250	RSRLCAPVRESHTYLIMPLGCC*FFLYYIFFGFFSVVFCLLSFYSP FFSFVSSVSFV*FWVF
7835	A	3	66	DAWEKKICETEDWLFEEIHQRISSSRMKRNKESLQDV*NTIKRTNIR IIGVIEKREKGRKLI*EIMAENSPNLGKDMSIQVYEAQRSPYRHS KKTSPKHMI IKLSKAKSRR*IRG
7836	A	3	146	HMVAGAVAGILEHCVMPIDCVKTRMQSLQPDPAARYRNVLEALWRI IRTEGLWRPMPRLNVSASCAGSAYALYFACSD*LTQLPAIAMCWRPS GGL
7837	A	2	329	VASGRRKNLLSKVTGLEVPESGTPDRPCSGRQSLNPPVTSFPNPSQR NRTPPPTTRQMATL*EALHGSHLPPPGRACRTSSPGPRTTRPQVSD RRAQSPTSIVGPHRP
7838	A	2	357	EAGAHT*ITMKNQRLKETVDDTVEVSDFTVSRNSAHEAFNTAFTTL AACAASIG*VLLYLYLTTCPC*CKTKRQNNMLHQSNANSSILRPGPA SDASADERNACARKRAVLLEPLKD
7839	A	3	266	ECWYTRHMPHPAQCFFYNAWNLFFPYRYLHLLDGNENYPCLVDA DGDVISFPITNSEKTKVGWHVCEHGVSSRLFPVELTQVC
7840	A	42	226	LLFSEMFFSFKVKTTSDLFVKVTSATSLQICKDVMDALILVSVGWL LLRNAFEREWCSAP
7841	A	1	507	LQLEAEEQRKQKQRQSVSGLHRYLHLLDGNENYPCLVDADGDVISFP PITNSEKTKVKTTSDLFLEVTSATSLQICKDVMDALILKMAEMKKY TLENKEEGSLSDTEADAVSQQLPDPTTNPSAGKDGPSLLVVEQVRV DLEGLSKVVYPSK\ADL\ATAPPHVTVVR
7842	A	51	342	PILVYRPDVPD*VAKDYASFRNYT*GPLLDRVFTTY*LMHHTQTVDF IRSRHAQFGGFSYGKMTVMEVEDLLDGLMDESDPDNLFLKSFA*KI AY
7843	A	44	1353	KMLYKNFIMQSQELTALWEAKVHPAMLGLDELGRSGCGHCTQADLRF GDAAGRDPGQDNDNRNTAEPAPPPPPRVMAAAAALRAPAQSSVTFEDV AVNFSLEWSLLNEAQGCLYHDVMLETLTLISSLGKRQTLHTRERPY ECIECGKAFAEKSSLINHRKVHSGAKRYECNECGKSFAYTSSLIKHR RIHTGERPYECSECGRSFAENSSLIKHLRVHTGERPYECVECGKSPR RSSSLLQHQRVHTRERPYECSECGKSFSLSRNLIIHQVHTGERHEC GQCGKSFSRKSSLIHLRVHTGERPYECSDCGKSFAENSSLIKHLRV HTGERPYECIDCGKSFRHSSSFRHQRVHTGMRPYK*SKFWKFSCPG FLLLQQRVHTGSRCECDKWGIFFS*NASFFT*KSAPTEEVPEFCN ECEKAFSPLSLVT
7844	A	2	354	NLLYQFWIHTEVINNGLPLELILNTRSHHRVHDGRNRYCIDKNYAGV LI IWDKSFGTFEAENEKVYGLTHPINTFEPIKVQFHHLFSIWTTFW ATPGFFNKFSVIFKGP*WGPCKP
7845	A	3	388	TVRVCACDHHGNMQSCHAEALIHAPAGLSTGALVAILLCIVILLETVV LFAALRRQRKKEPLIISKEDIIDNIVRYNDEGGGEEDTQAIDIRTLN NPVPI*DTHLRRCFAP*TSLYYHRATPTRSCYHP
7846	A	151	352	YCCTYYIFVLFI*SSCGLTLIFITCIILFGSISFFLFFFTIVFSIII VTTFKFRLLYSIIFLSYLLC
7847	A	2	265	VKPS*PLTGALSALLMTSGLAM*FHFHSITLLILGLLTINTPPVQKG LRYGIILFITSE/VFFFAGFF*AFYTPA*AYPQLGGTAQQDT
7848	A	1	156	GIRHEAYHIVKPS*PLTGALSALLMTSGLAM*FHFHLKKKKKIGSS FIAVG
7849	C	512	778	MTSGLSHVDFTSNSITLPHTRAYXTNTLNHIPPMMARMLTRRKAHTKG HHTRTCSKKAFRYGDKSYLFTSGSFFSSQGFLEPFLPLQA*
7850	A	15	613	LKTTHLLFQVSVGQESRCGLAKSSGSKSLTRVKVRGQPRWLCHLKAQ LGKDLLSSLTWLLAACGSSPVVGLWASAPGLLLASHHPRFSATWVF HKVAHNTAAGFMSTGKQEG*RDKITAKQKFASYNLISEVTTHHFLPY

				SIYEKQVTRSSPHTKERDSPRG*LSEKGDHWEPPQKLPATDVIALFY ENKHQTHYIHL
7851	A	66	357	KSMTDGHIQTVTNIRQLPARTLYTHWPREFSP*SPPLERMHTRGARR EARQKAPRIRDKRRGKSRVHCLGEELANGGGWDRIRWGKGERQGDG RV
7852	A	3	360	HASAHASQGDDQLERDHEN*DRFVRQVVGINNYRISEESGHPYNIF GKIFHDCADLDTSEH*LCKCDSFDKTLKPTINLVSYNRNFA*TNIDE NFRCGKSPSYSSCYSKHEELHNGM
7853	A	79	415	LSKGTGRKRDGLTLPAPHPAKTDPAAAPQGQPGVGVRRSSPPCPG/QR EQQGSAGSPGWMGGGCPVVS*PLKGQNPSPSSLGSGKSGFFSPPD PAVARGRRVRGEERGQVRE
7854	A	171	173	LTAEACLSFSPPLSSLGVSVCPPHHGGLGPAHPSALPQPPGCI FEA WPPRALT*PLSSPLTPPAPGHCRIRRGEEGASAAFPGLGTGLVLSF EDDHRLQD*QAHQSQPGASPTLCCFRGLHAGELLTPPTVQPG LFPESASKWPQLFGPRIILPGPPKGSPTTKAWPPGVCGQLPLVKGHP G*PSPASGRSRCEVSVSPSCPVLPLGWGCLAPAGCRSQHWRD
7855	A	27	263	FHCFSISNF*VANRSSLLIDFSVGLLKCKSFIFFNAILHYCLMMVC EYDSLFLSYMFLLIFFYFYIFIYLLFIHPY
7856	A	92	355	VLNSI*SGNQKSYANVYRLLYLDPIPKIYAEAYTP*NVNSTNLETK SPKTIQKFPEDREFKNDFFEKTNGDRETGAHPFLLFLV
7857	A	464	2848	GETGMSTALTHTTVAMRCPMLGGGGGPTYGPPQPGWHPDVHIMQH LPIQARLGSIAEIDLGVPPVPMKTFKEFLSLDDSVDETEAVKRYND YKLDFFRRQMQDFFLAHKDEEWFRSKYHPDEVGKRRQEARGALQNR RVFLSLMETGWFDNLLLDIDKADAIVKMLDAAVIKMEGGTENDLRIL EQEEEEEQAGKPGEPKKEEGRAGAGLDGERKTNDKDEKKEDGKQA ENDSSNDDKTKKSEGDDGKEKKEDSEKEAKKSSKKRNRKHSDDSF DEGSVSESESESESGQAEKEKEAEALKEKEKPKEEWEKPKDAAGL ECKPRPLHKTCSLFMRNIAPNISRAEIIISLCKRYPGFMVRVASEPQ ERRFFRRGWVTFDRSVNIKEICWNLQNIIRL/RECELSPGVNWDLTR VRNINGITQHKQIVRNDIKLAAKLIHTLDDRTQLWASEPGTPPLPTS LPSQNPILKNITDYLIEEVSAAAAEELGSSGGAPPEEPPKEGNPAEI NVERDEKLIKVLDKLLLYLRIVHSLDYNTCEYPNEDEMPNRCGIIH VRGPMPPNRIHGEVLEWQKTFEELTPLLVSRESLSEEAQKMGK DPEQEVEKFVTSNTQELGKDKWLCPLSGKKFKGPEFARKHIFNKHAE KIEEVRKEVAFFNNFLTDKAPALPEIKPAQPPGPAQILPPGLTPGL PYPHQTPQGLMPYGPQPRPILGYGAGAVRPAVPTGGPPYPHAPYAG RGNYDAFRGQGGYPGKPRNRMVRGDPRAIVEYRDLAPDDVDF
7858	A	1073	3541	GETGMSTALTHTTVAMRCPMLGGGGGPTYGPPQPGWHPDVHIMQH LPIQARLGSIAEIDLGVPPVPMKTFKEFLSLDDSVDETEAVKRYND YKLDFFRRQMQDFFLAHKDEEWFRSKYHPDEVGKRRQEARGAL\QNR LRVFLSLMETGWFDNLLLDIDKADAIVKMLDAAVIKMEGGTENDLRIL LEQEEEEEQAGKPGEPKKEEGRAGAGLDGERKTNDKDEKKEDGKQ AENDSSNDDKTKKSEGDDGKEKKEDSEKEAKKSSKKRNRKHSDDSF FDEGSVSESESESESGQAEKEKEAEALKEKEKPKEEWEKPKDAA GLECKPRPLHKTCSLFMRNIAPNISRAEIIISLCKRYPGFMVRVASEP QPERFFRRGWVTFDRSVNIKEICWNLQNIIRGARSLINRWCSRGKGL RAAVSLASGLRECELSPGVNRDLTRVRNINGITQHKQIVRNDIKLA AKLIHTLDDRTQLWASEPGTPPLPTSLPSQNPILKNITDYLIEEVS AAAAEELGSSGGAPPEEPPKEGNPAEINVERDEKLIKVLDKLLLYLR IVHSLDYNTCEYPNEDEMPNRCGIIHVRGPMPPNRIHGEVLEWQKT FEELTPLLVSRESLSEEAQKMGKDPQEVEKFVTSNTQELGKDK WLCPLSGKKFKGPEFVRKHIFNKHAEKIEEVKKEVAFFNNFLTDK PALPEIKPAQPPGPAQIIHVPRVVLPPGLTPGLPYPHQTPQGLMPY GQPRPILGYGVPPTGGPPYPHAPYAGRGNYDAFRGQGGYPGKPRNR MVRGDPRAIVEYRDLAPDDVDF
7859	B	145	226	MAVNCSEMRLKSSWNGCAIANEGDCHLEATSICSSTSFMMDLGEFRH

				CESSILLASTAX*
7860	A	136	1559	ILTMREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGSDQLQL DRISVYYNEATGGKYVPRAILVDLEPGTMDSVRSQPGQIFRPNFV PGQSGAGNNWAKGHYTEGAELVDSVLDVVRKEAESCDLQGFQLTSH LGGGTG/SPGMGT/LISKIREEYPDRIMNTFSVVP\SPKV\SDTVV EPYN\ATLSV\HQLVENT\DETYCIDNE\ALYDICFRTLKLTPT\Y GDLNHLVS\ATMSGV\TT\CLRFPG\Q\LNADLRKLV/VNMVPFPR L\HFFMPGFAPLHQPVESQQYRGSHKCRELTQQ/VSFDAKEH*WAAC GPPATGRYL\TVAA\AFRGRMSMKEVDEQMLN\QONKN*QLTLWEWF PQQCSRTACLFTSQPRGSRWAVHLSLGNRHSRSHRELFSQIFGSSF TWPCFRRKAF/LFWH/YTQEGHGTEMGVSTEG*EATLNDLRL*SIK QLPRMPTQEEEEEDFGEEAEAAA
7861	A	2	304	ARGLCPLGYTGLKCETDIDECSPPLCLNNGVCKDLVGEFICECPSGY TGORCEENINECSSSPWLNKGICVDGVVCYCTFV*GFCIFKFCSS CPLYTI
7862	A	1	345	GTSGTSRFL*DVLQMNDFGTRWRFYATVIYQKPQLKSLILE*RETW VLGTDGTLQTKEEKDPRLRKTLVYVAPLLVLGSDVLEALSGAAPLR LFLKDAIRDQARIGRAERTVL
7863	A	2	343	VRSAYPRRLNSLAGQRRHHLCHPLLPAGGARAPQPPQPPQLGAR PGPGRCRMRRRPQAPRAGRGAAALARAL*PLSSTASRRGACPGAAPSD SPEDPASDHGHSRPLGGRC
7864	A	1	338	QIDEIVTETLLTEAERGAQVYLTGTGFNLQAYMDLVLGTRAQYQIL LASPEVNGFFGAKGVAGAI PAAYVHIERQPFNDEC SL*QSRVQLSE YWRCSGRSLSMEFVRHDI
7865	A	174	363	WQFTFTFSKSIKDSKEEICYQLPRDTKIEDFGTGRPSRYPLVALLT LSDEDDREIMYYFHG
7866	A	1	1260	VRCRFPVRNSRVDPRVRMAAVFLVTLYEYSPLFYIAVVFTCFIVTTGL VLGWFGWDVPVILRNSEETQFSTRVFKQMRQVKNPFGLEITNPSSA SITTGITLTTDCLEDSLTCYWGCSVQKLYEALQKHVYCFRISTPQA LEDALYSEYLYQEY\FILSSDIPISTEN*TSYG*SVANLLIILGIL EACLLQNKHSPCIRTCSVYRISVSGTGAFRLIYPLALIIRLLMD KVPLTY*SFLGY*KHVYCFRISTPQALWSEYLYQEYHFIKDS KEEICYQLPRDTNIDDFGTVPRSRYPVALLTSLDEDDREIYDIISM VSVIHIPDRYKLSRILYQYLLLAQGFHDLKQLFMSANNFTPSN NSSSEKNTDRSLLEKVLSESEVEPSEENSKDCVVCQNGTVNW
7867	A	106	387	RWACSAEQKAEPAAGSSRTGGMGSACIKVTKYFLFLFNLIFFILGAVI LGFVWILADKSSSFISVLQTSSSSSLRMGAYVFIGVGAVTMLMGFLGW
7868	A	2	767	AVEFGLCSPTPTARAGDAGPAARSRKQNPQSPCCCVDDTWAQAEV GPVTSCTGFVEGSSRTGGMGSACIKVTKYFLFLFNLIFFILGAVILG FGVWILADKSSSFISVLQTSSSSSLRMGAYVFIGVGAVTMLMGFLGIG AVNEVRCLLGLYFAFLLLILIAQVTAGALFYFNMGKQEMGGIVTE LIRDYNSREDSLQDAWDYVQAQVKCCGWVSFYNWTDNABLMNRPEV TYPCSCVKGEEEDNSLSVRK
7869	A	149	421	CGTDKTFPWSCTVRENLSYSEELLSRRQICKKNNDPPGDRD*FDYS RSDYEHSSRRGRSYDSSMESNRNRDREKRERERDTRKRSRKSP
7870	A	1	445	GQDSRSRDNGPDGMEPEGVIESNWNIEVDSFDDMNLSESLLRGIYAY GFEKPSAIQQRAILPCIKGY/DCDLYETLTITQAVIFINTRRKVDWL TEKMHARDFTVSAMHGDMQKQERDVIMREFRSGSSRVLIITDLLARG IDVQQVSL
7871	A	2	363	ELDTLCDLYEP*PSPSIIIFINTRRK/VDWLTEKMHARDFTVSAMHGD MDQKQERDVIMREFRSGSSRVLIITDL\RIGRGRFRGRKGVAINMVTE EDKRTLRLDIETFYNTSIEEMPLNVADLI
7872	A	3	449	NLQEWKLDLTCLDYETLTITQAVIFINTRRKVDWLTEKMHARDFTVS AMVCLPAASLLWVCPSEVSYLKPGFLEPRCLPGLLHICFLFQHGDM QKQERDVIMREFRSGSSRVLIITDLLVSRGN**QRQKGGSKVIPSPRG HQCLSGK

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7873	A	236	534	SYAIYWLFFSSLAPKYIKMFVLDEADEMLSRGFKDQIYDIFQKLN SN TQVVLSSATMPSDVLEVTKKFMRDPIRILVKKEEVTLEGIRQFYINV EREWE
7874	A	1	366	AEIRDRSPCGELHVEREEWKLDLTCLDYETLTITQAVIFINTRRKVD WLTEKMHARDFTVSAMHGDMQKERDVMIMREFRSGSSRVLITDDL LV SRGN**QRQKGGSKVIPSPRGHQCCLSGK
7875	A	5	1285	FLRIMSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLS ESL LRGIYAYGFEEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISI LQQIELDLKATQALVLAAPTRELAQQIQKVVMAALGDYMGASCHACIGG TNVRAEVQKLQMEAPHIIVGTPGRVFDMLYR\RYLAP\KSIRMLVLN EADDEMLSRGFKDQIYDIFQK\LNSNTQ\VVLSSATMPFD\VLEVTKK FMRGP\IRILVKKE\ELTLEG\IRQFLHQPNWEEEWK\DT*CD\LY ET\LTIT\QAV\IFINTRRK/VWDWPHPRKMHA\RDFTVSRHAMGDM GPKGNETVIMEGSFRSG\S*QSF*LPT*PCWARGIDVPARFSLVI\N YDLPTNR\ENYIHR\IGSTVDRFGRKGVAINMVTEEDK\RALRTLGA SYNTSIEEMPLNV\ADLI
7876	A	3	380	MDTTPLSYSES*SDEYLVNTM*LQDAFCRGLVKGPNVLLKGPINAV IDVNLGLKQCLA*FKRYLECL*RLDVTLCVPP*IGGSDAPLPHNKD HK AADP*DYFQR*MSFYRQAHAAVLAVLPRLHH
7877	A	2	398	RESESCAAADTPALETLSFHGDWEIIEVFNRDLGSTYPDDLAL* MED VDFEEYEE*GYD*GWVLYPQEGVIGNMEGPDYS*VTFALHSSSVYR VSLDPKTYTLAVTGGYDDGAFVWLLTYG*LLFE*ASHE
7878	A	3	401	NSQVLLDSPIQLSKITENYECITELSGLLKREQSSTVNASNLE NDEA RLKAYLENRSEIDSLKTSNPIDL*EASISQAGSIN*SRF*SSGMNKS YDVRIDNFNGSIGDRILLTAANVILAWCRLYGLMRQNV
7879	A	1	424	PVLRVARERSLPGPQEGPHGRASESASPLAPSIAPSPPGPPALSASH IMGSQALRSPETPW*SPWDPPAPLDLVSPWQFPFGPHASATP*RSPL GLQTPQAPGSWAPHVPATPQASGLPAPHVTETP*ASS*LAMPVPETP
7880	A	156	312	LFSLACRYHYVPTCRNTSGILGFTVSVVTNAIPFIS*LSSFYYIYFL YNFG
7881	A	15	396	FGCLLQGRRLPKSHSPWQGGPGASGRPAQGHKKNR*RGQNPSNL SHPA PTPPWPGIKCPLPRAGPSLSSLLPGRVLCARPEFPLHGRGLEPSASL LPSALAPSPLRGLKGTERSRLKADQAWGGWKE
7882	A	2	102	NKILIKTNSRKK*KIE**RDNNQSNNNNKNNK
7883	A	3	399	NFLYTFLYFPNFV*SAHCF*NQKKKNKYFLLREKCLLNCFP HLYVAF YVYIPSIIFNLGSC*YLPSCSIFYVFIPLSHPLLFFFLC FSLFSLPF FLSLFCFPFLAFLFHPSPFILLDSSACLLCISCFH L
7884	A	190	341	DGKGLLQVCLPLQDVYKIGGIGTVPVGRVETGVLPKG\MV VNFA\PV NVTT
7885	A	377	1073	LQGHRLRTGAVLIVAAGVGEFESWYSPRMGRPESMPFLAYTLG VKRL \IVGVNKM\DSS*PPYS\QKRYEEIVKEGSTYIKKIGYNPD TVAFVP ISGWNGDNM\LEPSANMPWFKGWKVRKDG\NASGTTLEAL \DC\I LPPT\RPT*QSPCGLPSSRDV\YKIGG\ILGTVPVGP SGRLGVLPKG MGGSPAPVNV\TEVKICSEM\HHGRF*VEALSWG DNVGLSMFQGL LFCSK
7886	A	2	416	SVGDPCPSTASVDQCTIVP*PMEGPLLLYRRCIEGVGGIFLW DPQPS SPQHPGATPSTGEPGFPVVHQDLSHIQPPAAVVAALNNH KPPVRS*P PSATPEAFT*FSKCDLDEELSLRYCHAFSEC*HD IRPSHIHP
7887	A	1	360	TERFGM*GGEAVCLYEPPVSELLRRCGNCTRESWVVSFYLSA DHELL SPTNYHFLSSPKEAGGLCKAQITAIIFQQGDIFVFDLETS AVRPFVW WQVEAIPVDYLPSCFVMIIPTLYCSP
7888	A	152	379	WEGGGSGTILARRFWDLQAYRPHAQVPGFLR*SHLMAVGHA EATDLT ALTMLILTPEAWQLHTILYLSGLLAMLP
7889	A	302	565	YWLFDYFMIAEKILNGYFCCCC*DRSCPVAQAGELWHERGSL QPRPP GVKQCSYFSLSSWDRRHVPPHLANF*TFFCRDVSPVLP

7890	A	1282	4603	GSLPCLEHVSLNNPLSIIIPDYRTKVL AQFGERASEVCLDDTVTTEK ELDTVEVLKAIQKAKEVKSKLSNPEKKGGEDSRLSAAPCIRPSSSP TVAPASASL\ PQPI\LSNQGIMFVQEEALASSLSSTDSLTPHQPIA QGCSDSLESIPAGQAASDDL RDVPGAVGGASPEHAEPVQVVP GSGQ IIFLPFTCIGYTATNQDFIQR LSTLIRQAIERQLPAWIEAANQREEG QGEQGEED EEEEEEDVAENRYFEMGPPDVEEEEGGGQGE EEEEE EDEEAEEERLAEWALGADEDFLLEHIRILKVLWCFLIHVQGSIRQF AACLVLTDFGIAVFEIPHQESRGSSQHILSSLRVFCFPHGDLTEFG FLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMAML CSPILYGSHTSLQEFRLQLLTFYKVAGGCQERSQGCFFVYLVS DKR MVQTAAGDYSGNIEWASCTLC SAVRRSCCAPSEAVKSAAI PYWLLLT PQHLNVIKADFNPM PNRGTHNCRNRNSFKLSRVPLSTVLLDPTR SCT QPRGAFADGHVLELLVG YRFVTAIFVLPHEKFHFLRVYNQLRASLQD LKT VVI AKTPGTGSGSPQGSFADGQPAERRASNDQRQEVPAEALAPA PVEVPAPAPAAASASGPAKTPAPAEASTSALVPEETPVEAPAPPPAE APAQYPSEHLIQATSEENQIPSHLPACPSLRHVASLRGSAI IELFHS SIAEVENEELRHLMWSSVVFYQTPGLEVTACVLLSTKAVYFVLHDGL RRYFSEPLQDFWHQKNTDYNNSPFHISQCFVLKLSDLQSVNVGLFDQ HFRLTGSTPMQVVTCLTRDSYLTHCFLQHL MVVLSLERTPSPEPVD KDFYSEFGNKTGK MENYELIHSSRVKFTYPSEEEIGDLTFTVAQKM AEPEKAPALSILLYVQAFQVGMPPPGCCRGPLRPKTL LLSSEIFLL DEDCVHYPLPEFAKEPPQDRYRLDDGRRVRDLDRVLMGYQTYPQAL TLVFDDVQGHDLMGSVTL DHFGEVPGGPARASQGREVQWQVFPVSAE SREKLISLLARQWEALCGREL PVELTG
7891	A	1	286	SPPTVVPASASLPQPILSNQ GILGDE*VILVS*ACLLARPARKRGGC AVPSGA EARDTQERTPPARAPGDAELGVRSWENSSTRCFKSQKNIPT P
7892	A	3	419	PPPLWFNQDPHVESKGLAAGRVPVSTSQGR TQFRGSAPPPKDPLPRT GPSANRRVPHTFQPDISFPGSPKPPS*DRPHPNPSLRSLVSHSVHN QAGRWA KVQATARERKSDTKSIWLWRWRRILKRTRNSLYTLHG
7893	A	2	236	KKS NLRMLAEHGGSHL*SQLCRR LRQENHLISGGGGCSESTSHHCTP AWGTE*DFVSEK KKKKLTGWPDPSGRIKWWC
7894	A	3	254	LECNGTISAHCNLRMLMVSG*FSRLSLPSS*DYRRPRLRPANFCILVE MGFHHVQGAGLKLQTS GDLPLSLPKCWDYRRAHPLA
7895	A	1	185	RQSLALS PRLECSGAI IAHCSLEPLGLRQLCCLSLPKC*DYRHEPLS LACFLFLYPPEHLT
7896	A	1	182	KLVGLEPVSTYSIRVSAFTIVGNGNQFSNVVKFTTQESG*IQFLSLK CFFLYLTPFFSFS
7897	A	4	329	AGEGGLQALILRDGAWPQPPSGD*QVKGLEPLTPAPAGSSQGP GGP PIASSPVGQSKTDTATTTKVGPVGGGQPAPMHQQLPSPGDPAAEDA HTWGERSLSGMKGK
7898	A	115	408	HWKERGSLYPA*TOGSACVLPQGHLPRPQATPPTTAHLVPPQHCR PGPAAPAP*QGMSTPTTATLFSRLQGR LQLPMGAPSGQGPWLYCRGE GPRA
7899	C	128	253	MNSPDWELWQDN SPQDSCVLI PRTCDHAASRGRRDSSGVIE*
7900	A	856	1071	SFALVAQAGVQWHDLSLQPLPPRFK*FSHLSLPSSWDFRCPEPYWL IFVFLVETGFHHVDQAGLELLTSGD
7901	A	87	395	RSGGGVPPRNPPLGGRGGGFPQGP GFQITLSPKGKPLFFLKSQNF G*WAPPLKPPFKGG*TKKIFLTLEGGVPINGNFP PPPPPGGKNFFSK KKKKKKKK
7902	A	28	403	GGTIYGN CVVPATVPAGSPGVPVAVGGQPGPLPVL*RTSPETCPPLGV TTGSLCLAPYHSLSF GGHGLPGTPREAG*REGGNSLQLQLPNPKPFL PSRPEDPTWSPSSQGEELRRRKVRCDLKS LT
7903	A	50	543	GLFQKPGGTHVLPPAPKAVQASTDPPLKGGSPLLQGPWRRGRVGC AQKGGPGDRGSSLLFKPGDQGGPSLTSGQHSKSEAGVWQGLSWSPLG CGFLPEPHQRPLEPREGPRRAGVTPGLEHSSQSPEAPGDRNK*QSET

				TREKESTVSTKSPTLPKHGQLG
7904	A	1	610	SHKTNVQQCYCYCGGPGDWYLMQLQCCCKCKQWFHEACVQCLQKPMLE GDRFYTFICSVCSGPDY\LKRLP\LQWVDIAHLCLY\NLSVIHKKK YFDSELELMTY\INENWDRLHPGELADTPKSERIEHVLE\ALNDYKT MFMSGKEIKKK\KHLFGLR\IRVPPVPPNVAFKAEKEPEGTSHEFKL KGRKASKPISDSREVSNGI
7905	A	440	608	CVKLFLDTSQADTPKSERIEHVLEALNDYKTM*VDLFYVSL*GRHL VSIRNNGIV
7906	A	49	796	SHFIYFLTIWISSLVNEVC*SSPFLMNLQVVLYIFWLLLLLYELCCR IFSHFVVCLFTMFINIVTF*F*YLQIIVFLYG*LGFFYGYVKNIVNI LLLHAL*FCLSHFGFIPLGTIFNI*YEVIFLLL*G*SVVPALFIEKK QKQKTFLFLLL*SAFSVVYQYMQRSFMGSLLYWFFSCANVHSLHYF MIPKIFDI*YQSPFTSLLFINSWLFLVLCSSLYILEIAYHVSLLK AEHIENLIGVAMNL
7907	A	178	565	KGGATCPESPQDRKRRGNLDMEKLYSENEGMAHNGKMENE*QPQDQ RKPQVTLYSGRQEVKRGKDRKQGNRR*GNV*RIKGPESSEGEAKE GKSEREGESEMEGGSEREGKPEIEGKPESEGEPL
7908	A	3	415	VTGVLVYLAVERLISGDYEIDGGTMLSTSGCABAENIIMG*TLHQSG HGSHGTTNQ*EENPSVRAVFIHVIGDFMQSMGVLAAYIILYFKPEY KYVDPICTFVFSILRLGTTLTILRDVILVLMEGTPQGVYFTAV
7909	A	119	428	LESLSHKRSSPRHIVIRLSAKTKKSVLRAVRQKYQITYKRTPISSL VDCSAQTLQARRDLGPTFCLLKNNNPQIILYPVK*SFINEGKIVFF REISPERIC
7910	A	13	235	DLINKISKAAGYKINTEKSVAFLYTNSNQTEKEIKKAIPFTITTKNK TKYLGINLTKEV*ELYQENFETLMKGI
7911	A	39	141	LSIRGLNIIIKRQL*DWIKQDSTLCCP*EIH
7912	A	1	285	QQRPPGLRPPPHPRGQDQLWLKGWGAAQL*EGPSGGSRRGRVERE RGRRRKGRKGRA*RGTRKAGGEGRRRETALASPLRGHRSPQERPRPT L
7913	A	1	452	TAKTTFRNAHSKHL*NVCKPVEETQRPPTLQEIQKIDSYNTRK NCLGMKLREDGTYTGFIKVHLKLRPGTVPAGIRPQSIYDAIKEANL AVTIDKRTSYFLPLDAIKQLHISSTTTVSEGIQGLVKKFNGVDNPQK VALFKRIHK
7914	A	1	484	NVLCGNNQISDLGILLPEVCMAPEEKGDKDDQLNKETEDYLNLSLFEG \FLKVTEDSLSEYEDNQDDSDLLQDLSPEEASYSLQENLPSDESCLS LDDLAKRIEIAEVVPTGGLVLSILKKRNDTVGDHPAQMQHKPSKRRVR FQIIDDSDLQESLGFGDGL
7915	A	2	1121	HYATDRFPFERRVILLYYTYSYVPSFPSYTKCCFEFLTIFYSSSLE SKTCLGTESSKESQHTVEPLGSSPCCHQMDVQTDSPSLSVTAGKDHM EELLCSAEATLALHTQSSETAGSPSGPDSSDACCDDSLRLQLAQTEA CQDVARIEGIAEDPKVFLSSSKSKTEPLISPGCDRIPPALISEGKYSQ AQRKELRLPLRDASEALPTDQLENNELNELQOPDLTSDGKSPQAQA DSNGSENVLCGNNQISDLGILLPEVCMAPEEKGDKDDQLNKETEDYL NSLLKGLKDTEDSLSEYEDNQDDSDLLQDLSPEEASYSLQENLPSD ESCLSLDDLAKRIEIAEVNQR*STIKSKMAFKKHIVYVNLIALFL
7916	A	2	390	SDSRETRVVINKDSVFCLYCKLFGGKNQVKNENGCKDWHLSHIL SKHEESEMHNNSVKYSKLKSDLKKNKAIDAEERRLYENEEK*WCAV VVHVIYLSLFLGMMIRNLTLRKTSVLAIVSTIVL
7917	A	1	240	KRGEKAPETSKTTSTWRIPCRKRRLSNRDFPDLSTGEELPETCGSCL RRGSGREN*DAETWPAQCPECESKAAVSTRFLF
7918	A	3	422	EPLSSPLFCP*NQSKIHPPIFLAPTWPHPHFPFGPGQPPFPLSTG SHLV*QKPKGAHEHLSGIPPSLAQNPTWVPPHFGKRSSPHSATRPC KICPRLLAPSTLLTPSNLTGP*PLLPALPGLLGPPENFCTGCFL
7919	A	2	127	RFWDYGRIALVS*ADSESRFQRLSSTSSSGQDFFENELVGI
7920	A	1	346	DSRSPSPASPPTQ*CRPSSFPGPAPPRLWLAPPFCPPPPPHGYGPF

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				PARKRRGAALGLTRVLPPPGSAVRRSPGPGPGSAWDKTLKMKQKKFG RSVGLWRELIRDCSLAELLSA
7921	A	184	291	GRSLEASQSAGITGVSHSTRPIDILLIKAVYISLSH
7922	A	481	716	VFFFFFFETECRSIAQAGV*CSLRLPPPGSSDSRASVSRVAGIVGACH HAQLIFVFFVAMGFHHVGEAGLEHLTSSDLP
7923	A	4	423	VARERRLPGPQEGPHGRAAGSAPLAPSIAPSPPGPPALPASHILGS QALPSPETPW*SPWDPPAPLALVSPWQFPFGPPAPATP*RSPLGLQT PQAPGSWAPPVPATPQASGLPAPHVPETPWASS*LALPVPETPWDL
7924	A	3	437	GYLSEVVEENTPPKMEKEGLEIMIGKKKGIQGHYNscyLDSTLFLCLF AFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYGYVCATK IMKLRKILEKVEAASGFTSEEK/PAGQKVQDCYFYQIFMEKNEKVG VPTIQ
7925	A	3	187	VLAGELEDEACGCTDGTFRGTRYFTCALKKALFVKLKSCRPDSTRFA LLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGKKKG IQGHYNscyLDSTLFLCLFAFSSVLDTVLLRPKEKNDVEYYSETQELL RTEIVNPLRLIN*YCSRFPIRLSAVTL
7926	A	4	343	KLEN*KMVLKEIKEDLNKQTDILFS*LQRLITVRMSILPKLIYKFS APIQIPA*FL*IKIIKCMRGK*TRIAETASSSSSPSQSFILSPKL DHRGGITANCTPPWAIKGLL
7927	A	1	531	FYHADHAALKDEMEY*VFLQIKRYLYHGRLLCKHPDAALLAAYIIQ AEIGNHDSG*HPEGYSSKFQFFPKHSEKLERKIAEIHKTELSGQTPA TSELNFLRKAQTLTYGVDPHPCKDVSGNAFLAFTPFQFVVLQGNK RVHFIKWNEVTCLKFEGKTFYLYVSQKKKGIGSCPV
7928	A	115	348	KSCLNIFGLKQTTSSLRWNRVKK*AHTYG*QLIFNGAKIIHWIKYN PANGICYWISICKKVNLDPYLIPYTIQNGS
7929	A	4	430	AWLSALNSSLPATWSCCPSLGASHKLQWEATSPTVPPRAPSQVKCAA CEPTPLPCLPFQPPPSLSSQAQVLLTGHPG*GPLRRQGEGLLRS KGCQARLTQPNSEGGAVS*TGRPGDGAVGEAAPETTRDCTAPPA S
7930	A	1	380	GTRLLVRYTPKEPQVWTPTFVEVFGDLGQVGPE*C*HPEAKRMPCAQ DYLVSVLNQLCVLYEKTPLSDRDTKCTESLVNRRPCFSALEGDEAY DPQELNAETLTFHADICTLSEKERQIYKQTVL
7931	A	2	389	NVQKSLAFLYTNNSQVESQIRNAIPFTPATKRIKYLGIPLTRVHNV YNENYKTLLEKFREDPNKWNFPKSWVGRINIKMAMLSKAM*RFPR VHIKIPGTFTELKGPILKFIWNQKRAQIPRATRA
7932	A	72	373	TSTLKKLEEKQTSRRKEIKIPAEINAIENKQIEKISKTKSCSFK*S IKITNP*LKQ*TKEKI*INNIKNRGQVTMAFVAIKRISREYCO*LY TNKFNI
7933	A	2	259	KQWKPAAPPANPLPRGTSGPE*KGPHSDKAKPFPSPFFKKRQWGGAP SRSKKARGKQPPKGGHLKGPLRVVNGV*RAPLNRTAA
7934	A	3	335	QIKPPRLRDTPHSFTPYHPVRRGLVYFPPSAPSPAKGEQLHTRTRHNV LGSHPRRLPRSS*SSHRVTRGSLGSVPPARSTSYGSPSRQWDLACPL TPEGVWRTKNNKPEAL
7935	A	37	281	GPSPYTDPPTYP*LTLNLTNPRTNSTLPPTLHLPSPRPTSPSPST LPPSLVLRFFLKIQSGKRRAYPEHFWGQNGERKV
7936	A	13	234	DLINKISKAAGYKINTEKSVAFLYTNSNQTEKEIKKAIPFTITTKNK TKYLGINLTKEV*ELYQENFETLMKGI
7937	A	3	428	VLEELPISVLFNSSSVPAWQWLAHVYHSHGMMRAAQMCYIKTLQLAS QRRSWWAKLSSLWRLALLALKGCMANISNDYWPSLVQEBATEALKLC FCPLAVLLLALLQFKRMVST*TLCLLERVVYHPGPSKFIGSNWPAV
7938	A	132	395	ETNSLFGPQVKRQGNDLG*LNPPPRGFKKFSGLTLRRSGNYRPSPPR VFGE*GKRGLNWWAKGGLDLS*NNPPWPSPQARIMGES
7939	C	170	394	MYLGASSQLSPLYPELQAQEPMIQIPRPPHCGSIHWVGTSHSVPLQ PLKHRQRPLEYCPLPLHNTGQAALDQSG
7940	A	107	380	PPFVAQLGGKGNL*LNPPPRG*QFSSLGPPISGNYGPPPPSRVI

				FGFLRKKGVSPSGPGFGIPDLKIGPFNPPKGLG*RGGPWGPNO
7941	A	83	410	PEIISGFFFDHHGKLETPKRNFGNYPNTWKLSNTLLNDQGVIEGIS SSSLKWLKTNEKGNPTYQSL*DTAKAVLKGNLTAISAYIKNREKLQI NKQCI FNYPEKQEQM
7942	A	15	334	QHFWFNFHVTKDRINTGERQETDWKIFATYLMKKV*ISRKCYN SYKL VRKKQLNRKWAKEKNKQSQKKKQSGQ*TKTVQPQ*NKRNAD*RYYLS PISLAKSNKLN
7943	A	1	400	ESRLICQQMYMGEKPPFGCSCCEKAFSNKSYLLVHQQTHAEKPYGCN ECGKDFSSKSYLIVHQRHTGEKLHECSECRKTF SFHSQ LVIHQRIH TGENPYECCECGKVF SRIDQLVSHQKTHS*KQPYVCNEW
7944	A	46	364	SHLPNSSFEQKYAYEFVPGYQKHYTL SKFPWPF FAEMEKLILKFKWK S*SHITEAILRRKNKVGD LTLSDVKSSL*RYDNQLLSV*Y*YKHRI GPWDHGRPDIHL
7945	A	3	312	VCPCSQLNKAITSTTRCLRGFVCSSSYRRRARERGMKQTQRERER QR* RERQRRGEERQGGKREPHSRARGGGSRRERERVREL*SDSDRS LEREALLR
7946	A	225	722	GLAHSAVRHSSFWGHLQDSGPLVPPGAGQSGSLGLLAAEWVGKASPWG PAPACPTPHSEALVCSFRTSPPSTPHAHPGPVSGPASVLAALRLGLH LLRGCGGGTPTSPQTLQDEEAN*GHRGHGDRLLRLTQAPTAQPLWHR PWQKDWPNNLLRPLSFWCRRPPRP
7947	A	43	418	AYWGRKTPWLTISSFWPTPGSPYYDNGRPLCYSDSDAVLLCFDISRP ETGDSALKKVRDLQLSNL*LSMRTKKESGPCHECLLLTSRNGSQGRK RFAQGTISYSSSGTGTWVSLPHCLPPFLLSH
7948	A	2	221	AGPGGSPHGYVGSPLRISTRTHLCFAATRSLHIDPLIVLPLVDLKD RIII*NLWGLQPLPPASLLQPTALYS
7949	A	1	409	SPGTCGRRPQTM/PPGAPDFPAVEGRSLGLSPSQGGPAGAGGDAGPQ EDVRQPPGELAHGPLLPAQTG/SPGPQGLWLHRNPTS/GPPSQIGEG AEQGDGEGVADAPQIQCKNVLKIRRRKMNHKRYRKLVKKTRFLRRKV
7950	A	2	363	YSTSPAGQVGR LSPSQGGPAGAGGDAGPQEDVRQPPG/EAGSRPAAS CPDWIPG/AAGHVAPPQSYQCPSPQIGEGPGGT PETQADQVRERPEA HLAEGGAKGSPRRAGRPPRSTCGANESG
7951	A	337	1067	NLKAHPRRPFNPPLASGPFPLILAGADTW*GIGGWKPTSSLRVPGIQ SGAGSERGREPSSPGG*RTSSWGPASPPAPAGPPCEGERPRLPGPAG DVL*RETADPAAQHSMRQAKAGGRLPKERPSTAGKSGAPGAWSVGGG HRSQGSSTR LKLTVLRPPSGTSGPSPSRPRSAAATRRFLRTAPAGVL AAPDSALAQAPPKPKGDGFRGCGPWIYPQVQNRFR TTQGPDSQRADG SAGSRLRK
7952	A	127	440	SLRYTFLYTFPIILEHIIIVLMQQTCC LHGFISIYLLIHTFILQIHPF HTLFQQTCSIIQQLYFLV*YFAYVYTF LFILYLSYPFLYYY*ACFET FDSFNEIGRV
7953	A	2	341	MATSELSCEVSEENCERREAFWA EWKDLTLSTRPEEGCSLHEEDTQR HETYHQGGQCQVLVQRSPWLMMRMGILGRGLQEYQLPYQ RVLPLPIF TPAKMGATKEERGVPSTLC
7954	A	288	802	GVIMATSELSCEVSEENCERREAFWA EWKDLTLSTR/AEREGCSLHE EDTQRHETYHHQGGQV\LAQRSPWLMMRMGILGRGLQEYQLPYQ RV LPLPIFTP AKMGATNEEREDTPIQLQELLAETALGGQRVDRQEVAE ITKQLPPVVPVSKPGALRRSLSRMSQEAQRG
7955	A	72	489	HEAGSRMNGDHNSDVFSQD*QDFVQHFCQIGRVLTEDEMGHPEIGDA IARLKEVLEYNAIGGKYNRGLTVVAFRELVEPRKQDADSLQRAWTV GWCVE/ADDIMDSSLTRRGQICWYQKPGVGLDAINDANLLEACIYR
7956	A	1	236	GTRVAFRELVEPRKQDADSLQRAWTVGWCVELVRGVGQGRSFLQW W*LGWEGEWA*NLFLGCVCVSLSLVCYGOI
7957	A	317	1395	TGDQNSDVYAQEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARLKEV L\EYNAIGGKYNRGLTVV\VAFR\ELV\EPKQDA\DSLPA GPWTVG \WCVELLOAF\FLVADDIMDSSLTPGNRSCWYQKPGVGLDAINDG\

				NLL\EACIYRLLKLYCREQPYLNL\ELFLQSS\YQTEIGQTLDDL TAPP/QGNVDLSEFTEKRYKSI\VKYKTAFYSFYLP\IAAAMYMAGIDG EKEHANAKKILLEMGEFFQIQDDYLDLFGDPSVTGKIGTDIQDNKCS WLVVQCLQRATPEQYQILKENYQKEAEKVARVKALYEELDLPVFL QYEEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK
7958	A	3	484	ETPVPATSAAIRILVLLPSLRVTSPGRQGPSVDRVVFPPFKFRPERS RHAAAGPNVVRPQPKPHEVGGERGRPNAPANSFRSCSNLSPQYSLP KQNKSSSTNP*IPNKPTPPASPSGRTDGLSLLQPLPGSDGQASPTMRS SPAISSALEIEFGKTNPFH
7959	A	3	434	SGSSRPRGSAQPRPGPGACGMAAPTSE*SSPPAWQPRPPCGGLHHCP ACVHPHRDSGGSVPAPAAACCHTPHGRPWPEFEGQRPTQPPQGP VRPVLTLFAGRVASVPLVSLCAWASGSQPGPPSGGSGRALCTGLGAP PA
7960	A	2	332	VCKLQPQPLPAHSGSPNIHISQLCPSHAWGLLVLSGCVTFLESFF LCFALVLQRKSSSLGILSCPGSIFTALNSTNLYILGLGGFCLVFF* DRVSLCHPGWSEVVQS
7961	A	25	364	LFYLYHLLFFGFGLFLFLLIKLGSSLFINFSKKSVL*FTNWIYFSVL YFTDFCFIFIISFFGFSLIYFIIVGFPLKFIGFILSFI*ITVFYQQA QWLTVPVILWVAEVRGSL
7962	A	174	470	NGPP*RKKFFLSIPRKIWAPPGFF*/EGPPLFFFFFFLTESCSVA*P GMRWHNPGLLQPLPSGFKQFSCSLSPSSWDYRCPLPHANFFVVVFL VETEFC
7963	A	65	2774	PGKTGLGNMHAQRQFVVAAVRAEVRREHAVAKQALNRLKLAERVDDP ELQDSIQASLDSIREAVINSQEWTLRSIPELRLGLGDARSGKSSL IHRFLTGSYQVLEKTESEYKKEMLVDGQTHLVLIREEAGAPDAKFS GWADAVIFVFSLEDENSFQAVSRLHGQLSSLRGEGRGGLALAVGTQ DRISASSPRVGDARARALCADMKRCSYYETCATYGLNVDRVQFEVA QKVVTLRKQQLLAACKSLPSSPSHSAASTPVAGQASNGGHTSDYSS SLPSSPNVGHRELRAEAAAVAGLSTPGSLHRAAKRRTSLFANRRGSD SEKRLDSRGETTGSGRAIPIKQSFLKRSNGSNLNKEWKKKYVTLSS NGFLLYHPSINDYIHSTHGKEMDLLRTTVKVPGRPPRAISAFGPSA SINGLVKDMSTVQMGEGLEATTPMPSPSPSPSSLQPPPDQTSKHLK PDRNLARALSTVLSGQDYYPYFRDKETEAQIKICLAQGLKANCTPSG DLSPLSREPPSPMVKKQRRKLTTPSKTEGSAGQAEENFEFLIVS STGQTWHFEEAASFEERDAWVQAIESQILASLQCESSKVKLRTDSQS EAVAIQAIRNAKNSICVDCGAPNPTWASNLGALICIECSGIHRNL GTHLSRVRLDLDWPRELTLVLTAGNDTANRWESDTRGRAKPSR DSSREERESWIRAKYEQLLFLAPLSTSEEPLGRQLWAAVQAQDVATV LLLLAHARHGPLDTSVEDPQLRSPLHLAAELAHVVITQLLLWYGADV AARDAQVRTALFYARQAGSHLCADILLQHACPGEGGSAATTPSAATT PSITATPSPRRRSSAASVGRADAPVALHSWGRPTFTMGVLPKAKGK EKGISIESTK
7964	A	243	687	PHPIPHSEENFEFLIVSSTGQTWHFEEAASFEERDAWVQAIESQILAS LQCESSKVVRV*GGVEDWPQELTLVLTAGNDTAEVV*EESRGV* EGGGAWRQSQCPQPSLQLRTDSQSEAVAIQAIRNAKNSICAHASA DAWVEA
7965	A	3	370	PSDPEVAGDPIFPPGPPSCPEVKDKTKSSISLGWKPPAKDGGSPIKG YIV*MQEEGTTDWKRVNEPYKLITWECCGPNLKELRKYRFRVKAVN EAGESEPRDTTGEIPATDIQEEPEVFID
7966	A	3	78	FKIQNLIASTVRTVMVADCSRFDSPDLLLEAGDPATSPCRIFDLGSD NEEVVAIPDPSPHPKEGLSYSLSVLLGRSLPRCLISCIYPLCLSVAS GPHKFY*PHCQHRPHGDGGRLQPLRQP
7967	A	195	345	NDISANPAIKKFWKLPKCPTTEGWLNT*LYIHLVEYYATLKVCGDLY VR
7968	A	2	802	WRNSADVWWYCGGPLLDTLPSNWSGTCTLVQFAIPFALAFLOPEKEK PQHRKIREAPYGSFDSQVYLDATGVPQGVPHKFAQDQIAAGFESIF

				WWVTISKNIIDWINYIYYNQORFINYTRDAVKGIAEQLGPTSQMAWEN RMALDMILAKKGGVCVMIKTQCCTFIPNNTAPSGSITRALQGLTALS NELAKNSGVNDPFGWLERWFGKWKGIASILTSLAARIGVVILFGC *VTPCIRGLVQRLIETVLTKTSLSSPPPYSD
7969	A	113	362	WLHAPECFSQCPSQSPS*LGCQGPESDPPDRSVVGPPLSQAGSPGR PGGTVITLCCCLWPHLAPLFLHLWSPGKCTSLLVVQHS
7970	A	1	955	MTQPFNYSAFERIIFAGSPGHTVFSSERSLLVRPRSHPEPKGEHYVT GSPTPENQRTSAAMSKPHSEAGTAFIQTOQLHAAMADTFLEHMCRLD IDSPP/RRPLPATPQKPPWPWRPPSSAAVGP*SSPSLADVKSQV LVTCCCLACHCHWQREEWVLVTLGQGCCLSVSEFRV
7971	A	113	716	RSLGPCQHSWQSSPGGPRPQPRPGLGPCTAQGRCHGTGGPDE/TWV GFRVTAMMGARGRYL/AHLVSRLEMWGSYIRVHFTRPQEVPSGRSN SSPSHPAQ*GLWPLQHLRRTPEARAAPHIPSPSAC*VTICPLPPF HRPRDQDHLAPARSASPTVP\POPMVGRTPTP*TLTQRGSPGPMSP APIPLAANDSDKPSST
7972	A	244	1510	KFPFKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGEFKL LKAEEVAKLWGLRKNKNTNMNYDKLSRALRYYYDKNIIKKVIGQKFVY KFVSFPEILKMDPHAVEISRESLLLQSDCKVSPEGREAHKHGLAVL RSTSRNEYIHSGLYSSFTINLENPPDAFKAIKREKLEPPEDSPPV EEVRTVIRFVTNKTDKHVTRPVVSLPSTSEAAAASAFCLASSVSAKIS SLMLPNAASISSASPFSSRSPSLSPKSPLPSEHRSFLFLEACHSDSDS LEPLNLSSGSKTKSPSLPPKAKK\PKGLEISAPPLVSGTDIGSIAL NSPALPSGSLTPAFFTAQTPNGLLL\TPS\PLL\SSIHFW\GSL*SK FVPLSPARLQGPSTLQFPTLLNGHMPVPIPSLDRAASPVLLSSNSQ KS
7973	A	1	1230	MGEIAFPICASVMVGFDLQHGMEASITLWQFLLQLLLDQKHEHLICW TSNDGEFKLLKAEEVAKLWGLRKNKNTNMNYDKLSRALRYYYDKNIIK KVIGQKFVYKFVSFPEILKMDPHAVEISRESLLLQSDCKASPEGRE AHKHGLAALRSTSRNEYIHSGLYSSFTINSLQNPDAFKAIKTEKLE EPPEDSPPVEEVRTVIRFVTNKTDKHVTRPVVSLPSTSEAAAASAF ASSVSAKISSMLPNAASISSASPFSSRSPSLSPNSPLPSEHRSFL EAACHSDSLEPLNLSSGSKTKSPSLPPKAKKPKGLEISAPPLVLSG TDIGSIALNSPALPSGSLTPAFFTAQEMMVHVYSDSTRYQDLWELGY VHPLVSSVLSHYCRPMVLKVSMMQNNLLEDAHLHI
7974	A	3	360	LPAPGARPEWLLFPAPVVGVLWCWTPQSIISLHFFLNVPVGTLS SSSSP*RT*LPMTLS*VGAVSGFKPISRPEPHSGHNSPSLSQPSL TILVSSNSPGSGKARGPQCPQAWL
7975	A	194	373	LFG*LKAPPPGLKQFSGLSLRRSGNYGPPPPPPVYFFVFLKKNGFPL VTQGGNLNRTWG
7976	C	238	459	MQGVISPSTSTSLFVFLALVLPASHXPPQPPPLPGPPSEIAHLTTVR RGAALANVNHENISDTDENKLNAFVTA
7977	A	1	505	AGGAGEETPHQESQRQGCALPQEPPLYPPCPAIHPPPLPLGGLLLFP SLPSLALSCMVPPPWAAQEGI*MENHQPPEKKRLWGPPPPANSFP PLNPHLFQAGTGCPPCPREVPTSPPPWAEPPLPGPPSEIAHLTTVR RGAALANVNHENISDTDENKLNAFVTA
7978	A	39	141	LSIRGLNIIIKRQRL*DWIKQDSTLCCP*EIH
7979	A	8	533	FNYLLKFKIRPPHAFQMFPMSSQGKEGPETAESLSHHGCLSL*R* EISWAPPTCGAFPSSAATLGASVPLGASVPLGAAGMQRGRGRHRI PGDTWGLLLPGAGGTAESPAHNWEP*TSVPPSRPGHPSGSPAGLQSGR PPL*GDCEWGRKAGKGHAY*VPGPELHTLPLSDP
7980	A	1	9786	DGRVKYTLNKNLSKIEIPLPFGGKSSRDLMLETVRTPALHFKSVGF HLPSREFQVPTFTIPKLYQLQVPLLGVLDSLTVNSLYNWSASYSG GNTSTDHFSRLRARYHMKADSVVLLSYNVQSGSETTYDHKNFTLSC DGSRLRHKFLDSNIFSHVEKLGNNPVSKGLLIFDASSWGPMQMSAV HLDSKKKQHLFVKEVKIDGQFRVSSFYAKGTGLSCQRPNTGRLNG ESNLRFNSSYLQGTNQITGRYEDGTLSTSTSDLSGIIKNTASLKY

				<p> ENYELTLKSDTNGKYKNFATSNKMDMTFSKQNALLRSEYQADYESLR FFSLLSGSLNSHGLELNADILGTDKINSGAHKATLRIGQDGI STSAT TNLKCSLLVLEENELNAELGLSGASMKLTTNGRPFREHNAKFSLDGKAA LTEL SLGSAYQAMILGVDSKNIFNFKVSQEGKLKSLNDMMGSYAEMKF DHTNSLNIAGLSLDFSSKLDNIYSSDKFYKQTVNLQLQPYSLVTTLN SDLKYNALDLTNNGLRLLEPLKLHVAGNLKGAYQNNKHIYAISSA ALSASYKADTVAKVQGVFESHRLNTDIAGLASAIDMSTNYSNDSLHF SNVFRSVMAPFTMTIDAHTNGNGKLALWGEHTGQLYSKFLKAEPLA FTFSHDYKGSTSHHLVSRKSI SAAL EHKVSALLTPAEQTGTWKLKTQ FNNNEYSQDL DAYNTKDKIGVELTGRTLADLTLLDSPIKVPLLLSEP INI IDALEMRDAVEKPQEFTIVAFVKYDKNQDVHSINLPFFETLQEB FERNRQTIIVVLENVQRNLKHINIDQFVRKYRAALGKLPQQANDYLN SFNWERQVSHAKEKLTALTKKYRITENDIQIALDDAKINPNEKLSQL QTYMIQFDQYIKDSYDLHDLKIAIANIIDEIEKLSLDEHYHIRVN LVKTIHDLHLFIENIDFNKSGSSTASWIQNVDTKYQIRIQIQEKLQQ LKRHIQNIIDIQHLAGKLKQHIEAIDVRVLLDQLGTTISFERINDVLE HVKH FVINLIGDFEVAEKINAFRAKVHELIEREYVDQOIQVLMCLKV ELAHQYKCLKETIQKLSNVLQQVKIKDYFEKLVGFIDDAVKKLNELSF KTFIEDVNFKFLDMLIKKLKSFYHQFVDETNDKIREVTQRLNGEIQ LELPQKAEALKLFLEETKATVAVYLESQDTKITLI INWLQEALSSA SLAHMKAKFRETLEDTRDRMYQMDIQQELQRYLSLVGVYSTLVTYI SDWWTAAKNLTDFAEQYSIQDWAKRMKALVEQGFTVPEIKTILGTM PAFEVSLQALQKATFQTPDFIVPLTDLRIPSVQINFKDLKNIKIPSR FSTPEFTILNTFHIPSTIDFVEMKVKIIRTIDQMLNSELQWPVPI YLRDLKVEDIPLARITLPDFRLPEIAIPEFQLPHISHTIEVPTFGKL YSILKIQSPLFTLDANADIGNGTTSANEAGIAASITAKGESKLEVLN FDFQANAQLSNPKINPLALKESVKFSSKYLRTHEGSEMLFFGNAIEG KSNTVASLHTEKNTELSNGVIVKINNQLTDSNTKYFHKLNIPKLD FSSQADLRNEIKTLLKAGHIAWTSSGKGSWKWACPRFSDEGTHESQI SFTIEGPLTSFGLSNKINSKHLRVNQNLVYESGSLNFSKLEIQSQVD SQHVGH SVLTAKGMALFGEKAEFTGRHDAHNGKVIGTLKNSLFFS AQPFEITASTNNEGNLKVRFPLRLTGKIDFLNNYALFLSPSAQQASW QVSARFNQYKYNQNF SAGNNENIMEAHVGINGEANLDFLNIPLTIPE MRLPYTIITTPPLKDFSLWEKTGLKEFLKTTKQSFDSL SVKAYQYKKNK HRHSITNPLAVLCEFISSQISKFDRHFENRNNALDFVTKNSINETKI KFDKYKAEKSHDELPRTPQIPGYTVPVVNVEVSPFTIEMSAFGYVFP KAVSMPSFSILGSDVLVPSYTLILPSLELPVLHVPRNLKLSLPHFKE LCTISHIFIPAMGNNTYDFSFKSSVITLNTNAELFNQSDIVAHLLSS SSSVIDALQYKLEGTRRLTRKRGKLALATLSLKNFVEGSHNSTVSL TTKNMEVSVAKTTKAEIPILRMNFKQELNGNTKSKPTVSSSMEFKYD FNSSMLYSTAKGAVDHKLSLESLSYFSIESSTKGDVKGSVLSREYS GTIASEANTYLNKSTRSSVKLQGT SKIDDIWNLEVKENFAGEATLQ RIYSLWEHSTKNHLQLEGLFFTNGEHTSKATLELSPWQMSALVQVHA SQPSSFHDFPD LGQEV ALNANTKNQKIRWKNEVRIHSGSFQSQVELS NDQEKALHDIAGSLEGHLRFLKNIILPVYDKSLWDFLKL DVTTISGR RQHLRVSTAFVYTKNPNNGYSFSPVKVLADKFITPGLKLNDLNSVLV MPTFHVPFTDLQVPSCKLDFREIQIYKKLRTSSFALNLPTLPEVKFP EVDVLT KYSQPEDSLIPFFEITVPESQLTVSQFTLPKSVSDGIAALD LNAVANKIADFELPTIIVPEQTIEIPSIKFSVPAGIVIPSFQALTAR FEVDSPVYNATWSASLKNKADYVETVLDSTCSSSTVQFLEYELNVLT HKIEDGTLASKTKGTFAHDRDFAEYEEDGKYEGLQEWEGKAHLNKS PAFTDLHLRYQKDKKGISTSAASPAVGTVMGMDDEDDDFSKWNFYYS PQSSPDKLTIFKTEL RVRESDEETQIKVNWEEEAASGLLTSLKDNV PKATGVLYDYVNKYHWEHTGLTLREVSSKLRRNLQNNAEVWYQGAIR QIDDI D VRFQKAASGTTGT YQEWKDKAQNLYQELLTQEGQASFOGLK DNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPFQFPKPGIYTREE LCTMFIREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRKHKL </p>
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				IDVISMYRELLKDLKSEAQEVFKAIQSLKTTEVLRNLQDLLQFIFQL IEDNIKQLKEMKFTYLINYIQDEINTIFNDYIPYVFKLLKENLCLNL HKFNEFIQNELQEASQELQQIHQYIMALREEYFDPSIVGWTVKYYEL EEKIVSLIKNLLVALKDFHSEYIVSASNFTSQLSSQVEQFLHRNIQE YLSILTDPDGKGKEKIAELSATAQEI IKSQAIATKKIISDYHQQFRY KLQDFSDQLSDYIEKFIAESKRLIDLSTIQNYHTFLIYITELLKKLQS TTVMNPYMKLAPGELTIIL
7981	A	27	13822	VPFVAAAEEPAQPARAARPRGRSPGAAPPQAMDPFRPALLALLA LPALLLLLLLAGARAEEMLENVSLVCPKDATRFKHLRKYTYNYEAE SSGVPGTADSRSATRINCKVELEVPQLCSFILKTSQCILKEVYGFNP EGKALLKKTKNSEEFAAAMSRVELKLAIPGKQVFLYPEKDEPTYIL NIKRGIIISALLVPPETEEAKQVFLDFTVYGNCSTHFTVKTRKGNVAT EISTERDLGQCDRFPKIRPTGISPLALIKGMTRPLSTLISSSQSCYT LDAKRKHVAEAIKCEQHLFLPFSYKNKYGMVAQVTQTLKLEDTPKIN SRFFGEGTKKMGLAFESTKSTSPPKQAEAVLKTQVBLKLTISEQNI QRANLFNKLVTELRLGLSDEAVTSLLPQLIEVSSPTTLQALVQCGPQ CSTHILQWLKRVHANPLLIDVVTYLVALIPEPSAQQRLREIFNMARDQ RSRATLYALSHAVNNYHKTNPTGTQELLDIANYLMEQIQDDCTGDED YTYLILRVIGNMGQTMEQLTPELKSSILKCVQSTKPSLMIQKAAIQA LRKMEPKDKDQEVLLQTFLLDASPGDKRLAAYLMLMRSPSQADINKI VQILPWEQNEQVKNFVASHIANILNSEELDIQDLKKLVKEVLKESQL PTVMDFRKFSRNYQLYKSVSIPSLDPASAKIEGNLIFDPNNYLPKES MLKTTTLTAFGFASADLIEIGLEGKGFEPTLEALFGKQGFPPDSVNKA LYWVNGQVPDGVSKVLVDHFGYTKDDKHEQDMVNGIMLSVEKLIKDL KSKEVPEARAYLRILGEELGFASLHDLQLLGLKLLMGARTLQGIQPM IGEVIRKGSKNDFFLHYIFMENAFELPTGAGLQLQISSSGVIAPGA AGVKLEVANMQAELVAKPSVSVEFVTNMGIIIPDFARSGVQMNTNPF HESGLEAHVALKPGKLFIIIPSPKRPVKLLSGGNTLHLVSTTKTEVI PPLIENRQSWVCKQVFPGLNYCTSGAYSNASSTDSASYPLTGDTR LELELRPTGEIEQYSVSATYELQREDRALVDTLKFVTQAEQAKQTEA TMTFKYNRQSMTLSSSEVQIPDFDVLGTLIRVNDESTEGKTSYRLTL DIQNKKITEVALMGLHSCDTKEERKIKGVISIPRLQAEARSEILAHW SPAKLLLQMDSSATAYGSTVSKRVAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDPKSLHMYANRLLDHRVPQDTMTFRHVGSKLIVAMS SWLQKASGSLPYTQTLQDHLNSLKEFNLQNMGLPDFHIIENLFLKSD GRVKYTLNKNLSKIEIPLPFGGKSSRDLMLETVRTPALHFKSVGFH LPSREFQVPTFTIPKLYQLQVPLLGVLDLSTNVYTNLWNSASYS NTSTDHFSRLRHYHMKADSVVDLLSYNVQGSGETTYDHKNFTLSCD GSLRHKFLDSNIFKSHVEKLGNNPVSKGLLIFDASSSWGPMQMSASVH LDSKKKQHLFVKEVKIDGQFRVSSFYAKGTGLSCQRPNTGRLNGE SNLRFNSSYLQGTNQITGRYEDGTLSTLSTSDLSQSGIIKNTASLKYE NYELTLKSDTNGKYKNFATSNKMDMTFSKQNALRSEYQADYESLRF FSLSGSLNSHGLELNADILGTDKINSKAHKTALRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASMKLTTNGRFREHNAKFLDGAAL TELSLGSAYQAMILGVDSKNIFNFKVSQEGKLKLSNDMMGSAEMKFD HTNSLNIAGLSLDFSSKLDNIYSSDKFYKQTVNLQQLQPYSLVTTLNS DLKYNALDLTNNGLRLLEPLKLHVAGNLKGAYQNNIEKHIYAISAA LSASYKADTVAKVQGVFESHRLNTDIAGLASAIDMSTNYNSDSLHFS NVFRSVMAPFTMTIDAHTNGNGKLALWGEHTGQLYSKFLKAEPLAF TFSHDYKGSTSHHLVSRKSI SAALHKKVSALLTPAEQTGTWKLKTQF NNNEYSQDLDAYNTKDKIGVELTGRTLADTLDDSPIKVPLLLSEPI NIIDALEMRDAVEKPQEFTIVAFVKYDKNQDVHSINLPPFETLQEYF ERNRQTIIVVLENVQRNLKHINIDQFVRKYRAALGKLPPQANDYLS FNWERQVSHAKEKLTALTKKYRITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANIIDEIIEKLSLDEHYHIRVNL VKTIHDLHLFIENIDFNKSGSSTASWIQNVDTKYQIRIQIQEKLQQL KRHIQONIDIQHLAGKLKQHIEAIDVRVLLDQLGTTISFERINDVLEH

				VKHFVINLIGDFEVAEKINAFRAKVHELIEREYVDQQIQVLMDKLVE LAHQYKLKETIQKLSNVLQQVKIKDYFEKLVGFIDDAVKKLNELSPK TFIEDVKNKFLDMLIKKLKSFYHQFVDETDNDKIREVTQRLNGEIQAL ELPQKAEALKFLEETKATVAVYLESQDTKITLIINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDIQQELQRYLSLVGQVYSTLVTYIS DWWTAAKNLTDFAEQYSIQDWAKRMKALVEQGFVPEIKTILGTMP AFEVSLQALQKATFQTPDFIVPLTDLRIPSVQINFKDLKNIKIPSRF STPEFTILNTFHIPSFTIDFVEMKVKIIRTIDQMLNSELQWPVPDIY LRDCLKVEDIPLARITLPDFRLPEIAIPEFIIPTNLNDFQVPDLHIP EFQLPHISHTIEVPTFGKLYSILKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDQANAQLSNPKINPLALKESVKFSSK YLRTEHGSEMLFFGNAIEGKSNTVASLHTEKNTLELSNGVIVKINNQ LTLDSNTKYFHKLNIPKLDFFSSQADLRNEIKTLLKAGHIAWTSSGKG SWKWACPRFSDEGTHESQISFTIEGPLTSFGLSNKINSKHLRVNQN VYESGSLNFSKLEIQSQVDSQHVGHSVLTAKGMALFEGGKAEFTGRH DAHLNGKVIGTLKNSLFFSAQPFETASTNNEGNLKVRFPLRLTGKI DFLNNYALFLSPSAQQASWQVSARFNQYKYNQNFSAENNENIMEAHV GINGEANLDFLNIPLTIPEMRLPYTIITTPPLKDFSLWEKTLKBEFL KTTKQSFDSLVAQYKKNKHRHSITNPLAVLCEFISQSISKSFDRHFE KNRNNALDFVTKSYNETKIKFDKYKAEKSHDELPRTFQIPGYTVPV NVEVSPFTIEMSAFGYVFPKAVSMPSFSILGSDVRVPSYTLILPSLE LPVLHVPRNLKLSLPDFKELCTISHIFIPAMGNITYDFSFKSSVITL NTNALFNQSDIVAHLLSSSSSVIDALQYKLEGTRRLTRKRGLKLAT ALSLSNKFVEGSHNSTVSLTTKNMEVSVATTTKAQIPILRMNFKQEL NGNTKSKPTVSSSMEFKYDFNSSMLYSTAKGAVDHKLSLESITSYFS IESSTKGDVKGSVLSREYSGTIASEANTYLSNKSSTRSSVKLQGTSKI DDIWNLEVKENFAGEATLQRIYSLWEHSTKNHLQLEGLFFTNGEHTS KATLELSPWQMSALVQVHASQPSSFHDFPDLGQEVALNANTKNQKIR WKNEVRHSGSFQSQVELSNDQEKALHLDIAGSLGHLRFLKNIILPV YDKSLWDFLKLDTTISIGRRQHLRVSTAFVYTKNPNNGYSFSPVKVL ADKFIIPLGLKNDLNSVLVMPFTFHVPTDLQVPSCKLDREIQIYKK LRTSSPALNPLTLPEVKFPEVDVLTKEYSQPEDSLIPFFEITVPESQL TVSQFTLPKSVSDGIAALDLNAVANKIADFELPTIIVPEQTIEIPSI KFSVPAGIAIPSFQALTARFEVDSPVYNATWSASLKNKADYVETVLD STCSSTVQFLEYELNVLGTHKIEDGTLASKTKGTFAHRDPSABEYED GKYEGLQEWEGKAHLNIKSPAFTDLHLRYQKDKKGHISTSAASPAGT VGMDMDEDDDFSKWNFYSPQSSPDKKLTIFKTELVRRESDEETQIK VNWEEEAASGLLTSCLKDNVPKATGVLYDYVNKYHWEHTGLTLREVSS KLRRNLQDHAEWVYQGAIREIDDIDERFQKGASGTTGTQYQEWKDKAQ NLYQELLTQEQQASFGQLKDNVFDGLVRVTQEFHMKVKHLIDSLIDF LNFPRFQFPGKPGIYTREELCTMFIREVGTVLSQVYSKVHNGSEILF SYFQDLVITLPPFELRKHKLIDVISMYRELLKDLKSKEAQEVFKAIQSL KTEVLRNLQDLLQFIFQLIEDNIKQLKEMKFTYLINYIQDEINTIF NDYIPYVFKLLKENLCLNLHKNFNEFIQNELQEASQELQQIHQYIMAL REEYFDPSIVGWTVKYEELEEKIVSLIKNLLVALKDFHSEYIVSASN FTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEIIK SQAI\ATKKIISDYHQFQRYKLQDFSDQLSDYYEKFIAESKRLIDLS IQNYHT\FLIYITELLKKLQSTT\VMNPYMKLAPGELTIIL ELFGIIALQTIAYSILWDLKFLMRNLALGGGLLLLLAESRSEGKSMF AG\LMFMTLLHFDASFFSIVQNIQVGTALMILVAIGFKTKLAALTLVV WLFAINVYFNAFWTIPVYKPMHDFLKY
7982	A	40	401	
7983	A	1	900	FRAAGAGADGREPASERASRAEPPAVAMGQNDLMGMAEDFADQFLRV TKQYLPHVARLCLISTFLEDGIRMWFQWSEQRDYIDTTWNCGYLLAS SFVFLNLLGQLTGCVLVLSRNFVQYACFGLFGIIFLY\TIAYSILWD LKFLMRNLALGGGLLLLLAESRSEGKSMFAG\VPTMRES SPKQYMQ GGRVLLVLMFMTLLHF\ DASFLFLVQNIQV\ TALMI\ LVAIGFKTK

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				L\AALTLVVWLFAINVYFNAFWTIPVYK\PMHDFLKYDF\FQTM SVI GGLLLV\VALGPGGVSMDEKKKEW
7984	A	2	398	GRVGRPTRPPTRPPTRPPTRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SS SSGPPFGVSPCVPEILKSSSPRIGCPRN*AFPFKRGNL
7985	A	5	230	IGNFKNVFSIVNITTRQNTSTDIENTLNKNTHV*NTVSNS*YTVFSSA CGTFTKISHLLRH*TSLDKF*KLDVLWS
7986	A	1	366	NPSIVGGQDLCKGNYKTQIKDLLADGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPAGPMKTPTSFLIELGKTIVQFL*NQKRV*ITKVILSKK PQKTENKTKLEAFHSTLCYLPSNYATRL
7987	A	3	363	ISKKKFFLKGFFFLGFF*KKPPFFFFPPPPPG*RGKKKIFFFFWVKK NPLEKNFFSLFLKKGPPPTPPGGFFFFFKKKRAPQGGGPPKIFFFFFF FFFFFFFFFGDGVLLCCPGWSAV
7988	A	2	360	GLPS*HYSPPQLPH*SHSHTIAPKAEKANRKETHFSRSPQQISGRG PPQDKSLAKVDFLDQLRPMVGHSLGRGPGHLPKHMPTPEQIQEEPEA HIHLPLVCEQLPLLPWEDFVYGSSR
7989	A	490	583	NH*SPMFGYCICVCFETESCSVAQAGVQWYNRGSQPLPGPKGFVC LSLPSSWDYRRRPP
7990	A	1	129	QPGPEGKIRFFLKIPNLTPSGGKSLKFPLFKRVKPENCLSLRG*GCN *PGPEGKIRFFLKIPNLTPSGGKSLKFPLFKRVKPENCLSLRG
7991	C	96	380	MWIPFSKFLVXXX XX F
7992	A	202	499	ILGFVQWHDHSSPQPKTPGLKQSSCLNFLSS*DNRHMPPGLANFFIF VEMGSCYVAQACLELLGSSNPLASVSQNAIGTSMQCTQLFLLLLNR FPAFL
7993	A	1	206	NSSVFLHLQALGIPHLAYVSVFPPTPG*GSGHGRSLLSISVQGGLP PQRSPASPFLDIIHQGPW
7994	A	2	349	TCHRRKRKRNRPRHGEVGLGYPTDESAFAPSAPALGPGEPRVPGSSSGR ASGH*WYPNAVESP*EEGEL*GRRGETLVAEKKKKPRHGEVGPSPM EKKCLPISP*AGPRGPRRPWF
7995	A	269	365	GHLAIGHPPF*MSFNHGRKTRTWNYLGSSEQ
7996	A	1	314	PSRSFISNH*PHQDV*PRFFNGIHL*YSHTPGINHVEPEPNSTRSKA CWEGFGSSNSGNGSFLGAR*VDVQEVLTITWRVIRVWN*CFGRNSAP MAQSKSSSES
7997	A	65	355	YFYIYFSIYHFIAPPYYFSLVFLHLVCPYLSSFLSR*KIHVCLKDPK VNFS*TIPKLSKLELLESISLFFL*NVDIFIILEIILYLYSAILKRV YF
7998	A	1	957	MGLLLKASSLASVTGFCLLQEGPDQEVFYLLLFVNYFSAKQLLAYR CFVEMGSEILGPTLSETRPEALPPPSNETPAVSDSKEKKNAAKKKC LYNFQDAFMEANKVVMATSSATSSVSCATTQSSNSQFRVSSKRPP SVARGDPDCEGHRCEGVYDPQDDGDESADEDCSEHSSSTSTSTN QKEGKYCDCCYCEFFGHGGNGFVLVLAIMRAAADTPALSAGEPSFRR KEPSTVEMIEERPSCCDCSTLKSSAHTSQSYSRFRILTIGPDWEALGE KPCVPVQKTRDCWSAENTVCPFRSVQHRGTHDGPRP
7999	A	97	4146	EKEPYEISAEADREPQQLQNYWSEVRYTVRCIYRQAGTPLADDQDQ SLVPDKEGVKELVDRLCERDPYQLYQRLEQQAREYVLEMKVRLRLQL SAAAKVKAPSGLQGPQAHQFISLLLEEGALCQAARSISTFLGTLE NEHLKKFQVTWELHNKHLFENLVFSEPLLQSNLPALVSQIRLGTTH DTCESTYSTLLQRYQRSEELRRVAEWELECKRIDAYVDEQMTMK TKQRMLETEDWELFKORRFIEEQLTNKKAVTGENNFTDMRHVLSRL SMPDCPNCNYYRRACDDCSLHILTCGIMDPPVTDDIHIHQPLQV DPAPDYLAERSPPSVSSASSSGSGSSSPITIQQHPRLILTDSGSAPT CSDDDEVAPLSAKFADIYPLSNYDDTEVVANMNGIHSELNGGGENMA LKDESPQISSTSSSSSEADDEEADGESSGEPGAPKEDGVLGSRSPR TEESKADSPPPSYPTQAEQAPNTCECHVCKQEASGLTPSAMTAGAL

				PPGHQFLSPEKPTHPALHLYPHIHGHVPLHTVPHLPRPLIHPTLYAT PPFTHSKALPPAPVQNHTNKHQVFNASLQDHIYPSCFGNTPEWNSSK FISLWGSEVMNDKNWNP GTFLPDTISGSEILGPTLSETRPEALPPPS SNETPAVSDSKEKKNAAKKKCLYNFQDAFMEANKVVMATSSATSSVS CTATTVQSSNSQFRVSSKRPPSVGDV FHG I SKEDHRHSAPAAPRNSP TGLAPLPALSPAALSPAALSPASTPHLANLAAPSF PKTATTT PGFVD TRKSFCPAPLPPATDGSISAPPSVCSDPDCEGHRCENGVYDPQQDDG DESADEDSCEHSSSTSTSTNQKEGKYCDCCYCEFFGHGGPPAAPT RNYAEMREKLRLRLTKRKEEQPKMDQISERESVVDHRRVEDLLQFI NSSETKPVSSSTRAAKRARHKQRKLEEKARLEAEARAREHLHLQEEQR RREEEDEEEEDRFKEEFQRLQELQKLRAVKKKKKERPSKDCPKLD MLTRNFQAATESVPNSGNIHNGSLEQTEEPETSSHSRHMNHSEPR PGLGADGDAADPVDTRDSKFLLPKEVNGKQHEPLSFFFDIMQHHKEG NGKQKL RQTSKASSEPARRPTEPPKATEGQSKPRAQTESKAKVVDLM SITEQKREERKVNSNNNNKKQLNHIKDEKSNPTMEPTSPGEHQONS KLVLAE SPQPKGNKKNKKKKGDRVNSIDGVSLLLPSLGYNGAILA HCNLR L PGSSDCAASASQVVGITDDVFLPKDIDLDSVMDETEREVE YFKRFCLDSARQTRQRLSINWSNFS LKKATFAAH
8000	A	97	2728	EKEPYEEISAEADREPQQLQNYWSEVRYTVRCIYRQAGTPLADDQDQ SLVPDKEGVKELVDRLCERDPYQLYQRLEQQAREYVLEMKVRLLRQL SAAAKVKAPSGLQGPQAHQFISLLLEYGALCQAARSISTFLGTLE NEHLKKFQVTWELHNKHLFENLVFSEPLLQSNLPALVSPIRLGTTH DTCSEDTYSTLLQRYQRSEELRRVAEEWLECQKRIDAYVDEQMTMK TKQRM LTEDWELFKQRRFIEEQLTNKKAVTGENNFTDTMRHVLSSRL SMPDCPN CNYRRRCACDDCSLHILTCGIMDPVTDIHIHQPLQV DPAPDYLAERSPPSVSSASSGSGSSSPITIQHPRLILTDSGSAPT CSDDDEDVAPLSAKFADIYPLSNYDDTEVVANMNGIHSELNGGGENMA LKDESPQISSTSSSSSEADDEEADGESSGEPGAPKEDGVLSRSR TEESKADSPPPSYPTQAEQAPNTCECHVCKQEAAGLTPSAMTAGAL PPGHQFLSPEKPTHPALHLYPHIHGHVPLHTVPHLPRPLIHPTLYAT PPFTHSKALPPAPVQNHTNKHQVFNASLQDHIYPSCFGNTPEWNSSK FISLWGSEVMNDKNWNP GTFLPDTISGSEILGPTLSETRPEALPPPS SNETPAVSDSKEKKNAAKKKCLYNFQDAFMEANKVVMATSSATSSVS CTATTVQSSNSQFRVSSKRPPSVGDV FHG I SKEDHRHSAPAAPRNSP TGLAPLPALSPAALSPAALSPASTPHLANLAAPSF PKTATTT PGFVD TRKSFCPAPLPPATDGSISAPPSVCSDPDCEGHRCENGVYDPQQDDG DESADEDSCEHSSSTSTSTNQKEASSCTNK
8001	A	1	2295	MGLLLKASSLASVTGFCLLQEGPQDQEVFYLLLFVNYFSAKQLLAYR CFVEMGSEILGPTLSETRPEALPPSSNETPAVSDSKEKKNAAKKKC LYNFQDAFMEANKVVMATSSATSSVSC TATTVQSSNSQFRVSSKRPP SVGDV FHG I SKEDHRHSAPAAPRNSPTGLAPLPALSPAALSPAALSP ASTPHLANLAAPSF PKTATTT PGFVDTRKSFCPAPLPPATDGSISAP PSVCSDPDCEGHRCENGVYDPQQDDGDESADEDSCEHSSSTSTSTN QKEGKYCDCCYCEFFGHGGPPAAPT SRNYAEMREKLRLRLTKRKEEQ PKKMDQISERESVVDHRRVEDLLQFINSETKPNFVLVLAIMRAAA DTPALSAGEPSFRRKEPSTVEMIEERPSCCDCSTLKSSAHTS QSYSR FRLTIGPDWEALGEKPCVPQKTRDCWSAENTLEEKARLEAEARARE HLHLQEEQRREEEDEEEEDRFKEEFQRLQELQKLRAVKKKKKER PSKDCPKLDMLTRNFQAATESVPNSGNIHNGSLEQTEEPETSSHSR RHMNHSEPRPGLGADGDAADPVDTRDSKFLLPKEVNGKQHEPLSFF DIMQHHKEGNGKQKL RQTSKASSEPARRPTEPPKATEGQSKPRAQTE SKAKVVDLMSITEQKREERKVNSNNNNKKQLNHIKDEKSNPTMEPT SPGEHQONS KLVLAE SPQPKGNKKNKKKKGDRVNSIDSKNLDPII HGAFTDLLSPTTQ
8002	A	97	4027	EKEPYEEISAEADREPQQLQNYWSEVRYTVRCIYRQAGTPLADDQDQ SLVPDKEGVKELVDRLCERDPYQLYQRLEQQAREYVLEMKVRLLRQL

				SAAAKVKAPSGLQGPQAHQFISLLEEYGALCQAARSISTFLGTLE NEHLKKFQVTWELHNKHLFENLVFSEPLLQSNLPALVSQIRLGTTH DTCSEDTYSTLLQRYQRSEELRRVAEEWLECKRIDAYVDEQMTMK TKQRLMTEDWELFKQRRFIEEQLTNKKAVTGENNFTDTMRHVLSSRL SMPDCPNCNYYRRRCACDDCSLHILTCGIMDPVTDIHIHQLPLQV DPAPDYLAERSPPSVSSASSSGSGSSSPITIQHPRLILTDSGSAPT CSDDEDVAPLSAKFADIYPLSNYDDTEVVANMNGIHSELNGGGENMA LKDESPQISSTSSSSSEADDEEADGESSGEPGAPKEDGVLGSRSPR TEESKADSPPPSYPTQQAQAPNTCECHVCKQEASGLTPSAMTAGAL PPGHQFLSPEKPTHPLHLYPHIHGHVPLHTVPHLPRPLIHPTLYAT PPFTHSKALPPAPVQNTNKHQVFNASLQDHIYPSCFGNTPEWNSSK FISLWGSEVMNDKNWNPFTLPTDISGSEILGPTLSETRPEALPPPS SNETPAVSDSKEKKNAKKKCLYNFQDAFMEANK\VVMATSSATSSV SWTANTVQSSNSQFRVSSKRPPSVGDVFGHISLGD\QKNSAPAAPRN SPTGLAPLPALSPAALSPAALSPASTPHLANLAAPSFKTATTTTGF VDTRKSFCPAPLPPATDGSISAPPSVCSDPDCEGRCENGKATVDPQQD DGDESADEDSCEHSSSTSTSTNQKEGKYCDCCYCEFFGHGGPPAAP TSRNYAEMREKLRLRLTKRKEEQPKMDQISERESVVDHRRVEDLLQ FINSSETKPVSSSTRAAKRARHKQRKLEEKARLEAEARAREHLHLQEE QRRREEDDEEEDRFEKFQRLQELQKLRAVKKKKKERPSKDCPK LDMLTRNFQAATESVPNSGNIHNGSLEQTEEPETSSHSRHMNHSE PRPGLGADGDAADPVDTRDSKFLLPKEVNGKQHEPLSFFDIMQHKK EGNGKQKLRTSKASSEPARRPTEPPKATEGQSKPRAQTESKAKVVD LMSITEQKREERKVNNSNNNNKKQLNHIKDEKSNPTPMEPTSPGEHQ NSKLVLAESEPQKGNKKNKKKKGDRVNSIDVFLPKDIDLDSVDM DETEREVEYFKRFCLDSARQTRQRLSINWSNFSLLKATFAAH
8003	A	1	450	GVPIYKRHIEGF*PGLNGPLKFNGPSSSSSSDGLRLFGSGGGQSPN WVPLGSYQGRSRPVPPGGSSAEPFPPSPASGGTHVPQLRALPPLHGH SAAHPHLSLALTVPVPPVVRTL*GHWGPGPPTLDAPPSPSHLQVPLSS QGGIPPHWT
8004	A	16	303	GENPLMRWPEALPGVFKTCFSPPT*GYGGGLMFLCHHADSINFSAFQ PINNADFIVPIEIEGTTTHQVSCQPDHTQPRGWGVCLLPHLYWGPPPI SG
8005	A	146	809	RIFSLCSAALSCKHGNPQDCSRRAPGNVPAAISRAPSLVLGLRARTV TRKGGLRPRKGEQGPIPSPSDPAVKGPGAEPGQARFAPVYQILIGAP RWEPLSTGGYTVSGSSPVVEVGTRANQPRQ*ALPASHLPPLASRSS SSSHLYTAAPPLVSRGSGGSAGRALDSSFPQHSKAKPRPSAGLEAPG HWGRTGGDRRKGTGGEPTTFAEVEALPASARP
8006	A	111	371	FGPGPPL*SPLF*GSSSSHSGVGK*NPSFLPGGTPVFFKNPKFPPPW GGPPVSPLFWGGETGNWGNPGGGTLEGPGYPPLALPGGK
8007	A	85	394	DWRRRRRDSRSS*REDCQSTIYVRKRAKSNWCWSKEKS KSHERDSI PIRIEKRMRSRSKGRDHENVKEKEKQSDSIGNDQEGSR SREKSNQF DSKSNERDH
8008	A	2	2255	AAQGRRRARVTWRRQMPLAQLKEPWPLMELVPLDPENGQTSGEAGL QPSKDEGLVKEISITHVKAQSEKADPSHFELKVLGQGSFGKVFLV RKVTRPDSGHLIYAMKVLKATLKVRDRVRTKMERDILADVNHFPVVK LHYAFQTEGKLYLILDFLRGGDLFTRLKVEVMFTEEDVKFYLAELAL GLDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGLSKEAIDHEKKAY SFCGTVEYMAPEVVNRQGHSHSADWWSYGVLMEMLTGS LFPQGKDR KETMTLILKAKLGMPQFLSTEASLLRALFKRNPANRLGSGPDGAEE IKRHVYSTIDWNKLYRREITPPFKPAVAQPDFTFYFDEFTSRPPY ESSWQPPPELGPNTWFGVPSVATGLMEDDGKPRAPQAPLHVSQQQL HGKNLVFSDGYVVKETIGVGSYSECKRCVHKATNMEYAVKVIDKSKR DPSEEIEILLRYGQHPNIIITLKDVEDDGKHVYLVTLMRSGELLDKI LRQKFFSEREASFVLHTIGKTVEYLHSQGVVHRDLKPSNIIYVDESG NPECLRICDFGFAQLRAENGLLMTPCYTANFVAPEVLKRQGYDEGC

				DIWSLGILLYTMLAGYTPFANGPSDTPPEILTRIGSGKFTLSGGNWN TVSETAKDLVSKMLHVDPHQRLTAKQVLQHPVWTQKDKLPQSLSHQ DLQLVKGAMATYSALNSSKPTPQLKPIESSILAQRVRKLPSTTL
8009	A	1	1845	MAEGDAKGDKAKVKDEKPAPPKPEPKPKKAPAKKGEKVPKGGKKGAD AGKEGNNPAENGDAKTDQEGPAAQLQGVWTADSLQLSAPGLASDADS LLAQDHILPHPSSSPRAAPIRKFTTITWFSHINCSLRTGHDDNGG FVEQKGGKVRDRVRTKMERDILADVNDHPFVVKLHYAFQTGEGKLYLIL DFLRGGDLFTRLSKEVMFTEEDVKFYLAELALGLDHLHSLGIIYRDL KPENILLDEEGHIKLTDFGLSKEAIDHEKKAYSFCGTVEYMAPEGSA LMSPPGCCFRAKLGMPQFLSTEAQSLLRALFKRNPANRLSGSPDGAEE IKRHVYSTIDWNKLYRREIKPPFKPAVAQPDFTFYDTEFTSRTPK DSPGIPPSAGAHQLFRGFSFVATGLMEDDGKPRAPQAPLHVVQQLH GKNLVFSDGYVVKETIGVGSYSECKRCVHKATNMEYAVKVIDKSKRD PSEEIEILLRYGOHPNIITLKDVEDDGKHVYLVTELMRGKELDKIL RQKFFSEREASFVLHTIGKTVEYLHSQGEWKWALRPNYLRSCWLGRY PLSLRGSNSDPSQLEFP SNKCSAPLRGSERGVGGAAAAGAVGTRAE RHKN
8010	A	12	452	SEPP*ITSVDPVRVGNASTGYGKIWLDDVSCDGDSEDLWSCRNSGWG NNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGA VGILC ANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGG EASLW
8011	A	121	342	QNESVVMKTFILAVFKLPLKIRQIKCIYIFYN*ELKLYSVILKYFFL YDFRPVCLVLSEIPFMSTWFLLVSTFR
8012	A	3	385	EKGPLSPKVLFNHLCQKAPRFKDFQQQDSQELLHYLLDAGRTE*TKR IQASILKAFNNPTTKTADDETRKKVKTYGKEGVKMNIFIDRIFIGELT STVMCEECANISTVKDPFIDISLPIIEERVSKP
8013	A	18	280	KCRSRN*TA*FHRLNAKALSLTLLNVYQKKHLVEILSYHNCDSQTR NAPELDCLIRLQAQNIQQRHIVFLTGKESTPKLSTMNIGM
8014	A	3	271	FFLRQSHSVT\ RLECTGAI*AHCNLCPLGSSDSPASAS*VAGITGMC HHARLIFVFLVETGFHHVQAVLELL/NLMICPPQPPKVLGLQA
8015	A	609	921	FYLSEEAFFFFFETES/HLLSPRLECSGMMSAHCNLRPLPGSSDSP ASAS*VAGITGGHHPAQLIFVAF/MYQPGFCHVGQAGQQLLA*VIC LPQPPKVLGITGA
8016	A	140	347	FPPICYLLEIGSHSVVQAGVQWHRHSAQYP*IEHKQSSCVSLMSS* HYSHVPPSPGNILL*RRGSCV
8017	A	2	349	AGVPPGNPPLWGGEGGSGPRGGGLKPGFPQGRGNPFFFKKSQPTPPGG GPPLIPPPWGGGAGGSPLPQGRFQ*TKIGPPSPRGGKKKKPPFPKK KKKKKKRKEKSEMPGMVNLNA
8018	C	282	497	MGSFQSHHTKWQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXPGGGPGAQFPL
8019	C	267	473	MGSFQSHHTKWQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXTGGGPAPI
8020	C	435	821	MKSRVIGWASGLKNEIFFFFFFFWRDRYRAMPLRLVLNLLFLIEPP VSILVKHWDYRHEPPPPRXRLPFCMMRLEGPHCFRDFATIYKKQSVR TVAGLFSCLIKFSAHTNLDQRIWDLNPISGYFPN*
8021	A	121	818	HSKGSQVQSPGPEPSSAGPKPGAQPQTWGLAAPEEGREGGKCGRHC RNSKPLSQPCAGVWSGRGAEEGGAGPDHPARPTGPPSSPSCSAGLPD L**GLKPPLEASSMDPGFVLEGGPRVREGVCQDGI*A*ELEEVPSPG GSATSGAATLSDRRGGNGASQARLP*PSHWLPRAK*APQG*ASPGSP TACPAHPHSWKGSAGPGMGRGRVVGDRGGAWGTGSHCNPTPSS
8022	A	11	369	SFTCCFQMHTKLLCLNTLCNTFLSTGAFFLIVLTWLSPIAVRLSLNV ISERPFLFILSVVDPCAHIYLSLLFVS*VLPQYVIALFVPHKRM*E TMYACLPVCP*LLTACLEHNCSIFI
8023	A	3247	5031	EGLRGTAALLTGGGRGP*GQPQQ/PGGPASSPSPAAPGPAAEPACS TALWPTVSLRAPSPCPPQRAQGYGSWG/GEPP/NSMASGGDG/EPL SQGLAPAGTPGLARLQPGHWAWSLWPSLRGFPGGPQTGQSPLSQPH

10646

				SALTGRGRSPGALGPPPPQRPHPQRPAPDPARPQR*TPLTAGATTRPQ HLPQGNCRCSLLLLFLLLLFLLLLFLLFFLILFFLFIPLLLLL FLLPISLRLNRSQWDLGGGEQHVREAHPPDPVEQPRPFSVIGEVSE VLVGQTQRHSSWEAHLKWRHGEHLGLEVIGPLPNPRKAWMPHLLQ LGPRDAEHRGHESVVASSEGRVAPVGRPHRAALSRAAALNEGTTGAR GAAAAGVRVMLRLQRGGGEHGGRRQSSQGAVPREGVPRESVLLQLSLW ACGVRLSPSRAGSRVQG
8024	A	87	569	KQPPPHGESAAWAATSRPGWLLCRPAEGRTPGWTAFDVHPTLMQKL PEHSGNFSGQSPPCQLEALPRPSTCPLGSSRGSGREGPLPPT*ELFP NGQSVRCQVGPGYDSWCPGPGPAPCPPT*P*GPQALTSAPGPNK HPGLELGRRRGERAPGPF
8025	A	2	348	KALACPTCCVLGVHHAHSVAGGFPGRPLVRRHIAPAGHQVTLSTFLH PTLCHPKSNCTPCGSRRAVPTPTPLPAPGPQAFCPVPGSHWLAWSP RGRSPPTSVAPTQPY*QPPSC
8026	A	3	361	HEGTVQQPQARGLYEDLLMSEGENDEDDAGSDDNGDNIFSAIHLSES GRSDA*PGGIRPKQSRMLKENTRMVMDNEERLLFYEGDCGEASHGL EDSCLSYGSYEDPDPKWNTQNTSFC
8027	A	2	424	LFWSPQTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERHFD LSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVD PVNFKLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
8028	A	3	456	PQTQREPTMVLSPADKTNVKAAGKVGGAHAGEYGAEALERMFSLFPT TKNYFPHFDSLHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSD LHAHKLRVD\PVNFKLSHCLLVTLAAHLPAEFTPAVHA\SLDKILA SVSTVLTSKYR
8029	A	3	198	RQSGSVTQPGVQWNNLGLL*P*PPGLKQSSYLSSPSSWDYRCVPTR LANSYFKFI*YVFFCLF
8030	A	1	346	LFAQPNPVTFKIRIYCMSKDIIDKVRARPPWEKICANHVNKGLGS RIYKVLLLE*KNIVRLNQKANAQFYAGYKLCRYKFSNKSIVNE*KV LLFMR*EYIPVSTHFICCVIL
8031	A	60	525	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEADCAVLIVAAGVGEFEAGICKNGQTREHALLAYTLGVKQ LIVGVNKMDSSTEPPYSQKRYEEIVKEVSTYIKKIGYNPDTVAFVPIS GWNGDNMLEPSAN
8032	B	68	679	MGKEKXHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLGVKQLIVGVNKMDSGTGIAILTGDFPSLEPRHVSTWLQHVVTIPTR NWHKCYCVGVVANFLN*
8033	A	53	1497	KLPLKAKMGKEKTYINL\AVIGHVDSGKSTTTGHLIYKCGGIDKRTI EKFEKEAAEMGKGSFKYAWVLDKLKAERERGITIDISLW\KFETSKY YVTIIGAPGHRDFIKNMITGTSQADWCCPELLLVGGEFEAGISKNG QT\REHALLAYTLGVKQLI\AGANKMDSSTEPPYSQKRYEEIVKEV\S TYIKKIGY\NPATVAF\VPISGWNG\DNMLEP\SANMPWFKGWKVS\ RKDWQCQLGTTLEALDCILPPTRPTDKLLRLAFQ\DA*QNGGIGTV P\VG\RVETGVLKPG\MGVTF\APVNVYNGK*KSVEMHHEAFECKLF PG\DKCGAFNVK\NVSVKDV\RRGNVAGDSKNDPPMEA\AGFTAQVI ILNHSGQISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPK FLKSGDAAIIDMVPGKPMCVESFSDYPPPLGCFAVRDMRQTVAVGVIK AVDKKAAGAGKVTSAQKAQKAK
8034	A	3	309	RFTGHYRMLSGEKPYEWIEWGKRLSSNTALTQHORIHTGENPFECKE CGKAFNQKITLIQHQRVHTGEKPYEC*ACGKTRFWGGRF ILHQNLPT QKTPVQA
8035	A	3	366	RDSVVEILFEQDNKEQSVATLILDSLIQCPIDTRKQLAENLEMMFDV GKTQPPLLKRAFSTEK*KFD*/TINLASYQIFNQL*ANCTKYVGCFV IEDYSGSEIILCLLFALIYNSFDFVSLV
8036	C	310	546	MGIMSVPPHPQNVDPYPLDGEKILHILGFNPEIQLWEILFEQDNGRAI

				SWPLLILGFPLYSVPIGHQGRQLGRRNLGRS*
8037	A	97	333	HRIRPICSPQYMEKVYVTNNNYRILEIDMNFPPPETEGVGGQVLE VMPHEELKPSIFFFF*DRVSLCHPGWSAVVQS
8038	A	250	378	TESLYLNTIKATYEKFTANITLNNEMLKAFSLRLDTR*EHSLS
8039	A	280	759	GYINNGGRKRRTELKPTPRSCRAEGGGVEGGPPACPPPTNCLQRLQ PHLGSCTEISGQERE*GYINNGGRKRRTELKPTPRSCRAEGGGVEG GPPACPPPTNCLQRLQPHLGSCTEISGQERESGGGEGNSGPNRVH GFSKAGHGLGVGEEEEERQLWL*TGRKQRPNIPIRRLPQASLHLPPA SPCQPAVPGALSSPRRWPQPPASHSCSPSPRHTKS
8040	A	1	401	ILVLDPPPQPPKLLSVKGNPEDFIFRQFFFSYPLFPFPPFSYAKPP VSNETPFPHPRFSKLLSQGPADMPPLPGSLP*LLHYSACMLHHLF CSLAHCAFRLLSQGCQYLHGLMHMFRSGHMHYAAGR
8041	A	32	379	CVYTFIC*EISGLFPVWG*YRK*GSSSSSSSSSSSSSSSHFNKYSS CMFNFF*NC*TVLQSGCTILLHHWCMRVLSP*CCQHLAVFFSIIA ILLSV*LHLTVIFICIPQITS
8042	A	30	436	DGSSLCRPGWSAEQDCVSSGGEKKKKGRDNIEDEACSSRPSR*LFEE NIHLVHALIEEDQLANI IDISAGSAYTILDEKLTLSKRFTRWVPKPL PSDQLQTRAEFLMEILNGWDQDPEAFLQRIVTGDET*FYQR
8043	A	3	342	IPKPMAKLPFMKYRDLHTNLLYSRMETGPKHIPMTLLKIMEDIAIG MDNLSLMNYLYLELTARNCMERDDMTDCEADFGLSRKRYSGENYLHC RIANRPV*GSAIESLAHR
8044	A	3	380	LIKXHVDFDLATNVQEEKIAALEDFAQLITAGHYAKGDI FSRNEV LDRWRRVKTQMIKRA*V*KSQTLQQFNRDVDENEAWISEKLHTASD DSYKDPTNIQLCKLLSKHQKHQAF*TELPAT
8045	A	169	375	SSSSLPLHITNNPLHQQLPPLPAYTGAEGDPCALLS*YCLIHLN TEAVNNIITFLGKQPKRYDKV
8046	A	27	289	RSPKTHGGRRWGMVRPGTAPT/PCCPHRPQLP/CQPLLGPPE*SL EGRSSSLDSCMEESQTHAAPACTWCSGPR*PWMGPAARCSG
8047	A	3	284	LFLWRRQLTLTENPRWWPTLGDGQARDCSDACCPHRPQLPSSHCSQT KSSPIPEVPRPPKHR*GGVCAGPSHLPGGPGSSPSPCPWPGLF
8048	A	459	1020	EPGRGAEQGGVPGGKGPETSAAAPTAREPERVPGGA\PPAPECAC AELVAAPAPAGGSL\PAGPRPWERPRWAAGAP/QGDKGPGEAATSPA /RGDSGVEPRGGGVPLPRHAGPQARRCEPTLPHDLYSQVQPEHRAA G/LHPRSSGTI*APCTTCR\AA*V*DSSIPESREELRPSKKRSFRS EKEK
8049	A	3	419	VTCKAFAQAQALIVHQI IHTGKKPYDCGACGKDFREKVHLVRHQRT HTGEKPYDRSERGKAFSHKSDLI IHHRVHTGEKPYECCECGIAFSQK SPLI IHCR IHTGERPYECIKCGKAFYHK*QLSIAHRAHTGDIAG
8050	A	29	223	LIKKLASCGGEHLYS*LLKRLRWEN*SSLGV*GCGEL*SQHCTPTWV ME*GPAQKHKNKTKLL
8051	A	194	373	ICQPLSLSTANHPVLCLCFTHKNLHIFIAALFIIAKSWKQP*CTSV DEWIWGLAPLY
8052	A	1	325	FFFFF*DRVSLLLPKLECNGTISAHCNLRPLGSSDSPASASSSFTI HVAPLPQLRHY*IFYDGRSLYAG*YSQNLLIYSAPRQPQYHKDMN KILDSIQRSYTKI
8053	A	228	481	QFFRNTIFF*DRVSLLLPKLECNLSAISAHNLCPLGSSDSPASASRV AGITGTCHHTRL\ FVFLVETGFYHVSQSGLLELTSGD
8054	A	175	431	LIVKMPFLK*SWKIF*MSK*VMLIH*GFVFLFVC\FF*DRVSLLLP RLECNPI SAHRNLHLPDSSDSPASAYIKGFVRQLSHEE
8055	A	257	453	TKGGGYTQRTAIQFILFIYLFYIY*DGVSLLLPRLE*NGAISAHCNLH LPGSSDSQKTKKNFCTQ
8056	A	277	1230	ISFHLSTFGAPSSFFFFFEMEFSLLLPRLECNGAISAHRNLRLPGSSD SPASASPVGWYRHVHPRSANFVFFSRDGVSPCWGLVSNRPQMI PPSRPPKVLDTGLATMPGLCLANFCGRNRVSLMCPSPWSELKQSTCL SLPKCWDYRRRAVPGLFILFLLRHRCPILTQDEVQWCDHSSLQSTP

				EIKHPPASASQSSWDQRHAPLHLANFYFYF*FFETES\HSVT\RLC SGAILAHCNLCPLPGSSYPAPAS*VAGTTGAH/RRLANFFVFLVEMG FHHVRQVDARSLDLVICLPRPPKVLGLQDVSHRPAFY
8057	A	1	467	FFFLF*EGVSLLLPRLECSGAISA/HCNLHLPSSSDSPASASQEDGI TGVRYHAWLIL/VFLVEIGFHHVGQADLKP*PQVIHPLFFFFLRQS FALVAQAGVQWCDLSSLQTPPPRVQGILLAQPPPEYLVAFTGMRHHT RLFFFFAFLVETGFHPC
8058	A	274	321	EEEEEEEEEEEEEDQE
8059	C	69	254	MDHLYNXXXXXXXXXXXXXXXXXXXXXXXXXXEIQFXXXERERNKNP FPAGDDIISRGVGQ*
8060	A	32	169	NPVPPYPLCPALVFFLLLIYLLIY*PSPLLRMSAPAGKGFLLSL
8061	A	417	490	GDDFFFLRDRVLLCHPGWNAVVS
8062	A	424	579	RQVNMAEGIIHDTETKMEEFKDQLPADECNKLEEEISKMRELLARKD SETGE
8063	A	1	2157	GFQKRCRHRIAQLFAVGALVCCLVLLHLSAMISASRAAAARLVGAAA SRGPTAARHQDSWNGLSHEAFRLVSRRDYASEAIKGAVVGIDLGTTN SCVAVMEGKQAKVLENAEGARTTPSVVAFTADGERLVGMPAKRQAVT NPNNTFYATKRLIGRRYDDPEVQKDIKNVPFKIVRASNGDAWVEAHG KLYSPSQIGAFVLMKMKETAENYLGHATAKNAVITVPAYFNDSSQRQAT KDAGQISGLNVLRVINEPTAAALAYGLDKSEDKVIAYVDLGGGTFDI SILEIQKGVFEVKSTNGDTFLGGEDFDQALLRHIVKEFKRETGVDLT KDNMALQVRREAEEKAKCELSSSVQTDINLPYLTMDSSGPKHLNMKL TRAQFEGIVTDLIRRTIAPCQKAMQDAEVSXSDIGEVILVGGMTKMP KVQQTVDLFGRAVSKAVNPDEAVAIGAAIQGGVLAGDVTDLVLLDV TPLSLGIETLGGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVC QGEREMAGDNKLLGQFTLIGIPAPRGVPQIEVTFDIDANGIVHSA KDKGTGREQQIV\IQSSGGLSKDDIENMVKNAEKYAEEDRRKKERVE AVNMAEGIIHDTETKMEEFKDQLPC/ADECNKLEEEISKMRELL\AR KDSETGENIR\QAASS\QQAS\LKLFRNGLTKMGS*AEEGSG\SS GHWGNKREDSKGREKPVN
8064	A	500	753	NGVLAPAVQAGVQWRDPGSPPPPPPGFRRFCLSLSSWDYSHAPPR PANFVFLVEMRFLHVGQAGLELPTSGGLPALASQSAG
8065	B	1	1713	MALWRGSAYAGFLALALTWRDRKKKFPGDDEAPGVKRTWAAGAGMRG RQWLKRVEVVCTGRSANTVCAGVRAAGLVEKSPPPSLSRVGRFRF CGDLDCPDRVLAEISTLAKMVECTGSTLGGGGYKKILKLADAKFVE EHGKKDIDSPTFLSSASSWSSSSAYGSRPPGGFELKLIGQQGESG DVKATVAVLSFILSGAAKHSVDGKSLASELQQLGLPKHAASPCCCY EEKQSPLOKHLRVCSLRTWSLAARVAEGTAETVDPSPAPKTSVWSSR VCWGRLLATISPSVNETDTGCMEDRRLVVCWPWRAQCHMKAWGWRHP EEGGTHSGAPSAVLQALAVAIQLGGHLADPLLQVDPLSSCGAVSLDI LIYLVFYRTASVPETYIVKTLFKKLESQSLIQSNVLRSSNSMKAER GEEAAKEKSEASRGWFMRFKERSCLHNIKMQGEAASADVEAAASYPK DLAKITDEHGYTKQQVRCIQNSLLLEGNAEEVRKIIVCSMSPPLKPG GPVTLVEEFLCASKASVSAVSGWISKWRNWQEIIRQEEERDRASLPD LQASES*
8066	A	1	3053	MRPGFVVSVMVEGVPGEPPYPVLCTPWPBGHDLPASRAALAQGRS WSLHRMIGQDSGRRRSRRQHFAPGTSSGLRSAPGLTRAGPAPPEAVS PSHVIVDSADLAGPEKEIPGPWLPRAMYEAAGVKRAWAAGAGMRGRQ WLKRVEVVCTGRSANTVCAGVRAAGLVEKSPPPSLSRMGRFRFCG DLDCPDRVLAEISTLAKMVECTGSTLGGGGYKKILKLADAKFVEEH EGKKDIDSPTFLSSASSWSSSSAYGSRPPGGFELKLIGQQGESGDV KATVAVLSFILSGAAKHSVDGKSLASELQQLGLPKGAQAQPPPATSR ASFPYPQSTRPARAAVMRRSKAPLQKHLRVCSLRTWSLAARVAEGTA ETVDPSPAPKTSVWSSRVCWGRLLATISPSVNETDTGCMEDRRLGVQ ALACTVPHDGLGWRHPEEGGTHSGSPLEHLEPKKLSLTFAIPGTRP LIMMKVDPNPLRGLKEQSEFILSPDARKGSSGDGEVQRNLVPAAVNP

				YVMIFLPALFRVLVLA AVFGQLKEYQQRKSPGIPAGAKTKKKKTDSS PETTTSGGCHSPGDSQYQELAVALESSSVTINQLNENIESLKQKKQ VEHQLEEA KKTNNEIHK AQMEQLETINILTEKADLKTLYHTKRAA RHFEESKDLA GRLQYSLQR IQELERALCAVSTQQQEEDRGHCLSSP DQNFSLFTIQSSSCREAVLQRR LQQT IKERALLNAHVTVQV TESLKQV QLERDEYAKHIKGERARWQERMWKMSVEARTLKEEK RDIHRIQELE RSLSELKNQMAEPPSLAPPAVTSVVEQLQDEAKHLRQE/VGRSGGKA PVPGGKQSGLESP*QGTAE TPGAGGDAPRAGGAESAGAGETV*TKR EASGAEDATGAG*EAAKAGAEATQTGGEAAKGGEAAKAGKEAVGP GGEAVEEGGEATKAGGEARALPEPQARQAAGRATVQLRGSEQREKER TAVGAASKGAAGEARRGEGDAVHGHL SAADL
8067	A	330	452	EADQYLLWGPEPFPPTPDPEPTRLPLGESPA GADRAGHP
8068	A	3	347	PEWVPPSSGWRQPQAFMWHCARQGLHTTSLSSMPQVSVSFTEGEMV AKSLPQHTRLDHTEVLGA AEGSTVSAVPSATRAARDHVRRLQTRKCF CKGALLLLITAARAGRVLWG
8069	A	3	1279	TAEETSGTSAGRNNVIFPAYNMTAGFGGHS DAENNEKKSALQLEQQV KELQEKLDEVKEMSQYQELAVALESSSVTINQLNENIESLLALVEHS VKVAALDVAEGGAASGAGLQVAEAEALPLTHTVSAFVFGPVGRGTGVG PSEGPAGGRRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQP HEVSVHINAHRL EISVDQYPHTSNRGVLSYLEPRGSLLLGGLDAEA SCHLQEHRLGLIPGATNVSL LGCMEDLRVNGQRQGLREALLTRNMAA GCRLEEEYEDDAYGHYEA FSTLAPEAWLAMELPEPCVPEGLPPVF ANFTQLLTISP LVVAKGGTAWLEWWHVQPTLDLIGAELRKSQCSAPC GSGVQRRLVKCVNTQTGLPEEDSDQCGHEAWPESSRPCGTEDCEPIE SP
8070	A	1	496	LLGVAPSRAFQEEILR/DRASFHE/RPNLFALKHPTSKAECTAEKCY RVTKGRGIFPSGSPFKSVTLEDGKTFIPGQGNNA YVFPGVALGVIAG GIRHIPDEIFLLTAEQIAQEVFEQHL SQGRLYPPLSTIRDVSLRIAI KVL DYAYKHNLD SYTWPKEAMNVQTV
8071	A	228	448	RAGIPTTRLFPVGVAAIAGAFTEQILRDMASFHERPIIFALSNPTSK AECTAEKCYRVTEVSGESFLPPAERT
8072	A	3	1877	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGCHSK PGPARPVPLKRGYDVTRNPHLNKGMAFTLEERLQLG I HGLIPPCFL SQDVQLLRIMRYRERQQSDLDKYIILMTLQDRNEKLFYRVLTSDVEK FMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKGHLATMLNSWPED NIKAVVVT DGERILGLGDLGCYGMGIPVGKLALYTACGGVNPQQCLP VL LDVGTNNEELLRDPLYIGLKHQRVHGKAYDDLDEFMQAVTDKFG INCLIQFEDFANANAFRLLNKYRNKYCMFNDDIQGTASVAVAGILAA LRITMKNLSNHVVFVQGAGEAAMGIAHLLVMALKEGVPKAEATRKI WMVDSKGLIVKGRSHLNHEKEMFAQD\HPESNSLDEVVRLVKPTAII GVAAIAEA\FTEQILRNMA SF\RRAPIIFALSNPPRKAECTA\EKCY RVTEGPRGFFASG\SPF*GVLIWEMGKTFIPGGRGNNA\YVFPG\VA TG\VA\GGIRHIP\DEIFLLDSRAKL PQEVSEQHL\SQGRLYPPLS TIRDVSLRIAIKVL DYAYKHNLV\SYYPEPKDKEAFCKIPGSYTPDY DSFYT/VDSYIWAQ GKAMNVQTV
8073	A	325	587	VGHIILLRGTLGFPWFYTSWAELLRFLLFSGIGVGGVREQGLTSPR LKSRGVITAHCNLELLGSSSPASAFQGARITGVHHPAN
8074	A	124	343	NHFQHDFTTSDQQHCISNQPSPLLHPHPSQYQCQAAYPHPPHCHNAH GTGAKLSPSPRPPLPQGPLTRISC
8075	A	32	487	SRRHGSSLWGKVNVEDAGGETLGRLLVVPWTQRFDFSFGNLSSASA IMGNPKVKAHGKVLTS LGDAIKHLDDLKGTFAQLSELHCDKLHVDP ENFKLLGNVLVTVLA I HFGKEFTPEVQASW/QEDGDWSGQCPVLQIP LSSLPMMQSFQ
8076	A	3	573	FCPRGQEFGEKNLLVLPDAHGVISQRRTKATI\TSLWGK\VNVE\DA GGET\LGRL\LVVYP\WT\QRFFD\SFGNLSSASAI\MGNP\KVKAH G\KKVLTILGRCCQSTLDDLKGTFAQL\SELHCDK\LVDPENFKLL

				G\NVLVTVL\AIHF\GKDFTPEGCRASW\QKMGD\FSGQCPV\LQ\I PLKPLGP*IQ\SFGQ
8077	A	2	347	ARGRKIQTHMPKDHSDIPDINRAHIINDAFNLTSAHTVPDTLALINT LFLIDQRQYMPWEAVLSSLSYFKLMFDRSHVYSPMNNYLNLTPLF IHFTNNTINWMEIPEHLMHDY
8078	C	213	263	MGFHHVSQDCLDLTS*
8079	C	637	1452	MGIAAASVLGDLAVVFGMHVPAQADGQDHPQELDGHGTHAHAEDDAQ VLLQPRHLHLLHAALLVHRPVLRVVATLGPVAGGLAEALPHRKAVVLF PLDFAGTGVGDLRAIHELSSVCPVVEADPAAALHLSLHVVPGLQAV LATAVVSNELSHDATHLLQLAHVEVEEGPGRHLGNEDQEESKVQ PQQAADLVGDAAQEAHEHSDCPHADEDIGPHPKRAGGGLQDRDET ALVGQDPHPEAQDHCAQDKEDQVEEEEKVFGDFDTG*
8080	A	226	314	KWNSRPGVVAHTCNPSTLGGRGGQITRSG
8081	A	2	350	KTLLFFFFFRFEPHLLTSMICGLVYNQPPQHLVHILLKRRIWPQG NILGINKRPGTVAHTCNPSTLGGRGGRITRSGVRD*PGQHSESPSL PTIQKNYPGVMAGACNPSSYSGG
8082	A	172	287	IVYASEEKI*TFQEQGWPGAVAHTCNPSTLGGRGGRITRSGDRDHPG *HRPP
8083	A	14731	15032	IAGCRPGAVAHSCNPSTLGGRGGQI/TLRSGV*DQPGQYGETPSLLK IQKLGRGGRRLKSQLLREAEAGESLEPGRQFAVSRHRATALQPGNR ARLHLKK
8084	A	1	193	GTSFYLYRKGYSLSKVVPFSHYAGTLLLLLARVACLLGIVRWAYPH FPQFLAISSPIHLYLTS
8085	A	1	346	VAAEIPALNWNQNGLCRLPGHTGPLESPASPRPPGCGDRPATDFLAR GVAGCHGRERQPDIGGHGAARPPQSKSPWGCVSANCGAGHSCRLSGC RALPCLTPGSWSWRKDSQISC
8086	A	3	522	LTDDEMRRLNIPVLQDDGFLFLWVTGRAMELGRECLNLWGYERVDEI IWVKTNLQRIIRTGRTGHWLNHGKEHCLVGKGNPQGFNQGLDCDV IVAEVRSTSHKPDEIYGMIERLSPGTRTIELFGRPHNVQPNWITLGN QLDGIHLLDPDVVARFKQRYPDGIIISKPKNL
8087	A	1	840	HMELPYGTLTDDEMRRLNIPVLQDDGFLFLWVTGRAMELGRECLNLW GYERVDEI IWVKTNLQRIIRTGRTGHWLNHGKEHCLVSSSQAQFNR WSTKKNHLISY*EKVQRCGFIR*SVILW*AG\GVKENPQGFNQGLDL *CDRS*GMCFSGLQSFHIFVGYQLFMVGCILIPRFFLI*IIINIIGKG LGIAILCNLKKQLVFIS*VRSTSHKPDEIYG\MIERLSPG\TRKIEL FGRPHNVQPNWITLGNQLDGIHLLDPDVVARFKQRYPDGIIISKPKNL
8088	A	13	323	AESTCPYYNGTPGSGRRPPVPLPPFLWGGPLSSLRSHYQHPSPYCRL AGSGNADGWVPVAVPDPGIRWHAQALRHSSPCLTLQPQLLYPLILWQ ATYARDALA
8089	A	3	218	QEGQKRDVCEHHGKKLQIFCKEDGKVICWVCELSQEHQGHQTFRINE VVKECQVGSKIEEERAESRRWYLM
8090	A	3	332	HEVRFFVVDICPAEQYGAGHLSTAFHLSDMLQNPSEFAQSVKSL EAQKQSIESGSIAGGEHLCFMGSGREEEDMYNMVLAHFLQKNTEYV SIASGGFMALQQLA
8091	A	3	334	HEDEFKPLVGDPHNLMDPNRELFDQLGEYKFQNALLFHYTKTVPHVS TPTLVEVSRNLKVGSTCWKHPESKRMPCAEEYLSAVLIHLCVLHEN TLFRDRVIKCTESLV
8092	A	1	1431	MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFA IARRLAQDGAHVVSRRKQONVDQAVATLQGEGLSVTGTVCHVGKAE DRERLVATAVKLHGGIDILVSNAAVNPFSGIMDVTEEVWDKTL VKAAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFS PYNVSKTA LLGLNNTLAIELAPRNIRVNC/LAPGLIKTSFSRM\LGEPEDCAGIV SFLCSEDASYITGETVVNLSVMFTGGGVCRAASWKEGGTGTPRTPRE SPRQREPGETSSDTQENKVWNGLPANPQRPAAEQPVRRKTNKQKGI ASTSAKDSINIRTKDIHTKTPSIGHQHQRPKVDKTTKMERNQSKKA ETSRNQNVSSLPKEYKSSPAREQNWMENKFDDLTDSVFRRSVITNYT

				QLKEHVLTHCKEAKNLDKMLNEWLTRMKNLEKSLNDLMELITTVQEL HEGYTSFNS
8093	A	195	434	TSVPSCVRCRYIILRSSSALTNIILGTHSNSSFFHASSSALHSCCFPF FSWLQTLDDINVKAPALMTKAVVPEMEKRGYRE
8094	A	43	1601	SMHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHVVVSSRKQONVDQAVATLQGEGLSVTGTVCHVGKA EDR\ERLVATAVKLHGGIDILVSNAAVNPFFGSIMDVTEEVWDKTL INVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSFYNVSK TVLLGLTKTLAIELAPRNIRVNCLAPGLIKTSF\SRMLW\MDKEKEE SMKETLR\IRRLGEPEDCAGIVSFLCSEDASYITGETTVNLSVMFTG GGVCRAASWKEGGTGTPTPTPRESPRQREPGENQARSSPRMALRPEFP PESASTSWMGPEPVGNRERPCPKPARKVGASPRALRRLGSATRMLSRA ALRAGVGARAPRPGGGRGAHATATVWSGLASAAALTARALLKRSGLAC AAAPQRCGWRRLLCSSSLGSRGQGGQAHARGAHLRVVRYGTASVFGTPR LVASQIQHVPSGPAPRPGASHPATPSIQTLRQPLHLSPDIAVPGASS AGAGA
8095	A	2	172	ARDNQHDQLQEWEEHLQEHTNVTWVGNTIKPHSLPSHTVWTCFSCF HTPCVAYRG
8096	A	3	825	KPCMMDDTGMSCSDHVTVDSPYVAVRIADETSINTRSFSKFGVMSA DATPLHVARSGNDTEDFSNSPSACSDIYGESISSHFTTESTGKLIESLS DCASSLPKIKIAGSNYNTFLDSELSMLNGTKVLSDSAVGIDLGSTGD TTEALHELRTAEFEKTEEQDASGSIEFGVSFPDRESSMETSIEPKA TETSRTGEGITAIEESWESMFNDDGDCLDPRLQLQELSGNTKSRESIQE PRSDYYNHEVPDIDLSDCFEFPHVIEIYDFPQEFRTEDL
8097	A	2	469	TVLCATGGGAYKFEKDFRTIGNLHLHLKLELDCLVKGLLYIDSVSFN GQAECYYFANASEPERCQKMPFNLDOPYLLVNVNIGSGVSI LAVHSK DNYKRVGTGSLGGGTFLGLCSLLTGCESEFEEALEMASKGDSTQADKL VRDIYGGDYERFGL
8098	A	1	2694	MTSEGVPSARAVLALYENDLKALRTLCSCLPGFEGQRCIEINPDDCED NDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPENLNCQHEA KCIPLDKGFSCECPVPGYSGKLCETDNDCCVAHKCRHGAQCVDTINGY TCTCPQGFSGPFCEHPPMVLLQTSPCDQYECQNGAQCI VVQOEPTC RCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDK DNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQ FHSVELVTLNQTNLNVVDKGT PKSLGKLQKQPAVGINSPLYLGAPFW FGMDIGGTLVKLSYFEPIDITAEEEQEEVESLKSIRKYLTSNVAYGS TGIRDVHLELKDITLFGRRGNLHFIRFPTQDLPTFIQMRDKNFSTL QTVLCATGGGAYKFEKDFRTIGNLHLHLKLELDCLVKGLLYIDSVSF NGQAECYYFANASEPERCQKMPFNLDOPYLLVNVNIGSGVSI LAVHS KDNYKRVGTGSLTGCESEFEEALEMASKGDSTQADKLVRDIYGGDYE RFGLPGWAVASSFGNMIYKEKRESVSKEDLARATLVITNNIGSVAR MCAVNEKINRVFVGNFLRVNTLSMKLLAYALDYWSKGQLKALFLEH EFGYNIGVISAPETVIQDFLSYTLKERSEDSPSEVLLMSWPWSSVAI FPNGDMIGSFLLHSLSTTLAAQNLLKLISNFSKVSGYKINAQKSQAF LYTNKRQTESQIMSELPFTIASKTIKYLGIQLTRDVKOLFENYKPL LNEIKEDTNKWNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMT FFRELEKTTLKFTWNQKRAHITKSILSQKNKAGGITLPDFKLYYKAT VTKIA
8099	A	346	461	TLHKKTFFYYLEQLILKYGMHQNTLRIKEIHGELKLSI
8100	A	3	1560	SSLWRRQPELKAYRTMEYMAESTDRSPGHILCCECGVPI SPNPNIC VACLRSKVDISQGIKQVSI SFCKQCQRYFQPPGTWIQCALESRELL ALCLKIKIAPLSKVRLVDAGFVWTEPHSKRLKVLTIQKEVMNGAIL QQVFVVDYVVQSQMCGDGHESEKLDKDFWK\AVIQVRQKTLHKKTFFY LEQLILKYGMHQNTLRIKEIHDGLDFYYSKQHAQKMFELQCTVPC RYKASQRLISQDIHSNTYNYKSTFSVEIVPICKDNVCLSPKLAQSL GNMNQICVCIRVTSAILHLDIPNTLQVADIDGSTFWSHFPNSLCHPKQ

				LEEFIVIECSIQDIKRAAGAGMISKKHTLGEVWVQKTSEMNTDKQY FCRTHLGHLLNPGDLVLGFDLANCNLNDEHVNMNSDRVPDVVLICK SYDRTKRQRRRNWKLKELARERENMDTDDERQYQDFLEDLEDEAIR KNVNIYRDSAIPVESDTEDEGAPRISLAEMLEDLHISQDATGEEGAS MLT
8101	A	1	171	GTSISKNRLLSIKTFLYWTILGFSAFIFFFGSYLLIGKDTSLLGNG QMFRNCTFDA
8102	A	3	231	RRQAQIAAGRVLVVALFGGCGGLHSRLDGAAI/CLPGHCHGSRVEVT YETHQCGLVGLKLLRGGREQSDRGGSLGLT
8103	A	48	532	NLMNICRGPCLLPGAPFMRDLAAVA/SVGLP/LVRRQAQVAAGRVLV VALFEGCGGLHS\RLDGAAICLPGHCHGSRVEVTYEAPQCGLVGLKL LRGGREQSDEGGSLGLT*DAQLGPGAHEPEIRAWE*TAVIISLVLS LEPRDQGGRVARLGAREAINP
8104	A	3	421	AAEASVGL/PLLRQAQIAAGRVL/VVALFGGCGGLHSRLDGAAICL PGHCHGSRVEVTYETHQCGLVGLKLLRGGREQSDRGGSLGLT*DGQL GPSAEDYTISSCPHLTGIVGLIPGLDSADQGGRVPRLGARESVRDT
8105	A	94	582	LSHPLPL/LGRQAQIAA\GRVLVVALFGGCGGLHSRLDGAAICLPGH CHGSRVEVTYETHQCGLVGLKLLRGGREQSDRGGSLGLT*DGQLGPS AEHQSVSVPSLTVIISLILRLEVGDGEVAVSPRAGAREAIRNSAPLV VASTTFKPHQVPRGLSCLLLMPRDVVPTVSTAQSAGEPDRGSQGSRG RG
8106	A	2	332	GSLOGLPGQSFSFGGLPLLGRQVRVAAGRVLV\VALFGGFGGLHSR\ LDGAAICLPGHCHSSRVEVTDQTH*CGLVGLELLRGGREQSDSGVGL GLTQDGLRSTSEDKVC
8107	C	30	653	MTCSPLLLTLLIHCTGSAHVSILTQPPSVSAAPGQITISCSGSRLN VGNYFVSWYQQLPGTAPKILIYDNDKRPSGVPARFSGSKSGTSATLA ITGLQTGDEANYCYGAWDTSLDNWVFGGGTEVTVLGQPKAAPSVTLF PPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNKYAASSYLSLTPEQ*
8108	A	484	632	PWSHFRRF*LTMRIFIEGLLSAGARRA/WMPWGGRDPSPGILQL*SP V\GGVRDENL*TFCRGHCLLHGAPFMRDLAAVAVGLPLLRQAQVA AGRVLVVALFGGFGGLHSRLDGAAICLPGHCHSSRVEVTDQTH*CGL VGLELLRGGREQSDSGVGLGLT*DGDLGPTSEDSKGATTSKRAAVII SLVVSLEPRDCQGGRRVGRHGAREAINP
8109	B	27	1337	MAWTPLLLLFPLLLHCTGSLSQPVLTSQSSASASLGSSVTLTCTLSS GHSDYIIAWHQQLPGKAPRSLMKVEGDGSYKTGRGVDPDRFSGSSGA NRYLSISNFQSEADYQCQAWDSSTAHSDTGRCGIVGRPPVRQWCP LLLLGLAMVAHGLLRPMVAPQSGDPDPGASVGSSRSLRSLWGRLLL QPSPQRADPRCWPGRFWSEPSQLCYVFGTGKTVLGLQPKANPTVTL FPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKP SKQSNKYAASSYLSLTPEQWKSHRSYSCQLQWGLGLGASQGGFLYE PVSQCVMVFGGGLKTLVLGQPKAAPSVTLFPPSSEELQANKATLVCL ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPE QWKQAQKLQLPET*
8110	C	54	410	MEGAHEEAVSSLLPSPAGGGGCEPARREESSYRIKMTQXXXXXXXXX XXXAC RQQEDRLGQCCSLHLQCLAQSRCH
8111	A	1	175	LSHFDSVTGFLSAGRLTPSTPSWRWKEDAHRPFLMQAIDGNVRQCES TPEHFWGPLWD
8112	A	1815	2017	GQGAVAHT\CNPSTLGGQGGRITLRSVQVQNPQDQHGETLSLLNISGV WWRAPVIAAFQEAETGESLEP
8113	A	1109	1482	YQGLAAWQRKKNRLRHMIEDRQGCHNNHNGKDQDQKGPPLTPNPWA DGSRTQNFPSCRKMGPGAVAHACNPSILGGQGGADHLRSQVRDQPGQ HGTPVSTKKKKKKKKKKKKKLAGHGGSL
8114	A	266	400	VVEEVECLLLLNDMTVYLEHPKDSSKLLLELVNAFSKVSRYIV
8115	A	6	363	PFAPAAGIRHEVNMGQKQEILDLFSSVLYECVTQETPEMLPAYIAMD

				QAIIRRLGRREMSETSELWQIKLVLEFFSSSRSHQERLQNHPRKGLFMN SEFLPVVKCTIDNTLDQWLQVGGD
8116	A	688	1127	AALAQHCTLEVGGAGSGGTQAISSPLVAGRFTGIREATCVRARPWD RELHYVPVPSRGGRWDLSSSGSGEKRRLLSKPVCSQIKSSFNPQSA PDSSSNISAGGGGHGKPAQQRLPDREACLLFRLFPMFSLDCRRGSR CGEGR
8117	A	2	312	LKGGPFSDSYRLFQFHFHWGSTNEHGSEHTVDGVKYFAELHVPHWNS AKYSSLAEADSKADGLAIGAMKKDDKANPPLDHVQGVGRADRNFG IEVLSDALI
8118	A	2	51	QNASCFCWCCCCCRNW
8119	A	203	366	IESPEANSCIDGQLLFDGGIRIAHWAKDSSSSSSSSSSSSSTCRMRK LDPYHTP
8120	A	152	315	IESPETNSCIDGQLLFDGGIRITHWAKDSSSSSSSSSSSSSTCRRIQ LDPYLTP
8121	A	11	381	RLHRFFLGESEQSPASSSSSSSSSSITPSQTRQHGPLRSIMKDLHSD DYEEESYEVDNDNDNDKMERPANR*RTSRVTSLSDGSDSESRSS* PLHYEPPPPLLYTNNQILEVESPI THSL
8122	A	124	1924	ITAEGGRRRGYHTTPQQTSGPPGMASCSVQVKLELGHRAQVRKPP TVEGFTHDWMVFVRGPEHSNIQHFEKVVFHLHESFPRPKRVCKDPP YKVEESGYAGFILPIEVYFKNKEPRKVRFDYDLFLHLEGHPVNLH RCEKLTFFNNPTEDFRKLLKAGGDPNRSIHTSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSTFSKPKHLMKEHKEKPSKDS REHKSAPKEPSRDHNKSSKESKKPKENKPLKEEKIVPKMAFKEPKP MSKEPKPDSNLLTITSGQDKKAPSKRPPI SDSEELSAKKRKSSEA LFKSFSSAPPLILTCSADKKQIKDKSHVKMGKVKIESETSEKKKSTL PPFDDIVDPNDSVDEENISSKSDSEQSPAS\SSSSSSSFHTIPGP GQQGPL\RSIMKDLHSD\NEEEADEAEDSDNDSEMERPV\NRGGS RRV\SLSDGSDSESSSASSPLHHEPPPPLLKTNNDQSWKWKSPK QSK\SD*GKLNGEC*QGLT*MELVGAFTRGFRIDFEEERHILQQIVN LIEETGHFHTNTTFDFDLCSLDKTTVRKLQSYLETSGTS
8123	A	2	319	VPGAGLGRVAWEIAMLGACQGNWSFFMLFSSNFVLNRCSEINKYK LYPWIHQFSNNRRSADQIRPIFFPDVDPHSLPPGSNFSMTAGDFQEI YSECSKSKSSV
8124	A	1	323	VHCLGADLLEINNNPCYWGMVKYAAEALLEGKPEGTFLLRDSAQED YLFSGSFRYRSLSLHARIEQWNHNSFDADHPCVFHSPDITGLLEHY KDPSACMFFEPLL
8125	A	31	118	TFLAQNVQLCFPPYPSPGVLPFKKEPDDS
8126	A	1	4938	MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKT VKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGLVIWDSVHPCYTV FHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGF IEN MFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTTQGDVLMPLA IQLPVSQPVPTIQGEPIPVATQPSVVPVHSGAHFLPVGQPLPTPLL PQYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQPLLTASSATTA AIPGVSTVVPSQLPTLLQPVTLQPSQVHPQLLQPAVQSMGIPANLQ AAEVPLSSGDVLYQGFPRLPPQYPGDSNIAPSSNVASVCIHSTVLS PPMPTEVLATPGYFPTVVQPYVESNLLVPMGGVGGQVQVSPGGSLA QAPTSSQAVLESTQGVSVQVAPAEVAVAQATQATQPTTLASSVDSA HSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSRSRSRHEKTSRP KLRI LNVS NKGDRVVECOLETHNRKMVTFKFDLDGDNPEE IATIMVN NDFILAIERESFVDQVREIIEKADEMLSEDVSVEPEGDQGLSLOGK DDYGFSGSQKLEGEFKQPIPASSMPQIQIGIPTSSLTQVVHSAGRRFI VSPVPESRLRESKVFPSEITDTVAASTAQSPGMNLSHSASSLSLQQA FSELRRQMTEGPNTAPPNFSHTGPTFPVVPFLSSIAGVPTTAAT APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGLPI PPVSESPVLSSVVSSITIPAVVSISTTSPSLQVPTSTSEIVSSTAL YPSVTVSATSASAGGSTATPGPKPPAVVSQQAAGSTTVGATLTSVST

10654

				<p>TTSFPSTASQLCIQLSSSTSTPTLAETVVVSAHSLDKTSHSSTTG FSL SAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGP TSTPLLPQVPSIPPLVQPVANVPAVQQTLIHSQPPALLPNQPHTHC PEVDSDTQPKAPGIDDIKTLEEKLRSLFSEHSSSGAQHASVSLETS VIESTVTPGIPPTAVAPSKLLTSTTSTCLPPTNLPLGTVALPVPV TPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTLPSE QLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAGPVSMAAP TAITEAGTQPKGVSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQ KEGKNKSEDAKSVHFESSTSESSVLSSSSPESTLVKPEPNGITIPGI SSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTANKVGRFSVSKTE DKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPS SDPEAAFLSRDVGSGSPHSPHQLSSKSLPSQNLSQLSNSFNSSY MSSDNESDIEDLDKLELRRLRDKHLKEIQDLQSRQKHEIESLYTKL GKVPPAVIIPPAAPLSGRRRRPTKSKGSKSSRSSSLGNKSPQLSGNL SGQSAASVLHPQQTLPHPGNIPESGQNQLLQPLKPSPSNDLYSAFT SDGAISVPSLSAPGQCAKENCASEQVTFKPGRRTRFLSTPCLALC V</p>
8127	A	472	4356	<p>PPTCSNPSFSLSQGFPPRLPPQYPGDSNIAPSSNVAVCIHSTVLS PPMPTVLATPGYFPTVVQPYVESNLLVPMGGVGGQVQVSSGGLSA QAPTTSSQQAULESTQGVSVQVAPAEVAVAQATQPTQLASSVDSA HSDVASGMSDGNENVPSSSSGRHEGRTTKRHYRKSVRSRSRHEKTSRP KLRI LNVSNGDRVVECQLETHNRKMVTFKFDLDGDNPEEATIMVN NDFILAIERESFVDQVREIIEKADEMLSEDVSVEPEGDQGLSLOQK DDYGFSGSQKLEGEFKQPIPASSMPQIGIPTSSLTQVVHSAGRRFI VSPVPESRLRESKVFPSEITDTVAASTAQSPGMNLSHSASSLSLQQA FSELRAQMTEGPNTAPPNFSHTGPTFPVVPFLSSIAGVPTTAAAT APVPATSSPPNDISTSVIQSEVTVPTTEGIAGVATSTGVVTSGLPI PPVSESPVLSSVVSSITIPAVVSISTTSPSLQVPTSTSEIVVSSAL YPSVTVSATSASAGGSTATPGPKPPAVVSQQAAGSTTVGATLTSVST TTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTSHSSTTG FSL SAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGP TSTPLLPQVPSIPPLVQPVANVPAVQQTLIHSQPPALLPNQPHTHC PEVDSDTQPKAPGIDDIKTLEEKLRSLFSEHSSSGAQHASVSLETS VIESTVTPGIPPTAVAPSKLLTSTTSTCLPPTNLPLGTVALPVPV TPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTLPSE QLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAGPVSMAAP TAITEAGTQPKGVSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQ KEGKNKSEDAKSVHFESSTSESSVLSSSSPESTLVKPEPNGITIPGI SSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTANKVGRFSVSKTE DKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPS SDPEAAFLSRDVGSGSPHSPHQLSSKSLPSQNLSQLSNSFNSSY MSSDNESDIEDLDKLELRRLRDKHLKEIQDLQSRQKHEIESLYTKL GKVPPAVIIPPAAPLSGRRRRPTKSKGSKSSRSSSLGNKSPQLSGNL SGQSAASVLHPQQTLPHPGNIPESGQNQLLQPLKPSPSNDLYSAFT SDGAISVPSLSAPGQGNKATIIIVQKQ</p>
8128	A	2	237	<p>ISGQEGQLQAVLASDYSFAQFRYLQRLLLVHGRWSYFRMCKFLCYFFY KNFAFTLVHFWFGFFCGFSAQTVYDQWFITL</p>
8129	A	503	639	<p>LLLLFSLLFHRSLLFIPFRLLGIIITKDLRHMAQTANQDPASI</p>
8130	A	464	2848	<p>GETGMSTALTHTTVAMRCPMLGGGGPTYGPPQPWGHDPVHIMQHHV LPIQARLGSIAEIDLGVPPVPMKTFKEFLSLDDSDVETEAVKRYND YKLDFFRRQMQDFFLAHKDEEWFERSKYHPDEVGKRRQEARGALQNR RVFLSLMETGWFDNLLDIDKADAIKMLDAAVIKMEGGTENDLRIL EQEEEEEQAGKPEPSKKEEGRAGAGLDGERKTNDKDEKKEDGKQA ENDSSNDKTKKSEGDGDKEKKEDSEKAKKSSKKRNRKHSDDSF DEGSVSESESESESGQAEKEEAEALKEKEKPEKEEWEKPKDAAGL ECKPRPLHKTCSLFMRNIAPNISRAEIIISLCKRYPGFMRVALSEPQP</p>

10655

				ERRFFRRGWVTFDRSVNIKEICWNLQNI RL/RECELSPGVNWDLTRR VRNINGITQHKQIVRNDIKLAAKLIHTLDDRTQLWASEPGTPPLPTS LPSQNPILKNITDYLIEEVSAAAAEELGSSGGAPPEEPPKEGPNPAEI NVERDEKLIKVLDKLLLYLRIVHSLDYNTCEYPNEDEMPNRCGIIH VRGPMPPNRI SHGEVLEWQKTFEKLTPLLSVRESLSEEEAQKMGRK DPEQEVEKFVTSNTQELGKDKWLCPLSGKKFKGPEFARKHIFNKHAE KIEEVRKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQILPPGLTPGL PYPHQTPQGLMPYQPPRPPI LGYGAGAVRPAVPTGGPPYPHAPYGAG RGNYDAFRGQGGYPGKPRNRMVRGDPRAIVEYRDL DAPDDVDF
8131	A	2	434	RLRVFLSLMETGWFDNLLLDIDKADAIVKMLDAAVIKMEGGTENDLR ILEQEEEEQAGKPGEPSKKEEGRAGAGLDGERKTNDKDSEKEAKK SSKKRNRKHSDDSFDEGSVSESESESESGQAEEKEEAALKEKEK PKE
8132	A	1073	3545	GETGMSTALHTTVAMRCPMLGGGGGPTYGPPQWGHDPVHIMQHHV LPIQARLGSIAEIDLGVPPVMKTFKEFLSLDDSVDETEAVKRYND YKLD FRRQMQDFFLAHKDEEWFERSKYHPDEVGKRRQE\SRGALQNR LRVFLSLMET\G\WFDNLLLG*TKLIAIVKMLDAAVIKMEGGTEND LRILEQEEEEQAGKPGEPSKKEEGRAGAGLDGERKTNDKDKEKKED GKQAEENDSSNDKTKKSEGDGDKKEKKEDSEKEAKSSKKRNRKHS DDSFDEGSVSESESESESGQAEEKEEAALKEKEKPEEWEKPK DAAGLECKPRPLHKTCSLFMRNIAPNISRAEII SLCKRYPGFMRVAL SEPQPERRRFFRRGWVTFDRSVNIKEICWNLQNI RGARSLINRWCSRG KGLRAAVSLASGLRECELSPGVNRDLTRRVNRINGITQHKQIVRNDI KLAAKLIHTLDDRTQLWASEPGTPPLPTSLPSQNPILKNITDYLIEE VSAEEEEELGSSGGAPPEEPPKEGPNPAI NVERDEKLIKVLDKLLY LRIVHSLDYNTCEYPNEDEMPNRCGIIHVRGPMPPNRI SHGEVLEW QKTFEKLTPLLSVRESLSEEEAQKMGRKDPEQEFVTSNTQELG KDKWLCPLSGKKFKGPEFVRKHIFNKHAEKIEEVKKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQIIHVPVRVVLPPGLTPGLPYPHQTPQGL MPYQPPRPPI LGYGVPTGGPPYPHAPYGAGRGNYDAFRGQGGYPGK RNRMVRGDPRAIVEYRDL DAPDDVDF
8133	A	188	391	RRNRAWISRKTGFTRTQRRPRTYKRRNYQTYRNMWLWAQMQRDST RAGVCDRQLRKRGARELSH
8134	A	1	998	MAVMLHSAKWPLPVQQGLTMQPPLPSKHISERSEEDSRQPLYSVIL IFYEAGFAILVFDKTD FQPKVKRDKEGHI IMVGSMQQEELTILNI YAPNTGASSFIKQVLGDPQRDLDSHTII VGD FNTPLS ILDRLMRQKI NKDIQDLNSALDQVDLID IYRTLHPKSTEYTFFSAPHHTYSKIDHII GSKTLLSKCKRTEIITNSLSDHSAIKLELRIEKTQNH TTTWKLNLI PLNDYVWVNEIKAEINKFFETNENRDTMYQNLWD TAKAVFRGKFIAL \NGHRRK*ERSKINTLTLQLKELEKQE QTHSKASRRQEITKIRAE LK EIDS
8135	A	1	1674	MNSALDQLDLIDIYRTFHPKSAEYAFFSALHHPYSKIEHII GSKTLL SKCKRMEIITNNLSHSEIKLELRIKKLTQNRSTWKLNNLLNLDY VNNEIKAEINKFFETKENKDTSCAPSSRLV LGAKGHAHMFYATLW MHAIPEFSVEMATAWSESASLDHSPILSFLPQEFPADRDGSLALHST YESLRLSASSWTVNPLRGINMMPSSLAPSSQCGPKCKETPLELVFV IDSSSVGPENFQIIKNFVKTMADRVALDLATARIGI INYSHKVEKV ANLKQFSSKDDFKLAVDNMQYLGE GTYTATALQAANDMFEDARPGVK KVALVITDGQTDSDRDEKLT EVVKNASDTNVEIFVIGVVKNNDPNFE IFHKEMNL IATDPEHVYQFDDFTLQDTLKQKLFQKICEDFDSYLVQ IFGSSSPQPGFGMSGEELSESTPEPQKEISELSVTRDQDEDDKAPE PTWADDLPATTSSEATTTPRPLLSTPVDGAEDPRCLEALKPGNCGEY VVRWYDYDKQVNSCARFWFSGCNGSGNRFNSEKECQETCI QG
8136	A	3	363	HEGLKMLHTTPIATACLDADLYLLTEVHCPKELGACMPTGLTVDRAT DAGDGALVLSKRRSQALIITLRAEGCVMLPQTDPEPELIATDNGKAA DTTDAGDSFVGALAFYLA YPNLSL

8137	A	3	174	PELRAELFESLQEQPGALPVPGPSRSAPSSPAPRRTKQVSSGWTALR DPDQAEGCC
8138	A	3	328	NTSQYHGVGYTGLGCETDIDECRPLPCLNNGVCKDLVGEFICECPSG YTGORCEENINECSSTPCLNKGICADGVAGYRCTCVKGLARNMIPMF LWCLTNLYTTAYYY
8139	A	1	82	IRSQLENEKVAQLYADLDGGFFLPTLLF
8140	A	2	373	SVSDKGGISPAAIKECQVQIAYHDQKRQVVPVSTRGFNNKHLRESL CSDPLKETNSDEQHSTSALTEVEMNQPHATELMVTS DHIVPGDMAR EPVEETTKSPSDVNISAQPALSNFISQLV
8141	A	1	352	GTRGNSDELDEPIKTVFADVAFVKKHNLMSLNSINWSRVLVQMAHFF FAYFQCTPSLDTHPLPLLVVSLFFSTYLFHTFFVTPLFLIFLSSSSH FHLSIYLSSIILSSHSFSSYTL
8142	A	2	396	ARGSKCKHPEAKRMPCAEDYLSVVLDSLCLVLEKTPVSDRVTKCCT ESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKK QTALVELVKHKPKATKEQLKAVMDDFAAFVQKCKAD
8143	A	4274	5256	HTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPPLP RLVRPEVDVMCTAFHDNGETFLKK*VIRCL*FKIKKHGVTP*ANTL* KLP*KYFQH*DLEVLL**FFKEVVFDTTKFYTAKNMIKDILKFIET GYNLSQKFIDKFFNVFRYVYVMVVIDFVLVSNIIILPKFNHLC THT HTHHTLTLFSTYLNDRDKTIMCKLSLIG*L\ESLEFGGSGENV DYN YFCNIVCYRK/ADCFSLKFRYLYEIARRHPYFYAPELLFFAKRYKA AFTECCQAADKAACLLPKVLCTRIEKKSLLSNLILSLWLDLGTLSV
8144	A	23	136	SFHVFAQPDNLNLSRDLPALASQSTGITGMSHQCPG
8145	A	1	248	GTRSCENIHLHSEAVLCTVPNDLLKLNSELNIEWKQAISSSTVLGKVI VQPDHNTGLIAGVVLIIITALLLLLGFI LRYNIED
8146	A	2	229	KLATPPAAQESSRRRSRKGHLPAVPQPYEHGYPVSGGFAMPFVSLYH ILTTSFSSHAVDISLDMCCFILLPSLL
8147	A	3	231	TAAGCQLVASCDIAVASDKSSFATPGVNVGLFCSTPGVALARAVPIK VALEMLFTGEPISAEALLHGLLNKVLL
8148	A	30	217	FRWSEQSGQMAEMIRMAKVPIVWNHGSIVSPQPQMIWLIVGAKHKD LWKLLIALNKITIWE
8149	B	49	754	MAGAAPRLPWSRPHGSCGWPMQPLQGPGRRAVAAAEVATPVFMPV GTQATMKASRPNSWTLWVAASAWEYLP SGSKAGGTAAPFDGVAGVSV RGDGGGLRFRSPYDGNETLLSPENPCRSRMRWAPGVVTGALLQVNPL AGPVHAAHQRPDKQNLFAIIQVGWTOISGPPALKRFGSAWHSRAFLT HCCTVTTTRPCTTSRPOHRLPAELMSAVRTSIVEKRFPSDGT SWAP X*
8150	A	1	593	RQSRWREQLPRLSWRLVPRIMRLVAECGRSRARAGELWLPHGTVATP VFMPVGTQATMKGITF\EFLDALGCRICLG\NTYHLGLRPGPEL\IQ KANGLPRLS*IWPSLILLNGTAAVFQMVSLVSLSEVTEEGVRFRSPY DGNETLLSPEKSVQIQNALGSDIIMQLDDVVSSTVTGPRVEEAMYS IRWLDRCICSH
8151	B	374	613	MTALDLFLTNOFSEALSILKPRTKESMYHSLTYATILEMQAMMTFDP QDILLAGNMMKEAQMLCQRHRRKSSVTDSFSSL*
8152	A	2	1922	VETPPQGSVHSGHLGSVVGDPHTGTGNAGERGPRGKGARVLALDSGG MDSSPSLPLIRTPESSLHEALDQCM TALDLFLTNOFSEALSILKPRT KESMYHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRK SSVTDSFSSLVNRPTLGQFTEEEIHAEV CYAECLLQRAALTFLQGSS HGGAVRPRALHDP SHACSCPPGPRQHLFLLQDENMV SFIKGGIKVR NSYQTYKELDSLVSQSYCKGENHPHFEGGVKLGVA FNLTLSMLPT RILRLLEFVGFGSGNKDYGLLQLEEGASGHSFRSVLCVMLLLCYHTFL TFVLGTGNVNIEEAELKLPYLNRYPKAIFLFFAGRIEVIKGNIDA VSDGGPGRGWGSLGVSQTSRKSGTCDILRDRIDWGRGGGPRENQPS RGRRGPSGRAAWEDKGGGGICGAWDFDWEI*DCSIAVEGGGRCLRE AEVRKAHLFRA*RLGWSLVPLHYSSLLLHFVTKNQSPRRGLYLSF TSCKT*EVKPGLEARSPGSWGPT*A*HRAGPLCPGGVPVCCGVGRFG

				GCRGVGAGWAPVRLTRRCLQAIRRFEECCEAQQHWKQFHMCYWELM WCFTYKGQWKMSYFYADLLSKENCWSKVG
8153	A	1	285	QNEASRKNKKKEKSTSKYEVLTVQEPPIEDAEFPNLAGASERED SLETRDIECTWASLEDLKFPCLKVHLAEENGLLHSGFWGALTFFSL S
8154	A	3	409	NTTAATVAPFSSPVFTLSSTPQTIQRTVSKESLLVSHPSVQTKSPGG LSIQNEPLPPGPTEPTPPPTFSIPSGNQFQPRCESPIVSPITRIQ NPVAFLLSSVLPSIPAIPLTNAMGLPRAPSMPSHVLAYINI
8155	A	1	390	NLLQAIIDSLSGEDKREHRGKEEALVLDTKKDLKQITSHLLDMLVSK KVSQGRDQALNLLKNVPRKDLAIHDNSRTIYVVDNGLRKILKVVG QVPDLPSCLPLTDNTRMLASILINKLYDDLRCDDPER
8156	A	17	221	GSGPPHSAPPKGWFFSHHSEPEICLPPPRNKELPLPRRHSGLGPPLSL FKRRPPYFVHFLSFPFYPYLS
8157	A	2	367	NQRHMLGHHAEMEIRLLKANNTLLKMGYHLELPGPRMVVTNLLTRN QDKQRQKRQEEQKQQLKEQKLIAMLENGLGPPGMWELLGGPKPD SRMQEFFQPPPPRPNPQNVFQSQRSE
8158	A	1270	1692	TETKINFQNVKAMDLIHLFIYLFYFVFETESRSIGRLEFSGTISAHC NLRPLDSSNSPASAYLVAGTTGARHHARLI FVFLLETGFHHVGPWS RSLDLVIPP RP PKALGLQGGATAPGLSSVQFLKRNLPVVFQHKQ
8159	A	2	261	RPRRSSSTS*SPH*PPAVAAAPSGAPPWGLSCPRRPRAPPAAAPPEA LGQGPSTGRGAAEVAGAAGSRPPQPFYSDFQSRFCCIKS
8160	A	44	463	PPAVAAAPSGAPPWGLSCPRRPRAPPAAAPPEALGQGPSTGRGAAEV AGAAGSRPPQPPSCGSGRPSSPRSCPPPLPCFPSSLPPGTRPPH RHLPPVSTPGQRAAASPSYIASARNGRSGEGCKCARSLALRGAD
8161	A	2	319	TAIWKDQKAITQGGKYKLSKEDKGGFFLEIHKTDTSDSGLYTCTVKN SAGSVSSSKLTIKAIKDTEAQKVSTQKTSEITPQKAVVQEEISQK ALRSEEIKMSE
8162	A	1	349	RRRLVVVSGFAVPPPCLEVPLLGFAWVLGTGTAPSGWGDWDRMPSWY SCLPSMWGQKEQVLPRAGSWGFWPGSVRGENCPPVPQAPQLPPAQF LHSRLFCQGRPHRVPPGFARV
8163	A	38	369	GLYMVNGPPHFTSTVFPRVNIISVTNKGLLHSDLLKAGSLEFSPK NTVLATRQPYTTCKDGTAGIPNLQLYDVKTGTCLKSFIQKGMHNWCP SWSEDETLCARNVNNE
8164	A	43	376	LSMANGPPHCTECTAFPPRESGKNCKVCIFNTDGTLVAVRTGQKADII SVSSKGLLHSHFYLLKAVCLEFSPKNTAL*TGLPYSTSKDATAGIPNL QLYDVKTGTCLKSFLQK
8165	A	22	192	GPGSALVNSHPSGFSFRDNMAPSTPLLTVRGSEGLYMVNGPPHFTES TVFPRYDLFC
8166	B	852	931	MYSPPSDPRTVKSGVDGAMLSRKEKPLG*
8167	A	1	202	NHVFLFICFGDGVSLCCPGWSRTPGLKQSSCLGLPGCWDYRYEPACP FYKQVFSNVTSSRADVSVTP
8168	A	2	330	SICRAMKLEPYFTLYSKINLKWVIDLNIISKTVKLQENNIRENNLDI SLGKDIYLYLTAKAQSMKAKIYKYWYTKLKIFCTTKNRVNRMKRQP TNWEKIFISHMYDKR
8169	A	1	283	AAWILKARALTEMVYIDEIDVDQEGIAEMMLDENAIA/PSSTPITQA GRPITGFLRPSTQSGRPGTMEQAIPTPTAYTARPITSSSGRFVRLG T
8170	A	1	770	QAAWILKARALTEMVYIDEIDVDQEGIAEMMLDENAIAQVPRPGTSL KLPGTNQTGGPSQAVRP\TSHSEKPI TGFLRPSTQSGRPGTMEQAIR TPRTAYTARPITSSSGRFVRLGTASMLTSPDGPFFIN*SRLNLTKYSQ KPKMAKALPEYIFHHENDVKTALELAALSTEHSSQYKDWVWKVQIEKR YYRLGMYREAEKQIKSSLKQQEMVDTFLYLAKVYVSLDQPV TALNLF KQGLHKFPGEVTL LCGIARIYE
8171	A	2441	2706	FCFGLSCSLPPFFFFFEMESRSVAQAGVQWCDLSSHLPLPPG\SS NAPASASRVAGTTGAYHQCLANFGFVFLVETGVSLCWLGS

8172	A	1258	1733	ILFWIIQLNLECEFSWRLRQGRGIMLFFFPFLFFFETESHVAQTG VQWCDLGLSLQPPPP\GLSDSPALASSVSWITDVRHHLWLI FVFLVET GFRHVQASLKLPTSGDLPTLASQSAGITGVSHYAWLI FVFLVETEF HHVGQAGLELLAPSDPPA
8173	A	3	376	WYVVPPEHGQRLDRLARELFPGSSRCCGAFLRHKVALISPTVLKENG IPFNRI TQEAGEFMETFPYGYHAGFNHGFNCAEA INFATPRWIDYGK MASQCICGKARVTFSMDAFVRILQPERYDL
8174	A	196	390	RRGELLTRLAGFPSYFLLPLLESWPLTIRDEAQLTLQAQRPLVSET VLDAFWGSKPVGALFVLS
8175	A	927	1137	KRREENRGQTLQFTDAIPDKMPRAWPGAVTHACNPSTLGGRGRMRTR SGDRDHRGQHGETPSLLKIQKK
8176	A	84	307	AFKSVNLNNYMAVFISLYKNYYNLSHISNSTGFYPIFVSYFIMTI IHDLCIFPLSEDYSGSCFVCGSGSGS
8177	A	3	383	DIKILIASPSATHIHKETTRATSSPYRDTQSRTASPNRAGKGVIEQT EKSHPRSPNVLSAALSQRTTVPEEELNPKILALQNAQRKRKMEHDGS LFQAVGI /DLACRL /LGQSMDESGLPQLTSYDCEV
8178	A	2	691	TVTVFQQTQIQEPTANATTTTATTDELKTVTKDRMEDIKILIASPSP THIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEKSHPRSPNVL SVALSQRRTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLL QQPDDHAATTSLSWKRVKGMQSSEQNGMEQKTIIMLIPSDLACRL LGA SMDESGLPQLTSHDCEVNAPIQGSRNLLQGEELLRALDQVN
8179	A	2	203	SSRRLRATCGDKLRRFDENFGAPDKRLKAEPAPPAAPSTPALPPAV PKQLPAPPASPPSSAGDSVI
8180	A	1	62	QHDEEVCLDEM RDALKEKVT
8181	A	116	334	ITSKKHTNQERKMKKPLVPKGFTIEFSQLCKKL RVPVFMKPFQKYGE RGLFLNGFYEPGLTLIPKFGKNPGG
8182	A	55	351	QWSYLPQVMFTGENIP\ VHPHVYSNGHICLSILTEDWSPALSVQSVCL LSIISMLSSCKEKRPPDN SFYVRTCNKNPKKTKWYHKGFEHRDIH KGKKM
8183	A	3	474	DGSIMASMQRKLQKELLALQNDPPPGMTLNEKSVQNSIT\QWIVYME GAPCTLYEGEKFQLLFKCRRYPFDSSQGMFTGENITDHPHVYSNGH MCLSILTKNWFPALSVQSVCL\SIISMLSSCKE\KTTDHPDNSFYVR T\CNKNPKKTKWYHDDTC
8184	A	1	232	WRQGLT LSPRPECSGAIMAHCNLGLLASSHTPTSPSRVAGITGVRPH PAFFLMLAFLLLDQLQKQLILCHLISSEFN
8185	A	3	369	HERKAQPAGEGRTHMTKSDSLPSFRVSTLPLESHHPDPNTMGGASHR DRALSVTATVRETNNDPAPTQPPHASNHelayNVSLPSHLTLLISH HLLHLII IYSSCDIIYHYNTHGQHDAH
8186	A	1	203	GTRNSG DY EILYWDIPNGCKLIRNRSDCKDIDWTTYTCVLGFQVFG VWPQSGDGT DINALVRSHNI
8187	A	2	335	ARVKRLGMFNIQHCKKLSSWVLLMKYLG NATAI FFLPDEGKLQHLEN ELTHDIIITKFL\ETFLHFPKLSITGT YDLKSVLGQLGITKVFSNGA DLSGVTEEAPLKL SKAD
8188	A	1	855	EYRRFLVDRHLQLTTGNGLFLSEGLYLVDKFLEDVGRLYHSEALT VN FGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGK WERPFVEKDT EEEFDHVDQVTVKVPMMKRLGMFNIQHCKKLSSWVL LMKYLG NATAI FFLPDEGKLQHLENELTHDIIITKFL ENEDRRSASLH LPKLSITGT YDLKSVLGQLG\ITKV\FGRGSQHEKRRTEATKECKRT QNNRGTERVATAT*THNQKRKRAQQGNTREKENGKQRQEGPFVFLMI EQN
8189	A	3	157	QIRNCC LRAWEKIQDLGTTYQS FNSIRQGSKEPYPDFIARLQDAAQK ALTD
8190	A	3	362	LTWSACYWRDILRIQLWIAADILLRMLEEALLYSEYQNI SNTGLSSQ GLLILAELIPA KRTLARLLVIIVSLDYGIEKPHLGTVMHRVIGLRL LYLIFADAEGGIRDIEGSNHSAGGL

8191	A	3	335	LTWSACYWKDILRIQFWIAADIRLGMLEKAVLYSEHQNIRNTGLSSQ GLLIFAESIPAICKRTLARLLVIAASLDYGIIEKPHLGTGMHRVIGLML LYLIFANAESVIRVIG
8192	A	174	363	WQFTFTFSKSIKKDSKEEIIYQQLPRDTKIEDFGTGPRSRYPPLVALLT LSDEDDREIMYYFHG
8193	A	1	1144	VRCRPVYRNSRVDPRVRMAAVFLVTLYEYSPLFYIAVFTCFIVTTGL VLGWFGWDVPVILRNSEETQFSTRVFKKQMRQVKNPFGLEITNPSSA SITTGITLTDCLEDSLLTCYWGCSVQKLYEALQKHVYCFRISTPQA LEDALYSEYLYQEY\FILSSDIPISTEN*TSYG*SVANLLIILGIL EACLLLQNKHSPCIRTCSVYRISVSGTGAFACRLIYPLALIIRLLMD KVPLTY*SFLGY*KHVYCFRISTPQALEDALWSEYLYQEYHFICKDS KEEIIYQQLPRDTNIDDFGTVPFRSRYPPLVALLTSDDEDDREIYDIISM VSVIHIPDRTYKLSCRILYQYLLLAQGGQFHDLLKQLFMSANNFTPSN NSSSE
8194	A	2	499	DIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIMKCDVDIRKDLANTVLSGGTT MYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLST FQQMWISKQEYDESGPSIVHRKCF
8195	A	3	486	LCYVALDFEQEMATAASSSSLEKSYQLPDGQVITIGNERFRCPEALF QPSFLGMESCGIHETTFNSIMKCDVDIRKDLANTVLSGGTTMYPGI ADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMW ISKQEYDESGPSIVHRKCF
8196	A	80	1281	LPAQKLDTCDEDETTALVCDNGSGLVKAGFAGDDAPRAVFPISVGR PRHQGVMMVGMGQKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEK IWHHTFYNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPA MYVAIQAVLSLYASGRTTGIVLDSGDGVTHNVPIYEGYALPHAIMRL DLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDFEN EMATG/APS IHPPMEKSYELPDG\QVITIGNERFRCPTL\FQPSFI GM\ESAGI\HETT\YNSIMKCDIDI\RKDL\YAN\NVMFGGHPRLYP WEFAD\RMQERDSPALAPQAPMEDQGFIRPRRSKYS\ VWIGRLPSW PSLSHLPSKMWITEAGSTDEAGPFSSNRKCF
8197	A	2	228	GRVDGNWAVNEGLSIFVILVWLGLNVFLFVWYYRVYDIPPKFFYTRK LLGVSINSIPCNIGWFTFLIRHSCSSC
8198	A	1	369	GTSSEPVELLSSNSSLRPAEPRFSLVDATSLHIESLSLGDGEIYTCQ EILNVTQWFQVWLQVASGPYQIEVHIVATGTLPNGTLAARGSQVDF SCNSSSRPPPVVEWWFQALNSSSESFGHN
8199	A	1	416	NQTHYALQASLISLDFYEKHFDIYYPLSKLDLIAIPDFAPGAMENWG LITYRETSLLFDPKTSASDKLWVTRVIAHELAHQWFGNLVTMEWWN DIWLNEGFAKYMELIAVNATYPELOFDDYFLNVCFEVITKDSL
8200	A	2	397	LNTGEQKDMTEFFTDLITKIEEMSPELKNTVKSFLGGVITNNVSLD CEHVSQTAEFFYTVRCQVADMKNYESLDEVTIKDTLEGDNMYTCSH CGKKVRAEKACFKKLPRILSFNTMRYTFNMVTMMKE
8201	B	1	555	MESTYMPINSGLDKENVESECKAYNPRPFCKTYTMDKQPLNTGEQKD MTEFFTDLITKIEEMSPELSLRCEELHLHAENLSRRVWELLMLLPTC PNMLMAFQNISDEQGSYSDLYPDSDDSSSEDQVENSKNWSCKISSNF TSSSSKTIWYFSAVWEQLRYTLDNNVLKKSIIQKDSSEYBYD*
8202	A	1	901	MSLSSGASGGKVDANPVETYDSGDEWDIGVGNLIIDLDADLEKDQQ KLEMSGSKVEGIPAPNAVATLPDNIKFVTPVPGPQGKEGKSKSKRSK SGKDTSKPTPGTSLFTPSEGAASKVEVQGRSGDGANAGGLVAAIAPK GSEKAAKASRSVAGSKKEKENSSSKSKKERSEGVTCSEKDPGVLQP VPLGGRRGGYDGSAGVDTGAVEPLGSIAIEPGAALNPLGTPKEPEEG ENECRLKKVKSEKMESPVSTPAVLPIHLLVPVNNDISSPCEQIMV RTRSVGVNTCDVSGSRA
8203	A	1	407	AFFMARKAMGGHWTFSWLLCNFQITIQDINVIGTDYLTVLNAMHRCV CLLRPVVNNHHTVSPVPTGMIGPWVMAALLTLPIIRVTTVPKTV TVACTFNFSPTNDPIERINVADAMLTARGIIRFIIDFSAP

8204	A	2	1149	PDLELPRARPQLVNSPGADKMETNSSLPNTNISGGTPAVSAGYLFLDI ITYLVFAVTFVLGVLGNGLVIWVAGFRMTHTVTTISYLNLAADPCF TSTLPFFMVRKAMGGHWPFGWFLCKFVFTIVDINLFGSVFLIALIAL DRCVCVLHPVWTQNHRTVSLAKKVIIGPWVMAALLTLPIIRVTTVP GKTGTVACTFNFSPWTNDPKERINVAVAMLTVRGIIRFIIGFSAPMS I\VAVSYGLIATKIHKQGLIKVQVRP*GALSFA\KAFFLCWSP\YQ \VVP**PTSQESREVNCKGMYQRKLGIA\VDVNKVPLAFFNS/CAF NPMVLVF\MG\QDFRERLIHALPAKSGRGPLTFDFNPKPVPQLTNST LPS\AEVALQAK
8205	A	2	387	NGMLGNRFKSGFI FKVYLQETAGETWSVEQVCSWLVEKNLGELVHRF QEEEVSGAALLALNDRMVQQLVKKIGHQAVLMDLIKKYKQNTQGLKS PENPKKAALVMQTEAARDYRDEESSSPARHGEQM
8206	A	2	294	IQGGLDADLRATCLEEMTKRDVPGFAIGGLSGGESKQFWRMVALST SRLPKDKPRYLMGVGYVVDREARALPVGSGFLGTPYPAWGGGIWGR TQV
8207	A	541	713	SEVSAMVFLFFFF/CFFEMESRSAAQAGVQWCNLSLQALPPRFTPF SCLSLPSSWDY
8208	A	2	1730	KKSIQQLVPEYNEKQTPESLPQNSNPDPWHTNLTLSDETCQRSKNLK VGDKSPSVSPSPENQSATKELGQMNLTREKMDTGVVLLSGNDTLH DLCQSQLPENKESKEDYVLYTLVSSLTERLDFAAEQDLELTSEEEQ ERLKGCEKQPDKAIFKTCSPTEKTPKKQNKQINLPLLHLQKTSQE PEMAKDCDREDIPIYPVLPHVQKSEEMRIEQGKLEWKNQLKLVINEL KQRFGEIYEKYKIPACPEEEPLLDNSTRGTDVKDIPFNLTNNIPGCE EEDASEISVSVILLAYQESKKDTFCLCEHLLKKNHCDQLTVKLKQ MENMVSVLQNELSETKKTKLQLELQKIEWEKELYDLRLALKQENEEK RNADMLYNKDSEQLRIKEEECGKVETKQQLKWNLRRLVKELRTVRN NLDLVVQERNDQAQQLSEEQDARILQDQILTSKQKLEMAQKKRNPE FHSAAKNLQAESEKQILSLQEKNEKELMDEYNHLKERMDQCEKEKAGR KVVMREFQQEWTDLKQQTSEATSRCHINLDETQDSKKKLGQIRSE VCMKHNMSTVNL
8209	A	1	183	RTRGRTRGILCHMQISYAQVETMRQSI EELHYELEYVLQPHHLQV VWENHLCIFFYYLK
8210	A	3	320	RAALVLGGPKFASKTPRPVTEPLVLLSGMQLAKLIRQRKVKCIDDVQ AYINRIKDVNPMINGIDKHFEEAMNEAHAVHQKLAEKHVDVISLKN TWTFLVVALNA
8211	A	2	198	STLIVTHALHKVKVGKSPVVRGWLSGKVSPLCHFSTMTPLPPSYNTS EFLRIKWSKIEVDITGIH
8212	A	110	364	QGDSLDDTWWNQQLPKESLSWFQSLSPGIGFVDGSSCGAVREELAA LTVHCLIFRFPCLGLGKGMDDGSLERILVGEILLTSQ
8213	A	1	849	MPESWLAFFPPYGDIKKVVGLQLKEGLHQNLTMQDSIQIFDFQLPGL LRPSSVLWTLKPYHTAGLASDRDSYKGILACMPCMFGSRRSPLRDIK SHQADLELEVKNSLDTIHRLESELKKQSKIQSOMKVEKAHLEEBIAE LKKSQAQDKAKLLEMQESI KDLSAIRADLANKLAEERAKKAVLKDL SDLTAQAKSRDEETATIITQLKLERDVHQRELKDLTSSLQSVKTKHE QNIQELMKHFKKEKSEAENHIRTLLKVPLLNYPDDTEGIFLVAHEVNA A
8214	A	1	993	MWVWTAEGPTIPQFLHSVGRTVQAANPGEWVLEMPGYLSACGAERVF IYYNICPGRMGLHWLLNQEYKHISIEEEHLRRMEEARLQLKDQLLCLE TEQESILGVIGKEIDAACKTFKSDSVEKLKNI FMLAIDTVSTRVVVL CSSIDYALRVYGGSNFTDYGLESELKKQSKIQSOMKVEKAHLEEBIAE ELKKSQAQDKAKLLEMQESI KDLSAIRADLANKLAEERAKKAVLKDL LSDLTAQAKSRDEETATIITQLKLERDVHQRELKDLTSSLQSVKTKH EQNIQELMKHFKKEKSEAENHIRTLLKVPLLNYPDDTEGIFLVAHEVNA KA
8215	A	23	627	SIKCTLVSIYILIILGWQRKNCFI FYHRTYKIKYSILILF SRLKKEA PAKEQEPVSKEIARPNMAERETETSNSSESKQDKAASSKEKNGCNANS

				FEGSSTTKSEESITVSDKENETCLADQETGSKNIVSCDSNIGADKVE KKKQIQHVQCQEMELKMCQSSENIILSDQIKDHNSSSEARFSSKNIKDL RLASDNVSIIDFFF
8216	C	79	171	MDISGTKCDFTVQVQLRFLSETKATQPTN*
8217	A	3	632	HASADLWADISQRFRETCFAFALTPQQVQQISSMDISGTKCDFTVQ VQLRFLSETSCPDQEDHFPNLCVKVNTKPCSLPGYLPPTKNGVEPK RPSRPINITSLVRLSTTVPNTIVVSWTAEIGRNYSMAYLVKQLSST VLLQRLRAKGIRNPDHSRALIKEKLTADPDSEIATTSLRVSLLCPLG KMRLTIPCRALTCSHLQCFDG
8218	A	1	188	NTIVVSWTAEIGRNYSMAYLVKQLSSTVLLQRLRAKGIRNPDHSRA LSTYDKLISLIQLFC
8219	A	1	2295	VFEVVERVEELRRKWPVAVGKLDGSGIGVVTYPYADQVFRIRAE LRKK RLSDVNVERVLNVQGGKQFRVFLSTVRTRHTCKHKQTPIKKKEQLLE DSTEDLDYGFLSNYKLLNTAITRAQSLVAVVGDPIALCSIGRCRKFW ERFIALCHENSSSLHGITFEQIKAQLEALELKKTYVLNPLAPEFIPRA LRLQHSGSTNKQQQSPPKGSLHHTQNDHFQNDGIVQPNPSVLIGNP IRAYTPPPPLGPHPNLGKSPSPVQRIDPHTGTSILYVPAVYGGNVVM SVPLPVPWTGYQGRFAVDPRIITHQAAMAYNMNLLQTHGRGSPIPYG LGHHPPVTIGQPQNQHKEKDQHEQNRNGKSDTNNSGPEINKIRTPEK KPTPEKQLP RPPFPPI PQHTLLNQQQNNLPEQPNQIPQPNQAGPNN AFFNSAVAHRPQSPPAEAVIPEQQPPPMLEGEHSPLRAIAQPGPILP SHLNSFIDENPSGLPIGEALDRIHGSVALETLRQQQARFQQWSEHHA FLSQGSAPYPHHHHPHLQHLQPPLGLHQPPVRADWKLTTSSAEDEVE TTYSRLEIDEEAGEEKEASRGWFMRFKERSHPHNIKVQGETASANI EAAASYPEDLAKIIDEDGYTKLQIFCVDKTASYWKMLSRTFSSAPPK TVKPPEDQLKSENLEVSSSFNYSVLQHLGQFPPLMPNKQIAESANSS SPQSSAGGKPAMSYASALRAPPKPRPPPEQAKKSSDPLSLFQELSLG SSSGSNGFYSYFK
8220	A	143	5972	VMEDRRAEKSCEQACESLKRQDYEMALKHCTEALLSLGQYSMA DFTG PCPLEIERITIESLLYRIASFLLQKNYVQADEDCRHLVGEGLAGGED AFRAVLCCMQLKGKLQPVSTILAKSLTGESLNGMVT KDLTRKTLLS ETETATSNALSGYHVEDLDEGSCNGWHFRPPPRGITSSEEYTLCKRF LEQGICRYGAQCTSAHSQEELA EWQKRYASRLIKLKQONENKQLSGS YMETLIEKWMNSLSPEKVLSECI EGKVEHNPDLSVTTSKKSHQWT TFALTCKPARMLYRVALLYDAHRPHFSIIAISAGDSTTVQSVQEPEN CQEWIGGKMAQNGLDHYVYKVGIAFNTEIFGTFRQTI VDFGLEPVL MQRVMIDAASTEDLEYLMHAKQQLVTTAKRWDSSSKTIIDFEPNETT DLEKSLIRYQIPLSADQLFTQSVLDKSLTKSNYQSRLHDLLEYIEEI AQYKEISKFNLVQLQILASFMLTGVSGGAKYAQNGQLFGRFKLTET LSEDTLAGRLVMTKVNAYVLLPVPKQKLVTQGTKEKVYEATIEEKT KEYIFLRLSRECCEELNLRPCDTQVELQFQLNRLPLCEMHYALDRI KDNGVLPFDISMTPTIPWSPNRQWDEQLDPRLNAKQEAVALAITTPL AIQLPPVLIIGPYGTGKTFTLAQAVKHILQQQETRIILIC'THSNSAAD LYIKDYLHPYVEAGNPQARPLRVYFRNRWVKTVHPVVHQYCLISSAH STFQMPQKEDILKHRVVVTLNTS QYLCQLDLEPGFFTHILLDEAAQ AMECETIMPLALATQNTRIVL AGDHMQLSPFVYSEFARERNLHVSL DRLYEHYPAEFPCRILLCENYRSHEAIINYTSELFYEGKLMASGKQP AHKDFYPLTFFTGARGEDVQEKNSTAFYNNAEVFEVVERVEELRRKWP VAVGKLDGSGIGVVTYPYADQVFRIRAE LRKKRLSDVNVERVLNVQGGK QFRVFLSTVRTRHTCKHKQTPIKKKEQLLEDSTEDLDYGFLSNYKL LNTAITRAQSLVAVVGDPIALCSIGRCRKFWERFIALCHENSSSLHGI TFEQIKAQLEALELKKTYVLNPLAPEFIPRALRLQHSGSTNKQQQSP PKGSLHHTQNDHFQNDGIVQPNPSVLIGNP IRAYTPPPPLGPHPNL GKSPSPVQRIDPHTGTSILYVPAVYGGNVVMSVPLPVPWTGYQGRFA VDPRIITHQAAMAYNMNLLQTHGRGSPIPYGLGHHPPVTIGQPQNQH QEKDQHEQNRNGKSDTNNSGPEINKIRTPEKKPTPEKQVDLESNPQN

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				<p>RSPEsrpsvVYPSTKfPRKdNlnPRHlnLPLPAPHAQYAIPNRHFHP LPQLPRPPFPPIPQOHTLLNQQQNNLPEQPNQIIPPQPNQVVOQQSOLN QQPQQPPPPQLSPAYQAGPNNAFFNSAVHRPQSPPAEAVIPEQQPPP MLQEGHSPLRAIAQPGPILPSHLNSFIDENPSGLPIGEALDRIHGSV ALETLRQQQARFQQWSEHHAFLSQGSVPYPHHHHPHLQHLPPPLGL HQPVRADWKLtSSAEDEVETtYSRFQDLIRELSHRDQSETRELAEM PPQSRLLQYRQVQSRSPPAVPSPPSSTDHSSHSFNFNDSNRDIEVA SNPAFPQRLPPQIFNSPFSLPSEHLAPPPLKYLA PDGAWTFANLQON HLMGPGFPYGLPPLPHRPPQNPFVQIQNHQAIGQEPFHPPLSSRTVS SSSLPSLEEYEPGRGPRPLYQRRISSSSVQPCSEEVSTPQDSLQCK ELQDHSNQSSFNFSPESWNTTSSTPYQNI PCNGSSRTAQPRELIA PPKTVKPPEDQLKSENLEVSSSFNYSVLQHLGQFPPLMPNKQIAESA NSSSPQSSAGGKPAMSYASALRAPPKPRPPEQAKKSSDPLSLFQEL SLGSSSGSNGFYSYFK</p>
8221	A	3	755	<p>KYVNNFILKNFPALLSTGEFLKL PFERLAFVLSSNSLKHCTELELFK AACRWLRLEDPRMDYAAKLMKNIRFPLMT PQDLIN YVQTVDFMR TDN TCVNLLEASNYQMPYMQPVMQSDRTAIRSDSTHLVTLGGVLRQQQL VVSKELRMYDERAQEWRSLAPMDAPRYQHGI AVFLYVVGGSNY DTKGKPAVDTVFRFDPRYNKWMQVASLNEKRTFFHLSACKAHLYAVG RHSAA GELATVECYN</p>
8222	A	57	272	<p>HIFLT SWNFYINRELHLNNLRLVLPFELGKLFQLQTLGLKGMTSIF VLLMVCEYVFESKEAKLSARGFF</p>
8223	A	1	218	<p>PTRPGKYIVTGGEDDLVTVWSFVDCRVIARGHGHKSWVSVA FDPYT TSVEEGDPMEFSGSDEDFQDLLHFG</p>
8224	A	180	293	<p>WVPFFCDLRQGPVYPITGGFRQPYPSLSVDTMSR</p>
8225	A	76	551	<p>IKMSGKANASKNAQQLKRNPKRKDNEEVVLS ENKVRNTVKKNKNH LKDLSSEGQTKHTNLKHGKTAASKRKTWQPLSKSTRDHLQTMMESVI MTILSNSIKEKEEIQYHLNFLKKRLLQQCETLKVPPKKMEDLTNVSS LLNMERARDKANEGLA</p>
8226	A	3	145	<p>SDGSASKGKHYFSEP VHILKRAFARTVSGVSHVLKNLSFSLQSSDTF</p>
8227	A	16	548	<p>QLNGRSIRHEVM SHRKFSAPRHGSLGFLPRKRSSRHRGKVKSF PKDD PSKPVHLTAF LGYKAGMTHIVREVDRPGSKVKNKKEVVEAVTIVETPP MVVVGIVGYVETPRGLRTFKTVFAEHISDE/CRLPLRQKKAHLMEI HVNGGTVAEKLDWARERLEQQVPVNPVFGQDE MIDVI</p>
8228	A	3	348	<p>TRHIVREVDRPGSKVKNKKEVVEAVTIVENTPMVVVGIVGYV/ETPR/ GLRTFKTVFAEHISDECKRRFYKNWNKSKKIDLKFIDTTSKLCHGRL QTMEKKAFMGPLKKDRIAKEEGA</p>
8229	A	1	956	<p>VNHAPAHASDGVM SHRKFSAPRHC\SLGFLPRKRSS\RHRGKVKSF MDDPSK\PVHLTAF\ LGYKAG\MTHIVRE\VDR\ PGSKVKNK\ EVVE \AVTIV*DTTHWCLLGIVGYVGNPSEGLRD/TFKTCLLLEHISY*MP RRRFL*RIWALKS*EGRPLPKYCKEIGKDED\GKKPAWKDFQQH*K KLLAQVHPCSIAQTQ\MRLPL\ RQK\KAHLMEIQV\NGGTVARES DWAREKLE\QQVPVNQVFGQDEMI\ DVI\GVTKGK\GFKGVTRS\WP TN*LPFKA\HLG\LSRVACFGAWHPARAHWHVARAGQKGYQPYTLV HSDL</p>
8230	A	1	375	<p>QNI AHIIGPPNRCEHAAWIINDLFQSCRRGPPGPPGGPGMPQGARAR ERGQGTWDTPGGQMSFSIPAHKSGLVIGLGGDNVKAITQQT GALVEI SRQLPPTGDPNYKLLIIRGSPQQIDHTKPR A</p>
8231	A	1	399	<p>LDVKLIEGLVVKAGT TVRFP AIIRGVPVPTAKWTTDGSEIKTDEHYT VETDNFSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPG PPTGPINILDVTP EHTISWQPPKDDGGSPVINIYIVEIQ</p>
8232	A	2441	2706	<p>FCFGLSCSLLPFFFFFEMESRSVAQAGVQWCDLSSHLPLPPG\SS NAPASASRVAGTTGAYHQCLANFGFVFLVETGVS LCLWLGWS</p>
8233	A	1275	1749	<p>ILFWIIQLNLECSEFSWRLRQGRGIMLFFFFPFLFF FETESH SVAQTG VQWCDLGLSQPPPP\GLSDSPALASSVSWITDVRHHLWLIFVFLVET GFRHVQASLKLPTSGDLPTLASQSAGITGVSHYAWLIFVFLVETEF</p>

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				HHVGQAGLELLAPSDPPA
8234	A	3	200	DALAFVIKVFAAEEVDGCSVTTGS/HNHSVASGSNHRTRFCFTVYLS SIVSWRY*SCRCRECRGRAF
8235	A	1	1214	PGSPIVKS AKFVTDLLLHF IKDQTCYNI IPLYNSMKKKVLSDSEDEE KDADVPGTSTRKRKDHPRRRLRNRAQSYDIQAWKKQCEELLNLIFQ CEDSEPFRRQPVLDLLEYPDYRDIIDTPMDFATVRETLEAGNYESPMEL CKDVRLIFSNSKAYTPSKRSRIYSMSLRLSAFFEEHISSVLS DYKSA LRFYKRNTITKRRKKRNRSSSVSSSAASSPERKKRILKPQLKSESST SAFSTPTRSIPPRHNAQINGKTESSSVVTRSRNRVVDPVVT EQPS TSSAAKTFITKANASAI PGKTI LENS VKH SKALNTLSSPGQSSFSHG TRNNSAKENMEKEKPVKRKMSSVLPKASTLSKSSAVIEQGCKEQR FLYQGPFFQVNGHGGQPSKLVKRGPGKET
8236	A	24	183	PVPEIKVVPPLPPTIMEEVPLSGTDADLLVPYDIYVLS PCCNLKCL IQACL
8237	A	256	491	PPMLGKDKKEKEKALKRKITKEEKELRLLRPL YQFMSCKEFDDLFE NMHKEKMLRAKIRELQRYRRNGITKMEESA E
8238	A	243	385	DISHLSADGYSSSDSFTSDPEQIGSNVTRQRSVFLSMKSMNLNYLAAF
8239	A	3	404	SCYGFNVRGQV\SDGGQLRSINGELYAPLQH\NHVNVEGATHKQVVD LIRAREKELILTVLSVPPEADNL YPSDDSLGQSFYDYTEKQAVPIS VPYKHXVEQNGEKFVVYVNYMAGRQLCSKRYRQFALHQN L
8240	A	1	706	GGGGGGSVLHCAGNGGGGGPRVVRIVKSESGYGFNVRGQVSEGGQ LRSINGELYAPLQHVSAVLPGGADDRAGVRKGDRILEVNHVNVEGAT HKQVVDLIRAGEKELILTVLSVPPEADNLDP SDDSLGQSFYDYTEK QAVPISVPYKHXVEQNGEKFVVYVNYMAGRQLCSKRYREFALHQN L KREFANFTFPRLP GKWPFSLSEQQLDARRRGLEEYLEKVC SIRVIGE
8241	A	323	497	DRVSLCCPGVQWHNLGSLQPLPPWFKRFSLLSLPSSWDHRRMPHPA NPCILSRHGVL
8242	A	1	483	GRDLWDDEEMAKAQSHDCVPVLSEHPLYILYTS GTTGLPKGVIRPTG GYAVMLHWSMSSIIYGLQPGEVWAAASDLSWVVGHSYICYGPLLHGNT TVLYEGKPVGTPDAGAYFRVLAEHGVAALFTAPT AIRAIRQQDPGAA LGKQYSLTRFKTLFVAGRTM
8243	A	2	740	QMAHAVMIRDIGSNSPVSKLAGVLVKHG IKKGDTTVVIYMPMIPQAMY TMLACARIGAIHSLIFGGFASKELSSRIDHV KPKVVVTASFGIEPGR RVEYVPLVEEALKIGQHKPKIL IYNRPNMEAVPLAPGRDLWDDEEM AKAQSHDCVPVLSEHPLYILYTS GTTGLPKGVIRPTGGYAVMLHWSM SSIIYGLQPGESQTPSGGIPEEVIIVIGDDSSMLALVELPVRQIVEM EDSDTDNPD PV
8244	A	249	390	VANIKKETHIVVYKDEREISVDEKHDFKDGICTLLITEVG DYKCKM
8245	A	24	428	GQEKLVPPSVELDVKLIEGLVVKAGTTVRFP AIIRGVPVP TAKWTTD GSEIKTDEHYTVETDNFSSVLT IKNCLRRDTGEYQITVSNAAGSKTV AAHLTVLDVPGPPTGPINILDVTPEHMTISWQPPKDDGGS
8246	A	1	240	TPSRCCCCRSAPTLVGVRTRGFNIPKQVSRSGLYRSPSPMDNLNRPS LKQVEKFVGSIPDKVKKKYFSGQGLRKVRTF
8247	A	935	1150	QRRRGRGWTCGSTLREDGHLPEPAFLHSAQEPRSGALACGKATGEH RAPRRPPGRVRS PAHPEPCPSSGV
8248	A	190	584	KIKHRPEEPRWAAAGASAGPGA AEVAPPRPGTVAPGANGMTDSAT ANGDDRDP EIELFVKAGIDGESIGNCPFSQRLFMILWLKGVVFNVT T VDLKRKPADLHNLAPGTHPPFLTFNGDVKT DVNKIEE
8249	A	201	364	MILYKSSLYVFPYCNQLFLTAVNFTEVNEENKNDLFQEVFSS IETL AFTFGNM
8250	A	1	1122	MHKDWVFDVSGEHKEALLHELQLCDSTLKPAAHGQTRLVDLSLSEH KAQGTGAHVYEEHQVSVSR TDDVGCVPSECLRACGA EVGCSNIAY PKLVMELMPIGLRGLMIAVMLAALMSSLT SIFNSSSTLFTMDIWRRL RPRSGERELLVGRTGIPSTPPAPQSRLSFLLPETPPLERYLLGLV MDLWL VIVALIGVSAWI PVLQDSNSGQLFIYMQSVTSS LAPPVTAV

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				FVLGVFWRRANEQGAFWGLIAGLVVGATRLVLEFLNPAPPCGEPDTR PAVLGSIHYLHFAVALFALSGAVVVAGSLLTPPPQSVQIENLTWWTL AQDVPLGTKAGDGQTPQKHAFWARVCGFNAILLMCVNIFFYAYFA
8251	A	1	1197	MHKDWVVFVDSGEHKEALLHELQLCDSTLKPAAHGQTRLVDLSLSEH KAQGTGAHVYEERHQVSVSRRTDDVGCVPVSECL\RACGAEVGCSNIA YPKLVMELMPI/GFSGAGDFPGPPLSNPLFLEAFDPSGLRGLMIAVM LAALMSSLTSIFNSSSTLFTMDIWRRLRPRSGERELLLVGRGTGIPST PPAPQSRLSFLLPETPPLERYLLGLVVM DLWLVI VALIGVSVAWIPV LQDSNSGQLFIYMQSVTSSSLAPPVTAVFVLGVFWRRANEQGAFWGLI AGLVVGATRLVLEFLNPAPPCGEPDTRPAVLGSIHYLHFGVALFALS GAVVVAGSLLTPPPQSVQIENLTWWTLAQDVPLGTKAGDGQTPQKHA FWARVCGFNAILLMCVNIFFYAYFA
8252	A	1	624	MGCGIEFVTKSSKAIATTKTKIDNWDLIKELLHSKRNYQYSKQTIYKE LCGCSERSQGEVEILNLEPLDEGASMHPCCDDTYCGPPESEPEVKAV ANFLRKHRKHIRAYLSFHAYAQM LLYPYSYKYATIPNFRCVESAAYK AVNALQSVYGVRYRYGPASTTLCSSAGSGNQIDTRQVKQEKSIQILL ILCVQDLHNRVKSKEVAKAR
8253	A	88	627	PHGPKTMEEGGSTGSAGSDSSTSGSGGAQQRELERMAEVLVTGEQLR LRLHBEKVIKDRRHHLKTYPNCFVAKELIDWLI EHK EASDRETAIKL MQKLADRGIIHVCDEHKEFKDV KLFYRFRKDDGTFFPLDN EVKAFMR GQRLYEKLMS PENTLLQPREEGVKYERTFMASEFLDWL
8254	A	3	439	SIYASPDKRNQTHYALQASLKLDFYEKYFDIYYPLSKLDLIAIPDF APGAMENWGLITYRETSLLFDPKTSSASDKLVWTRVIAHEL AHQWFG NLVTMEWWNDIWLKEGFAKYMELIAVNATYPELQFDDYFLNVCFEVI TKDS
8255	A	1	401	SPRTGGGGGQSPAPAGERTMHCLGAEYLVSAEGAPRQREWRPQIYR KCTDTAWLFLFFLFWTGLVFIMGYSV VAGAAGRL LFGYDSFGNMCGK KNSPVEGAPLSGQDMTLKKHVFFMNSCNLEVKG TQLNRM
8256	A	220	415	KYAFVLVHIYASIWEERRLFTTENTPIKYGSQIFTLVQPIHLPQKVA VVHCWGHQKGQDEIGQKN
8257	A	2	359	HEMLDKAPVLKVI VNSLKNMINTFVPSGKVMQV VDEKL PGLLG NFP GPFEEEMKGIAAVTDIPLGKVHLEALKKKVIKFFYKFPLRCDIHTAQ VLYVLDIQHRCCMSLDIHTAQVHRS
8258	A	1	1270	RTRGRTRGELVLESGEWRWLLERCPRGGAVAILLA AVVS\CAV\SQ HAPPWTEDCRKSTYPPSRPTYRGAVPWDTI/HVLDLPPYKRWDELML DMPV/LSKVI VNSLKNMINTFVP\SGKIMQV VDEK/LPGLLG NFP PFEEMKGIAAV/SLDIPLGEIISFNIFYELFTICTSIVAEDKKGHL IHGRNMGF\GVF\LVWNINNDTWVITEQLKPLTVNLDFQRNNTKTVFK ASSFAGYVGMLT\GFKPGLFSLTLNERFSINGGYLGILEWILGKKDA MWIGFLTRTVLENSTSYEEAKNLLTKTKILAPAYFILGGNQSGEGCV ITRDRKESLDVYELDAKQGRWYVQTN YDRWKHPFFLDDRRTPAKMC LNRTSQENISFETMYDVLSTKPVLNKLTVYTTLIDVTKGQFETYLRD CPDPCIGW
8259	A	108	988	TARGSKARSGGTRWSLGPSSSGGRRSQPLVISRAV*H*GKSSRHQ PLYSGHPLGPVSHRGGPGPVRQPAAT*RPACASKLVQ PWH*WGPG* LGSQPALAGHLCRTGCEESHHTCFPGYVKP*RL*ALPGGRPV*VGER ARARPDEPREAAGFCGTEEQPHTDPAHPRLKRDCL/PSVSQA AVSTT ASAGFPPAWAASAGFPPTWTPNLSPATLGMQRSSCALTFRRICRFLS DNKWMQRSITSM AIWICNGSGGSTSGRVSFSSTLGGTDCSSSSL SKS ETFPSATSFSLR
8260	A	1	319	GVKNNHPQIPALPRFKKSLPASVSQA AVSTTASAGFPPAWAASAGFP PAWAASAGFPPTWTPNLHRAHSLVCKTERSRTQSSKPYWAPTMCW STLRLEQKR PCH
8261	A	19	373	AVFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF\SSSSSSFFFF SFFLFFFFFKLKE LRLVI*PLNPEN*ESCPLFSPVNL DMP*TFKDKRW KVNWARSTSRQOLLESARTKSWAEREGGTRWRW

10665

8262	A	227	420	KNFLPNCSAKELFFFFFFFFFFFLLLLLLLLLYFKP/MI*WFKHLAF PLLAFILSPAL*RGVFHH
8263	A	400	582	VLVSFGVLLLLLFIFFTSFSFLFFFFLLFFFFFFFFFFFFFFFFFFFF FFFFFFFFFLLLLLLLLLCH
8264	A	1205	1681	SSLIFLLSSLISSMNRSISSPSPIISMLSTSLGTSPPKPGAGGAQ TPLTFPPGSWYSPPPKAGASCTGAFSTTLFSLGTFMSLFFPVFFF FFFIFIFFFFFFFFLLLLLLLLLLYFKFGARGGLPRACA TLPLALQGVTSMAVLMV
8265	A	1	403	KSLQYSNTGDMILVVSGSCHAKVIDRDGFEVMECIKGDQYIVDMANT KGHTAMLHTGSWHPKIKGEFMTCSNDATVTTWEVENSKKHKSVMFKPR TMHGQKVIPTTCTYSRDGNLIAACQNGSIQIWRNLTVH
8266	A	3	399	LEKQMEKAHEDSEKLRREIVLPMKEIEELKAKLLRAELIQEIQRPP RHAPSLHGSTELLPLSRDPSPPLEPLEELSGDGGPAAEFAHNCDD ASISSFSLGGVGSSSSLPQSRQGLSPEQEETASLVS
8267	A	36	448	NFMDVFTWSLPFVGEKVTDLFLNVLSICSDDELMTGEDQFDGSAA RKEIIRNKIRAIGKMARVFSVLREESESVLTLKGLTPTGMLPSGVLA GGROTQLSAIRGFSPPHRI CSFEEAKGLDRINERMPPRKDAVQ
8268	A	1	453	RHERHERHEELMTEGEDQFDVGSAAARKEIIRNKIRAIGKMARVFSV LREESESVLTLKGLTPTGMLPSGVLAGGROTQLSATVEAIEAEKAIR GFSPPHRICSFEEAKGLDRINERMPPRKDAVQDGFNSL\NTAHATE NHGTGNHTAQ
8269	A	644	809	VWNRLIEYCKHACPKLEPFSLFIPKVGSAARKEIIRNKIRAIGKM ARVFSVLR
8270	A	37	235	SHSSLPCSASSPPALVSPGSFSGLVYKNVTPVYVYALKGVRNCCTKR GCLIRKGPWPHHPMTGAGL
8271	A	2	230	EDKTISDQESFREVITAMDVMQFTKEEVWEVSRLLAGILHLGNIEFI TAGGAQVSFKTGKIMPACPPRSLCSPWET
8272	A	516	695	GLSHQIILNRFYLYKSSRLGAMAHACNPSTLGGRGQLIMRSGVRGQPV QHGTKPYLLKIQ
8273	A	2	435	GRSDRNSSEEGTAEKSKKLRTTNEHSQTCDWGNLLQDIILQVFKYL PLLDRAHASQVCRNWNQVFHMPDLWRCFEFELNQPATSYLKATHPEL IKQIIKRHSNHLQYVSFKVDSSKESAEACDILSQLVNCSLKTLGLI STA
8274	A	3	417	RQAWHKAGLHAADWAGRARSLLGDSHTSWSAGSIPGKHYQAVGLHLW KVEKRRVNLPRVLSMPPVAGTVCH\AYDREVHLRCELSPGYLLAVPS TFLKDAPGEVLLRVFSTGRVSLSAIRAVAKNTTPGAALPAVERGT
8275	A	308	614	HGSHGIALRPRQSQAQPLVHKVCCFQEEQMGAPGKGPCEGSRICRL LAQGLGFHLVCLDRV*HLAPHCSLSLHGCGPHDVPFLVAKRSFLGLE GPLSSPP
8276	A	11	161	LFFPDNLEDETEDDDLFETEFRQYKRTYYMTKMGVDVVSEYVFANAF ILK
8277	A	163	437	HLAGNMPPKQELGSGVGELAMCAPSEKFLNMGAPLGVLGLVVFVSSL GSMFLPPTTEAGATLYSLAMYGGVLVFSMFLLYDTQKVIKRAQV
8278	A	1	660	MALWTLRPTPLLVTCMLICAPGVMGAVVAPLTLGGPLLIRAAWYTA GIVGGLSTVAMCAPSEKFLNMGAPLGVLGLVVFVSSLVDQMGRWFVA GGAAGVLGALCYGLGLSNEIGAIEKAVEYWFNSFVCHSNQQNACSH ELHDERLLGDMGLPILHAMLLRRLPSVDSQNALSSIMLLHTALPLTK ALTQLKKCSSGLMLMEFTGLTMFPIILKQLD
8279	A	2	1246	SCSAPEELCSLRPTLGARRGNCEAKVTGDRAFQICSDVLGAPPPMLA ARL\VCLRTLPSRVFHPAFTKASP\VVKNSITKNQWLLTP\SREYAT *T*/RLGIRAWGELGQELKEGSIGNHSMGKNILKFSDSGEELVA\G GA\VVGLSICAYLLALGL/GLN*DLGAI*KRL*FGPQYVK\DRI\H STYM\YLAGGVLGLTA\LSAIAIQNRLFFMELP*WRLLGWTIGVD LWQPWLGAGMLVRSIPYDQSPGPKHLAWLLHSGVMGAVVAPLTLGG PL\LIRAAWY\TAGIVGGLS\TVA\MCAPSEKFLNMGAPLGSGAGVS

				VFVSSIGI*CFPPPTD/TVAGATL\YSV\AMYGGISSFLSMFLLYDT PESKSSRAEVSPMYG\VQKYDPI\NSML\SIY\MDTLNIFMRVATML ATGGNRKK
8280	A	325	432	GVSGALTVLMKDALKPNLMQTLVSRVTPAFLNWF
8281	A	1	293	EKGHTRTAQFDISVASEIMAVLALTTSLDEMRERLGMVAVSSKKGE PVSAEDLGVSGALTVLMKDAIKPNLMQTLVSRVTPAFLNWFVTVRA EWL
8282	A	1	366	PTRPRLGNLRPRLGNPPILRHQGVRESAVCAEAMAAAAPVAADDNKR RRRPGADSISSYEAQITALKQERQQQQQDCEEKERELGRLLKQLLSRA YPLDSLEKQMEKVGIGMASLLPWDLEEC
8283	A	780	891	KYSIFSDFLADQAACYVQAIQWILHYHYHGVQSWW
8284	A	44	155	GSPVKNKFYVHNDMFRYEDEVFGDSEPELDEGEVTLKI
8285	A	336	416	LAARRQEQRATVRALGFWAFSLQAKE
8286	A	1	294	KLDTVVEFPPIRGLNMSEFVCNMSARPYVYDLIAVSNHYGAMGVGHY\ KAAYVLFYQRRDDEFYKTPSLSSSGSSDGGTRPSSSQGFGDDEACS MDTN
8287	A	302	486	MVFPPPLVFQTKAAYVLFYQRRDDEFYKTPSLSRSGSSDGGTRPSSSQ QGFGDDEACSMMDTN
8288	A	1	620	AYEKHVSMQLPQKKKKTVALRDCIELFTTMETLGEHDPWYCPNCKK HQQATKKFDLWSLPKILVVHLKRFSYNRYWRDKLDTVVEFPPIRGLNM SEFVCNLSARPYVYDLIAVSNHYGAMGVGHYTAYAKNKLNGWYF DSNVSLASEDQIVTKAAYVLFYQRRDDEFYKTPSLSSSGSSDGGTRP SSSQGFGDDEACSMMDTN
8289	A	1	804	MGPQRGYPYPQAWNHQPKGECPLDAAAGPAWSCAPAGAQQQLPRLH PHAPSREGLSTVGSI CSPQVDIGLNNGDMSDSVGSLKYICPSSPKEK SLFSFLYTEICLQGLVGKEGSSQMVGLISWRRLYCVLRGGKLYCFY SPEEIEAKVEPALVVPINKMLEREREGERAERNPSQENKEWRRPGQF ALEMEGPSLRGPALRLAGLPTQQETIRAMDKDAKKRIHNFVINV PGQAITQIFAVDNREDLQKWMEAFWQHFFDLK
8290	A	164	399	TAISHLSSEWSYLCILALVIGALFSSFGVMFSSMVLMLVDVYLCLV IKELGFYISLCSLGLFVPIILLGKTLQAFKGN
8291	A	1	2226	MDKFWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRT EAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFIIEGHVVIPIRIHPN SICANNTGVYILTYNTSYDYTCFNASAPPEEDCTSVTDLPNAPFDG PITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDVSSGSSSERSS TSGGYIFYTFSTVHPIDEDSPWITDSTDRIPATTLMTSATATETA TKRQEAWDWFSWLFLPSESKNHLHTTQMAGTSSNTISAGWEPNEEN EDERDRHLSFSGSGIDDED FISSTISTTPRAFDHTKQNDWTQWNP SHSNPEVLLQTTTRMTDVRNGTTAYEGNWNPEAHPLIHHEHHEEE ETPHSTSTIQATPSSTTEETATQKEQWFGNRWHEGYRQTPREDSHST TGTAASAHTSHPMQGRTPSPEDSSWTDFFNPISHPMGRGHQAGRR MDMDSSHSTTLQOPTANPNTGLVENLDRGTPLSMTTQQSNSQSFSSTSH EGLBEDKDHPTTSTLTSSNRNDVTGGRDPNHSEGSTTLLEGYTSY PHTKESRTFIPVTSAGTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHP SGGSHTHGSESDGSHSGSQEGGANTTSGPIRTPQIPEWLIILASLL ALALILAVCIAVNSRRRCGQKKLVINSNGAVEDRKPSGLNGEASK SQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV
8292	A	876	1104	HFDNCSNCMVTAASAHTSHPMQGRTPSPEDSSWTDFFNPISHPMGR GHQAGRRMDMDSSHSTTLQOPTASPNTEG
8293	A	2	427	AIPNHKDPSTQFHHWYLTDWKSGDQYQSLSSSSSTATGTTVIECTQ VQGSSESLASPSTSRATTPSLSIEVEAREISSPGRPPGLMSPSSGY SSQSETPTPTVMSLTLGHLPPSSSVVRVPVPERKSSLPPTSPME
8294	A	1	128	DKEIFSKSFLSHFILLHISGSLPKVHPRYDLGDGDSMAKSGSI
8295	A	33	279	PPVPNSSRRPTRPPTRPRTSYEKQGYLLLPVFSIVLEVLARAIQ TEIKSVQMGKEEVKLSLVVCVYLKMRKSCGIHQ

8296	A	198	781	QERLPSGIRPLSGNIRVATAMPPTARPGSRGCPIGTGGVLSSQIKV AHRPVTQOGLTGMKTGTGKGPQRQILDKSYLGLLRSKISELTTEVNK LQKGIEMYNQENSÝVLSYEKRAETLAVEIKELQGQLADYNMLVDKLN TNTEMEEVMDYNMLKAQNDRETQSLDVIFTERQAKEKQIRSVEEEI EQEKQA
8297	A	1	441	AYVKLSKVLNIFYVANADDSSKTELLFAALKALKYLFRFIIQSRVLYL RFYQSKDGDEFNNSIRQLFLAFNMLMDRPLEEAVKIKGAALKYLPS IINDVKLVFDPVELSVLFCKFIQSIPDNQLVRQKLCNMTKIVESTLF RQSECK
8298	A	132	702	WWWGHQRQGVGHGDEAGPDTTPAIIITTMDFNVTKPVEYLINPII TQFFPTLLLWCFSALLPTIVYSGFFEDHWTRSGENRTTMHKCYTLL IFMVLLLPSLGLSSLDLFFRWLFDKKFLAEAAIRLESGFLPNNGAFL KNYVIASPFIGNAMDLLRIPGLLLMYMIRLCLTRSAERENVKQHAY E
8299	A	303	617	AKPSSGFECRSRAFLSKECGKQLGPSSSSALSLSGSFFHLGAPS*PR TPRKSDGARCRRPHPPSSMIGVQLLLGGCLAQHPHRAQLLDADVPTT ISIKHVKGQP
8300	A	50	258	NHVNFCFCFCFSDRGEIKLGINVIKRIHVIRKIFPPFRTEASLASRR EQKREQYRQVKAHVQKEDRRVQ
8301	A	110	180	CFPAAPDEDSTTNITKKQKWTVE
8302	A	187	571	GDSRSRVTRRQDTAWNAWSASHCRRLSASSRSPLTGPASVGGMAATG ANAEKAESHNDPVRLLNPNIAKMKEDILYHFNLTTSRHNFALFGD VKFVCVGGSPSRMKAFIRSGARHCGHNRAAGSYL
8303	A	2	150	FVDLLISNIAKMKEDILYHFNLTTSRHNFALFGDVKVRGQVLTWPWN LA
8304	A	227	857	GDSRSRVTRRQDTAWNAWSASHCRRLSASSRSPLTGPASVGGMAATG ANAEKAESHNDPVRLLNPNIAKMKEDILYHFNLTTSRH/NFPQALF GDV\KFVC\VGGSPPSRNEKPSSGCRLGA\ELGLDCPGRDYPNICAGT DRYAMYKVGVPVLSVSHGMGIPSIISIMLHELKLLYYARCSNVTIIRI GTSGGIGLEPGTVVITEQAVDTCFK
8305	A	2	358	MAFLWLVCFCALVGATFGCGVPAIQPGLTGLSRIVNGEDAIPGSWPW QESLQDRTGFHFCCGSLISENVVTAHCGVKTTDQVVGAGEFDQGS EKNVQVLKIVQVFNPKFNSFTVR
8306	A	1	714	TPKRAPKKKMAISGVPVLGFFIIAVLMSAQESWAIKEEHVIIQAEFY LNPDQSGEFMFDFDGDEIFHVDMAKKETVWRLEEFGRFASFEAQGAL ANIAVDKANLEIMTKRSNYTPIINDKFTPPVVNVTLRNGKPVTTGV SETVFLPREDFHFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWE FDAPSPLPETTENVVLCALGLTVGLVGIIIGTIFIIGLKRKSNAEER GPL
8307	A	225	384	ITFLFIKNPTFDSECYFFPHSLPCTLPYFPPEFDAPSPLPETTENVV CALGL
8308	A	2	862	FLSVLPHSRALLTPKRAPKKKMAISGVPVLGFFIIAVLMSAQESWAI KEEHVIIQAEFYLNPDQSGEFMFDFDGDEIFHVDMAKKETVWRLEEF GRFASFEAQGALANIAVDKANLEIMTKRSNYTPIINVPPEVTVLINS PVELREPNVLICFIDKFTPPVVNVTLRNGKPVTTG\VSET\VFLPR \EDHFFR\KFHYLPF\LPSTEDV\YDCR\VEHWGLDEPLLKHWEFDA PSPL\PETTENVVLCALGL\AVGLVGIIIGTIFHHSRELKRSNCRQKR KGGLCKAQWR
8309	A	2	224	INNSLFIKKGPTALQPQHRTRPWTATASPARGFATSMPSRLAATV AGCGIPDSGRPAPTRDSQNMASPPDWH
8310	A	1	3253	MELSVTLVSRAPRGLPVFRQLNTAIAVSQMSSGQCRLAPLIQVIQD CSHLYHYTVKLLFKLHSLPADTLQHRDRFHEQFHSLRNFFRRASD MLYFKRLIQIPRLPEGPPNFLRASALAEHIKPVVVIPEEAPEDDEEPE NLIEISTGPPAGEPVVADLFDQTFGPPNGSVKDDRDQIESLKREV EMLRSELEKIKLEAQRYIAQLKSQVNALEGELEEQRKQKQKALVDNE QLRHELAQLRAAQLEGERSQGLREEAERKASATEARYNKLKEKHSEL

				VHVHAE LLRNADTAKQLTVTQQSQEEVARVKEQLAFQVEQVKRESE LKLEEKSDQLEKLEKRELEAKAGELARAQEALSHTEQSKSELSSRLDT LSAEKDALSGAVRQREADLLAAQSLDDFSPTS KLQRLLAESRQMVTD LELSTLLPISHENLTGSATNIRKCCLOSCSHGLIAKPSATLIQHVL LFIAEGTLRVEGSYSFTATAPDTALDSDGEPGQPLCNFNAKLTSGC DRGRLWHPRQRPVRRFSEQQRSHRCGPATALFQAARAHPPSPGLQWP AISISKAINTEAPVKEKHARRILGRLLDPGVGHSHGHTPREVGFTF WSTPLGCRCPAVHSQLEFCHVLKGPRECTHGCLMPQQHVVCCFRNSPA AMVQPORLLHSRTRTVGTGLLSPANLPNPQRI PKRMPPAPPGDPAPP GIGNGACPLQSMAGPSGYI QDTGSAISSIQOTSTPQCSRENQAKALC PPGTSLTPEVLQCIQIAGPPGLSGLTVCVLMQTSSPDSSAAGLGEP RNLRPATGSLTTEVPGLWSCHISQLESQEQLRQLLDEQFSVFRGA AAEA AVILQDAVSKLDDPLHLRCTSSPDYLVSSAQEALDAVSTLEEG HAQYLTSLADASALVAALTRFSLAADI ING GATSHLAPTD PADRL IDTCRECGARALELMGQLQDQALRHMQASLVRTPLQGILQLGQAAV DGGGRRLLPLSDSHPHQELKPKSLDVRQEELGAVVDKEM/AATSAAI E DAVRRIEDPQLLHR/H**R*GAVTRGGLHLEGHQSLLSWSRQAIRLL VTST
8311	A	3	3253	ESRGRSRTKAGGGGRMNSIKNVPARVLSRRPGHSLEAEREQFDKTQA ISISKAINTEAPVKEKHARRI ILGTHHEKGAFTFWSYAIGLPLPSS SILSWKFCHVLHKVLRDGHPNVLHDCQRYRSNIREIGDLWGHLDHY GQLVNVYTKLLLT KISFHLKHPQFPAGLEVTDDEVLEKAAGTDVNNIF QLTVEMFDYMDCELKLSSES VFRQLNTAIAVSQMSSGQCRLAPLIQVI QDCSHLYHYTVKLLFKLHSCLPADTLQGHRDRFHEQFHS LRNFERRA SDMLYFKRLIQIPRLPEGPPNFLRASALAEHIKPVVVIPEEAPEDDE PENLIEISTGPPAGEPVVADLFDQTFGPPNGSVKDDRLQIESLKR EVEMLRSELEKIKLEAQRYIAQLKSQVNALEGEQRKQKQKALVD NEQLRHELAQLRAAQLEGERSQGLREEAERKASATEARYNKLKEKHS ELVHVHAE LLRNADTAKQLTVTQQSQEEVARVKEQLAFQVEQVKRE SELKLEEKSDQLEKLEKRELEAKAGELARAQEALSHTEQSKSELSSRL DTLSAEKDALSGAVRQREADLLAAQSLVRETEAALSREQQRSSQE QG ELQGR LAERESQEQLRQRLLEQFAVLRGAAAEAGILQDAVSKLD DPLHLRCTSSPDYLVSR AQEALDAVSTLEEGHAQYLTSLADASALVA ALTRFSLAADI ING GATSHLAPTD PADRLIDTCRECGARALELMG QLQDQALRHMQASLVRTPLQGILQLGQELKPKSLDVRQEELGAVVD KEMAATSAAI EDVRRIEDMMNQARHASSGVKLEVNERI LNSCTDLM KAIRLLVTSTSLQKEIVESGRGAATQQEFYAKNSRWTEGLISASKA VGWGATQLVEAADKVVLHTGKYEELIVCSHEIAASTAQLVAASKVKA NKHSPHLSRLQECSTRVNERRAANVVASTKSGQE QIEDRD TMDFSGLS LIKLLKQEMETQVRVLELEKTLEAERMRLGELRKQHYVLGASGSPG EEVAIRPSTAPRSVTTKKPLAQKPSVAPRQDHQLDKKDIYPAQLV NY
8312	A	1	673	SKSELSSRLDTLSAEKDALSGAVRQREADLLAAQSLDDFSPTS KLQRL LLAESRQMVTDLELSTLLPISHENLTGSATNIRKCCLOSCSHGLIAK PSATLIQHVL L LFIAEGTLRVEGSYSFTATAPDTALDSDGEARPGAA FATSMPPSSRLAATVAGCGIPRQRPVAGGYGGGWHRCTRD SQNMGKPR LTGHGQLNRPVTASFPLRKQLTVGVSSPQE QGMYGH
8313	A	177	395	ETPGGFKDNLHAVICLAENSVGPNATRPDDIHL LFSGKTVEINNTDA EGTLVLADGV PYACKDLGADI I LDM
8314	A	177	402	ETPGGFKDNLHAVICLAENSVGPNATRPDDIHL LHS GKTVEINNTDA EGTLVLADGVSYACKDLGADI I LDMAT
8315	A	3	831	QKNTHYMMIFDAFVILTCLVSLILCIRSVIRGLQLQQEFV NPFLLHY KKEVSVDQMEFVNGWYIMII ISDILTIIGSILKMEIQAKSLTSYDV CSILLGTS TMLVWLGVIRYLGF FAKYNLLILTLQAALPNVIRFCCA AMIYLYGFCGWIVLGPYHDKFRSLNMVSECLFSLINGDDMFATFAK MQQKSYLVWLF SRIYLYSFISLFYIMILSLFIALITDTYETIKQYQQ

				DGFPETELRTFISECKDLPSNGKYRLEDDPPVSLFCCCKK
8316	A	1	473	LIPSDRPLIASTHACADSNDLKVIIISAVGPVFSSVHDLKELTEEQG RDYHAEVFQTC SKVALEMLFTGEPISAEALLHGLLSKVPEAELOE ETMRIARKIASLSRPVSLGKATFYKQLPQDLGTAYYLTSQAMVDNL ALRDGQEGITGFLQKR
8317	B	549	602	MWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSNDLKVI IISAEGPVFSSGHDLELKEEQGRDYHAEVFQTC SKVMHNRHPVP VIAMVNLATAAGCQLVASCDICRGERQDLFCHSWVPRKVALEMLLT GEPISAEALLHGLLNKGGPEAELOEETMRIARKIASLSRPGVSLGK ATFYKQLPQDLGTDYYLTSQAMVDNLALRDRQEGITAFHLKRKPVWS HEPV*
8318	A	1	350	PCCSHPNVAVLGVOQTLEEMDFQGIWSAALNGDLGRVKHLIQKAEDP SQPDSAGYTALHYASRNGHYAVCQFLLESGAKCDAQTHGGATALHRA SYCGHTEIGRLLLSHGSPKVG
8319	A	272	364	YYKCGAQFALVTLTGLGTATAFTVAVTRWR
8320	A	1	322	IFGELLLFLHHQYPGDIGCFAYFLNLLTLKPGEAMFLEANVPHAYL KGGEPHFSSEPHCHPCWALFPYLDKGRRRRVKETPKDLAALTSEGSW AQQATAGRDDECI
8321	A	37	344	PPAPDTPDTPPTYGLTLLTNPRNTSLPPTLHLPSPRTPSSPPSTS LPPSLVLGFFLKIQSGKRRAYPEHFWQNGERKAQPSVHAPVNSASA YVDAAANS
8322	A	3	414	SARLHTVYRVPRLNHPPEEIGCHSRVPGSAHPSEKPPSAPASAPQNV FSTTVSSGYNTKKIGPRLNIQLKKGTEGLGFSITSRDVTIGGSAPIY VKNILPRGAAIQDGRKAGDRLEGNVDLVGKSQEEVVSL
8323	A	37	438	SLPRGGFRCCLVHTTANRPSLDAHLGGRKHRHLVELRAARKAQGLR SVFVSGFPRDGD SAQLSEYFLAFGPVASVMDKDKGVFAIVEMGDVG AREAVLSQSQHS LGHSLRVPPPEQKESRAPPPNPQRSGP
8324	A	2	425	GRVGKLRKMMIIAENKKDMSGHYQNALYLGDGNSRGRILKNCGQKSL AYFTSATHGLYEDTESLKETFDPKKETIPIHYPNARLLQPPAPILPL DTNWTLLTVSNGFFEGTIARKGKGVLAAACIDIVTGSIGWRRGVKL
8325	A	543	848	KSQSECPDSVQRDVLSSGRHTHVKRKKVTFLEEVTEYYISGDEDRK GPWEEFARDGCSVQKRIQETEDAIGYCLTFEHRERIGNRLQGTCKG LNVLKQC
8326	A	2	242	PPDCSRAACPVLCSGNGQYSKGRCLCFSGWKGTECDVPTTQCIDPQC GGRGICIMGSCACNSGYKGESCEEAPRYIPKKE
8327	A	2	246	AVPDCSRAACPVLCSGNGQYSKGRCLCFSGWKGTECDVPTTQCIDPQ CGRGICIMGSCACNSGYKGESCEEAPRYIPKKE
8328	A	294	402	IIHLYFCVFFEDHSDNPLGAAVTLAHELGHIFGWI
8329	A	259	350	PSGESWPSMGHRLIPGIRCGPNNREESGDR
8330	A	2	410	RPPPPVSSVPGPGRDQLGVTPLSGRHSLCCWVRIVFPESDGAP*MA SFPPRVNEKEIGKLLNLVDHTEVVRDLTFAPDGSILIVSASRDCTL RVWDLKDDGNMMKVLRGHQKLVSACAFSPDSSMLCSVGASKA
8331	A	453	684	SLRFVLSVFCQSLLGKAESSKYDTRETPKAWKESAAPPELLGWA\HS SGLTCDIKCCRARDLPWSGPKIHTSV MCPSS
8332	A	1	92	FFFFFFFFFFFFFFFFFFFFFYKSLIKLKNKI
8333	A	67	301	LGLLALATTPQLIFVFFVKMGPDWSRIPELKQSTHGLPKCWNHRHK PLCNTFQSYFYPTWYNCHPSCCKIKVKWRQV
8334	A	3	276	SDCTWTINLPIGFGVHLQFVNFSTETIH DYLEVRSGSSETSTVIGRL SGPQIPSSLFSTTHETSLYFHS DYSONKQGFHIVYQGRNNKK
8335	A	1	564	MSLGCFSSETWTPNGSVGMYTSAIQMSVFSFAALGGQTEVQFGNMPR RGTVSSNERSHYSGGGITVLRKEKGRNRHIDTCHCVR IAYSVQYS NMLCRERVENTSHPGEMQVTIQNLMPATVYIFRMAQNKHGSGESSA PLRVETQPEAISDVHYLQILVLPNTTLLSSSADELISYFRGYSSR
8336	A	1	364	KSQLMCQMYMGKEKPFGRCCCEKAFSNKSYLLVHQQTHAEKPYGCN ECGKDFSSKSYLIVHQRIHTGEKLHECSECKRTFSFHSQLGHIHQRIH

				TGENPYECCECGKVFSKKDQLVSHQKT
8337	A	3	103	GTLCDDSSQTQTEWMTSIFIAQVRDLFELSSRV
8338	A	1	744	VNGVPSRSPRLVASGDDSDVSLQRMVQNEQEPMEKSIDAVIATAS APPSSSPGRSHSKDRTLGKPDSSLVPAVASDSCNNSISLLSEKLTSS CSPHHIKRSVVEAMQRQARKMCNYDKILATKKNLDHVNKILKAKKLQ RQARTGNNFVKRRPGRPRKCPLQAVVSMQAFQAAQFVNPELNRDEEG AALHLSPTVTDVIEAVVQSVNLNPEHKKGLKRKGWLLLEEQRKKQK PLPEEEEEQENNR
8339	A	3	266	VGWQQGVPEPPPGKAVTVPLRPADPFKGKKAPARSGFPALFPGDPPG EESLGRRRPGSSPLTPLSIPEVIKIFVPPAPQKSGHFFSF
8340	A	481	637	LFLPFSRVLLERLIVNRPHWPGLLITFIELIKNPAFKFWNHEFVHCA PGRVG
8341	A	1	3335	LNLKFEIEVLCKNLALDINELKPGNLLKDKDRLKNLDEQLSAPKKDV KQPEELPPITTTTTSTTPATNTTCTATVPPQPQYSYHDINVYSLAGL APHITLNPITPLFQAHPQLKQCVRQAIERAVQELVHPVVDRSIKIAM TTCEQIVRKDFALDSEESRMRIAAHHMMRNLTAGMAMITCREPLLMS ISTNLKNSFASALRTASPOQREMMDQAAAQLAQDNCELACCFIQKTA VEKAGPEMDKRLATEFELRKHARQEGRRYCDPVVLTGYQAERMPEQIR LKVGVDPKQLAVYEEFARNVPGFLPTNDLSQPTGLAQPMQAWAT DDVAQIYDKCITELEQHLHAIPPTLAMNPQAQALRSLLVVLSRNS RDAIAALGLLQKAVEGLLDATSGADADLLRYRECHLLVLKALQDGR AYGSPWCNKQITRCLIECRDEYKYNVEAVELLIRNHLVNMQQYDLHL AQSMENGLNYMAVAFAMQLVKILLVDERSVAHVTEADLFHTIETLMR INAHSRGNAPEGLPQLMVVRSNYEAMIDRAHGGPNFMMHSGISQAS EYDDPPGLREKAHEYLLREWVNLVHSAAGRDSTKAFSAFVGQMHQOG ILKTDDLITRFFRLCTEMCVEISYRAQAEQQHNPAANPTMIRAKCYH NLDAFVRLIALLVKHSGEATNTVTKINLLNKVLGIVGVLLQDHDVR QSEFQQLPYHRIFIMLLELNAPEHVLETINFQTLTAFCTNFHILRP TKAPGFVYAWLELISHRIFIARMLAHTPQQKGWPMYAQLLIDLFKYL APFLRNVELTKPMQILYKGTLRVLLVLLHDFPEFLCDYHYGFCDVIP PNCIQLRNLILSAFPRNMRLPDPTPNLKVDMLEINIAPRILTNFT GVMPPQFKKDLDSYLKTRSPVTFLSDLRSNLQVSNPEGNNRYNLQLIN ALVLYVGTQAIHAIHNKGSTPSMSTITHSAHMDIFQNLAVDLDEGR YLFNLAIANQLRYPN\SHTHYF\SCT\MLYPFCRGPFRKPSQEQITR VLLERLIVNRP\HPWGLLITFIELIKNP\AFK\FW\NHGICYTCAPG NSEKLFPVGSAQWLAWGQEGQGPSKLIGRGTGLPS
8342	A	1	520	KMDSTEPPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPISGWNGDN MLEPSANMPWFKGWKVTRKDGNASGTTLLEALDCIL/PPTRPTDKPL RLPLQDVYKIGGIGTVPVGRVETGVLKPGMVV\MHHEALSEALPGDN VGFNVKNVDVKDVRGNGAGDSTNEPTMEANGFT
8343	A	1	443	AYTLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKEVSTYIKKIGYNPD TVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEALD CILPPTRPTDKPLRLPLQDVYKIGGIGTVPVGFAPVNVTTTEVKSVM HHEALS
8344	A	41	666	PLHLAEEKNGYNPDVAFVPISGWNGDNMLEPSANMPWFKGWKVTRK DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDDYKISGWNGDNMLE PSANMPWFKGWKVTRKDGNASGTTLLEALDCILPPTCPTDKPLRLPL QDVYKIGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTTEVKSVMHHE ALSETLPGDNVSFNVKNSVC
8345	A	2	396	ADIERLRMRVMMAATHASASISGWNGDNMLEPSANMPWFKGWKVTRK DGNASGTTLLEALN\CGIGTVPVGRVETGVLKPGMEVTFAPGNVTTE VKSVEKHHEALSEALS\GDNAGFNVKNVSVKDVRRGNV
8346	A	1	461	MLLEALDCILPPTRPTDKPLHLPLQDVYKIGGIGSVPVGRVETGVLK PGMVVTFAPVNVTTTEVKSVMHHEALSEALPGDNVGFNVKNVSVKDV RHGNVAGDSKNDPPMEAAG\RAVRDMRQTAVAGVIKAVIDKKAAGAG KVTKSAQKAQKAK

8347	A	1	743	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCSSIDKRTIEKFEKETA EMGKGSFKYGWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVPIVAAGVGEFEAGISKNGQTREHALLAY TLGVKQLIVGVNKMDSSTEPYPYSQKRYEEMWLREVSTYIKKIGYNPDT VAFVPISGWNGNMLEPSANMPWFKGWKVTRKDGNASGTMLEASQ TIHLWVALLFVI
8348	A	208	947	NWFKGWKVTRKDGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK IGGIGTVPVGRLETVGLKPGMVVTFATVNVTTTEVKSVENHLVAPLDC PRTP\FGPTRPSTYIKKIGYY\PDTLAFEPISGWNGDDMLEPSANMP WFKGWKVTRKDGNASGTTLLEALDCILPPTRPTDKPLRLTIQDVYKI GGIGTVPVGRVETGVLKPGMVVTFAPVNGTT*VKSVMHHEALSEAH SVDNVGFNVKNV
8349	A	1	1434	RGITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLI VAAGVGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSSTEPYP SQKRYEEIVKEVSTYIKKIGYNPDTVAFVPISGWNGDNMLEPSANMP WFKGWKVTRKDGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYKI GGIGTVPVGRVETGV/LEVPISGWNGDNMLEPRANMPWFKGWKVTRK DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYKIGGIGTGPVGR LETGVLKPGMVVTFAPGNVTTEVKSVELLHEALSEAFPGDNVGFNVK NVSVDVRRHGNVAGDSKNDPPMEAAGFTAQVILNHPGQISTGYAPV LDCHTAHIACKFAELKEKIDHRSKGKLEDGPKFLKSDAAIVDMVPG KPMCVESFSDYPSLGCFAVRDMRQIVTVGVIIKAVDKKTAGAGKVTKS AQKAQKAK
8350	A	1	1254	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLI VAAGVGEFEAGISKNGQTREHALLAY TLVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEAL DCILPPTHPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTTTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNVA GDSKNDPPMEAAGFTAQVILNHPGQISTGYAPVLDCHTAHIACKFA ELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP LGRFAVRDMRQTVAVGVIIKAVDKKAAGAGKVTKSAQKAQKAK
8351	A	1	1195	MQSERGITIDISLWKFETSKYYVTIIDAPGHRDFIQNMITGTSQADC AVLIVAAGVGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDS EPPYSQKRYEEIVKEVSTYIKKIGYNPDTVAFVPISGWNGDNMLEPS ANMPWFKGWKVTRKDGNASGTTLLEALDCILPPTRPTDKPLGLPLQD VYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTTTEVKSVEMHHEAL GEALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFPAQVIL LNHPGQISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKF LKSGDAAIVDMVPGKPMCVESFSDYPPPLGCFAVRDMRQTVAVGVIIK VDKKAAGAGKVTKSAQKAQKAK
8352	A	1	2471	MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAA EMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAY TLGVKQLIVGVNKMDSSTEPYPYSQKRYEEMWLREVSTYIKKIGYNPDT VAFVPISGWN\GDNMLEPSANMPWFKGWKVTRKDGNASATTLEALD CILPPTRPTDKPLRLPLQDVYKIGGIGTDPAGRVKTGVLKPGMV/VA PFAPVNGTTEVKSVEMHHEALSE/ALLLGDKGAFNVKNVSVKDVRRG \NVAGDSKNDPPMEAS\GFTAQVILNHP\SQKNARHMPLELDCHTA HIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCV SFSDYPPPLGRFAVRDMRQTVAVGVIIKAVDKKAAGAGKVTKSAQKAQK AK
8353	A	184	819	ETEIKNASRGKTETSKLKQNLEEQDLRLMQQLQDLEECREELDTDEY EETKKETLEQLSEFNDSLKKIMSGNMTLVDELSGMLAIQAAISQAF KTPKVIRLCGKK/HHPVQLRPR*AEMDRDLMVGKLERDLYTQKVEI LTALRKLGEKLTADDEAFLSANAGAILSQFEKVESTDLGRPPSYMNYL

				LDSHPSKNIDVPSKISFLLKIQDL
8354	A	1	387	GTRSGNMTLVDELSGMQLAIQAAISQAFKTPEVILLFAKKQPGQLRT RLAEMDRDLMVGKLERDLYTQQKVEILTALRKLGEKLTADDEAFLSA NAGAILSQFEKVSTD LGSGDKILALASFEVEKTKK
8355	A	3	1022	FLASLQWVQTSSFSSEKFVITDLLKPTSVNLSKSFVQLCSIAGGSL RPTPEIQEVKTPEELETFMLKHGENIIDTLGAEVDRLEKELKSGSLV PCIPAAPAVTKRQGTAPAIASVGGSPKPWQLPRGVGPVGAQKSRT VWKS LPRFQRMYGKHLDAQNDRSTDLSHSAPGKATDTQCQPLKAAS GLYP AELKRWSCPWLEPTFCISVTWSDLEQLRKIRRRSPHEDTESF TVYLRSDVEAKSLEVWGSPEALAREKKLRKEAIEYREKGSINSATL I/EFSRYLS DTRY/RTRSCAWCLKICKI IPTMANSCSPNTCSLCLL YSSPALPWTLKFA
8356	A	4	516	PLWWSNVIIAATCMGLTSITGNPLYDSLGS LGVGTLLGMVSAFLIYT NTEALLGRSIQEQQVRLTELENDPSVRAIHVDKATDLGLGKVRFK AEVDFDGRVVTRSYLEKQDFDQMLQEIQEVKTPEELETFMLKHGENI IDTLGAEVDRLEKELKKRNPEVRHVDLEIL
8357	A	1	248	GSTHASERRQKTTTRTKVIPAASEEQLLLVELVRSISVMRAETVIQ TVKEVLKQPPAIAKDKKHLSEVCM LQFFYAIQR
8358	A	3	4135	IPMVVSDFDLPDQQIEILQSSDSGCSQSSAGDNLSYEVDPETVNAQE DSQMPKESSPDDVQVVFDLICKVVSGLVESASVTSQLEIEAMPP KCSIDIDPEETIKIEDDSIQSSQNALLSNESSQFLSVSAEGGHECVA NGISRNSSSPCISGTTHTLHDSSVASIETKSQRQSHSSIQFSFKEKL SEKVSEKETIVKESGKQPGAKPKVKLARKKDDDKKSSNEKLKQTSV PFSDGLDLENWYSCGEGDISEIESDMGSPGSRKSPNFIHPLYQHVL LYLQLYDSSRTLYAFSAIKAILKTNPIAFVNAISTTSVNNAITPQLS LLQNLARHRISVMGKDFYSHIPVDSNHNFRSSMYIEILISLCLYYM RSHYP THVKVTAQDLIGNRNMQMSIEILTLFTELAKVIESSAKGF PSFISDMLSCKKVQKVILHCLLSSIFSAQKWHSEK MAGKNLVAVEEG FSEDSLINFSEDEFDNGSTLQS QLLKVLQRLIVLEHRVMTIPEENET GFDVVS DLEHISPHQPM TSLQYLHAQPITCQGMFLCAVIRALHQHC ACKMHPQWIGLITSTLPYMGKVLQRVVSVTLQLCRNLDNLIQQYKY ETGLSDSRPLWMASIIPPDMILTLEGITAIHYCLLDPTTQYHQLL VSVDQKHLFEARS GILSILHMIMSSVTLLWSILHQADSSEKMTI AAS ASLT TINLGATKNLRQQILELLGPISMNHGVHFM AIAIAFVWNERRQN KTTTRTKVIPAASEEQLLLVELVRSISVMRAETVIQTVKEVLKQPPA IAKDKKHLSEVCM LQFFYAIQRIPVPNLVDSWASLLILLKDSIQL SLPAPGQFLILGV LNEFIMKNPSLENKKDQRDLDQDVTHKIVDAIGAI AGSSLEQT TWLRRNLEV KPSPKIMVDG TNLES DVEDMLS PAMETANI TPSVYSVHALTLLSEVLAHLLDMVFYSDEKERVIPLLVNIMHYVVPY LRNHSAHNAPS YRACVQLLSSLSGYQYTRRAWKKEAFDLMFDP SFFQ MDASCVNHWRAIMDNLMTHDKTTFRDLMT RVAVAQSSSLNLFANRDV ELEQRAMLLKRLAFAIFSS EIDQYQKYL PDIERLVESLRLPQVPTL HSQVFLFRVLLLRMS PQHLTSLWPTMITELVQVFLLM EQELTADED ISRTSGPSVAGLETTYTGNGFSTSYNSQRWLNLYLSACKFLDLALA LPSENLPQFQMYRWAFIPEASDDSGLEVRRQGIHQREFKPYVVR LAK LLRKRKKNPEEDNSGRTLGWEPGHLLTICTVRSMEQLLPFFNVLS QVFNSKVTSRCGGHSGSPILYSNAFPNKM KLENHKKPCSSKARQKIE EMVEKDFLEGMIKT
8359	A	2	418	KEFSELVARIDYNDGEFLLIEAADFLPKWLDPENSTNRGFFCHGELC IIPAPIKFGAESWLPPTTPPTIPQALNIIITAHSEKILASKSIPSVVNR RITGYPEKIQASLNRAHCFLPAGIVAVLKQRPRLVAAAVQAFL
8360	A	43	239	AYWGRKTPWLTISSFWPTPGSPYYDNVRPLCYSDSDAVLLCFDISRP KTVD SALKKVRLDQLSNL
8361	C	141	356	MSFDCGFGTLPLLLSPICCLGSYSNKVIS PGLXXXXXXXXXXG GALL KDPWGGPIFPGGGKKFFFLFGGGF*
8362	C	22	159	MRGVFPLFPLKXXXXPKGLKIXXXGPI MSPQKKVPFQKSQGGF*

8363	A	64	240	TLKFWKEGGPPISPPQKKGPFPKIPRGGL*GPPKKKKNFSFPPPVKL GPPKGIFKRAPP
8364	A	19	471	TPRQARHEGEDFVSVSPQHLHKFLASIDLNIENEKQVYNAAIKWLLA NPQHHSKWLDETLAQVRLPLLVDPLMGVGAKEQIVQNLKCRDLLD EARNYHLHLSSRAVPDFEYSIRTTTPRKHTAGVLFCVSGRGSGDPFR SIECYSINKN
8365	A	3	401	HASANAGDSRAIIVRNGEIIIPMSREFTPETERQRLQLLGFLKPELLG REFTHLEFPRRVLPKELGQRMLYRDQNMGTWAYKKIELEDLRFPLVC GEGKKARVMATIGVTRGLGDHSLKVCSSSTLPIKPFLLSC
8366	A	186	840	NFTLQKQTAGWIWPMSCSLTTLGLEHSLPRPATEPLERPSRSHIAPT EYSQLVPLSSCGEGLPLPQATITSHSHPEAGPGLEARTPELQLFS GQLSFWSAAEETKTRPPQARATKPPKPKSSWQORSCISSESETPGLP IDFPSCPYPALVRLPLRSSLSQQEVVRVPQGSRAKSLPAREWEAWPHP ATATVRAWAWPCSGVPLMERGGSRSRGPR
8367	A	7	633	PTITNVWSETSQELADGLRRGSQGDSVQONGPPRKHIVERYTEFYHV PTHSDASKKRLIEDTEDWRPRTGTTQSRSFRI LAQITGTEHLKESEA DNTEKANNSQEPSPQLASSVASTRSMPELSDPTSGRPGVTSLTAA AFKPVGSTGVIKSPSWQRPNOQVPSTGRISNSAAYSQSVAPANSALG QTQPSDQDTLVQR*PTITNVWSETSQELADGLRRGSQGDSVQONGPP RKHIVERYTEFYHVPPTHSDASKKRLIEDTEDWRPRTGTTQSRSFRI LAQITGTEHLKESEADNTEKANNSQEPSPQLASSVASTRSMPELSDP TSGRPGVTSLTAAAFKPVGSTGVIKSPSWQRPNOQVPSTGRISNSA AYSQSVAPANSALGQTQPSDQDTLVQRAEHIPAGN
8368	C	78	386	MTHLEAQNKIKGCTGSLNMTLQASAAKPEPGSCSKAHSHQVRFRD FSGASRGTRIEDPRVTVNTQNGKIPPKRPPRKPHCGALYRVLSCTHF TVMPARRD*
8369	A	20	443	SASVAVVGEFGPAQLGLGLHLPNPNGKPGSSQWSPVPGSSTVALLCPR PATASELIKFPPLSSQAQNSCKWSYIRKGPASSIPSPFLASADSCRV VSCPDQPRAPCRGQCWPGGVGAASALPWQPAPSLTFIPASYSAPTRP
8370	A	49	354	SCHIIPSLTFTFTRFIQSPVTLRLSQVILILQWAIASSTLDRDAN CSVMRFVRDLIHTGVANDVSIKMI PFLNLSFYLLSLCHSLGENQHPS ISFLDLYW
8371	A	239	402	IESPETNSCIDGQLLFDGGIRITHWAKDSSSSSSSSSSSSSTCRRMK LDPYLTP
8372	A	141	351	HTTASPFWQGLTNVRCRNTSLTTFQVIPDLDGWFHAQPVQLQLLSP VTEFILPPSLVLPLPGESHFL
8373	A	239	474	MRMVTWWRGVFLATSPSP/RPSQLEKQYALYRKATSPN*FAPNCY PDPQPHLG*LAPVAHVPL*QRRKAESPSSN
8374	A	1	740	MVSDIRKEDGMNVLPKYIPNVGVNFSFAGVYLASETLPGSFAHPEA TSRGAVATGTTHLASAVEPNGDSWCKQRSRVSVHYIRINITGWVCT CCDIERNIMLSPSLNIRNNITARLRPKTGTQMPLEQRYTGIDENAH VVERRVF/RVPALHLRRPSQLEKQYIALYRKATSPN*FAPNCYPDPQ PHLDR LAPVAHFPL*Q*KAESPSSN*VARGTCTS*LSKPRTVWKD PVARNRPPVGPT
8375	A	803	985	GLALTPTTAGGGGLTALRRGSLEPGRGRGWLLL PVSQEVCTTPAILG VISSPPRILGTR
8376	A	1	319	VDDLLLGHPTAVGCTKGTDALHRHLED CGYKVSKKKAQICRQQPWAS VDWELYVDGNSFFNPQGERGAGCAVTLDTVVEARSLPQATAAQKAE LIAFIGALELSE
8377	A	339	808	GSQSQQGNRGWFSVPASRGVPPPAVMGVLRARGGRGAGSQSPPPGGC LPPMRWGSGATRSGLWWETSDGLEPTPSRRWWGSS*TL/GGSPVQV Y*LVTPDSGSSH*KANSFCLSGDNLIGKKASFRSKQVNQLSSAGSKP NNVDGLGTGCKVSV
8378	A	588	2278	GWAHGGEACFCVPALHLCRPSQLEKQYPVLY*KATSSN*FAPNYYPD P*PHLG*LPPW
8379	A	779	986	ELQLYWLCKKPPIDIRSHWKSC*AGISTSRCLQLPKR*GSGVL PAD

				SMMRGKV\SRSAWHRSLSWSSPL
8380	A	179	795	PAFFLIPGCAPPVG**IPSNVPAVGRS\DFFSWTPYTHSPPDAGVEH PFPWRTRLPWGVPAKGHQRTGATRSLSGFWWDTSGGLEPTPPRRWWS S*TLBEARSKCTE**HLTPDLPTERTASGSQGRIC*RKHLS/WSK QVKQLSSAGSNPSNVYGLG/DCWM*SHCSLLNQAQILSRPVVGLRL GNRQEGSVPWRLTRNYHSGKS
8381	A	1	1029	MGSCMARASPMGATPCFAAVGPIDCQAEERHTVWDWVVALPTAAVG DPIGQPIQYARSTCEAGVGELHIQDALPEDHGYTCLAEALGQVSC SARVTVREGTSPGPKGKTGHCGLSVSPGLMKELALMENVAEPPGSVK LSARTVQVQPSLALSVPAGHGGEHCGASGLGVDDLLGHPTAVGCA TGTDAPHRHLEDCEGYKVSKKKAQICQQQHDARQGPVPPGIIQAYGAA PFEDLQVDFREMPKCGGNKYVVLVLRGTYSGWVEAYPTRTEKTREVT VLLRDLIRRFRPPLWIGSDNGPAFLAALVQKTAQIQNNITGGVYTL CDIDSHIILFRSGY
8382	A	989	2798	EENCRNRLGLQGRHPQLLQIASQVFNRYAVSRKENGKENGQARP HADLFVSCSNQRGPRKEARERGPWERNSAWLSEFAALMTFCWDTPRQ SGVPREQMPYTAPGGLWVEGVQEESDLPADGVSKGWPPCWRALAA TALLVQEAANKLTGLRNLNIKASRAVVTLMTKGGHWTDLARLIKYQT LLCENPRITIEVCNTHLPASLLPVSESTVEPDCVEMLDSVDSSRPDL RDQAWASGDWKLIVYVGSFFNPQGERGLQVDFTEMPKCGGNKHVL VLGRTYSGWVEAYPTRTEKAGEVIPVLLRDVIPRFRPPLWIGSDNGP AFLAALVQKTAKPALALLSLSLSMYLVTVLRNLPSILAVSSDCPLHT PMYFFLSNLCWPDIGFTSAMVPKMIVDTQSHSRVISHAGCLTQMSFL LLVACIEGMLLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFL SLDLSQLHSWIVLQLTIIKNVEISNLVCDPSQLNLACSDSVINNIF IYFDSTMFGFLPISGIFLSYKIVPSILRISSSDGKYKAFSTCGCHL AVVCWFYGTGIGMYLTSAVSPPPRNGVVASVMYAVVTPC
8383	A	2	397	SILKLPQWLKGLLAFLVKPLLPRLSAFLSNMKSRSAGKLWELQHEIE VYRKTVIAQWRALDLDVVLTPMLGPALDLNAPGRATGVVPVTTVTAE DEAQMEHYRGYFGDIWDKMLQKGMKKSGLPVAVQCV
8384	A	3	1773	PGGRQQQAEGIMVOYELWAALPGASGVALACCFVAAVAALRWSSGRT ARGAVVRARQKQORAGLENMDRAAQRFRLOPNDDLSEALLALPLPQLV QKLHSRELAPEAVLFTYVGKAWENVKGTNCVTSYLADCEQLSQAPR QGLLYGVFVSLKECFTYKQDSTLGLSLNEGVPACDSVVVHVLKLQ GAVPFVHTNVQSMFSYDCSNPLFGQTVNPNWKSXSPGSSSGGEGAL IGSGGSPGLGLGTDIGGSIRFPSSFCGICGLKPTGNRLSKSGLKGCYV GQEAURLSVGPMARDVESLALCLRALCEDMFRDPTVPPLPFREEV YTSSQPLRVGYETDNYTMPSPAMRRVLETQKSLAAGHTLVPFLLP SNIPHALETSTGGFLSDGGHTFLQNFKGDFVDPCLGDLVLSILKLQ WLKGLLAFLVKPLLPRLSAFLSNMKSRSAGKLWELQHEIEVYRKTVI AQWRALDLDVVLTPMLAPALDLNAPGRATGAVSYTMLYNCLDFPAGV VPVTTVTAEDAEQMEHYRGYFGDIWDKMLQKGMKKSGLPVAVQCV ALEWQEEVCLRFMRVERLMTPEKQSS
8385	A	660	774	PSWLVTLLLLPSSAGKLWELQHEIEVYRKTVICQWRA
8386	A	27	374	SSPPAWQPRPPCGGLHHCAPCVHPRDSSGVSPPAPAACCHTPHGRPW PEFEGQRPTQPPQGPAPVVRPVLTLASGRVASVPLVSLCAWASGSQ PGPPTGSGRAICTGLGAPPA
8387	A	685	769	EQHFLPLRLILKQEHPELAVLADSVDLQE
8388	A	305	426	HWHKKNQIDQWIKIKNPKNPTTYRELIFGQGAQNNTWGK
8389	A	308	411	HWLKNQIDQWIRIKNPETNPHTYSELIFDKGAK
8390	A	3	503	LVILDYIIRNTDRGNDNLVRYEKQKCEKEIDHKEKSWIDDEFLIK IAAIDNGLAFFFFKHPDEWRAYPFHAWLPQAKVPFSEIRNLILPYI SDMNFQDLCEDLYELFKTDKGFDKATFESQMSVMRGQILNLQALR DGKSPFQLVQIPCVIVERSQGGSGQ
8391	A	4	318	NKKSQSESEGQLSQGLKPASFQPGVVVIHPPGVSrvPTVALGTCQPPS SQEQIPSHRSFSPDTEMGVSPAGSGSLETANTHPAGPAGHLSCPVG

				SQVKPAVAGGK
8392	C	340	474	MSRQWIPXSRQKFEADCPGESGSSGKRTLTRSWCRSCCCVLXNXS
8393	B	317	702	LAEWRPREPMQRKLKVTSLPGLTVVITEQAVDTCFKAEEQIVLGKR VIRKTDLNKKLVQELLLCSAELSEFTTVVGNTMCTLDIFYEQGRLDG ALCSYTEKDQAYLEAAYAAGVRNIEMESSVFAAI*
8394	A	209	582	EQNWMLRVWMCWICFFLPYALLCAPWLPFCNFILFYTPAISBDVWL FFPPGLGSPGLTVVITEQAVDTCFGRVLSRIVLGKRVIRKTDLNKKL VQELLLCSAELSEFTTVVGNTMCTLDIFYER
8395	A	227	1302	GDSRSRVTRRQDTAWNWSASHCRRLSASSRSPLTGPASVGGMAATG ANAEGAESHNDPCVRLNPNIAKMKEDILYHFNLTTSRHNFTLFW FKFGLFGGNP\SRMKPFI\RCLGPEIGLDCPVRDYPN\ICAGTRYA MYKVGVPVLSVSHGMGIPSIISIMLHELKLLYYARCSNVTTIRIGTSG GIGLEPGTVVITEQAV\DTCFKAEEFKQI\VLGKRVIR\KT\DLNKKL VQELLL\VSALSEFT\TVVGNTMCTL\DFYE\GQGR\LDGALCSY TEKDKQAYLEAAY\AARVPQLFEMESSVFA\AMCSACGLQAAVVCVT LLNRLEGDQISSP\RNVLSEYQQ\RPQRLVSFYIKKKLSKA
8396	A	3	339	QWYSFNDQHVSRITQEDIKKTHGGSSGSRGYSSAFASSTNAYMLTY RLKDPARNAKFLEVDEYPEHIKNLVQKERELEEQEKRQREIERNTCK IKLFLHPTKQVMMENK
8397	A	2	376	NHEKDDNSLKIISNASCCTTNWLTPLAKGIHDFNGIVEGLMTTVHAIT ATQKTGDGPGS\NWGVMAAGLSKTSSLPPLG/LGKAGGKVIPELNGK LTGMAFRVPTGNVAGVDLTCLRLKPKGYDDIK
8398	A	3	1141	IRHEVRQSAASSFASPAEPHRSDTMGKVKVGVNGFGRIGRLVTRAAF NSGKVDIVAINDPFIDLNYMVYMFQYDSTHGKFHGT\VKA\ENGKLV I\NGNPITIFQEPKIPSKIKVGGDAGRLKYV\VEFHAVFTT\MEKG LGASFCRGGAKRVNQSLPPSG*CPPCFGHGV*TIEKYDNSLK\IISN \ASCTTNCLT\PLAKVIHDFNG\IV\EGLMTTVH\AIT\ATQKTGVW ALPGNCG\VMGPRGSSRTSSLPPLAAAKAVGKVNPLSLNG\EAHLGM GFRVNPANV\SVVDLTCRLEKPAK\YDDIKKVVQASEGPKLGILGY TEHQVVSSDFNSDTHSSTFDAGAGIALNDHF\VSRLISWYDNEFGY\ SNR\VVDLMAHMASKE
8399	A	1	374	QFEFSIDSFQIILDSLLLFQGSSTPMSEAFHPTVTGESLYGDFTEA LEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGRFRPRPSTDVRLQRY MCSRFFIDFPDLVEQRRTLERYLEAHFGGA
8400	A	127	420	VLLSIFPQRDVDNLPCQLHLFLSFNNISSFDRVSCLDSSSLSDITF DGNPIAQESWYKHTVLQNMMLRQLDMKRITEEERRMASVLAKKEEB KKRE
8401	A	3	509	KNRIKKISNLENLKSLDVLDLHGNQITKIENINHLCELRVLNLARNF LSHVDNLNGLDSLTELNLNRHNQITFVRDVDNLPCQLHLFLSFNNISS FDSVSCLDSSSLSDITFDGNPIAQESWYKHTVLQNMMLRLR*DMEG EFTGRRKGVWHLF*PKKGGKRKEPGKS
8402	A	2	385	LKIIACLSLITNMVGAITGGLPELASRLTRISAVLLEGMMKETFNL KEVLNSIGIQTCVEVNKTLMERGLPTLNAEIQANLIGQFSSIEEDN PIWSLIDKRIKLYMRRLCLPSPQKCMPPMPGG
8403	A	1	431	ERVGNVCSLEISNIQKGEYGMCHAVNIIGEAKSFANVDIMPQEER VVALPPPEFCRSKYGFKGRRQRTKN*FR\IFEMPPRFIMPICDFKI PENSDAVFKCSVIGIPTPEVKWYKEYMCIEPDNIKYVISEEKGSHTL IIR
8404	A	1	12064	MVVEWLHDGKPLEAANRLRMINEFGYCSLDYGVAYSRDSGIITCRAT NKYGTDHSTATLIVKDEKSLVEESQLPEGRKGLQRIEELERMAHEGA LTGVTTDQKEKQKPDIVLYPEPVRVLEGETARFCRVGTGYPQPKVNW YLNGLIRKSKRFRVRYDGIHYLDIVDCKSYDTGEVKVTAENPEGVI EHKVKLEIQQREDFRSVLRRAPRPEFHVHEPGKLQFEVQKVDPRV DTTETKEVVKLKRAERITHEKVPEESEELRSKFKRRTTEEGYEAITA VELKSRKKDESIEELLRKTKDELLHWTKELTTEEKKALABEGKITIP TFKPKDIELSPSMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPEC

				<p> EWYKNGVKIERSDRIYWYWPEDNVCELVIRDVTAEDSASIMVKAINI AGETSSHAFLLVQAKQLITFTQELQDVVAKEKDTMATFECETSEPFV KVKWYKDGMVEHGEDKRYMHSDRKVHFLSILTIDTSDAEDYSCVLVE DENVKTTAKLIVEGAVVEFVKELQDIEVPESYSGELECIVSPENIEG KWHNDVELKSNKYTITSRGRQNLTVKDVTKEDQGEYSFVIDGKK TTCKLKMKPRPIAILQGLSDQKVCEDIVQLEVKVSLESVEGVWMKD GQEVQPSDRVHIVIDKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSG RVSVYSVDVITPLKDVNVEIEGTKAVLECKVSVDPVTSVKWYLNDEQI KPDDRQVAIVKGTQKQRLVINRTHASDEGPKLIVGRVETNCNLSVEK IKIIRGLRDLTCTETQNVVFEVELSHSGIDVLWNFKDKEIKPSSKYK IEAHGKIYKLTVLNMMKDDDEGKYTFYAGENMTSGKLTVAGGAISKPL TDQTVAESQEAFFECEVANPDSKGEWLRDGHKLPLTNNIRTVKIKKT LKNLTVTETQDAVFTVELTHPNVKGQWIKNGVLESNEKYAISVKG TIYSLRIKNCIAVDESUYGFRGLGRLGASARLHVETVKI IKPKDVT LENATVAFEVSVSHDTVVPKWFHKSVEIKPSDKHRLVSEKVKHKLML QNISPSDAGEYTAVVGQLECKAKLFVETLHITKTMKNIEVPTKTAS FECEVSHFNVP SMWLKNGVEIEMSEKFKIVVQGLHQLI IMNTSTED SAEYTFVCGNDQVSATLTVTPIMITSMKLDINAEKDTITFEVTNY EGISYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGDAADYTFV AGKATSTATLYVEARHIEFRKHIDIKVLEKKRAMFECEVSEPDITV QWMKDDQELQITDRIKIQKEKYVHRLIPSTRMSDAGKYTVVAGGNV STAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDVAHWYKD GIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYTFVAGRNRSSV TLYVNAPEPPQVLQELQPVTVQSGKPARFCAVISGRPPKISWYKEE QLLSTGFKCKFLHDGQEYTLLEAFPEDAAVYTCEPKNDYVPEVVS PDQEMPVYPPAIITPLQDTVTSSEGQPARFQCRVSGTDLKVSWSYKDK KIKPSRFFRMTQFEDTYQLEIAEAYPEDEGTYTFVASNAVQVSSTA NLSLEVSVFKKEPLGQKPSFIQPLSSLRVHNGETVRFHARVSGIPKPE IQWFHNQQLILPTKDVVFHFEEESTGMALMLIVDAYSEHAGQYSCKAA NSAGEATCAATLTVTPKVQALDRQSSGKDVRESAKSQAVADSSFTKE ESKISQKEIKSFQSSSYEYEVQVFESVSQSSIHTAASVQDTQLCHTA SLSQIAESTELSKECAKESTDDSFIDVTWTHEGAKIEESERLKQSQN GNIQPLTICNVQLVDQGLYSCIVHNDGERTTSAVLSVEAPESILHE RIEQEIEMEMKELFSEGESEHSEDRDTRDAFSDSEDIDHKSMAAKRYA SRISSTSSWPEYFKPSFTQKLTFKYVLEGEPPVFTCRLIACPTPEMT WFHNNRPIPTGLRRIKAEISDLHHHSSSLEIKRVQDRDSCSYRLAI NSEGSAESTASLLVIQKGQDEKYLEFLKRAERTHENVEALVERGEDR IKVDLRFETGSPFNKKQDVEQKGMRTIHFKTMSAKKTDYMYDEEYL ESKSDIRGWLNVGESFLDKETKVKLQRLREARKTLMKCKKLSLLDTS SEISSRTLSEASDKDILFSREDMKIRMSDLAESYKVDHSAESIVQ NPHALSNQMDQNI ESEELPTSFTQIVDEEIFQTEIRMSQEALVKESL PKDHLYGEILVNENTQARGQLEEIMANTTIGESSTYITNVCEKEEVY ETPENVSQAITPHASESFGTLVNVEESEEEIASERIKKODLRELQLSA STRIDEFKTEQKEENMRFFENSFRKRPQRCPPSFLQEI ESQEVYEGD SCNFVCHFGQYPQPIVTVWYNNDMPIPRNQNFIIHSLENYSILTLSSV HHQNEGSITCVLFNQYGTVKTTSMKVKAKQKHDVKAHKVPVFDYL DEEEELALVFDQAKGAHPSMSQEGQTNLHLLKTNPPVPPSGDTLLS FPVEIQVTAATPIEQDKESKEVFQTEELEPKAMPQDQVTSQPKHRF VFLSDITNEPPKMLQEMPKHARCREGDSIILECLISGEPQPVVTFWQ NGVLLKQNKQKFQFEEVNCSHKLYIKDVNSQDSGKYKCAENNSGAVE SVSDLTVEPVTYRENSQFENIGEYGYKYSRDQQLQDQGESVRAHFYD YPAGPFTPWTVNKEYSVRDYFQSLETIEQIDQKEQVRCIPREKIPR FVHGASRTIKISKPIRAEFIQCAEGKERHVSSEKSLHQAEGTVYPP VDDFSDVTIKKEIRNMFGLGRSEKENVQECAQSDYLPNIHSERISD SYNTKDSSAIVYEESLGEEIHYPGKKVKHRIIEFEKLHVEKGVLEKR PTRTSIVNPPQKKIDDKAFSLKQRESRSSNLNANMYQAEKMSPTES DSSNIAINLKLSSQTHKEFDQAQEREQQEKISLIDKPAISKRAEHES </p>
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				PITFDLKQFHTQIKHTDVKFQELDSGQPBEAYFKIQHPADTENIVFD LKQMYSHIGDPALEFQGGQETREQQEIHYKEKIPSPETLPQDTHNISK SVQNNVFASQEISSSQELSNRTMVEKSSIDENSISLEKEVRHVQEON LDILKTDLSLKSFSEEIYSESCALLPTSSADIEETDLSEKSCPLENG GRSSISHLKKAASEEKPLGVGEMEEECTLEPELAAPFKQDGGTQEYT DATLEDHRGDVQEADTLHRQLSLSQCFPLLMTEEQQNPGEQISTNIH ASGEEKCYEEVQVQNEASFSTLEGEMIETSFQSNIPKLDEAHTTEAA ESETSLTQYLLAAGKREVPETKDTRDQAKLVQSESITSMEEVEVTFN TVYEYNNQKQESLGRPLSPESDISIGVGSTTSEEISELDQFYTPPSS VEYFESPKSPDLYFNPSDITKQSSIHSGGETVERYSTPLGEVAERYS TPSEGEVGERYSTPPGETLERYSTPPGETLERYSTPPGETLERYSTP PGETLERYSTPPGETLERYSTPPGEALERYSIPTGGPNPTGTFTKYP SKIEREDGTPNEHFYTPTEERGSAYEIWRSDSFGTPNEAIEPKDNEM PPSFIEPLTKRKVYENTTLGFIVEVEGLPVPGVKWRNKSLEPDER IKMERVGNVCSLEISNIQKGEGEYMCHAVNIIGEAKSFANVDIMPQ EERVVALPPPVTQHVMEDLEHTTSSRTPSPQEIIVLEVELSEKDVK EFKQVKIVTVPEFTPDHKSIMIVSLDVLFPNFVDPNMDSREGEDKEL KIDLEVFEPPRFIMPICDFKIPENSDAVFKCSVIGIPTPEVKWYIV YMCVEPDNIGDVISEEKGSHTLTTRNVCLSDSATYRCRAVNCVGEAI CRGFLTMGDSEIFAIAKSKVTLSSLMEELVLKSNYTDSPFEPQVW EGPPRFIKGISDCYAPIGTAAYFQCL
8405	A	2	384	DDTRYHTMQAAVDAVARVTGQHPEVPPAFWNNAFTLLSAVSLPRREP TVSSFYVKRAELWDTWKVAHLKEHRRVFQAMWLSFLKHKLPLSLYKK VLLIVHDAILPQLAQPTLMIDFLTRACDLGGAL
8406	A	1	1677	KRPKLKASKRMTCHKRYKIQKKVREHHRKLRKEAKKQGHKKPRKDP GVPNSAPFKEALLREAELRKQRLEELKQQQLDRQKELEKKRKLETN PDIKPSNVPEMEKEFGCLKTENKAKSGKQNSKKLYCQELKKVIEASD VVLEVLDARDPLGCRCPQVEEAIQSGQKKLVILNKSDLVPKENLE SWLNYLKKELPTVVFRASTKPKDKGKITKRVKAKKNAAPFRSEVCFG KEGLWKLGGFQETCSKAIRVGVI GF PNVGKSSI INSLKQE QMCNVG VSMGLTRSMQVVPLDKQITIIDSPSFIVSPLNSSSALALRSPASIEV VKPMEAASAILSQADARQVVLKYTVPGYRNSLEFFTMLAQRRGMHQK GGIPNVEGAAKLLWSEWTGASLAYYCHPPTSWTPPPYFNESIVVDMK SGFNLEELEKNNAQSIRAIKGPLHANSILFQSSGLTNGIIEEKDIHE ELPKRKERKQEEREDDKSDQETVDEEVDENSSGMFAAEETGEALLR RLQQVNSLQGLLSWIKSLKRMMLMTSVQIMCNRMTAFYDFFF
8407	A	2	2580	GQKKLVILNKSDLVPKENLESWLNYLKKELPTVVFRASTKPKDKGK ITKRVKAKKNAAPFRSEVCFGKEGLWKLGGFQETCSKAIRVGVI GF PNVGKSSI INSLKQ\EQMCNVGVIHGGLQSGMQVPLD\KQITIID\ SPSFIVSPLNSSSALALRSPASI\EVVKPM\EAASAILFQAD\VRQV VLKYTVPGQLQGILWEFFT\MLAQRKEVWHQKGG\IPKLEGAAKLLW SEWTGASLAYYCHPPTSWTPPPYFNESIVVDMKSGFNLEBLEKNNAQ SIRGENCVSLLSSADRPVELLPVYMGLLSFPAIKGPLHANSILFQS SGLTNGIIEEKDIHEELPKRKERKQEEREDDKSDHETVDEEVDKKL DSMGSKRRRATSPSSSVSGDFDDGHHSVSTPGPSRKRRRLSNLPTVD PIAVCHELYNTIRDYKDEQGRLLCELFIRAPKRRTDSEIYEDAVELQ QFFIKIRDELCKNGEILLSPALSYTTKHLHNDVEKERKEKLPKEIEE DKLKREEEKRVEGIIQRLHYCTNPDSKPKYPAQRTPQIHLQGEVLFY ESKFRTELEVTVVLDTHIISINQPDYEVVSQPIDLMKIQKLMEE YDDVNLLTADFQLLFNNAKSYKPDSPPEYKAACKLWDLYLRTNEFV QKGEADDEDDDEDGQDNQGTVTEGLLKISITQKIRPVVILFHYGESW NLLRADQRLIFAKSWPRASRYQQGHQDLFILRSDLPSQVFIRDKLME RRNRRTGRTEKARIWEVTDRTVTRTWIGEAVAAAAADGVTFSVPVTPH TFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEYVTKVFALDVAARH RVQFAMPESDAVAMLKQLS
8408	A	2	259	VFLSEQDEVLLIQEAKRECRGSWYLPAGRMPEGETIVEALYREVKEE

				AGLHCEPETLLSVEERGPSWVRVFLARPTGMAHLEAV
8409	A	1	257	RTLLVPGLGGQRKPPPPFRPGGANGDKAPPPAPTTPPGIPRCAAQESLG AAASGQVPWCSRGPPAPGPLRSVCRAEGRPPYHAPFF
8410	A	3	367	IMKDRWMNVGHEEEELKPYTEPDPDFNDTKRIDIMVTMGFARDEIND ALINQKYDEVMATYILLGRKPPEFEGGESLSSGNLCQRSRPSDDLNN STLQSPAHLKVQRSISANQKQRRFSDH
8411	A	2	244	EFSDALGYLQLLNSCSDAAGAPAYSFSISSSMATTTGVDPAKWWAS LTAVVIHWLRRDEEAAERLCPLVEHLPRVLQES
8412	A	2	339	PRVRPRVRPRVRGRVGCSDAAGAPAYSFSISSSMATTTGESAPAVLA PFSAPPCSVTESGDPSSAGVDPVAKWWASLTAVVIHWLRRDEEAA ERLCPLVEHLPRVLQESE
8413	A	2	182	RAFATMGETVMSVKIIRNRLTGIPAGYCFVEFADLATAEKCLHKLING KPLPGATPVRTFR
8414	A	2	382	CRTLCEGPQRFEEYEYLGKAGLYEAIADHYMQVLVCQHECVRELAT RPGRLSPIENFLPLHYDYLQFAYYRVGEYVKALECAKAYLLCHPDDE DVLDNDVYYESLLDDSIDPASIEAREDLTMFV
8415	A	59	572	SGRPPFFFFSATGACLFPPGPGRGLGAEYRQRHWGTWVWHGLELGR GSNREGCARACRDWSHPPTERGPSSGHGGITSARLTGTGTGERLRSGC VQGLVGMGRPVDRA*SVLEPGGTPGRANWALDVEKLGK*ENKSL WVSRP/RQRCDRQDRPWERPRLQVTPRIARQ
8416	A	3	1735	LCTRKLGRKLGPLEGYSRAAAYYSGDYERAVRDLEAALRSHRLRE IRTRCARHCAARHPLPPPPGEGPGAELPLFRSLLGRARCYSRSCETQ RLGGPASRHRVSEDVRSDFQRRVPYNLQRAYIKLNQLEKAVEAAHT FFVANPEHMEMQQNIENYRATAGVEALQLVDREAKPHMESYNAGVKH YEADDFEMAIHFQALREYFVEDTECRTLCEGPQRFEEYEYLGKAG GLYEAIADHYMQVLVCQHECVRELATRPGRLSPIENFLPLHYDYLQF AYYRGSGNFKEPNKDCFYVDALLPENRNQILTQILQSANLSANKLFT VGGQIAIYLCQAQELLVGEYVKALECAKAYLLCHPDDEDVLDNDVY ESLDDSIDPASIEAREDLTMFVKRHKLESELIKSAEGLGFSYTEP PFKDKVTSARAFLSPMRNVASSTVESHHTQFRALEVKAQQNERNWQ ASELPRGNVVEGQKENGFLGSSAHAQHKTLLIYGPQGMPTLVKMF FTQSTDNANLFQKHPHRHNQKCFSSYLGPFKSTSKIDCHTDEKTEI QIFETNYLRPRGD
8417	A	2	442	LTSSVDLYFGAHHPLHVTMLPNPSHLEAVNPVAVGKTRGRQQRQDG DYSPDNSAQPGDRVICLQVHGDAFCGQGIPTFTLSNLPHPKIGG SVHLIVNNQLGYTTPAERGRSSLYCSDIGKLVGCAIIVNGDSPPEV VRATR
8418	A	412	569	LSLSAAAAAGRYGGTFQNVSLQLPITLKNFFQPTEMASQDFFQRWKQ LSNPQ
8419	A	2	2812	RGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKK YVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIGYLFISVLNS NSELIRLINNAIKNDLASRNPTFMGLALHCIAVSGSREMAEAFAGEI PKVLVAGDTMDSVKQSAALCLRLRYRTSPDLVPMGDWTSRVVHLLND QHLGVVTAATSLITLAQKNPEEFKTSVSLAVSRLSRIVTSASTDLQ DYTTYFVPAPWLSVKLLRLQLCYPPDPAPVRGRLTECLETIILNKAQE PPKSKKVQHSNAKNAVLFEAISLIHHDSEPNLLVRACNQLGQFLQH RETNLRYLALESMTLASSEFSHEAVKTHIETVINALKTERDVSVRQ RAVDLLYAMCDRSNAPQIVAEMLSYLETADYSIREEIVLKVAILAEK YAVDVTWYVDITILNIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAK TVFEALQAPACHENLVKVGYYILGEFGNLIAGDPRSSPLIQFHLHLS KFHLCSVPTRALLSTYIKFVNLFPEVKPTIQDVLRSDSLRLNADVE LQORAVEYLRLLSTVASTDILATVLEEMPFFPERESSILAKLKKKGP STVTDLEDTKRDRSDVNGGPEPAPASTSAVSTPSPSADLLGLGAAP PAPAGPPPSSGGGLVDVFSASVVAPLAPGSEDNFARFVCKNNG VLFENQLLQIGLKSEFRQNLGRMFI FYGNKTSTQFLNFTPTLICSD LQPNLNLQTKPVDPTVEGGAQVQVNNIECVSDFTEAPVLNIQVHGS

				GGT\FQN\VSLQLPITL\NKFFQP\TEMASQDFF\QRWEGSL\SNPQ QGSCRNIPSKAKHPMDTEVTKAKIIGFGSALLEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYR\LTRTSKEAVS\Q\RLCELLSA QF
8420	A	2	398	SKKRKRQEEKHVCKKHNVLTFFCQKDLELLCPRCSLSTDHHCWV PIKKAASYHRKLEYNAPRKERVELTEKVITMQTRKSLELKKKVKH RAEEVKPEFEQLRLFLQNEQETVLRHLQDEQMDILPQL
8421	A	3	440	IASRNVPLTLIDLPGIPTGAAGNQPADIGDNIKTLIKKLIQRHETI RLAVVPRIVDIAATEALTMAQEVDPEDRTIEILTKPDLVDKGTDNK AVDVVRNLVLHLKKAHMIVKCRGQQGDPDQMSLPETLPRDKIFFENH PYIK
8422	A	3	356	NDEQAPAQSLLTTPRPAAIMPLRSVPSASPSPPSASSTGLHAAPQAF PVPTGPRPDRSLELHWPSGKLQAPHYCLQTLVIWTCSPSRLGGGPSP RSGKCLRPSQLWSMHLFPFPHRS
8423	A	3	341	LKLYPNETIVGNGSPSQTNNGAMLIWIKRKIHVGTKSYPASVSKVA GKKGTRLHAQRFLVHLERTGGKCHYTMIKGSIHLEYTAIIIIYAPNI RTPKYIKQTLTKLKGEIK
8424	A	1	338	LLRVYSFMALKMYHQLPTQVSSSTALNLQHQLPTGSPDARPSKWNIN SPRFPAPRPSTCNISSPPGLQMHSPTGTSTPRRVSRCTACKLEHQ LPSGLQLHSPQTATAAAS
8425	A	1	70	GNYGSGPGYSSRGGYGGGVDA
8426	A	62	375	GRGGFFLGPRGPKKKTPGGEGFTRFFDPGWGKGPEKKTPPPWGKGG PKMNLWGAGKIKFLEIKGKSFRGTTPNFFGPPLFFSPPKTQPGN FLDFSFKLN
8427	A	2	375	PRCQQPVFAEKVSSLGKNWHRFCLKCERCHSILSPGGHAEHNGRPY CHKPCYGALFGPRGVNIGGVGSYLYNPPTPSPGCTTPLSPSSFSPR PRTGLPQGGKSPPHMKTFGTGETSLCPGCGE
8428	A	2	460	PGRPTRPTSPSNTPASISPKLNVEVKKEVDKEKAVTDEKPKQKDKPG EEEEKCDISSKYHYLTENDLEESPKGGLDILKSLENTVTSAINKAQN GTPSWGGSYPSIHAAYQLPNMMKLSLGSSGKSTPLKPMFGNSEIVSPT KNQTLVSPSS
8429	A	1	342	RLTVLLPLLLFKVCFRSTTPCTSHPSQLCLPVSPSPPPQACLSLTARI LPTPTPRQITPPKSLTGTNLGTLPIIRNTLDEAPTRRILAVAAEFSG MCLILLGWLIIFFKSRISG
8430	B	212	587	MKGGSFKYAWVLDKDKADRERGITIDISLGKFETSKYYVTIIDAPGH RDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAYT LGVKQLIGGVTKMDSTEPFRRKRYEIVKGX*
8431	A	1	1386	MDIKKGITDISASLRVESGWEARTRKEKTHINTVIIIGHVDSGKSTTT GHLIYKCGGVDKRTIEKFEKEAAEMGKCSFKYAWVLDKKAEREHGI TIDISLWKFETSKYYVTIIDAPGHRDLIKNMITGTSQADCAVLIVAA GFGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPYPYSHK RYEEIVKEVSTYIKKIGHNTDTVAFVPVSGWNGDNTLEPSANMPWFK GWKVRKDGNASGTTLEALDCILPPTRPTDKPLCLPLQDVYKIGGI VNVATEVKSVMHHEALSEVLPGDNVGFNVKNVSVKDVRRGNVAGDS KKDPPMEAAGFTAQVIIILNHPGQISAGYAPVLDCHTAHIACKFAELK EKTDHRSGKKLEDGPKFLKSGDAAIVDMVPGKPVYVESFSDYPPLGR FAVHDIRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK
8432	A	66	1574	KLTPLPKPWESVKTHINL\AVIGH\VDSGKS\TTTGHLYKCGGIDT KNHLKNLTKEAAEMG\KGSF\KYAWVLDKKAERERGITIDISLWKF ETSKYYVTIIDAPG\HRDFIKN\MITGTSQA*PGLGGPLFGG/CSPL IVAAG\VGFEFEAGISKNGQ\TREHALLAYT\LGVKQL\IVGC*QKWD ST\EPTPTAQKKILKEIVK/EKVSTFH*RKFGYNP\DTVAF\VPNFL VWN\GDNMLGAQVPNMPWFQGDGKVTCKD\GNASGTTLLWRALDCIL P\PTRPTDQAPLR\LPFQ\DVLPKIGGYLGTWFLVWPEWETGVL/RN PGMGVTF\APVNVTT\EVKSVEMHHEALSEA\LPGDNVGFNVKNVSV KDVRRGNVAGDSKNDPPMEAAGFTAQVIIILNHPGQISAGYAPVLDCH

				TAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMC VESFSDYPPLGRFAVRDMRQTVAVGVKAVDKKAAGAKVTKSAQKA QKAK
8433	A	2	265	AIQPRLVAVSKTKPADMVIEAYGHGQRTFGENYVQELLEKASNPKIL SLCPEIKWHFIGHLQKQNVNKLGMKSEFLIKRENIMPTE
8434	A	3	318	GTRDLPALQPRLVAVSKTKPADMVIEAYGHGQRTFGENYVQELLEKA SNPKILSLCPEIKWHFIGHLQKQNVNKLGMKIKLNMKTKLFCCHIAS TTLGRESNF
8435	A	2	896	VGPRGMWRAGSMSAELGVGCALRAVNERVQQAVARRP/RGDLPAIQP RLV\AVSKT\KPADM\VEAYGHGQRTFGENYVQEL\LEKAS\NPKI LSLCPEIKWHFI\GHLQKQNVNKLMAVBNL\FML\ETV\DSVKL\ADK VNSSW\QRK\GSPERLKVMPGFNTSREEIYLFVSLSLEGKHG\LPP SETIAIVEHINAKC\PNL\EFVGL\MTLG\SFGHDLSSQGNPDFQLL LSLPEETVVK*RI PADQVELSMGLSADMQHAVEVRSTDVWIRSTVP GEPDYSKKPTDKCAADV KAPLEVAQEH
8436	A	202	349	HRPRQSQNTCFNWKCHHSRPAPLRLPAPEPRPFGPTQPDPPGIQPD LP
8437	A	1	129	DLSCHSHGEATQKHSEKCKASCTHMFITALFLIAKHWNQPTCL
8438	A	3	389	PQTVAATTVPNTSWAPTTS LGPAKDKPGLRKAQGGGSTFTSQGG TPDATAASGAPVSPQAAPESKRPHHGD PQDGPSHRDSWLTVPGTS RPLSTSSGVFTAATGPTPAAFDTSVSPPSRGFLR
8439	A	505	693	QAQNLSPVTPSTSFTVIRNVQFKILD AVVAQEPLHRGAGQIIPTARR VVYSAFLMGARDLGCN
8440	A	46	3454	AGESIMDTLDYDEFGNYIGPELDSDEDDDELGRETKDLDEMDDDDDD DDVGDDHDDHDPGMEVVLHEDKKYPTAEVYGVPEVETIVQEEDTQPL TEPIIKPVKTKKFTLMEQTLPTVYEMDFLADLMDNSELIRNVTLG HLHHGKTCFVDCLIEQTHPEIRKRYDQDLCYTDILFTEQERGVGKIS TPVTVVLDPDTKGKSYLFNIMDTPGHVNFSDDEVTAGLRISDGVVLFID AAEGVMLNTERLIKHAVQERLAVTVCINKIDRLILELKLPTDAYYK LRHIVDEVNGLISMYSTDENLILSPLLGNVCFSSSQYSICFTLGSAFA KIYADTFGDINYQEFARKLWGDIFYNPKTRKFTTKAPTSSSQRSFVE FILEPLYKILAQVVGVDVDTSLPRTLDELGIHLTKHEELKLNIRPLLRL VCKKFFGEFTGFVDMCVQHI P SPKVGAKPKIEHTYTGGVDS DLGEAM SDCDPDGPLMCHTTKMYSTDDGVQFHAFGRVLSGTIHAGQPVKVLGE NYTLEDEEDSQICTVGRWLWISVARYHIEVNRVPAGNWVLIEGVQPI VKTATITEPRGNEEAQIFRPLKFNTTSVIKIAVEPVNPSSELPKMLDG LRKVNKSYPSLTTKVEESGEHVILGTGELYLDCVMHDLRKMYSEIDI KVADPVVTFCEVTVETSSLKCFATPNKKNKITMIAEPLEKGLAEDI ENEVVQITWNRKKLGEFFQTKYDWDLLAARSIFWAFGPDATGPNILVD DTLPSEVDKALLGSVKDSIVQGFQWGTREGPLCDELIRNVKFKILDA VVAQEPLHRGGGQIIPTARRVVYSAFLMATPRLMEPYFVEVQAPAD CVSAVYTVLARRRG\HVTQGCTHPKASPL*TIKAF\IPAIDSFGFET DLRTHTQGAQFSLSVFHHWQIVPGDPLDKSIVIRPLEQAPAPHLARE FMIKTRRRKGLSEDSVSIKFFDDPMLLELAKQDVVLNYPMSQQLLQA SDHTTWGNHLSDDSRNTFTCIVYLRNLTAACKMDDDDDDDDVGDDDD DHPGIALAAYRSPRPLVVACRRAQFFLTREQEDLSRGRRTGQAPVA DVQAQSRSSIDERRGPDHPYGC DHPKMNLKDSL DVAKPADAKNGNSI RLALTVSEA
8441	A	2	640	AVVVICSDASDMELMLVGGFFRCAGKVEVNVQAVGILCANGWGMNI AEVVCRLQECASAVTVSREPHFTERTLHILMSNSGCTGGEASLWDCI RWEWKQTACHLNMEASLICS AHRQPRLVGADMPCSGRVEVKHAYTWR SVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGLTWAKEFQC EGSETHLALCPIVQHPEDTCIHSR
8442	A	60	345	VECPLFCSWEETSESGTGSFLRGPVATERE GEC SFPPALSSCLPGA SSRPPFSLPPPPALS FHSPPPTPSDQVLPIAVPPPTPYLARVDL DL
8443	B	26	384	MHEALSEALPGDNVGFNVKNVSKDVRRGNVAGDSKNDPPMEAAGF

				TAQVILNHPGQISAGYALYWIAIVDMVPGKPMCVESFSDYPPPLGRF AVRDMRQTVAVGVKAVDKKAAGLAS*
8444	A	33	99	KLPLKAKMGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVLDKLKAERERGITIDISLWKFETSKYYV TIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNQQT\ REHALLAYTLGVKQLIVGVNKMDSSTEPYSQKRYEEIVKEVSTYIKK IGYNPDTVAFVPISGWNQDN\MLEL\CSNMPWFKGMK\VTRKDGA\ SGTTLLEALDCILPPTRPDKPLR\LPLQDVYKIGGIGTVPVGRVET GVLKPGMVVTFAPVN\VTTEVKSVMHHEALS\EALPGDNVGFNVVK CVVSRMFRRGNVAG\DSKNPPMEAAGFT\AQVILNHP\SQKNARH MPLELDCHTAHIACKFA*A*KRFDRRSG\KKL\EDGP*NSLKSG*C WPLVDMVPWASPMCV*EASQDYP\PLGRFWPFYMRQTALRLGVNQK QLDKK\AAG\AGKVHQSQAQA*KPKWERKRLISTLSSLD
8445	A	2	443	ANAALCQHPTGCQTSADLHWTLPPIRHSPPPPPLHILPPPRHRPPPP PLHIIPPPPPPFHSAQSSLRPLAPLHFSLSEHGHSARPPSTEHHPG QMGAGEAPPPPLPPPSQTRKYCRGRPPRRQNANCSCARPESLL PPLDPG
8446	A	76	413	LRLVNISNSFEYQNTGQDKMHVRSYIACELSVDFQWVLVTPHQCPGI VGVSEETSVSAKMMPRAVISWWEERNRSQRKGDEKHNHESQGIKFG ENFGRDFERGALSQPTY
8447	A	524	955	FCSMSSQKWSQAQPLSWRHSQGPVPSLPKALLFKGFLPGTAKPAC SAFREAAALAFIQDNKTAISEEKNGSRFLGPPSARLRGRPRAESPR PEPRARPRATQPGPAAPAAHATPPPGPAPAPYLVRGASGGRGNVRG PK
8448	A	3	208	AASTTPTRGCHAPSVHTAPHTAYVYTRPSGASAFASPPQSTVSVPD SNSSSPNHQGDGASQTSGEQI
8449	A	3	208	AASTTPTRGCHAPSVHTAPHTAYVNNKPVGASALASPQESTGRVSD SNSSSPNHQGDGASQTSGEQI
8450	A	3	329	TRNDERPAAEYEQPWEWKKEQIVRALSQVFEGERPSFREETVRQHH RQKSWTQKILKPALSDHSEGEKVDPGLPLEKQPWYHGAISRAEAESR LQPCKEAGYLVRNS
8451	A	56	325	FPLDSTGSELKQNILSFTGLPPAMQKVMYKGLPPEDKTLREIKVTSG AKIMGGGSPINGVLSVHTPIYSAHLDAKAEKNKKEPLCRQKQ
8452	A	33	159	QRLPRTPLTGQGTRLRHSQTLPVSKVYFKNYVPCRRLOS
8453	A	2	494	TVTIYSLFLFLVRNIHKNQCKTISVGVLFYITKLPLDISYKRGLT GEKRDKLALQSTARNIVFKIDFQHMDPWGKEEAFDTRGVCDERCSL LVPCPVSQVGRSLCYGLLYFRVKNRKNKVSLSTPPPQHPHPEPAVGC IWTCPAKPCFSLCSGGRLKPDMD
8454	A	130	716	LFARLPEAIPWRQKKESSAQIRLEPPSRAQGETGFSWLGPDTTHSRF WWWLGL/CGEGWAGIPLCFFSPRKYNTPI TRDFLGPPLTGQGNKKT\ NRSSQTLPIEKPLSLL*KLLPSLRERE*LFIGLGVRAVSPGSLIS GLGAQACPQ/GLPCLCLYPCLRGPGQDFPNQPRPQHPPSPQKPPSSP PHGSYVESLF
8455	A	1	578	GGRSVLPVDPRVRSHFPMTHGNTGLSAGLDASAQTT\SHELTIPNDL IGCIIGRQGAKEIRQMSGAIKIANPVEGSTDRQVTITGSAASIS LAQYLINVSLNAPSSQAASVTIPDHLSINLSQPSTPSSSSTTT PSLATAGTSDAPSSLENPSSDRPLCLQSAWHETHFPFGSPPPRLLLP ATPPL
8456	A	2	875	IITLAGPTNAIFKAFAMIIDKLEEDIS\SSMTNSTAASRPPVTLRLV VPASQ\CGSLIGKGCKIKEYTREYRGFRSKVAGDMLPNLTERA\IT IAGIP\QSIIECVKQICVVMLETLSQSPPKGV TIP\YRPK\PSSSPV ILQGGQPYTIQGYAIPQPDLTCLHQLAMQOS\HFPMTGNTGIQWH LNPASPRGSKAYW\AGL\DAQAQTTSSWNSPFPNGFDWAGIIGAFKG AKI\NEIRQM\SGAQIKIANPVE\GST\DRQVT\IT\GSAASISPGV NIIINVRLSSE\TGGMGSS
8457	A	3	376	HSSGLGGGVMLVHDIRRNESHLIDFRESAPGALREETLQRSWETKP

				GLLVGVPGMVKGLHEAHQLYGRPLPWSQVLAFAAAVAQDGFNVTHDLA RALAEQLPPNMSERFRETFLPFG\RPPLPGS
8458	A	1	1965	MAAENEASQESALGAYSPVDYMSITSFPRLPEDEPAPAAPLRGRKDE DAFLGDPDTPDSFLKSARLQRLPSSSSEMGSDGSPRETRKDPFS AAAAECSCRQDGLTVIVTACLTFATGVTVALVMQIYFGDPQIFQOGA VVTDAARCTSLGIEVLSKQGSSVDAVAALCLGIVAPHSSGLGGGG VMLVHDIRRNESHLIDFRESAPGALREETLQRSWETKVGTLDLLHPL LSGPPRLPWSQVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSEFR ETFLPSGRPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMV AEAQHAGGVITEEDFSNYSALVEKPCVGVYRGHLVLSPPPHTGPAL ISALNILEGFNLTSLSVSREQALHWVAETLKIALALASRLGDPVYDST ITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPTAAQVL IMGPDDFIVAMVSSLNQPFGLITPSGILLNSQMLDFSWPNRTANH SAPSENSVQPGKRPLSFLPTVVRPAEGLCGTYLALGANGAARGLS GLTQVLLNVLTILNRNLSDSLARGRLHLPDLQSNLLQVDSEFTEEEIEF LEARGHHVEKVDVLSWVHGSRRTNFI IAVKDPSPDAAGATIL
8459	A	4	267	DGVLCHLGTISAHCNLHLPGSSSSPASVSQIAGVTGVHYHVWLNFF LLVETWFCHVQADTPFLPKKKKKKAWSGVCAFKPRLLGRA
8460	A	10	465	TGPVAMGRVIRGQRKGAGSVFRAHVKHRKGAARLRAVDFAERHGYIK GIVKDIHDPGRGAPLAKVVFRDPYRFFKRTelfIAAEGIHTGQFVY CGKKAQLNIGNVLPVGTMPGTVIC\PVISKKVISSANRAVVGWVAG GGRIDKPILKA
8461	A	5	807	TGPVAMGRVIRGQRKGAGSVFRAHVKHRKGAARLRAVDFAERHGYIK GIVKDIHDPGRGAPLAKVVFRDPYRFFKRTelfIAAEGIHTGQFVY CGKKAQLNIGNVLPVGTMPGTVICCLGGEAWKTRGKLARASGNAT VISHNP\ETKKTRVKLPSGS\KKVISSANRAVVGWVAGWPELTNPS LKAG\RAYHKYKAK\RQRNCWP\RIRG\VAMNPVEHTFGGGQ/HPQH IASPPTIRRDAP/AGRKVGLIAARRTGRLRGTKTVQEKEN
8462	A	11	350	SILQKAKAKILEFATPTTKKEAQKFIFLFGYWRHMHMGNILQPLR AVTRKRYDFHWGQKESVAFQQAQAVQLTPDLWPINRNPVELQVAVL DQHANSLSLRQKQGGKRVPL
8463	A	305	676	RSKSDSAADLPSSRRARLSGTGEKASENKGDPVHL*ADGGFVPLEDSL CM*FPAWASSPSAALSIGLTVQVAGLQPLWAPWVWVPLGSTGRSSG ELEESEAGYLSSTDGLLGSFKEGCSSC
8464	A	352	784	DTADPPPYIQRACALAPPTASAPLHVVPVGVQGLIQAVALLVLI VLRKRIKLTVELFQITNKAISSAPFLFQPLWTFAILIFFWVLWVAV LLSLGTACGRPRCTGSLCSQRPFHQCQRAWLCGWADQQLNHFLIFRR CPS
8465	A	3	383	HEAYAPRIFFEGSRPPWVTPRSQQDCSEYLRFLLDRLHEEEKILKVQ ASHKPSEILECSETSLQEVASKAAVLTETPRTSDGEKTLIEKMFGGK LRTHIRCLNCTSTSQKVEAFTDLSLAFWPSSS
8466	A	1	233	GTRQEGNTTVLVEVNCETDFVSRNLKFQLLVQVALGTMHCQTLKD QPSAYSQVSLGFVSSVLNLLSSLGILLFLL
8467	A	3	358	HEWMHLTQPELQELTSLLTVNSEFVDWRKFLVTSMPWPIPLEELL ETLQKFKAVDKEQLGTITFEQYMQAGLWFTGDEDIKIPENPLEPLPF NRQEHLIEFFFRFADYEKDPQQL
8468	A	2	374	AREGLWKSFTPENTTKELFYKADGESCSSTSMYQEGKFPYRHMAES TQVLELPFKGDYITMGLILSKPKILAPVDKELTPKVLDPDWLDELED MMLVVMHPRLLIEDGFSLKDQLPDNGLVHL
8469	A	2	484	KFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHPEAKRMP AEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFH\VKHKPKATKEQLKAVMDDFAAFVEKCKADD KETCFAEEGKKLVAASQAAL
8470	A	2	435	GMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVF DEFKPLVEEPQNLIKQNCSELFEPDICTLSEKERQIKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCKADDKETCFAEEGKKLVAASQAAL

				LGL
8471	B	73	384	MFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFD EFKLLVEEPQNLIKQAWRVQIPECAISSLHQESTPSVNSNSCRGLKK PRKSGQOML*
8472	C	11	475	MFLYEYARRHPDYSVVLRLAKTYDAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTL SEKERQIKQTALVELVKHKPKATKEQLKAVXDDFXAFVEKCKGDX KGELLXRRXVXNLL
8473	A	1	608	EFSMLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVF LGMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKV FDEFVNRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIK QTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETCFAEE GKKLVAASQAALGL
8474	A	1	593	AKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAA DFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYE TTLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNCLEFQLG KFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHPEAKRMPC AEDYLSRGPRTSRMFAKTMLRQRMSSWAC/CLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNC LEFQLGKEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKH PEAKRMPCAEDYLSRGP
8475	A	1	1428	MKWVTFISLLFLFSSAYSRGVFRDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLF GDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPPLRLVR PEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFAKRYKAA FTECCQAADKAACLLPKLDELDEGKASSAKQRLKCSLQKFGERAF KAWAVARLSQRFPAEFAEVSKLVDTLTKVHTECHGDLLLECADDRA DLAKYICENQDSISSKLKECCEKPLLEKSHCIAE/HRNLGKVGSKCC KHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRR PCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKQTALVEL VKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETCFAEEGKKLVAAS QAALGL
8476	A	1	748	ADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNC LEFQLGKEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKH PEAKRMPVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKER QIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETCF AEEGKKLVAASQA
8477	A	1	1515	MKWVTFISLLFLFSSAYSRGVFRDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLF GDKLFVEVSRNLGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHE KTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHAD ICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEGKKLVAASQAALGLTCEACQEPGGLVVPPTDAPVS PTTLYVEDISEPPLHDFYCSRLLDLVFLLDGSSRLSEAEFEVLKAFV VDMMERLRISQKWVRVAVVEYHDSHAYIGLKDRKRPSSELRRIASQV KYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLMASQEPQRM SNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLS SVDELEQQORDEIVSYLCDLAPEAPPPTLPPDMAQV
8478	A	1	2931	MKWVTFISLLFLFSSAYSRGVFRRTPLGPASSLPQSFLKCLEQVRK IQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQ LAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI WQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVS YRVLRLHAQPGGGDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQ CPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLF GDKLCTVATL RETYGEMADCCAKQEPERNECFLOHKDDNPPLRLVRPEVDVMCTAF

				HDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTTECCQAADK AACLLPKLDELREDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQ RFPKAEFAEVSKLVTDLT KVHTECCHGDLLECADDRADLAKY ICENQ DSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLY EYARRHPDYSV VLLLRLAKTYETTLEKCCA AADPHECYAKVDEFKPLVEEPQNLIKQNCSELFQELGEYKFQNALLV RYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSV LNQLCVLHEKTPVSDRVT KCCTESLVENDEMPADLPSLAADFVESKD VCKNYAEAKDVFLGMFLY EYARRHPDYSV VLLLRLAKTYETTLEKCC AADPHECYAKVDEFKPLVEEPQNLIKQNCSELFQELGEYKFQNALLV VRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSV VLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKEF NAETFTFHADICTLSEKERQIKQTALVELVLCRCRSS *M\HAKAVM DDFAAFVEKCKADDKETCF AEEGKKLVAASQAALGL
8479	B	1	6124	MKWVTFISLLFLFSSAYS RGVFRDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQCCPFEDHV KLVNEVTEFAKTCVADESAENCDKSLHTLF GDKLCTVATLRETYGEMADCCAKQEPGRNECF LQHKDDNP NLPRLVR PEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAA FTECCQAADKAACLLPKLDELREDEGKASSAKQRLKASLQKFGERAF KAWAVARLSQRFPKAEFAEVSKLVTDLT KVHTECCHGDLLECADDR DLAKY ICENQDS ISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSL AADFVESKDVCKNYAEAKDVFLGMFLY EYARRHPDYSV VLLLRLAKT YETTLEKCCAAADPHECYAKVDEFKPLVEEPQNLIKQNCSELFQELG EYKFQNALLVRYTKKYLQCCPFEDHV KLVNEVTEFAKTCVADESAEN CDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPGRNECF LQHKDD NP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELL FFAKRYKAAFTTECCQAADKAACLLPKLDELREDEGKASSAKQRLKAS LQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLT KVHTECCHGD LLECADDRADLAKY ICENQDS ISSKLKECCEKPLLEKSHCIAEVENDE MPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLY EYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVDEFKPLVEEPQNLIKQ NCELFEQLGEYKFQNAAISSLHQEKVSRNLGKVGSKCCKHPEAKRMP CAEDYLSVVLNQLCVLHEKTPSFLKCLEQVRKI QGDGAALQEKLC TYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGFL YQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQ PTQGAMP AFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHQAQPGGGG DAHKSEVAHRFKDLGEENFKALV LIAFAQYLQCCPFEDHV KLVNEVT EFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQ EPERNECF LQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELREDE GKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLV TDLT KVHTECCHGDLLECADDRADLAKY ICENQDS ISSKLKECCEKPL LLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGM FLY EYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVDEF FKPLVEEPQNLIKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTL VEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVS DRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLS EKERQIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKADDK ETCFAEEDAPVSPPTLYVEDISEPPLHDFYCSRLDLVFLLDGSSRL SEAEFEVLKAFVVDMMERLRISQKWVRVAVVEYHDGSHAYIGLKDRK RPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIAL LLMASQEPQRM SRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIE KQAPENKAFVLSSVDELEQQORDEIVSYLCDLAPEAPPPTLPPDMAQV *
8480	A	241	348	SFFSQTQASEQLTKSKQGLALRTLPPVQFP PPPPRP
8481	A	2	191	VGRVGLELLASSDLPTSGSPSAGITGMSHCPWPNFLLI FIGYFTVL

				TPCEYYSGGMTVPLWL
8482	A	3	372	APQIKRHLEVKAS PSSLEGESSL SQOPTPLPQTFMAPKRLDKAKEAQ RTPSPGGGQPLSPLPHFTQELFTVPPVMPGHADTLLLKCPYPILRP APRPPAYRIHPVCQEAIGTLAILSALCS
8483	A	1	351	TLSTLRYADRAKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQG LGDIDIDIDPLIDDYSGSGSKYLKDFQNNKHRYLLASENQRPGHFSTA SMGSLTSSPSSCSLSSQVGLTSV
8484	A	44	455	HACERIHTGEKPYICFEWGSFFRKHSNLTQHQRHTGEKPHKCDECG KTFQTKANLSQHQRIHSGEKPYKCECGKAFQSPSLIKHQRIHTGE KPYKCECGKAFTQSTPLTKHQRIHTGERPYKCECGKAFIQK
8485	A	200	409	MRQDFEIIILFLFVSTLVCCSLVIKRMWPGAMAYACNPSTLGDGRGRQ ITRSGVQDQPGQYGETSSLLK
8486	A	1	110	PTRSGTFKSGVLYKGHGEIPNWADENSVDAAEVCAS
8487	A	48	464	QLGTRHNISASQVNAWHVAESAVNYSLGDEQGCSPWPNCNFPEYF TYSVLLSLLACSVFLQINCIGKLVMLAIELIYVLIVEVPGVTLFDN ADLLVTANAIDFFNNGTSQCPEHATKVALKVVTPIIISVFVLAAL
8488	A	1	721	MHWGVGFASSRPCVVDLSWNQSI SFFGWAGSEEPFSFYGDIIAFPL QDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHELLVIRKQGEI DSKDAIILHQFARPNNGVPSLSPFCLKMETYLRLMADLPYQNYFGGKL SAQGMKPWIEYNHEKVSGETEIIDFLEEKLGVLNLKNLGPHERAISR AVTKMVEEHFY\ALSWRWYHPVPTCPLQKFLQFVRQLMLFMRTSPSP ALPGH
8489	A	3	785	SCAACTGGLALLCFRPCVVDLSWNQSI SFFGWAGSEEPFSFYGDII AFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHELLVIRK QGEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRLMADLPYQNYF GGKLSAQGMKPWIEYNHEKVSGETEIIDFLEEKLGVLNLKNLGPHER AISRAVTMVEEHFYCLPAVNLCFWNKVQLPVLRLVIVLPLPAPPAS PLTGFLKCSLYPRAPYRSCSSSSGS
8490	A	5	302	FSNAERVGGLEEEERESVGPLRQDFSMSSSALIGVLVIAVAIATVIVI SLVMLRKRQYGTISHGIVEVDPMLTPEERHVNKMQNHGYENPTYKYL EQMQI
8491	A	1	2086	MAATGTAAAAATGRLLLLLLVGLTAPALALAGYIEALAAANAGTGFAV AEPQIAMFCGKLNMHVNIQTGKWEPTGTGKSCFETKEEVLQYQCQEM YPELQITNVMEANQRVSIDNWCRRDKKQCKSRFVTPFKCLVGEFVSD VLLVPEKQCQFFHKERMEVCENHQHWHVTVVKEACLTQGMTLYSYGMLL PCGVDQFHGTEYVCCPQTKIIGSVSKEEEEEDEEEEEDEEEDYDV YKSEFPTEADLEDFTAAVDEDEDEDEEVEEDRDYDYDTFKGDD YNEENPTEPGSDGTMSDKEITHDVKVPPTPLPTNDVDVYFETSADDN EHARFQKAKEQLEIRHRNRMDRVKKEWEEAELOAKNLPKAERQTLIQ HFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAAL QSDPPRPHRILQALRRYVRAENKDLRHTIRHYQHVLAVDPEKAAQMK SQVMTHLHVIEERRNQSLSLLYKVPYVAQEQEEIDELLQEQRADMD QFTASISETPVDVRVSSEEEIIPPFHPFHPFPALPENEGSGVGEQD GGLIGABEKVINSKNKVDENMVIDETLDVKEMI FNAERVGGLEEEERE SVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISH GIVEVDPMLTPEERHLNKMQNHGYENPTYKYLEQMQI
8492	A	3	2011	ANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPTGTGKSCFETKE EVLQYQCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKSRFVTPFK CLVGEFVSDVLLVPEKQCQFFHKERMEVCENHQHWHVTVVKEACLTQGM TLYSYGMLLPCGVDQFHGTEYVCCPQTKIIGSVSKEEEEEDEEEEE EDEEEDYDVYKSEFPTEADLEDFTAAVDEDEDEEVEEDRDY YYDTFKGDDYNEENPTEPGSDGTMSDKEITHDVKVPPTPLPTNDVDV YFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELOAKNLP KAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRM ALENYLAALQSDPPRPHRILQALRRYVRAENKDLRHTIRHYQHVLAV DPEKAAQMKSQVMTHLHVIEERRNQSLSLLYKVPYVAQEQEEIDEL

				LQEQRADMDQFTASISETPVDVRVSSESESEIIPPFPFPFPFALPEN EDTQPELYHPMKKSGVGGEQDGLIGAEKVINSKNKVDENMVIDET LDVKEMIFNAERVGGLEEEERESVGPLREDFSLSSSALIGLLVIAVAI ATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYEN PTYKYLEQMQI
8493	A	305	506	LFQVIDETLDVKEMIFNAERVGGLEEEERESVGPLREDFSLSSSALIG LLVIAVAIATVIVISLVMLR
8494	A	3	1588	EEEDYDVYKSEFPTEADLEDFTAAVDEDEDEDEEGEEVVEDRDYYY DTFKGDDYNEENPTEPGSDGTMSDKEITHDVKAVCSQEAMTGPCRAV MPRWYFDLSKGKCVRFIYGGCGGNRRNFESEDYCMVCKAMIPPTPL PTNDVDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE LQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAM LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRH YQHVLAVDPEKAA\QMK\SQVMTHL\HVIEERRNQSLSLLYKVPYVA \QE\IQEEIDELLQEQRADMDQFTASISETPVDVRV\SSDESEIIPP FHPFPFPFALPENEGSGVGGEQDGLIGAEKVINSK\NKVDEKHGPL NETLDVKEMIFNAERVGG\EEERESVGPLREDFSL\SSSALIGLLV IAVAIAT\VIVISLVMLRKRQYGTI\SHGIVE/VVDPMLTPEERHLN KMQNHGYENPTYKYLEQMQI
8495	B	73	1845	MAATGTAAAAATGRLLLLLVLGTAPALALAGYIEALANAGTGFAV AEPQIAMFCGKLNMHVNIQTGKWEPTGTGKSCFETKBEVLQYQCQEM YPELQITNVMEANQRVSIDNWCRRDKKQCKSRFVTFPKCLVGEFVSD VLLVPEKCQFFHKERMEVCENHQHWHVTVVKEACLTQGMTLYSYGMLL PCGVDQFHGTEYVCCPQTKIIGSVSKEEEEDEEEEEDEEEDYDV YKSEFPTEADLEDFTAAVDEDEDEDEEGEEVVEDRDYYYDTFKGDD YNEENPTEPGSDGTMSDKEITHDVKAVCSQEAMTGPCRAVMPRWYFD LSKGKCVRFIYGGCGGNRRNFESEDYCMVCKAMIPPTPLPTNDVDV YFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLP KAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRM ALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAV DPEKAAQMKSQVMTHLHVIEERRNQILSLLYKVPYVAQEIQEEIDEL LQEQRADMDQFTASISEHPCGRPGEL*
8496	B	55	274	MADANKAEVPGATGGDSPHLQPAEPPGEPREPHPAEAEKQQPQHSS SSNGVKMENDESAAKEKSDLKEKSTGX*
8497	A	3	754	FLFFEPHPAEARKQQPQHSSSSNGVKMENDESAAKEKSDLKEKSTGS KKANRFHPYSKDKNSGTGEKKGPNRRNVFISNIPYDMKWQAIKDLMR EKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKKALETMNKYDLG RRVNIKEDPDGENARRALORTGTSFQGSASHADVSGSLVNLPPSILNN PNIPPEVISNLQAGRLGSTIFVANLDFKVGWKKLKEVFSIAGTVKAG RY\KEDKDGQSRGMGT
8498	A	2	347	MPCDEEPSQLEELADFMELTPIEKYALNYLELFHTSIEQEKERTSE DAVMTAVRAWEFWNLKTLQEREARLRLEQEEADLLTYTREDAYSMEY VYEDVDGQTEVMPLWTPPTPP
8499	A	1	414	AWHEETHKVDLGLPEKKKNKKVVKPETRYSVLNNDYFADVSPLRA TSPSKSVAHQAPEMPLVKKKKKKKK\VSAAKGKVKRSQSKLRLRN TSP*VMTLRPPQQRK*SPKRR*SSQSSRSQ*KGKRRRGKRG
8500	A	1	1977	MEVDFKIRKVGQWTITLQEHFVSVLLFIEETHPENKPTSTAVEESHI SRDTVMVNFQCQLDWSKGYLEAYLTKINSICSHRFLLDGSVTCHDET GSSRDARDTVGTGVRVNDESVEQLGLRRTMWLGCIRGAAMAASVTVT AFAGRPRPGRSRNPRGWAGDSKWTSGSRRSWLSRGGGEISPTGMITK THF\VYLGLPEKKKKKRVVKEPETRYSVLNNDYFADVSPLRATSPS *\DVAHQAPEMPLVKKKKKKKGVSTLCEEHVEPTTLPARTEKS PSLRKQVFGHLEFL\RGKRKNKKSPLAMSHASGVKTSQ\DPQGEES TRVGKK\SKKHKKKKGGPGPHSL\PVQDPWFCEAREARDVGDTCSV GKKDEEQAALGQKRKRKSPREHNGKVKKKKIHOEGDALPGHSPSR SMESSPRKGSKKKPVKVEAPEYIPIISDDPKASAKKMKSKKKVEQPV

				IEEPALKRKKKKRRESGVAGDPWKEVVPSEMDFAVGELRETDTL EVLLEKKGNMDEAHIDQVRRKALQEEIDRESGKTEASETRKWTGTQF GQWDTAGFENEDQKLKFLRLMGGFKNLSPSPSRPASTIARPNMALGK KAADSLQQNLQRDYDRAMSWKYSRGAGLGFSTAPNKIFYIDRNASKS VKLED
8501	A	2	376	TAGFLLPQGLPCKYHLMYGSHLMPNVWRRTTTREPPLGDAEPNTRS LMWEVKRSSSGPWVFKSNIACHIPIFRITSTSSAYD/WPPTHSP**F SGIIPPCPHGCHQPFSDQDMVTFFLCQLPAHLH
8502	A	2	956	GLSQPKPRKETPIPSDTEEEEPQLQAHPVVCQKIEHEQPLGPQGLGQ GPPTVVEHTSYSAYTPTLWELAHPSLHQRLQVSRQLAQGKGDHILT EWLMAAMWTGWNDARELSKTVSKWQSYAELVEDTRDQRPVELAIHW YPTNVQQVLVLVGTADADYSLVYGKRDKFLGKAAYTDGYRGQSVKMTV DYQELNKVTAPLHAAVLSITDLMDDLTMELGQYHYAVDLANASLSD IAPESQEQFGFTWEGRWTFVLPQGYVHSPTICHGLVATDLATWKF PKGIRLFHYIDDIMLTSDSPADLEAVVPLLQOHLAA

Table 24

TISSUE ORIGIN	RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	8-9 105 140-142 144-145 180-183 220 230 292- 293 296-297 488-490 536 546-551 559-560 579 597-598 656-658 748-751 781 831-833 836-840 974 1048-1051 1107-1109 1185-1186 1206-1209 1287-1293 1297-1299 1305-1308 1316-1317 1334- 1335 1354-1355 1369-1370 1413-1414 1425-1431 1439-1441 1466-1470 1472-1477 1485-1489 1495- 1497 1501-1502 1518-1520 1561 1592-1595 1602 1607-1608 1610 1630-1634 1698-1700 1702-1710 1718 1726-1728 1781-1789 1809-1810 1813-1815 1824-1825 1854-1856 1890 1912 1950-1953 1970- 1971 1980-1984 2016-2017 2050-2052 2059-2060 2063 2068-2070 2079 2081 2131-2136 2186-2189 2262-2264 2266-2267 2276-2278 2315-2322 2341- 2346 2353-2357 2385-2386 2407 2417-2419 2430- 2434 2436-2438 2440-2441 2445-2451 2453 2469- 2470 2481 2487-2488 2511 2515-2516 2549-2550 2559-2565 2567-2568 2571 2587-2590 2623 2636- 2641 2644-2652 2655-2671 2679-2711 2716-2719 2722-2724 2731 2794 2798 2810-2811 2826-2834 2842-2848 2850-2851 2867 2913-2914 2917-2930 3102-3105 3112-3114 3133-3136 3152-3155 3163- 3164 3186 3262-3269 3276-3284 3287-3289 3298- 3300 3305 3308-3312 3386-3389 3402-3406 3454 3471-3474 3497 3508-3511 3524 3528-3530 3605- 3610 3638 3642-3643 3669-3672 3678-3679 3724- 3726 3733-3737 3782-3787 3840 3850-3860 3866- 3870 3901-3904 3991-3998 4042-4043 4048-4051 4055-4056 4061-4062 4080-4081 4128-4129 4170- 4171 4182-4183 4203-4204 4208 4216-4217 4225- 4227 4253 4266 4288-4289 4292 4327-4333 4415- 4417 4422-4426 4436-4438 4441-4443 4445-4447 4484 4502-4503 4510-4511 4514-4518 4553-4555 4566 4614 4629-4634 4691-4692 4733 4737 4774- 4776 4778-4779 4790-4795 4804-4805 4811 4843- 4844 4910-4916 4922 4950-4953 5013 5029-5033 5054-5055 5112-5113 5116 5146 5186-5189 5191- 5192 5216-5220 5236-5240 5255 5258-5262 5334- 5335 5343 5435-5440 5448-5451 5469-5471 5483- 5493 5687-5690 5692 5710 5723-5729 5757-5758 5818-5821 5829-5834 5848 5904-5914 5925-5930 5999-6000 6016-6020 6023-6024 6078-6084 6087- 6114 6119-6120 6180-6181 6305-6307 6348 6367- 6368 6385-6389 6399 6440-6446 6455 6662 6670- 6676 6691 6698 6751-6756 6780 6784 6811-6812 6845 6890-6894 6949-6953 6957 6987-6989 7001- 7002 7086-7087 7104 7152-7153 7281-7284 7310- 7311 7375 7398 7434-7447 7599-7600 7630-7633 7730-7737 7739-7741 7770-7772 7797 7921-7922 7958 8031-8033 8296 8361-8363 8372-8387 8430- 8432 8455-8456 8466
adult brain	GIBCO	ABD003	6-9 51 85 93 104 140-142 144-145 180-183 201- 209 213-215 230 250-252 272 275-276 280-282 298-321 330-340 345-349 360 370 383 395 402

10689

			416-418 425 466 488-494 498 527-529 537-538
			549-551 584 592 648 650-651 656-665 670 688
			714-715 718 726-728 735 752-756 759-760 767
			786-787 828-829 839-840 857-859 875-876 934-
			935 941-942 949-951 1000-1001 1022-1023 1037
			1185-1186 1190-1191 1206-1209 1216-1221 1227-
			1247 1261-1263 1287-1289 1297-1305 1314-1317
			1324-1333 1341-1348 1354-1355 1357-1358 1368-
			1370 1374-1379 1394-1395 1410-1414 1439-1441
			1448-1450 1453-1454 1460-1462 1465-1470 1472-
			1480 1485-1491 1514-1515 1540-1548 1557-1570
			1572-1574 1579-1580 1583-1595 1602 1610 1619-
			1620 1624-1628 1630-1634 1637-1642 1655-1658
			1671-1672 1675 1712-1714 1716 1718 1728 1781-
			1783 1786-1789 1809-1810 1813-1815 1817-1821
			1824-1825 1832-1834 1839-1840 1850-1863 1870-
			1874 1876 1890 1896 1904-1906 1912 1916 1921-
			1927 1937-1945 1950-1953 1958-1961 1969-1971
			1980-1984 1986-1991 2003-2004 2018-2019 2032-
			2036 2038-2044 2050-2058 2061 2063 2067-2073
			2079 2081 2087-2097 2112 2120-2121 2123 2131-
			2142 2155-2157 2165-2175 2182-2183 2186-2191
			2199-2200 2204-2207 2223-2224 2226-2230 2237-
			2239 2243 2255-2257 2266-2271 2276-2278 2282-
			2283 2290 2297-2305 2315-2322 2324-2327 2329-
			2333 2335-2336 2341-2358 2370-2372 2381 2385-
			2386 2398-2403 2407-2415 2433-2434 2440-2441
			2445-2451 2455 2458-2461 2469 2476-2477 2487-
			2490 2511 2514-2520 2526-2528 2543-2550 2557
			2567-2568 2571 2585-2586 2589-2590 2592-2596
			2619-2623 2625 2637-2641 2644-2647 2651-2655
			2658-2660 2665-2667 2671 2684-2688 2692-2696
			2698-2703 2712 2716-2743 2748-2756 2758-2771
			2776-2795 2801-2804 2810-2811 2814-2815 2823-
			2834 2850-2851 2867 2875-2879 2913-2914 2931-
			2946 2948-2971 2974-2979 3014-3016 3018-3023
			3034-3039 3043-3044 3066 3068-3071 3075-3078
			3088-3091 3093 3102-3105 3115-3116 3122-3133
			3137 3149-3150 3159-3160 3163-3172 3182-3183
			3251-3252 3274-3284 3287-3292 3298-3300 3305-
			3314 3346-3356 3371-3374 3384-3389 3400-3401
			3410-3411 3425-3428 3450-3452 3454 3456-3463
			3469-3474 3486-3488 3494-3497 3507 3512-3516
			3524-3527 3548-3553 3555-3557 3566-3567 3588-
			3593 3597-3599 3605-3610 3617-3619 3629-3632
			3638 3642-3643 3658 3660-3663 3675-3679 3687-
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			3798-3801 3841-3849 3866-3891 3901-3904 3926
			3931-3936 4009-4011 4042 4048-4051 4053-4056
			4058-4060 4065-4066 4073-4079 4082-4085 4092-
			4095 4097-4100 4107-4109 4128-4129 4132 4153
			4166 4170-4171 4173 4182-4183 4191-4193 4202
			4223-4224 4255 4286 4288-4289 4298-4322 4330-
			4333 4335-4353 4382-4384 4422-4426 4444 4448-
			4452 4484 4491-4494 4498-4503 4510-4511 4514-
			4518 4550-4553 4559 4566 4609 4621 4644-4645

			4662 4671-4673 4675 4678 4685-4690 4700-4703 4710 4737 4768-4769 4771-4772 4775-4776 4783 4785 4811-4836 4847-4850 4910-4918 4922 4924 4929 4934-4935 4937-4940 4955 4957-4961 4972- 4976 5019-5021 5032-5033 5043-5049 5076-5081 5098-5101 5107-5109 5167 5177-5183 5185-5189 5205 5208 5213 5216-5220 5224 5236-5240 5273 5283-5287 5297 5336 5343 5351 5359 5374 5391 5393-5401 5406-5409 5431-5434 5448-5459 5472 5475-5478 5485-5488 5492-5494 5496-5497 5499- 5506 5513-5520 5526-5545 5547-5553 5594 5616- 5617 5624-5626 5631 5639-5641 5658-5659 5673 5683 5687-5690 5721 5723-5729 5757-5758 5770 5777 5780-5782 5825-5834 5853-5868 5896-5898 5920-5921 5932 5940-5941 5945-5952 5956-5960 5969 5986 5998-6000 6003-6005 6014-6020 6023- 6024 6043 6047 6080-6083 6117-6120 6122-6127 6179 6195-6196 6203 6209-6210 6213-6217 6244 6256 6291-6292 6305-6307 6309-6311 6348 6378 6397 6399 6426-6431 6445-6453 6455-6459 6515 6519-6521 6523 6557-6559 6583 6600-6601 6607 6663-6664 6670-6676 6701-6702 6711-6712 6742- 6744 6759-6763 6766-6767 6776-6780 6784 6799- 6804 6808-6810 6828-6832 6840 6846-6848 6858 6861 6872-6874 6890-6894 6896 6909 6911-6917 6923-6924 6944-6945 6950 6953-6957 6960-6966 6970-6982 6987-6998 7001-7002 7014-7027 7029- 7033 7080-7083 7088-7090 7098-7102 7104 7111- 7112 7139 7151 7154 7168 7191 7227 7292 7310- 7311 7324 7334-7335 7346-7347 7375 7377-7384 7416-7417 7433 7438-7439 7443 7448-7454 7456- 7459 7461-7470 7485 7527-7531 7570-7573 7599- 7600 7626-7633 7672-7675 7698-7700 7732-7734 7742-7743 7757-7760 7780-7790 7797-7798 7850 7867-7868 7890-7891 7899-7900 7960-7964 8003 8023-8024 8031-8033 8062-8063 8089 8129 8175 8185 8194-8196 8227-8229 8257-8258 8261-8264 8319 8387-8396 8406-8407 8430-8432 8438 8455- 8456 8463-8464 8490-8495
adult brain	Clontech	ABR001	170 172-175 261 269-270 280-282 546-548 555 580-581 781 811-813 836-838 875-876 1021 1032-1035 1048 1122-1147 1261-1263 1275-1276 1314-1315 1347 1378-1390 1402-1407 1439-1441 1490-1491 1511-1513 1619-1620 1652 1655-1657 1780-1783 1801-1804 1854-1863 1876 1944-1945 1986-1991 2032-2035 2053-2058 2081 2112 2143- 2146 2255-2257 2266-2271 2282-2283 2297-2301 2315-2322 2370-2372 2433-2434 2495-2499 2549- 2550 2572 2648-2650 2704-2710 2744-2747 3066 3073-3074 3111 3137-3141 3152-3155 3221-3226 3276-3278 3355-3356 3358 3383 3481-3485 3508- 3516 3605-3610 3617-3619 3634-3636 3678-3679 3707-3713 3733-3737 3958-3960 4048-4051 4055- 4056 4058-4060 4073-4079 4086-4088 4163 4223- 4224 4249-4250 4289 4361-4362 4422-4424 4445- 4447 4498-4501 4551-4552 4671 4678 4759 4775- 4776 4791-4792 4840 4972-4976 4979 5216-5220

			5236-5240 5246 5312 5466 5475-5478 5497 5503 5631 5639-5641 5829-5834 5875-5881 5956-5960 5988-5992 6003-6005 6011-6012 6032 6157-6158 6174-6176 6455 6476-6479 6491-6499 6662 6670- 6676 6858 6897-6898 6960-6961 6970-6976 7014- 7027 7188-7190 7265 7464 7539-7549 7630-7633 7638-7639 7672-7675 7748 7757-7760 7773-7774 7907 8021 8202 8261-8264 8418-8419 8427 8466
adult brain	Clontech	ABR006	3-5 105 111 113 230 272 294-295 307-320 401 432-433 465 468 517 757-758 805 814-821 831- 833 1113-1117 1122-1147 1151-1152 1160-1162 1175-1176 1287-1289 1316-1317 1334-1335 1341- 1346 1399-1401 1421-1423 1439-1441 1460-1462 1490-1491 1540-1548 1562-1567 1579-1580 1602- 1608 1610 1626-1628 1702-1710 1726-1727 1765- 1767 1809-1810 1819-1821 1824-1825 1896 1912 1944-1945 1950-1953 2020-2027 2114-2119 2137 2290 2302-2305 2329-2331 2341-2343 2379 2385- 2386 2398-2403 2428-2429 2442-2451 2458-2461 2495-2499 2544-2548 2561-2565 2567-2568 2574- 2580 2589-2590 2592-2596 2612-2615 2636 2644- 2647 2671 2684-2688 2698-2703 2716-2719 2721 2810-2811 2881-2888 2905-2907 2951-2952 2978- 2979 3017 3029-3031 3045-3048 3095-3096 3115- 3116 3133 3165-3172 3218-3219 3262-3269 3280- 3284 3287-3289 3305 3311-3312 3334-3344 3346- 3348 3355-3356 3411 3454 3497 3548-3550 3606- 3610 3656-3657 3699-3701 3728-3729 3733-3739 3776-3778 3782-3784 3841-3849 3881-3882 3886- 3887 3904 4035-4040 4042 4053 4074-4079 4096 4102-4106 4164 4182-4183 4281 4289-4290 4343 4386-4387 4445-4447 4510-4511 4562 4702 4724- 4727 4828 4848-4850 4906 4928 4950-4953 4962- 4967 5022-5028 5034-5035 5107-5109 5223-5224 5255 5313-5314 5418-5420 5428 5431-5434 5452- 5459 5485-5488 5580-5581 5634 5723-5729 5829- 5834 5882-5885 5956-5960 5986 5993-5994 6001- 6002 6048-6050 6123-6127 6159 6243 6473 6563- 6582 6717 6936 6941-6942 7050-7053 7060-7062 7162-7165 7226 7346-7347 7377-7384 7446 7585- 7586 7595-7596 7630-7633 7748 8139 8227-8229 8253 8355-8356
adult brain	Clontech	ABR008	8-19 22-28 32 38 67 77-79 88 90 93 104-107 111 113 123-126 149-151 172-175 193-194 210- 211 217 227 230 241-243 250-251 269-270 286- 287 294-295 298-299 305 330-340 345-349 365 370 380-382 384-385 389-394 401-406 430-433 442-445 454-455 467 469-473 476-477 480-482 491-494 499-500 517 527-531 534-535 541-545 556 559-560 576-578 580-581 583 592 631 633- 634 688 692 714-715 719 757-758 811-813 830- 833 909-912 918 928 931-932 941-947 960-971 979-980 982-985 991-994 1011-1012 1014 1016 1038 1041-1043 1052-1053 1055-1059 1070-1105 1113-1120 1122-1149 1151-1152 1173-1176 1188 1190-1192 1213-1221 1244-1245 1261-1263 1275- 1276 1287-1289 1300-1302 1305 1311-1313 1316-

			1317 1334-1335 1341-1347 1354-1355 1359-1370
			1374-1379 1391 1396-1398 1402-1407 1413-1414
			1421-1423 1439-1444 1455-1462 1465 1490-1491
			1498-1500 1511-1513 1525-1537 1542-1548 1557
			1561-1570 1572-1574 1579-1580 1583-1595 1602
			1607-1608 1616-1617 1619-1620 1633-1634 1636-
			1641 1653-1658 1660-1674 1691-1692 1698-1700
			1702-1710 1726-1727 1759-1760 1765-1769 1781-
			1789 1801-1804 1806-1808 1813-1815 1820-1821
			1823-1825 1835-1840 1843 1854-1856 1861-1869
			1876 1878 1890-1893 1896 1906-1911 1921 1930-
			1932 1944-1945 1950-1953 1958-1961 1964-1966
			1970-1971 1980-1984 1986-1991 1998-1999 2001-
			2002 2016-2017 2020-2027 2032-2035 2050-2060
			2067-2073 2102-2107 2114-2121 2123-2126 2128
			2138-2141 2143-2147 2155 2165-2170 2174-2175
			2182-2183 2186-2198 2204-2207 2209-2217 2225
			2231-2233 2237-2240 2249-2250 2262-2264 2268-
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adult brain	Clontech	ABR011	384-385 1064-1065 1439-1441 1602 1950-1953 2258-2261 2268-2271 2810-2811 3133 3276-3279 3287-3289 3346-3348 3410 3623-3628 3642-3643 4229 4648-4652 4702 4841-4842 5107-5109 5359 5416 5829-5834 7392-7393 7509-7510 7599-7600 8355-8356
adult brain	BioChain Inst.	ABR012	14-19 26-28 140-142 384-385 416-418 1022-1023 1246-1247 1439-1441 1445 1448-1450 1575-1577 1712-1713 1896 1921 2079 2262-2264 2658-2660 2684-2688 2953-2959 3276-3278 3346-3348 5452- 5459 5829-5834 5853-5855 6456-6459 8397-8398
adult brain	Invitrogen	ABR013	384-385 1439-1444 1448-1450 2083-2085 2268-

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adult brain	Invitrogen	ABR014	264-265 345-349 786-787 2658-2660 2725-2727 2810-2811 2856 3064-3066 3133-3137 3149-3150 3760 4000 4048-4051 4061-4062 4092-4095 4429 4823-4824 4910-4916 5593 6032 6119-6120 7099- 7102 7152-7153 7158 7162-7165 7527-7531 7730
adult brain	Invitrogen	ABR015	549-551 559-560 1182-1183 2487-2490 2589-2590 2592-2596 2671 2692-2696 2731 2794 2913-2914 2974-2977 3017 3043 3065 3163-3164 3781 3901- 3903 3910-3919 4288 4854-4872 5452-5459 5475- 5478 5492-5493 5624-5626 6032 6119-6120 6464- 6466 6950 6957 7599-7600 8443-8444
adult brain	Invitrogen	ABR016	546-548 1022-1023 1050 2487-2490 2511 2559- 2560 2587-2588 2644-2647 2704-2710 2889-2893 2948-2950 2953-2959 3066 3073-3074 3138-3141 3779-3780 3798-3801 3904 3986-3987 4020-4026 4390 4793-4794 4922 5624-5626 6119-6120 6142 6954-6955 7099-7102 7162-7165 7470 7551-7554
adult brain	Invitrogen	ABT004	38 90 105-107 113 143 172-175 210-211 230 286-287 302 321 330-340 345-349 370-372 386 402 478 480-482 534-535 543-545 565-575 688 736-737 765 811-827 830 1113-1117 1151-1152 1181 1213-1221 1244-1245 1303-1304 1334-1335 1341-1346 1354-1355 1442-1444 1448-1450 1455- 1459 1465 1490-1491 1498-1500 1525-1528 1549- 1551 1562-1570 1607-1608 1619-1620 1633-1634 1691-1692 1728 1765-1767 1786-1789 1813-1815 1850-1851 1861-1863 1890-1893 1912 1921 1944- 1945 1998-1999 2020-2027 2067 2124-2126 2143- 2146 2165-2170 2262-2264 2282-2283 2289 2300- 2301 2307-2322 2328 2332-2333 2340 2347-2349 2398-2403 2420-2423 2440-2451 2482-2488 2522- 2525 2536-2537 2549-2550 2561-2565 2574-2580 2585-2586 2630-2633 2637-2641 2655 2658-2663 2671 2698-2710 2739-2743 2757 2776-2777 2810- 2813 2835 2842-2848 2850-2851 2874-2879 2913- 2915 2940-2946 3029-3031 3045-3048 3115-3116 3175-3177 3186 3221-3226 3259-3260 3262-3269 3276-3279 3308-3310 3346-3348 3386-3389 3416- 3418 3494-3496 3512-3516 3602-3604 3631-3632 3646-3652 3683-3686 3699-3701 3710-3713 3738- 3739 3785-3787 3794-3795 3798-3801 3841-3849 3886-3887 3904 3910-3919 3926 3938-3941 3950- 3955 4020-4021 4048-4051 4053 4058-4060 4063- 4064 4066 4082-4085 4092-4095 4102-4109 4143- 4144 4157-4162 4170-4171 4203-4204 4223-4224 4252 4263 4294-4295 4323 4366-4367 4378-4380 4433 4436-4438 4502-4503 4507 4520-4528 4556- 4558 4662 4672-4673 4676 4702-4703 4705 4715 4724-4727 4738-4741 4744 4768-4769 4796-4803 4806-4809 4826 4892-4898 4929 4943 4957-4958 5019-5021 5043-5049 5056 5107-5109 5116 5139- 5140 5147 5152 5226-5228 5284-5285 5288 5323

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adipocytes	Stratagene	ADP001	14-19 26-28 102-103 121 140-142 384-385 403- 406 408 463-464 468 527-529 579 645 650-651 696 828-829 937-942 1022-1023 1033-1035 1110- 1111 1151-1152 1160-1161 1206-1209 1213-1221 1244-1245 1294-1302 1327-1333 1354-1355 1391 1413-1414 1439-1441 1445 1465 1481-1484 1488- 1489 1511-1513 1558-1560 1562-1567 1572-1574 1592-1595 1602 1607-1608 1610 1619-1620 1659 1679 1691-1692 1712-1713 1726-1727 1774-1776 1781-1785 1824-1825 1870-1874 1894-1895 1912 1929 1934-1935 1962-1966 1968 1970-1971 1974- 1978 1998-1999 2079 2103-2107 2112 2128 2138- 2141 2182-2183 2223-2224 2231-2233 2244-2248 2262-2264 2268-2271 2282-2283 2285 2315-2322 2332-2333 2382-2384 2487-2488 2502-2508 2522- 2525 2567-2568 2574-2580 2603-2609 2630-2633 2642-2643 2656-2660 2722-2727 2731 2739-2742 2748-2749 2784-2786 2788-2794 2796 2817 2823- 2825 2867 2879 2974-2977 3014-3016 3018-3023 3036-3039 3054-3057 3073-3078 3102-3105 3111 3138-3141 3149-3150 3152-3155 3165-3172 3217 3259-3260 3274-3275 3280-3284 3287-3289 3306- 3307 3324-3332 3346-3348 3414-3415 3419-3421 3425-3428 3454 3469-3470 3498-3499 3507-3511 3524 3555-3557 3570 3600-3601 3605 3623-3628 3631-3633 3683-3686 3699-3703 3722 3728 3733- 3737 3771-3774 3794-3795 3986-3987 3991-3998 4048-4051 4057 4092-4095 4157-4162 4170-4171 4194-4195 4233-4240 4294-4295 4422-4424 4429 4436-4438 4484 4498-4501 4644-4645 4648-4652 4662 4715 4721-4723 4729 4734 4854-4872 4936 5015-5017 5019-5028 5065-5072 5080-5081 5098- 5100 5177-5179 5236-5240 5284-5285 5435-5437 5475-5478 5485-5488 5530-5545 5565-5566 5596 5616-5617 5639-5641 5714 5719-5720 5757-5760 5780-5782 5953 5999-6000 6038-6042 6112-6113 6123-6127 6161-6164 6297-6298 6385-6388 6407- 6411 6455-6459 6464-6466 6548-6549 6697 6703- 6704 6718-6721 6742 6799-6804 6828-6832 6840 6858 6943 6967-6969 6997-6998 7035 7086-7087 7105-7106 7179-7180 7248-7249 7251-7259 7281- 7282 7349-7350 7377-7384 7457-7459 7838 7859-

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adrenal gland	Clontech	ADR002	3-5 14-19 26-28 48 67 105-107 121 140-142 176 201-209 212 221-222 260 266-268 280-282 305 384-385 460-462 468 495 524-529 537 546-548 656-658 688 735 739 814-821 828-829 836-838 918 960-961 1005-1007 1010 1048 1110-1111 1185-1186 1206-1209 1244-1245 1261-1263 1297-1302 1341-1346 1439-1441 1445 1460-1462 1466-1470 1472-1477 1481-1484 1495-1497 1507-1513 1531-1539 1552-1555 1557-1560 1562-1570 1610 1612-1615 1619-1620 1624-1625 1635-1641 1655-1657 1675-1677 1693 1726-1729 1759-1760 1765-1767 1774-1776 1813-1815 1817-1818 1839-1840 1850-1852 1864-1874 1903 1913 1916-1920 1930-1932 1937-1942 1950-1953 1958-1966 1980-1984 1986-1991 2003-2004 2016-2017 2050-2052 2063-2066 2068-2070 2080 2095-2097 2112 2122 2124-2126 2131-2136 2142 2148-2152 2155 2158-2162 2174-2175 2223-2224 2249-2250 2262-2264 2268-2275 2286-2288 2291-2294 2300-2301 2315-2322 2335-2336 2344-2346 2358 2368 2379 2385-2386 2408-2415 2433-2438 2453 2474-2475 2487-2488 2495-2499 2509-2510 2512 2515-2516 2551-2553 2558 2571 2585-2586 2619-2622 2626-2629 2648-2650 2656-2660 2682-2683 2689-2691 2722-2724 2758 2778-2783 2788-2794 2796 2801-2804 2807-2813 2826-2834 2842-2848 2850-2851 2916 2940-2946 2948-2950 2960-2971 2973 2978-2979 3014-3016 3036 3049-3053 3058-3063 3072 3080-3085 3095-3096 3117-3121 3138-3141 3149-3150 3217 3221-3226 3250 3262-3273 3276-3279 3287-3289 3311-3312 3315-3318 3346-3354 3371-3372 3384-3385 3410-3411 3473-3476 3508-3511 3528-3530 3551-3553 3571-3587 3597-3604 3617-3619 3623-3628 3633 3638 3642-3643 3660-3663 3683-3686 3699-3701 3707-3709 3722 3733-3739 3779-3780 3788-3789 3841-3849 3886-3887 3928-3936 3983-3989 3991-3998 4012-4013 4015-4018 4027-4040 4042-4043 4061-4062 4070-4072 4082-4085 4127-4129 4132 4142 4157-4163 4167 4172 4252 4286 4294-4297 4331-4333 4348 4368 4429-4431 4498-4501 4510-4513 4520-4528 4566 4605 4609 4613 4691 4729 4738-4741 4745-4749 4752 4780-4782 4785 4791-4792 4804 4845-4846 4889 4908-4909 4937-4939 4954-4955 4993-4994 4996-5001 5005-5007 5022-5028 5056 5076-5079 5098-5100 5111-5113 5129-5131 5150 5161-5163 5177-5179 5194 5205 5209-5212 5247 5284-5287 5298 5312 5321-5322 5349 5352-5355 5392 5396-5401 5405-5409 5452-5459 5515-5516 5526-5529 5553 5569 5585 5588 5594 5619-5620 5674-5676 5683 5693 5697 5723-5729 5746-5753 5757-5758 5761-5763 5777 5798-5805 5835-5838 5856-5863 5872 5899-5903 5925-5930 5939 6008 6028-6031 6051-6057 6065-6068 6147 6165-6169 6209-6210 6221-6223 6234

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adult lung	GIBCO	ALG001	132-137 140-145 201-209 224 233-237 343-350 370 375 416-418 483-486 488-490 496-497 499- 500 527-529 549-551 645 650-651 673-675 693 723 757-758 767 839-840 842 857-859 921 949- 952 992-994 1014 1022-1023 1037 1041-1043 1067-1071 1110-1111 1160-1161 1185-1186 1206- 1209 1227-1243 1261-1263 1297-1299 1341-1347 1357-1358 1368-1370 1374-1377 1394-1395 1413- 1420 1439-1441 1446-1447 1453-1454 1465 1472-

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lymph node	Clontech	ALN001	14-19 144-145 197-209 280-282 380-382 469-473 488-490 527-529 532 549-551 597-598 641-644 648 694 714-715 724 790-792 834-835 857-859

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adult liver	GIBCO	ALV001	6-7 73 75-76 83 85 140-142 144-145 164-169 217 241-243 252 275-276 283-284 351-355 402 419-424 426-428 469-473 498 518-523 527-529 546-555 586-587 669 705-706 736-737 759-760 767 831-833 836-838 941-942 949-951 992-994 1011-1012 1022-1023 1106-1109 1173-1174 1200- 1209 1249-1253 1261-1263 1273-1279 1297-1299 1303-1305 1311-1313 1327-1333 1341-1347 1349- 1353 1359-1368 1399-1401 1453-1459 1466-1470 1472-1480 1498-1500 1507-1513 1516-1517 1531- 1537 1542-1551 1557 1568-1570 1572-1574 1583- 1585 1592-1599 1603-1608 1619-1620 1659 1671- 1672 1712-1713 1728 1784-1785 1790 1805 1813- 1815 1824-1825 1832-1834 1839-1840 1857-1860 1870-1874 1890 1912 1916 1950-1953 1958-1963 1986-1991 2016-2017 2050-2052 2059-2060 2063 2074-2075 2086 2112 2124-2126 2137 2158-2162 2171-2173 2182-2183 2195 2223-2224 2226-2227 2237-2239 2258-2264 2300-2301 2307-2322 2324- 2328 2332-2333 2375-2377 2382-2386 2388 2407

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adult liver	Invitrogen	ALV002	8-9 67 144-145 250-251 303 371-372 380-382 403-406 419-424 451 456-458 469-473 527-529 597-598 603-606 656-658 705 726-727 773 779- 780 905-912 1061 1066 1173-1174 1179-1180 1190-1191 1210 1244-1245 1249-1253 1261-1263 1273-1279 1287-1289 1303-1304 1311-1313 1349- 1353 1391 1442-1444 1448-1450 1460-1462 1498- 1500 1516-1517 1542-1548 1568-1570 1572-1574 1583-1591 1596-1599 1603-1608 1626-1628 1630- 1632 1658-1659 1673-1674 1678 1702-1710 1718 1728 1765-1767 1780 1784-1785 1791-1795 1813- 1815 1852 1854-1856 1896-1900 1912 1937-1942 1958-1961 1968 2001-2002 2038-2044 2064-2067 2074-2075 2095-2097 2112 2124-2126 2137 2148- 2152 2158-2162 2192-2194 2199-2200 2208 2229- 2230 2237-2239 2244-2250 2262-2264 2276-2278 2300-2301 2315-2322 2334 2337-2339 2369 2381 2417-2419 2436-2438 2454 2468 2482-2486 2513 2538-2542 2549-2550 2570 2574-2580 2583-2584

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adult liver	Clontech	ALV003	105 786-787 1277-1279 1596-1599 1602-1606 1813-1815 2884-2888 3065 3218-3219 3566-3567 4120-4121 4395-4396 4999-5001 5034-5035 6084 8430-8432 8468
ovary	Invitrogen	AOV001	6-13 20-21 38 40-43 48 51-54 68 91-92 104-107 113 139-145 160 164-169 180-183 193-195 201- 209 213-215 220-222 225 230 250-251 253-259 266-271 273-278 280-282 288-289 298-299 301 304-305 307-320 329-340 345-349 356-370 373 376 384-385 397-398 400 408-409 416-418 425 432-433 442-445 449 454-455 466 469-473 476- 477 488-495 514-516 527-535 537 543-554 556- 562 576-579 597-598 603-606 627-628 650-651 656-665 688-690 712-717 719 728 733-735 739 748-750 753 767-770 772 779-781 805 809 814- 827 831-833 836-840 842 857-859 874 877-879 881-882 887-891 920 923-927 930 941-944 949- 952 960-961 967-969 974 982-983 992-994 1000- 1002 1005-1007 1017-1018 1021-1023 1032-1035 1037 1055-1059 1061 1072-1106 1110-1121 1151- 1152 1160-1161 1163-1165 1177-1178 1182-1183 1187-1188 1194-1196 1206-1209 1213-1221 1227-

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Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	565-575 900-903 3188-3214 3942-3945 4456-4479 4854-4872
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC	BAC002	3188-3214 3942-3945 4456-4479 4854-4872 5925- 5930

Genomic DNA from BAC 393I6	Library) Research Genetics (CITB BAC Library)	BAC003	565-575 900-903 3188-3214 3942-3945 4456-4479 4854-4872
bladder	Invitrogen	BLD001	6-7 321 432-433 460-462 696 774 1033-1035 1110-1111 1306-1308 1439-1441 1455-1459 1511- 1513 1529-1530 1633-1634 1659-1669 1728 1759- 1760 1881-1882 1907-1911 1916 2018-2019 2061 2063-2066 2068-2070 2103-2107 2112 2143-2146 2209-2217 2223-2224 2302-2305 2315-2322 2353- 2357 2428-2429 2435 2585-2586 2630-2635 2729- 2730 2743 2842-2848 2860-2863 2905-2907 2913- 2914 2918-2930 2940-2946 2978-2979 3045-3048 3122-3132 3152-3155 3165-3172 3274-3278 3384- 3389 3612-3616 3699-3701 3722 3724-3726 3779- 3780 3788-3789 3794-3795 3798-3801 3850-3854 3876-3877 3922-3923 4015-4018 4022-4026 4090- 4091 4165 4436-4438 4697 4873-4876 4928 4972- 4976 4980 5098-5100 5139-5140 5213 5288 5290- 5292 5390 5687-5690 5705-5709 5714 5723-5729 6117-6118 6195 6213-6217 6299 6464-6466 6663- 6664 6703-6704 6785 7288-7289 7538 7551-7554 7612 7667-7668 7963-7964 8046-8048 8110-8113 8137 8387
bone marrow	Clontech	BMD001	1-2 14-21 36-37 44-46 52-56 94 105 108 114- 115 121 127-130 132-137 140-145 161 180-183 185 201-209 213-215 221-222 233-237 272 283- 284 290 296-297 351-352 384-385 416-418 434- 440 463-464 468 499-500 527-531 546-551 555 618-622 638-639 645 650-651 656-665 670 707- 708 726-729 778 786-787 790-792 828-829 831- 840 855-862 921-927 941-942 945-947 949-951 960-961 986 988 1017-1018 1022-1023 1032-1035 1037 1047 1050 1055-1060 1064-1065 1067-1069 1072-1105 1159-1171 1200-1209 1213-1221 1227- 1247 1249-1253 1261-1263 1294-1305 1311-1313 1327-1333 1337-1338 1341-1347 1357-1358 1369- 1370 1394-1395 1410-1420 1424-1431 1439-1441 1445-1450 1455-1489 1501-1502 1505-1506 1511- 1513 1525-1528 1540-1541 1549-1551 1557-1561 1568-1570 1575-1577 1579-1580 1583-1585 1592- 1595 1600-1602 1607-1608 1610 1619-1620 1622- 1623 1630-1632 1637-1641 1652-1654 1659 1671- 1672 1675-1692 1694-1696 1702-1718 1728 1784- 1785 1790 1798-1800 1809-1810 1817-1818 1820- 1821 1839-1840 1843 1849 1857-1860 1864-1874 1884-1889 1896 1901-1903 1912-1913 1916-1921 1930-1932 1934-1936 1943-1945 1950-1957 1962- 1963 1968 1973-1984 1986-1994 2003-2008 2014- 2015 2018-2027 2037 2045-2052 2063 2068-2070 2074-2075 2077-2081 2086-2094 2103-2107 2120- 2121 2124-2126 2128-2130 2137 2142 2158-2162 2165-2173 2182-2183 2190-2191 2199-2200 2204- 2207 2223-2224 2226-2227 2241-2243 2255-2257 2266-2267 2272-2280 2285 2297-2299 2302-2305

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bone marrow	Clontech	BMD002	14-19 44-45 51 84 94 132-137 144-145 162-163 172-175 233-237 261 275-276 283-284 377-378 384-385 495 499-500 586-587 650-651 755 790- 792 834-835 855-856 973 982-983 1022-1023 1110-1111 1172 1200-1209 1213-1221 1227-1243 1287-1289 1297-1299 1303-1304 1316-1317 1341- 1347 1357-1358 1369-1370 1374-1377 1415-1420 1446-1447 1465 1478-1480 1505-1506 1542-1548 1557-1560 1562-1567 1575-1577 1602 1607-1608 1671-1672 1694 1702-1711 1781-1783 1827-1830 1839-1840 1885-1889 1891-1896 1903 1907-1911 1916 1921 1934-1935 1944-1945 1985-1991 2003- 2004 2045 2063 2071-2073 2103-2107 2128 2137 2178-2181 2223-2224 2237-2239 2262-2264 2297- 2299 2302-2305 2315-2322 2337-2339 2350-2352 2382-2384 2392-2397 2407 2430-2432 2493-2494 2502-2508 2511 2551-2553 2558 2574-2580 2587- 2588 2592-2596 2636 2656-2660 2671 2731-2738 2744-2747 2817 2835 2853-2855 2857-2863 2867 2881-2883 2931-2934 2953-2959 2972 2974-2977 3014-3016 3037-3039 3064-3066 3071 3088-3091 3115-3116 3122-3132 3134-3136 3138-3141 3163- 3172 3181 3218-3219 3221-3226 3253-3258 3274- 3275 3280-3284 3290-3292 3306-3307 3315-3318 3334-3344 3346-3348 3370 3375-3380 3386-3389 3410 3412-3413 3419-3421 3477-3478 3481-3485 3517-3520 3540-3543 3548-3550 3605 3623-3628 3678-3679 3699-3701 3704 3738-3739 3748-3752 3760 3798-3801 3850-3854 3861-3865 3931-3936 3950-3955 3957 3986-3989 3991-3998 4000-4008 4015-4018 4035-4040 4061-4062 4092-4095 4128- 4129 4157-4162 4170-4171 4205-4207 4296-4297 4348 4377 4659-4660 4662 4674 4830-4835 4851- 4853 4873-4876 4889 4924 4937-4939 4984-4985 5080-5081 5114 5129-5130 5139-5140 5201 5232 5236-5240 5244-5245 5250-5254 5302-5305 5416 5452-5459 5485-5488 5504-5505 5588 5694-5695

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bone marrow	Clontech	BMD004	499-500 855-856 1003 1005-1007 1160-1161 1671-1672 1694 1916 1962-1963 3065 3270-3273 3313-3314 3376-3379 3904 5107-5109 5764 6613-6615 7615-7616 8031-8033 8430-8432
bone marrow	Clontech	BMD007	36-37 499-500 676-680 786-787 982-983 1022-1023 1337-1338 1424 1437-1438 1511-1513 1896 2492 3037-3039 3065 3227-3228 3346-3348 3595-3596 3605 3760 5999-6000 7615-7616 8102-8109 8117
colon	Invitrogen	CLN001	8-9 106-107 233-237 266-268 403-406 645 941-942 1290-1293 1300-1304 1374-1377 1439-1441 1446-1447 1616-1617 1765-1767 1784-1785 1813-1815 1912 1921 1930-1932 1958-1961 1970-1971 1985 2059-2060 2124-2126 2158-2162 2237-2239 2353-2357 2476-2477 2480 2515-2516 2574-2580 2587-2588 2598-2601 2603-2609 2669-2670 2698-2703 2817 2842-2848 2868-2873 2915 2978-2979 3014-3016 3033 3043 3095-3096 3313-3314 3349-3352 3386-3389 3623-3628 3639-3640 3693-3694 3728 3730 3743-3747 3841-3849 3904 3988-3989 4128-4129 4155 4223-4224 4252 4662 4672-4673 4780-4782 4910-4916 5157 5190 5250-5254 5280-5282 5343 5435-5437 5452-5459 5475-5478 5517-5518 5614-5617 5621-5622 5624-5626 5660 5686-5690 5714 5851-5852 6013 6065-6068 6077 6142 6236-6241 6353-6355 6443-6444 6501-6504 6560-6562 6586-6587 6703-6704 6734-6736 6799-6804 6925 6932-6934 6941-6942 6990-6992 7036 7079-7082 7099-7102 7188-7190 7255-7259 7303-7304 7398 7402-7403 7433 7662-7666 7676-7677 7770-7772 8102-8109 8227-8229 8413
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL016	144-145 193-194 641-644 1275-1276 1394-1395 1490-1491 1511-1513 1610 1671-1672 1986-1991 2074-2075 2095-2097 2850-2851 3217-3219 3486

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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			3986-3987 5425-5426 5554-5558 5829-5834 7465-7468 8031-8033 8430-8432
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL021	447 650-651 730-731 1003 1022-1023 1272 1349-1353 1402-1407 1439-1441 1446-1447 1495-1497 1511-1513 1784-1785 1796-1797 1896 2262-2264 2362-2364 2534-2535 2953-2959 3065-3066 3115-3116 3138-3141 3217 3302-3303 3456-3463 4120-4121 4180-4181 4484 5177-5179 5764 5829-5834 5971-5980 6414-6417 6877 7014-7027 7159-7160 7609-7611 7630-7633 8031-8033 8102-8109 8430-8432 8460-8461
Mixture of 11 tissues-mRNAs**	Various Vendors**	CTL028	2814-2815 4840 4950-4953 8430-8432
cervix	BioChain	CVX001	6-7 14-19 40-41 47 52-54 74 81-82 88 105-107 111 131 143 150-151 197-209 213-215 250-251 253-254 266-268 277-278 280-282 301 351-352 384-385 397-398 402 416-418 454-458 475 495 498 527-529 534-535 539 546-548 588-591 645 650-651 656-658 699-702 706 712-713 739 774 803-804 814-821 857-859 875-878 887-891 918 945-947 952 974 992-994 1005-1007 1016 1022-1023 1033-1037 1050 1072-1105 1110-1111 1160-1161 1163-1165 1182-1183 1194-1196 1206-1209 1216-1221 1227-1243 1246-1247 1249-1253 1287-1293 1297-1302 1311-1315 1334-1335 1347 1354-1355 1369-1370 1374-1379 1408-1420 1439-1441 1448-1450 1453-1454 1466-1470 1478-1480 1485-1487 1501-1502 1514-1515 1529-1539 1542-1551 1557 1561-1567 1572-1574 1586-1591 1600-1602 1610 1612-1615 1619-1620 1622-1623 1653-1657 1659 1671-1674 1676-1677 1694 1712-1714 1716 1718-1721 1726-1727 1730 1759-1760 1762-1763 1778 1798-1805 1809-1810 1820-1821 1824-1825 1844-1848 1850-1851 1854-1856 1864-1874 1883 1885-1889 1903 1912-1913 1916 1921 1930-1932 1936-1942 1968 1970-1971 1980-1984 1998-1999 2003-2004 2014-2015 2018-2019 2046-2052 2062-2066 2071-2075 2079-2080 2112 2114-2123 2131-2136 2156-2157 2165-2173 2182-2183 2186-2189 2201-2207 2226-2227 2243 2249-2250 2255-2257 2266-2267 2276-2278 2282-2283 2291-2294 2297-2299 2302-2305 2315-2322 2328-2331 2335-2339 2341-2349 2353-2357 2368 2375-2377 2381-2386 2389-2390 2404-2406 2416-2423 2428-2435 2458-2461 2469 2487-2488 2495-2499 2511 2514-2516 2522-2525 2543 2567-2569 2585-2588 2603-2609 2619-2622 2636-2641 2651-2652 2658-2663 2671 2704-2711 2716-2724 2731-2738 2750-2755 2772-

** The 11 tissue-mRNAs and their vendor source, are as follows: 1) adult trachea mRNA (Clontech), 2) adult pituitary gland mRNA (Clontech), 3) adult heart mRNA (Invitrogen), 4) fetal heart mRNA (Invitrogen), 5) adult placenta mRNA (Invitrogen), 6) adult brain mRNA (Invitrogen), 7) adult small intestine mRNA (Invitrogen), 8) fetal lung mRNA (Invitrogen), 9) adult lung mRNA (Invitrogen), 10) adult uterus mRNA (Invitrogen), 11) fetal brain mRNA (Invitrogen).

			2775 2778-2783 2788-2794 2796 2798-2800 2810-
			2817 2823-2838 2842-2848 2853-2855 2875-2878
			2889-2893 2915 2948-2950 2953-2959 2974-2979
			3018-3025 3036-3043 3054-3057 3066 3075-3078
			3080-3091 3095-3105 3108-3110 3122-3133 3137-
			3141 3149-3150 3161-3173 3175-3179 3217 3253-
			3258 3270-3273 3276-3284 3287-3289 3324-3332
			3334-3344 3349-3356 3373-3379 3399 3410-3415
			3419-3421 3424 3438-3449 3454 3475-3476 3479-
			3488 3491-3493 3497 3500-3503 3512-3516 3528-
			3530 3540-3543 3551-3560 3566-3567 3588-3590
			3605 3612-3615 3629-3630 3633 3638 3644-3645
			3653-3655 3660-3663 3669-3679 3687-3692 3705
			3710-3713 3717-3722 3724-3728 3730 3733-3739
			3767-3770 3788-3789 3798-3801 3850-3854 3866-
			3867 3883-3884 3888-3891 3896 3927-3936 3958-
			3960 3964-3968 4012-4018 4027-4044 4048-4051
			4054 4061-4062 4067-4073 4082-4088 4107-4109
			4163 4165-4167 4173-4175 4182-4183 4203-4204
			4208 4225-4227 4263 4266 4269-4270 4286 4294-
			4297 4330-4333 4336-4337 4343 4353 4360 4366-
			4367 4369 4377 4386-4387 4391 4418 4420-4424
			4429 4436-4438 4441-4443 4445-4452 4484-4485
			4496 4504 4510-4511 4529-4537 4550 4553 4556-
			4558 4562 4606 4609 4614 4625 4636-4639 4644-
			4645 4653 4658-4660 4662 4671-4673 4688-4690
			4692 4710 4719 4721-4723 4729 4734 4738-4741
			4765-4767 4771-4772 4779 4790 4804 4828 4841-
			4842 4848-4850 4873-4876 4882 4886-4888 4890-
			4891 4899 4901-4903 4905 4920-4921 4925-4926
			4934-4936 4940-4941 4949 4954 4957-4958 5005-
			5012 5015-5017 5019-5033 5039-5042 5050-5052
			5059-5060 5076-5079 5084-5097 5134 5138-5140
			5146 5148 5153-5154 5157 5159-5160 5184 5191-
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			5580-5581 5583-5584 5588 5590-5592 5594 5596-
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			5709 5713 5723-5729 5746-5747 5757-5758 5776-
			5777 5797 5809-5817 5823-5824 5853-5855 5875-
			5881 5920-5923 5932 5940-5941 5988-5992 5995-
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			6119-6120 6122-6127 6131 6165-6169 6174-6176
			6234 6236-6241 6267 6272 6297-6298 6301 6342-
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diaphragm	BioChain	DIA002	94 1206-1209 1311-1313 1357-1358 1402-1407 1561 1659 1870-1874 1950-1953 2156-2157 2262- 2264 2453 2493-2494 3740-3741 4484 5168-5173 5757-5758 7472 7953-7954
endothelial cells	Stratagene	EDT001	8-9 20-25 67 93 102-107 121 132-137 140-142 144-145 172-175 195-196 201-209 213-215 230 233-237 241-243 253-254 273-274 277-278 280- 284 296-297 304 345-349 371-374 397-398 403- 407 416-418 432-433 449 459-464 513 517 527- 531 546-551 580-581 597-598 633-634 641-645 650-651 656-658 661-665 720-721 733-735 757- 760 765 767 779-780 806-807 831-833 857-859 868-871 877-878 887-891 923-927 937-942 974 1005-1007 1016 1019 1022-1023 1033-1038 1044- 1046 1050 1070-1071 1151-1152 1160-1161 1172- 1176 1194-1196 1206-1209 1213-1221 1227-1247 1249-1253 1261-1263 1287-1302 1306-1308 1311- 1313 1316-1317 1324-1335 1339-1346 1348 1359- 1370 1374-1379 1391 1394-1414 1425-1431 1448- 1450 1453-1459 1465 1472-1487 1490-1491 1505- 1506 1511-1513 1525-1528 1531-1537 1540-1541 1549-1555 1557-1570 1572-1577 1579-1580 1583- 1585 1592-1595 1600-1602 1607-1608 1610 1616- 1617 1619-1620 1622-1628 1630-1634 1637-1642 1653-1658 1671-1674 1679 1691-1692 1698-1700 1702-1710 1712-1713 1716 1718 1726-1728 1759- 1760 1765-1767 1779-1795 1798-1800 1805 1809- 1810 1813-1815 1817-1818 1820-1821 1824-1825 1849-1851 1854-1856 1861-1869 1881-1882 1885- 1889 1894-1896 1907-1913 1916 1921-1927 1930- 1932 1934-1935 1937-1946 1950-1953 1955-1963 1967-1968 1970-1971 1980-1984 1986-1994 1998- 1999 2001-2008 2016-2019 2032-2044 2046-2052 2061 2063-2075 2077-2082 2087-2094 2103-2107 2112 2114-2121 2128 2131-2136 2138-2142 2147- 2154 2156-2157 2165-2175 2182-2183 2185-2194 2199-2200 2209-2217 2229-2230 2237-2239 2241- 2242 2249-2250 2255-2257 2262-2264 2266-2275 2282-2283 2285 2297-2299 2302-2306 2315-2322 2324-2327 2329-2349 2353-2358 2365-2366 2368- 2372 2381 2385-2386 2388-2390 2392-2397 2408- 2415 2417-2419 2428-2429 2433-2434 2445-2453 2458-2461 2468 2470 2482-2488 2493-2494 2509-

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Genomic clones from the short arm of chromosome 8	DNA from Genetic Research	EPM001	565-575 3188-3214 3942-3945 4456-4479 4854-4872
Genomic clones from the short arm of chromosome 8	DNA from Genetic Research	EPM003	3188-3214 3942-3945 4456-4479 4563-4564 4854-4872
Genomic clones from the short arm of chromosome 8	DNA from Genetic Research	EPM004	565-575 3188-3214 3942-3945 4456-4479 4563-4564 4854-4872 6712 7707
esophagus	BioChain	ESO002	144-145 973 1022-1023 1033-1035 1148-1149 1579-1580 2059-2060 2063 3163-3164 4490 6552-6554 6703-6704 7953-7954 8430-8432
fetal brain	Clontech	FBR001	264-265 386 656-658 1160-1161 1300-1302 2064-2066 2148-2152 2353-2357 2369 2389-2390 2442-2444 2656-2657 2689-2691 2731 2814-2815 2960-2962 3080-3085 3137 3227-3228 3639-3640 3840 3876-3877 3969-3970 4015-4018 4035-4040 4061-

			4062 4101 4263 4508-4509 4648-4652 4662 4806-4809 4917-4918 4954 5244-5245 5255 5686 5757-5758 5777 6452-6453 7416-7417 7626-7629 8227-8229 8413
fetal brain	Clontech	FBR004	272 280-282 992-994 1033-1035 1048 1610 1820-1821 1972 2062 2315-2322 2612-2615 2681 2711 2810-2811 2821-2822 2905-2907 3095-3096 3262-3269 3280-3284 3375 3410 3430 3620-3622 3729 3886-3887 3950-3955 4498-4501 4629-4634 4830-4835 4848-4850 4873-4876 4962-4967 5413-5414 5428 5721 5731-5735 6406 7357-7359 7794-7796 7837 8430-8432
fetal brain	Clontech	FBR006	8-19 22-25 30 67 77-79 93 105 113 143 150-151 180-183 193-194 279 286-289 294-295 362-363 366-369 384-385 402 430-431 439-440 480-482 488-490 517 527-529 534-535 580-581 583 586-587 688 692 828-829 880 899 934-935 941-947 982-985 992-994 1011-1012 1148-1149 1162 1190-1191 1206-1209 1227-1243 1311-1313 1334-1335 1339-1340 1359-1367 1396-1398 1402-1407 1413-1414 1455-1462 1490-1491 1498-1500 1511-1515 1518-1520 1525-1528 1531-1537 1558-1567 1579-1580 1592-1595 1607-1608 1616-1617 1622-1623 1636-1641 1671-1672 1680-1692 1702-1710 1781-1783 1813-1815 1820-1821 1823-1825 1835-1840 1844-1849 1857-1869 1876 1896 1912 1944-1945 1950-1953 1958-1963 1970-1971 2016-2017 2020-2027 2050-2060 2071-2073 2087-2094 2103-2107 2114-2119 2124-2126 2128 2137-2141 2156-2157 2165-2170 2174-2175 2204-2207 2209-2217 2223-2224 2262-2264 2315-2322 2324-2327 2379 2385-2386 2389-2390 2420-2423 2430-2432 2442-2444 2454 2493-2494 2509-2511 2551-2553 2558 2574-2580 2585-2588 2597 2625 2630-2633 2636 2644-2647 2651-2652 2656-2660 2722-2724 2739-2742 2744-2747 2776-2783 2796 2821-2822 2842-2848 2850-2851 2857-2859 2868-2878 2889-2893 2931-2934 2960-2962 3018-3023 3029-3031 3034-3035 3037-3039 3045-3048 3058-3063 3086-3087 3102-3105 3108-3111 3122-3133 3142-3147 3161-3162 3165-3172 3221-3228 3250 3276-3278 3280-3284 3287-3289 3305-3307 3346-3352 3355-3356 3358 3386-3389 3425-3428 3438-3449 3481-3485 3517-3519 3528-3530 3540-3543 3548-3550 3555-3559 3564-3565 3568-3569 3605-3610 3620-3622 3639-3640 3656-3657 3678-3679 3683-3686 3693-3695 3699-3701 3707-3709 3743-3759 3779-3780 3788-3789 3798-3801 3804-3805 3841-3849 3855-3857 3876-3877 3892-3893 3904-3909 3931-3936 3950-3955 3958-3960 3983-3987 4001-4008 4015-4018 4020-4026 4035-4040 4047-4051 4061-4062 4067-4072 4074-4079 4102-4109 4128-4129 4166 4170-4171 4177 4180-4181 4203-4204 4252 4271 4288 4361-4362 4369 4382-4384 4397 4436-4438 4514-4518 4520-4528 4536-4537 4559 4607-4608 4617 4629-4634 4662 4702 4705 4729 4738-4741 4773 4806-4809 4817 4830-4835 4873-4876 4917-

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fetal brain	Clontech	FBR503	2123 2358 2636 3560 3990 4804 6008 6957 8021 8031-8033 8430-8432
fetal brain	Invitrogen	FBT002	104 119 143-145 230 298-299 330-340 366-370 390-394 469-473 499-500 518-523 527-529 559- 560 650-651 688 712-713 716-717 720-721 733- 734 748-750 756 781-784 786-787 879 918 949- 951 989 1033-1035 1054 1062-1066 1160-1161 1190-1191 1213-1215 1244-1245 1290-1293 1311- 1313 1334-1335 1347 1359-1368 1448-1450 1465 1501-1502 1558-1560 1562-1570 1583-1585 1607- 1608 1691-1692 1768-1769 1781-1785 1791-1795 1813-1815 1839-1840 1912 1916 1921 1930-1932 1944-1945 1958-1961 1970-1971 2016-2017 2032- 2035 2038-2044 2059-2060 2067 2103-2110 2120- 2121 2137-2141 2165-2170 2190-2191 2209-2217 2223-2224 2268-2271 2276-2280 2282-2283 2307- 2322 2328 2334 2337-2340 2353-2357 2365-2366 2374 2389-2390 2392-2403 2436-2438 2440-2441 2476-2477 2480 2487-2488 2502-2508 2512-2513 2549-2550 2559-2565 2572 2583-2586 2630-2633 2636-2641 2648-2650 2655 2658-2660 2671 2682- 2683 2711 2713-2715 2739-2742 2776-2777 2795 2823-2825 2842-2848 2850-2851 2857-2859 2874- 2878 2881-2883 2902 2913-2914 2935-2939 2948- 2950 2960-2971 3026-3031 3037-3039 3058-3063 3080-3085 3097-3105 3108-3111 3165-3172 3183 3221-3226 3253-3258 3306-3307 3319-3323 3383 3386-3389 3399 3425-3428 3497 3522-3523 3555- 3557 3595-3596 3605 3620-3622 3631-3632 3637 3644-3645 3667-3672 3699-3701 3704 3723 3730 3779-3780 3782-3784 3794-3795 3798-3801 3841- 3849 3878-3880 3886-3887 3896 3901-3903 3922- 3923 3926 3938-3941 3950-3955 3983-3987 4015- 4018 4022-4040 4048-4051 4074-4079 4102-4106 4128-4129 4173 4229 4264 4271 4294-4295 4298- 4322 4341 4415-4417 4422-4424 4436-4438 4484 4505-4506 4529-4535 4544-4546 4556-4558 4662 4666-4667 4706-4709 4721-4727 4752 4768-4769 4827 4873-4876 4910-4916 4927-4929 4957-4958

10723

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fetal heart	Invitrogen	FHR001	94 499-500 1206-1209 1246-1247 1841-1842 1930-1932 2074-2075 2185 2268-2271 2315-2322 2636 3138-3141 3454 3560 3986-3987 4429 5236- 5240 5845-5847 6552-6554 7953-7954 8277-8279 8397-8398
fetal kidney	Clontech	FKD001	14-21 77-79 106-107 144-145 228-230 233-237 264-265 288-289 301 360 384-385 389 407 416- 418 468 537 559-560 601-602 641-644 785 795- 801 809 921 962-966 1005-1007 1064-1065 1070- 1071 1177-1180 1206-1209 1227-1243 1246-1247 1286 1311-1313 1368-1370 1415-1420 1439-1441 1445 1448-1450 1465-1470 1478-1480 1488-1489 1511-1515 1525-1528 1557-1561 1610 1675 1712- 1713 1716 1813-1815 1824-1825 1849 1870-1874 1896 1903 1916 1944-1945 1950-1954 1962-1963 2050-2052 2074-2075 2081 2138-2141 2158-2162 2165-2170 2223-2224 2243 2315-2322 2353-2357 2368-2372 2388 2420-2423 2428-2429 2487-2488 2509-2510 2513 2592-2596 2625 2716-2719 2744- 2747 2814-2815 2850-2851 2953-2959 3033-3036 3040-3042 3066 3108-3110 3133 3138-3141 3217 3253-3258 3279 3287-3289 3376-3379 3412-3413 3425-3428 3497 3560 3602-3605 3633 3678-3679 3683-3686 3696-3697 3699-3701 3722 3728 3743- 3747 3920-3921 3931-3936 3986-3987 4041-4042 4048-4051 4057 4061-4062 4167 4177 4253-4255 4266 4272-4273 4369 4395-4396 4422-4424 4445- 4447 4498-4501 4504 4520-4528 4538 4628 4644- 4645 4657 4692 4710 4731 4753-4755 4828 4837- 4838 4890 4930-4933 4991-4992 5022-5028 5150 5180-5184 5247 5280-5282 5376 5422 5517-5518 5526-5545 5630 5633 5673 5723-5729 5848 5853- 5855 5987-5992 6008 6058-6060 6069-6073 6084 6177 6179 6196 6234 6334 6361-6363 6406 6662 6665-6668 6703-6704 6738 6742 6799-6804 6871

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fetal kidney	Clontech	FKD002	144-145 212 1022-1023 1297-1299 1357-1358 1394-1398 1455-1459 1511-1513 1637-1641 1896 2003-2004 2018-2019 2038-2044 2074-2075 2223-2224 2382-2384 2778-2783 2823-2825 3138-3141 3287-3289 5920-5921 6464-6466 8031-8033 8075-8076 8430-8432
fetal kidney	Invitrogen	FKD007	14-19 264-265 384-385 549-551 982-983 1003 1022-1023 1038 1216-1221 1297-1299 1460-1462 1619-1620 1881-1882 2074-2075 2112 2511 2816 2823-2825 3066 3249 3274-3275 3400-3401 3605 3738-3739 3779-3780 4061-4062 4498-4501 5413-5414 5757-5758 5999-6000 6359-6360 7396 7662-7666
fetal lung	Clontech	FLG001	499-500 650-651 681-683 960-961 992-994 1033-1035 1311-1313 1557 1571 1619-1620 1671-1672 1921-1927 1944-1945 2003-2004 2302-2305 2329-2331 2408-2415 2454 2637-2641 2658-2660 2665-2667 2731 2814-2815 2856 2953-2959 2978-2979 3049-3053 3138-3141 3161-3162 3165-3172 3215-3216 3290-3292 3346-3348 3588-3590 3612-3616 3660-3663 3722 3931-3936 4042 4177 4269-4270 4395-4396 4422-4424 4445-4447 4648-4652 5015-5017 5155 5264 5377 5479-5482 5526-5545 5594 5631 5723-5729 5764 5798-5805 5825-5828 6285 6427-6431 6440 6663-6664 7152-7153 7246 7398 7672-7675 7953-7954 8022 8075-8076 8086-8087 8459
fetal lung	Invitrogen	FLG003	91 140-142 250-251 266-268 345-349 384-385 467 495 499-500 786-787 1014 1181 1213-1215 1286 1290-1293 1306-1308 1314-1315 1334-1335 1394-1395 1505-1506 1610 1612-1615 1659-1669 1702-1710 1784-1785 1823 1831 1839-1840 1891-1893 1921 1946 1958-1961 1980-1984 2020-2027 2112 2124-2126 2147 2192-2194 2315-2322 2353-2357 2362-2364 2368 2420-2423 2512 2551-2553 2585-2586 2603-2609 2642-2643 2704-2710 2720 2725-2727 2794 2913-2915 2953-2959 2978-2979 3054-3063 3065 3073-3074 3137 3217 3274-3278 3290-3292 3313-3314 3349-3352 3560 3605 3631-3633 3660-3663 3683-3686 3722 3743-3747 3926 3983-3989 4027-4034 4048-4051 4092-4095 4102-4106 4157-4162 4294-4295 4385 4395-4396 4436-4438 4520-4528 4563-4564 4672-4673 4693-4694 4724-4727 4738-4741 4851-4853 4873-4876 4929 4950-4953 5022-5028 5043-5049 5063-5072 5076-5079 5084-5097 5139-5140 5224 5264 5288 5452-5459 5506 5554-5558 5561 5714 5723-5729 5746-5753 5798-5805 5856-5863 5956-5960 5993-5994 6001-6002 6065-6068 6195 6603-6606 6653-6660 6757-6758 6766-6767 6910 7054 7144-7146 7152-7153 7191 7224 7550 7595-7596 7607 7625 7662-7666 7679 7698-7700 7723-7727 7770-7772 7805

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fetal lung	Clontech	FLG004	1244-1245 1439-1441 1511-1513 2003-2004 2112 2324-2327 2382-2384 2502-2508 2636 3623-3628 4203-4204 7799-7800
fetal liver- spleen	Soares	FLS001	1-9 14-19 22-25 29-37 48 55 57-79 100-101 104-107 113-115 118-122 131-137 140-145 157- 159 172-175 180-183 191 195 201-209 213-215 238 253-254 262-270 275-278 280-282 296-299 307-320 351-352 375-382 384-385 407 414-425 439-445 451 454-455 460-464 466 468-473 475 483-486 488-495 499-502 504-512 515-517 524- 531 546-551 576-579 582-583 597-607 610-613 615 623-630 641-645 656-658 661-666 668 671- 675 681-683 685-686 696 698 709 712-715 718 720-721 726-727 730-734 736-737 755 757-758 764 769 786-801 814-821 831-833 836-840 842- 861 863-873 875-876 905-912 917-920 923-927 941-942 948 960-966 974 976-977 992-994 1003 1005-1008 1020-1024 1032 1038 1041-1046 1064- 1065 1070-1105 1107-1111 1150 1160-1161 1181- 1187 1194-1196 1200-1210 1213-1224 1227-1247 1249-1263 1273-1279 1286-1293 1297-1313 1316- 1317 1324-1335 1337-1355 1357-1370 1374-1377 1380-1390 1394-1420 1424 1439-1445 1448-1450 1455-1462 1465-1494 1498-1517 1525-1537 1540- 1570 1575-1580 1583-1599 1602-1608 1610-1620 1624-1628 1630-1632 1637-1644 1653-1659 1671- 1672 1678-1679 1698-1700 1702-1714 1718-1721 1725-1730 1759-1778 1780-1789 1791-1795 1798- 1805 1809-1810 1813-1815 1817-1819 1823-1825 1827-1830 1839-1840 1844-1852 1854-1863 1870- 1874 1876-1877 1879-1880 1885-1890 1894-1896 1904-1905 1907-1913 1916-1927 1930-1932 1934- 1942 1944-1968 1973 1980-1984 1986-1991 1997- 2004 2016-2019 2030-2031 2036-2037 2045 2050- 2052 2062-2075 2077-2078 2081-2086 2095-2097 2103-2110 2112 2114-2122 2124-2126 2129-2137 2143-2146 2153-2154 2156-2175 2186-2189 2199- 2203 2208 2222-2224 2226-2227 2237-2239 2241- 2242 2244-2251 2255-2264 2266-2280 2285-2288 2291-2294 2297-2305 2307-2322 2324-2327 2337- 2346 2350-2358 2361-2364 2368 2370-2374 2379 2381-2387 2389-2390 2398-2403 2407 2417-2423 2428-2434 2436-2438 2442-2451 2453-2454 2458- 2463 2468-2470 2473 2476-2477 2482-2486 2489- 2490 2492-2494 2502-2511 2514-2521 2526-2556 2558-2560 2567-2568 2574-2580 2583-2588 2592- 2596 2603-2609 2616-2617 2625-2633 2636-2641 2651-2652 2656-2660 2665-2667 2671 2682-2683 2704-2711 2720-2727 2731-2742 2744-2749 2757 2776-2786 2788-2794 2796 2799-2800 2806 2812- 2819 2826-2838 2842-2848 2850-2851 2853-2863 2866-2879 2881-2888 2902 2904 2918-2946 2948- 2950 2960-2962 2974-2979 3014-3023 3034-3066 3071 3080-3091 3095-3096 3102-3105 3108-3114

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fetal liver-	Soares	FLS003	499-500 786-787 793-794 855-856 1003 1022- 1023 1200-1205 1249-1253 1277-1279 1349-1355

spleen			1516-1517 1784-1785 1870-1874 2315-2322 3065 3217 3507 3623-3628 3730 4070-4072 4395-4396 4484 4486 5022-5028 5107-5109 7108-7110 7797 8469-8479
fetal liver	Invitrogen	FLV001	3-5 20-21 105 140-142 191 210-211 230 280-282 345-349 419-424 479 488-490 499-500 527-529 583 625-626 656-658 712-715 733-734 765 786- 787 793-794 831-833 905-908 918 945-947 989 1003 1044-1046 1070-1071 1200-1205 1213-1221 1244-1245 1261-1263 1273-1279 1286-1293 1311- 1313 1337-1338 1348-1355 1359-1368 1424 1437- 1438 1442-1444 1455-1462 1498-1502 1542-1548 1561 1568-1570 1572-1574 1603-1608 1619-1620 1630-1632 1658-1659 1673-1674 1691-1692 1702- 1710 1759-1760 1764-1767 1780-1785 1791-1795 1813-1815 1839-1840 1861-1863 1890 1907-1912 1921 1930-1932 1944-1945 1955-1961 1970-1971 1995-1996 2059-2060 2120-2121 2124-2126 2137- 2141 2147 2156-2162 2220 2262-2264 2300-2301 2307-2322 2340 2365-2366 2468 2502-2510 2534- 2535 2538-2542 2549-2550 2574-2580 2587-2588 2651-2652 2658-2660 2698-2703 2711 2725-2727 2842-2848 2850-2851 2868-2873 2881-2883 2902 2913-2914 2918-2930 3037-3039 3043 3054-3057 3065 3108-3110 3115-3116 3217-3219 3305-3307 3313-3323 3346-3352 3358 3395-3397 3399 3410 3419-3422 3454 3522-3523 3605 3660-3663 3722 3742 3926 3942-3945 3961 3986-3987 3991-3998 4047 4082-4085 4102-4106 4122-4126 4209 4242- 4245 4293 4366-4367 4378-4380 4395-4396 4429 4480-4483 4486 4547-4549 4556-4558 4674 4676 4764 5019-5028 5034-5035 5065-5072 5076-5079 5098-5100 5107-5109 5153-5154 5241-5243 5351 5364 5393-5395 5416 5431-5437 5443-5445 5554- 5558 5585 5616-5617 5687-5690 5694-5695 5723- 5729 5748-5753 5780-5782 5856-5863 5882-5885 5940-5941 6003-6005 6044-6045 6051-6056 6058- 6060 6069-6073 6117-6120 6236-6241 6353-6355 6485 6508-6509 6548-6549 6718-6721 6742 6766- 6767 6805-6807 6872-6874 6909 6958-6959 7050- 7053 7080-7082 7086-7087 7151 7159-7160 7188- 7191 7205-7206 7231-7233 7373 7375 7418-7419 7465-7468 7474 7568 7570-7573 7615-7616 7658 7662-7666 7670 7672-7675 7698-7700 7748 7753- 7754 7799-7800 7867-7868 7929 7972-7973 8046- 8048 8077 8110-8113 8115-8116 8187-8188 8397- 8398 8418-8419 8430-8432 8457-8458 8466 8490- 8495
fetal liver	Clontech	FLV002	14-19 26-28 384-385 1796-1797 3334-3344 4063- 4064 4498-4501 4778
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fetal skin	Invitrogen	FSK002	144-145 260 283-284 307-320 330-340 351-352 407 425 552-555 580-581 909-912 1016 1110- 1111 1148-1149 1177-1178 1185-1186 1334-1335 1347 1369-1370 1488-1489 1505-1506 1659 1702- 1710 1781-1783 1854-1856 1870-1874 1894-1896 1916 1930-1932 2138-2141 2174-2175 2341-2343 2417-2419 2502-2508 2543 2558 2603-2609 2636 2658-2660 2665-2667 2682-2683 2698-2703 2801- 2804 2850-2851 2857-2859 2889-2893 2931-2934 2978-2979 3014-3016 3071 3138-3141 3165-3172 3250 3412-3413 3507 3728 3733-3739 3748-3752 3788-3789 3841-3849 3861-3865 3938-3941 3956 3988-3989 4009-4011 4020-4021 4048-4051 4080- 4081 4266 4629-4634 4783 4840-4842 4873-4876 4955 4957-4958 5236-5240 5448-5459 5621-5622 5687-5690 5714 5757-5758 5964-5966 6069-6073 6179 6182-6191 6455 6743-6744 6911-6915 7001- 7004 7432 7474 7570-7573 7720-7721 7955-7957 8031-8033 8414-8416 8459
fetal spleen	BioChain	FSP001	546-548 625-626 790-792 920 1022-1023 1357- 1358 1415-1420 1455-1459 1511-1513 1549-1551 1602 1679 1896 2003-2004 2223-2224 2453 3115- 3116 3163-3164 3274-3275 5416 6923-6924 7446 8430-8432
umbilical cord	BioChain	FUC001	3-5 14-19 26-28 42-43 48 93 105 114-115 128 140-142 144-145 164-169 193-194 196 213-215 221-222 296-297 307-320 355 370-372 387 416- 418 456-458 460-462 488-495 499-500 515-516 527-531 533 537 541-542 549-551 556 579 583 588-591 597-598 650-651 714-715 735 757-758 786-787 793-801 803-804 855-856 860-861 949- 951 1003 1022-1023 1033-1035 1064-1065 1110- 1111 1160-1161 1175-1176 1200-1209 1213-1215 1227-1247 1286-1289 1300-1302 1306-1308 1311- 1313 1337-1340 1354-1355 1359-1368 1374-1390 1408-1409 1424-1431 1439-1441 1465 1478-1480

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Induced neuron cells	Stratagene	NTD001	201-209 272 386 650-651 803-804 809 948 1033- 1035 1227-1247 1287-1289 1311-1313 1380-1390 1396-1398 1514-1515 1525-1528 1561 1568-1570 1652 1718 1798-1800 1813-1815 1854-1856 1912 1950-1953 1967 2003-2004 2030-2031 2223-2224 2255-2257 2341-2343 2353-2357 2385-2386 2482- 2488 2561-2565 2603-2609 2656-2657 2671 2732- 2742 2794 2798 2812-2813 2935-2939 2953-2962 2974-2977 3014-3016 3036-3039 3138-3141 3152- 3155 3253-3258 3262-3269 3274-3275 3279 3290- 3292 3296-3297 3425-3428 3497 3521 3548-3550 3560 3566-3567 3595-3596 3602-3605 3673-3674 3728 3733-3737 3779-3780 3804-3805 3888-3891 3958-3960 3986-3987 4001-4008 4043 4061-4062 4070-4072 4080-4081 4101-4106 4177 4292 4329 4484 4553 4827 4892-4898 4909 4922 4929 4950- 4953 5019-5021 5177-5179 5208 5244-5245 5315 5352-5355 5441-5442 5446-5447 5475-5478 5521- 5522 5559-5560 5664-5667 5683 5691 5705-5709 5999-6000 6119-6120 6279 6382 6385-6388 6443- 6444 6455 6464-6466 6588-6595 6695-6696 6785 6799-6804 6861 6946-6948 6950 6957 7014-7027 7045 7104 7152-7153 7162-7165 7377-7384 7439 7580 7735-7737 7809 7823 7989 8031-8033 8277- 8279 8413 8430-8432
Retinoid acid induced neuronal cells	Stratagene	NTR001	144-145 1005-1007 1022-1023 1160-1161 1246- 1247 1300-1302 1399-1407 1448-1450 1518-1520 1619-1620 1784-1785 1894-1895 1912 2018-2019 2095-2097 2120-2121 2223-2224 2262-2264 2315- 2322 2732-2738 2794 3133 3274-3275 5032-5033 5080-5081 5634 5673 6119-6120 7955-7957 8397- 8398 8430-8432
neuronal cells	Stratagene	NTU001	85 144-145 288-289 383 402 432-433 468 638- 639 650-651 803-804 836-838 934-935 970 1022- 1023 1064-1065 1072-1106 1246-1247 1316-1317 1341-1346 1455-1459 1466-1470 1511-1513 1540- 1548 1561 1619-1620 1637-1641 1658 1712-1713 1768-1769 1781-1785 1798-1800 1813-1815 1839- 1840 1850-1851 1861-1863 1894-1895 1897-1900 1907-1911 1930-1932 1950-1953 1955-1957 1964- 1967 2003-2004 2074-2075 2079 2103-2107 2192- 2194 2209-2217 2223-2224 2262-2264 2266-2267 2307-2322 2398-2403 2417-2419 2502-2508 2522- 2525 2536-2537 2549-2550 2567-2568 2658-2660 2698-2703 2796 2810-2811 2842-2848 2908-2911 2980-3013 3049-3053 3071 3080-3085 3108-3110

			3137 3165-3172 3274-3275 3279 3306-3307 3334-3344 3346-3348 3353-3354 3491-3493 3508-3511 3522-3524 3558-3559 3605 3699-3701 3723 3730 3802-3803 3871-3875 3892-3893 3946-3949 3958-3960 4048-4051 4057 4242-4245 4266 4547-4549 4565 4573-4602 4854-4872 4950-4953 4957-4958 5073-5075 5226-5227 5250-5254 5438-5440 5446-5447 5621-5622 5631 5634 5851-5852 5932 5964-5966 6203 6383-6384 6443-6444 6517-6518 6718-6721 6799-6804 6911-6915 6926 6941-6943 6950 6957 7303-7304 7310-7311 7570-7573 7743 7907 8031-8033 8151-8152 8159-8160 8163-8166 8397-8398 8408 8430-8432 8466
pituitary gland	Clontech	PIT004	26-28 106-107 416-418 454-455 786-787 992-994 1297-1299 1354-1355 1425-1431 1481-1484 1568-1570 1602 1619-1620 1922-1927 2003-2004 2112 2148-2152 2171-2173 2208 2241-2242 2266-2267 2511 2526-2528 2592-2596 2656-2657 2665-2667 2722-2724 2732-2738 2806 2918-2930 2940-2946 2978-2979 3037-3039 3165-3172 3274-3275 3279 3454 3477-3478 3486-3488 3497 3551-3553 3560 3605 3722 4015-4018 4043 4102-4106 4166 4353 4422-4424 4445-4447 4484-4485 4662 4699 4721-4723 4806-4809 4839 4908 4928 4957-4958 4972-4976 5301 5351 5448-5459 5523 5559-5560 5562-5563 5594 5988-5992 5998 6057 6282-6284 6305-6307 6489 6766-6767 6776-6779 6896 6943 6977-6978 7561 7747 8413 8488-8489
placenta	Clontech	PLA003	1185-1186 1261-1263 1357-1358 1511-1513 1784-1785 2074-2075 3054-3057 3138-3141 3904 3971-3982 4662 5022-5028 5241-5243 6464-6466 6634-6638 7068-7078 7188-7190 8430-8432
prostate	Clontech	PRT001	94 121 195 221-222 253-254 355 441 534-535 640 748-750 830 887-891 952 982-983 992-994 1033-1035 1193 1246-1247 1261-1263 1297-1299 1378-1379 1394-1395 1402-1407 1415-1420 1465 1481-1484 1525-1528 1538-1541 1549-1551 1561 1575-1577 1592-1595 1600-1602 1610 1624-1625 1658 1675 1680-1690 1813-1815 1849 1864-1869 1912 1930-1932 1962-1963 1980-1984 1986-1994 2003-2004 2036 2050-2052 2063 2112 2114-2119 2137 2165-2173 2268-2271 2315-2322 2324-2327 2341-2343 2370-2372 2375-2378 2388 2407 2430-2432 2455 2493-2501 2509-2511 2559-2565 2589-2590 2619-2622 2630-2633 2689-2691 2722-2727 2732-2738 2744-2747 2776-2783 2794 2810-2811 2835 2850-2851 2856 2867 2884-2888 2908-2911 2948-2950 3017-3023 3049-3053 3065-3066 3072 3134-3136 3149-3150 3227-3228 3274-3275 3279 3287-3289 3313-3314 3346-3352 3371-3372 3384-3385 3399 3411 3416-3418 3454 3469-3470 3473-3476 3481-3485 3507-3511 3631-3632 3673-3674 3678-3679 3722 3724-3726 3730 3765-3766 3788-3789 3869-3870 3892-3893 3904 3931-3936 4042 4061-4062 4174-4176 4216-4217 4246 4248 4255 4331-4333 4366-4367 4422-4424 4441-4443 4508-

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rectum	Invitrogen	REC001	253-254 264-265 416-418 459 469-473 580-581 736-737 775 1033-1035 1110-1111 1244-1245 1261-1263 1300-1304 1359-1367 1374-1391 1439- 1444 1446-1450 1465 1481-1484 1518-1520 1542- 1548 1571-1574 1626-1628 1691-1692 1694 1765- 1767 1781-1783 1831 1835-1838 1912 1921 1936 1972 1985 1998-1999 2063-2066 2068-2070 2158- 2162 2282-2283 2407 2436-2438 2511 2513 2522- 2525 2551-2553 2559-2560 2585-2588 2603-2609 2623 2630-2633 2636-2643 2658-2660 2672-2678 2692-2696 2731 2796 2812-2813 2820 2842-2848 2850-2851 2915 2948-2950 2953-2959 2974-2977 3049-3053 3066 3080-3085 3115-3116 3313-3314 3346-3348 3410 3454 3555-3557 3566-3567 3597- 3599 3605 3623-3628 3633 3641 3705 3717-3722 3740-3741 3798-3801 3888-3891 3904 3926 3931- 3936 4020-4021 4102-4106 4180-4181 4254 4331- 4333 4336 4388 4394 4498-4501 4556-4558 4648- 4652 4706-4709 4738-4741 4845-4846 4873-4877 4907 4957-4958 4962-4967 5111 5236-5243 5280- 5282 5297 5306 5343 5356-5358 5366 5402-5403 5406-5408 5435-5437 5452-5459 5475-5478 5504- 5505 5561 5621-5622 5673 5697-5701 5714 5723- 5729 5748-5753 5869 5882-5885 5971-5980 5988- 5992 6013 6198 6203 6244 6476-6479 6489 6613- 6615 6653-6660 6688-6689 6703-6704 6766-6767 6960-6961 6997-6998 7001-7002 7086-7087 7098 7251-7254 7310-7311 7321 7398 7424-7425 7496 7532-7537 7676-7677 7907 7914-7915 7923 8102- 8109 8185 8309-8312 8383-8385 8455-8456
salivary gland	Clontech	SAL001	10-13 55 105 144-145 172-175 272 283-284 307- 320 342-344 416-418 468 527-531 539 748-750 881-882 945-947 1160-1161 1163-1165 1213-1215 1227-1243 1261-1263 1300-1302 1305-1308 1311- 1313 1316-1323 1439-1441 1446-1447 1472-1477 1505-1506 1511-1513 1561 1602 1616-1617 1659 1694 1779 1784-1785 1801-1804 1813-1815 1958- 1961 1968 1985 1997 2028 2071-2073 2083-2085 2112 2148-2154 2156-2157 2220 2266-2267 2291- 2294 2307-2322 2385-2387 2420-2423 2453 2603- 2609 2626-2629 2651-2654 2682-2683 2731 2794 2796 2826-2834 2842-2848 2875-2878 2913-2914 2948-2950 2978-2979 3065 3163-3172 3280-3284 3287-3292 3425-3428 3469-3470 3473-3474 3479-

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			3480 3487-3488 3497 3522-3523 3528-3530 3560 3605 3612-3615 3623-3628 3722 3761-3764 3788- 3789 3791 3958-3960 3986-3987 3991-3998 4042 4061-4062 4110-4118 4128-4129 4264 4331-4333 4356-4359 4361-4362 4480-4484 4498-4501 4561 4573-4602 4629-4634 4731 4765-4767 4936 4943 4972-4976 5129-5130 5139-5140 5185 5290-5292 5441-5442 5523 5588 5614-5615 5624-5626 5631 5678-5679 5694-5695 5697 5757-5758 5851-5852 5949 6023-6024 6117-6120 6178 6285 6309-6311 6326-6333 6359-6360 6456-6459 6464-6466 6560- 6562 6627-6628 6663-6664 6718-6721 6925 7044 7150 7181-7184 7276-7277 7551-7554 8102-8109 8133-8135 8157 8403-8404 8430-8432
saliva gland	Clontech	SALS03	343-344 740-741 822-827 1446-1447 1568-1570 1827-1830 2123 2315-2322 2974-2977 8031-8033
skin fibroblast	ATCC	SFB001	416-418 1841-1842 1896 2315-2322 2823-2825 3454 3560 3605 3678-3679 3983-3985 4203-4204 4349-4350 5425-5426 5466 6957 7014-7027
skin fibroblast	ATCC	SFB002	416-418 650-651 1540-1541 1791-1795 1841-1842 2005-2008 2279-2280 2315-2322 2567-2568 3319- 3323 3560 3983-3985 5032-5033 5280-5282 5425- 5426 5631 6957 7014-7027
skin fibroblast	ATCC	SFB003	144-145 1540-1541 1791-1795 2174-2175 2315- 2322 2953-2959 5425-5426 6703-6704 6957
small intestine	Clontech	SIN001	38 42-43 119 195 283-284 296-297 432-433 534- 535 546-548 645 698 712-713 735 960-969 1072- 1105 1439-1441 1446-1447 1466-1470 1478-1480 1511-1513 1540-1541 1571 1637-1641 1658 1671- 1672 1675 1680-1690 1694 1770-1773 1781-1783 1813-1815 1819 1827-1830 1839-1840 1844-1848 1854-1856 1906 1912 1922-1927 1962-1963 2018- 2019 2122 2196-2198 2243 2300-2301 2307-2314 2350-2352 2369 2379 2430-2432 2598-2601 2626- 2629 2636 2658-2660 2689-2691 2725-2728 2748- 2749 2799-2800 2842-2848 2879 2913-2914 2953- 2959 3066 3161-3162 3280-3284 3287-3289 3324- 3332 3410 3487-3488 3537-3539 3620-3622 3633 3683-3686 3707-3709 3738-3739 3782-3784 3796 3878-3879 3883-3884 3888-3891 3904 3966-3968 4097-4100 4163 4165 4242-4245 4353 4422-4424 4444 4484 4542 4550 4573-4602 4605 4648-4652 4662 4666-4667 4710 4735 4745-4749 4765-4767 4841-4842 4920-4921 4936 5123-5124 5174-5176 5191-5192 5200 5255 5351 5366 5392 5507-5512 5526-5529 5554-5558 5594 5599-5601 5664-5667 5698-5701 5891 5895 5981-5983 6069-6073 6087- 6090 6276-6278 6342 6378 6448 6491-6499 6596- 6597 6634-6638 6863-6867 6941-6942 7310-7311 7335 7343 7398 7423 7461 7483 7761 7770-7772 7780-7790 7845 7907 8035-8036 8102-8109 8353- 8354 8367-8368
skeletal muscle	Clontech	SKM001	94 144-145 172-175 390-394 447 495 973 1003 1160-1161 1206-1209 1227-1243 1300-1302 1309- 1310 1374-1377 1396-1398 1439-1441 1561 1583- 1585 1691-1692 1695-1696 1718 1805 1819-1821

10754

			1827-1830 1839-1842 1850-1851 1861-1863 1936 2079 2095-2097 2231-2233 2262-2264 2329-2331 2353-2357 2453 2470 2544-2548 2668 2682-2683 2704-2710 2744-2747 2796 2835 2842-2848 2963- 2971 3036 3122-3132 3165-3172 3346-3348 3373- 3374 3386-3389 3450-3452 3507 3644-3645 3678- 3679 3910-3919 3926 4015-4018 4221 4360-4362 4395-4396 4484 4502-4503 4505-4506 4551-4552 4873-4876 4944-4945 5098-5100 5162-5163 5236- 5240 5284-5285 5352-5355 5360 5546 5599-5600 5616-5617 5624-5626 5723-5729 5769 5845-5849 6272 6305-6307 6407-6411 6552-6554 6814-6816 6861 7181-7184 7281-7282 7324 7328 7428-7429 7625 7802-7804 7863 7953-7954 8157 8161 8194- 8196 8367-8368 8403-8404
skeletal muscle	Clontech	SKM002	447 1540-1541 1827-1830 1841-1842 1962-1963 2836-2838 3983-3985 4514-4518 7014-7027
skeletal muscle	Clontech	SKMS03	1540-1541 1827-1830 1841-1842 2836-2838 8194- 8196
skeletal muscle	Clontech	SKMS04	1827-1830 1841-1842 2143-2146 2836-2838 3560 5723-5729 7780-7790
spinal cord	Clontech	SPC001	3-9 106-107 109 112 140-142 144-145 193-194 201-209 241-243 269-270 294-299 321 350 375 380-382 390-394 430-431 475 515-516 549-551 562 596 603-606 608-609 650-651 718 765 786- 787 984-985 1005-1007 1033-1035 1048 1064- 1066 1072-1105 1110-1111 1160-1161 1175-1176 1227-1243 1246-1247 1261-1263 1290-1293 1305 1311-1313 1348 1354-1355 1368 1380-1390 1394- 1395 1410-1412 1439-1441 1465 1472-1480 1490- 1491 1505-1506 1511-1513 1540-1541 1552-1555 1557 1586-1591 1600-1601 1612-1615 1619-1620 1637-1641 1659 1678 1718 1726-1727 1817-1818 1870-1874 1876 1896 1903-1905 1912 1916 1921 1930-1932 1944-1945 1947-1948 1950-1953 1958- 1963 1980-1984 2016-2017 2020-2027 2062-2063 2074-2075 2079 2086 2148-2152 2190-2191 2262- 2264 2268-2271 2282-2283 2302-2305 2307-2322 2324-2327 2353-2357 2408-2415 2440-2441 2454 2478 2480 2487-2488 2559-2560 2567-2568 2592- 2596 2603-2611 2651-2652 2655-2660 2671 2684- 2688 2698-2711 2725-2727 2732-2738 2744-2747 2788-2794 2796 2810-2811 2816-2817 2823-2825 2842-2848 2856 2868-2873 2879 2881-2883 2905- 2907 2918-2930 2935-2939 2948-2950 2953-2959 2978-2979 3049-3053 3065 3071 3086-3087 3137 3149-3150 3152-3155 3165-3172 3221-3226 3250- 3252 3274-3284 3287-3289 3355-3356 3386-3389 3410 3425-3429 3455-3463 3475-3476 3481-3485 3487-3488 3497 3507-3511 3555-3557 3560 3602- 3610 3612-3615 3642-3643 3658-3659 3675-3677 3705 3722 3733-3739 3742 3765-3766 3776-3778 3782-3784 3868 3878-3880 3885 3897-3900 3904 3910-3919 3931-3936 3938-3941 3966-3968 3986- 3987 4001-4008 4027-4040 4042 4048-4051 4061- 4062 4065 4092-4095 4101-4106 4131 4142 4150

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adult spleen	Clontech	SPLc01	6-7 56 105 121 345-349 351-352 432-433 941- 942 1005-1007 1148-1149 1249-1253 1347 1357- 1358 1369-1370 1394-1395 1442-1444 1478-1480 1511-1513 1558-1560 1610 1630-1632 1671-1672 1702-1710 1726-1727 1786-1789 1817-1818 1839- 1840 1894-1896 1950-1953 1980-1984 2003-2004 2014-2015 2020-2027 2037 2068-2070 2204-2207 2382-2386 2407 2417-2419 2495-2499 2597 2689- 2691 2698-2703 2821-2822 2839-2841 2857-2859 2963-2971 3071 3115-3116 3138-3141 3157-3158 3221-3226 3477-3478 3554 3605 3717-3721 3866- 3867 3881-3882 3988-3989 4061-4062 4648-4652 4662 4680 4830-4835 4841-4842 4910-4916 5005- 5007 5032-5033 5118-5119 5168-5173 5500-5501 5580-5581 5590-5592 5723-5729 5797 5882-5885 5892-5893 5964-5966 6077 6123-6127 6165-6169 6276-6278 6464-6466 6473 6757-6758 6799-6804 7001-7002 7274-7275 7412-7414 7609-7611 7748 7780-7790 8102-8109 8306-8308 8430-8432
stomach	Clontech	STO001	121 195 228 245. 449 656-658 1024 1206-1209 1402-1407 1439-1441 1446-1447 1671-1672 1680- 1690 1693-1694 1801-1804 1809-1810 1813-1815 1824-1825 1844-1848 1896 1962-1963 2241-2242 2276-2278 2286-2288 2353-2357 2379 2428-2429 2445-2451 2458-2461 2636 2665-2667 2669-2670 2744-2747 2778-2783 2814-2815 2842-2848 2940- 2946 2948-2950 2963-2971 2974-2979 3095-3096 3287-3289 3298-3300 3305 3324-3332 3334-3344 3359-3360 3399 3416-3418 3422 3475-3476 3487- 3488 3522-3523 3537-3543 3629-3630 3675-3679 3724-3726 3748-3752 3869-3870 3986-3987 4027- 4034 4274-4275 4498-4501 4529-4535 4753-4755 4823-4824 4873-4876 4889 5054 5200 5226-5227 5250-5254 5306 5310 5352-5355 5425-5426 5554-

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Mixture of 16 tissues- mRNAs***	Various Vendors***	SUP002	384-385 546-548 1022-1023 1070-1071 1113-1117 2636 2656-2657 2731 3066 4014 4061-4062 4929 5416 5466 7003-7004 7470 7551-7554 7764-7765 7949-7951 8430-8432
Mixture of 16 tissues- mRNAs***	Various Vendors***	SUP005	305 365 384-385 726-727 757-758 786-787 811- 813 2534-2535 2570 2656-2657 2665-2667 2807- 2811 2823-2825 3095-3096 3115-3116 3753-3759 3983-3985 4266 4377 4395-4396 4949 5448-5451 5554-5558 5694-5695 5705-5709 6957-6959 7029- 7033 7780-7790 7949-7951 8031-8033 8397-8398 8430-8432 8469-8479
Mixture of 16 tissues- mRNAs***	Various Vendors***	SUP008	576-578 726-727 730-731 806-807 1110-1111 2538-2542 2585-2586 2636 2642-2643 2651-2652 2656-2657 2671 2810-2811 2857-2859 2935-2939 2978-2979 4102-4106 4847 4873-4876 5547-5552 5554-5558 7091 7465-7468 7773-7778 8031-8033 8329-8332 8430-8432 8490-8495
Mixture of 16 tissues- mRNAs***	Various Vendors***	SUP009	726-727 730-731 786-787 793-794 2534-2535 2567-2568 2636 2656-2657 2823-2825 2935-2939 3037-3039 3043 3064-3066 3133 4000 5521-5522 5554-5558 5631 6065-6068 6990-6992 7152-7153 7949-7951 8397-8398 8469-8479
thalamus	Clontech	THA002	14-19 67 90 180-183 283-284 612-613 716-717 719 831-833 945-947 1151-1152 1324-1335 1347 1354-1355 1402-1407 1439-1441 1455-1459 1490- 1491 1538-1539 1558-1560 1619-1620 1691-1692 1702-1710 1726-1727 1759-1760 1781-1783 1791- 1795 1864-1869 1890 1907-1912 1921 1970-1971 2020-2027 2068-2070 2112 2131-2136 2148-2154 2251 2255-2257 2268-2271 2282-2283 2332-2333 2344-2346 2353-2357 2435 2521 2574-2580 2585- 2586 2610-2611 2637-2641 2658-2660 2682-2683 2697 2711 2739-2742 2748-2749 2796 2850-2851 2868-2873 2875-2878 2905-2907 2913-2914 2935- 2939 3122-3132 3137-3141 3173 3221-3226 3276- 3278 3280-3284 3287-3289 3308-3310 3346-3348 3456-3463 3487-3488 3497-3499 3605 3612-3615 3644-3645 3667-3672 3705 3717-3721 3748-3752 3798-3801 3983-3985 4035-4040 4043 4048-4051 4082-4085 4176 4180-4181 4218 4252 4296-4322 4378-4380 4415-4417 4419 4422-4424 4435 4520- 4528 4539-4541 4646 4721-4723 4784 4793-4794

*** The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human adult esophagus mRNA (BioChain), 16) human fetal umbilical cord mRNA (BioChain).

			4804 4972-4976 5065-5072 5168-5173 5226-5227 5236-5240 5280-5282 5284-5285 5302-5305 5324- 5325 5393-5395 5452-5459 5515-5516 5719-5720 5723-5729 5829-5834 5841 5937-5938 6025-6026 6119-6120 6243 6274 6361-6362 6467-6472 6486- 6488 6911-6915 6954-6955 6967-6969 7001-7002 7056-7059 7111-7112 7135 7188-7190 7421 7439 7470 7539-7549 7609-7611 7634-7636 7638-7639 7676-7677 7712-7713 7735-7737 7853-7854 7892 7989 8052-8057 8175 8227-8229 8282 8365 8490- 8495
thymus	Clontech	THM001	14-21 69 74 81-82 121 128 138 143 253-254 366-369 454-455 460-462 498 533 546-548 559- 560 603-606 670 698 714-715 814-821 831-833 881-882 1002 1005-1007 1017-1018 1021 1033- 1035 1206-1209 1227-1243 1261-1263 1300-1302 1341-1346 1368 1391 1399-1401 1439-1444 1446- 1447 1453-1454 1460-1462 1478-1484 1511-1513 1572-1574 1586-1595 1602 1610 1653-1654 1659 1680-1690 1715-1716 1726-1728 1768-1773 1809- 1810 1813-1815 1839-1840 1844-1848 1854-1856 1876 1930-1932 1937-1942 1958-1961 1992-1994 2003-2004 2038-2044 2053-2058 2063 2071-2075 2081 2103-2107 2137 2143-2146 2155 2174-2175 2192-2194 2218-2219 2223-2224 2226-2227 2229- 2230 2252-2257 2307-2314 2341-2343 2353-2357 2388 2416 2420-2423 2430-2432 2456 2458-2461 2502-2508 2585-2586 2619-2622 2626-2629 2636 2648-2650 2653-2654 2658-2660 2711 2739-2747 2794 2823-2825 2879 2889-2901 2931-2934 2948- 2952 2963-2971 3054-3057 3071 3088-3091 3122- 3141 3149-3150 3157-3158 3161-3162 3165-3172 3175-3177 3221-3226 3261-3269 3274-3275 3280- 3284 3287-3289 3298-3300 3311-3312 3349-3352 3373-3374 3399 3410 3454 3477-3478 3481-3485 3517-3519 3528-3535 3537-3539 3548-3550 3555- 3557 3560 3591-3593 3597-3599 3605 3612-3615 3633 3642-3643 3669-3674 3698-3701 3722 3730 3761-3764 3771-3774 3794-3795 3871-3875 3883- 3884 3926 3931-3936 3946-3949 3986-3987 3990 3999-4008 4015-4018 4042-4043 4052 4054 4092- 4095 4142 4145-4146 4185 4286-4287 4363-4364 4371 4378-4380 4422-4424 4484 4536-4537 4606 4658 4662 4692 4729 4732-4733 4742 4780-4782 4823-4824 4839 4886-4888 4890 4899 5002-5004 5008-5012 5019-5021 5032-5033 5060 5063-5064 5105 5125-5127 5129-5130 5136 5138 5157 5206- 5207 5223 5241-5245 5268-5272 5280-5282 5294 5337 5343 5352-5355 5364 5366 5425-5426 5428 5472 5474-5478 5489-5491 5500-5501 5514 5526- 5529 5547-5552 5599-5600 5605-5607 5631 5683 5686 5692-5693 5705-5709 5714 5746-5747 5764 5777 5780-5782 5797-5805 5842-5843 5853-5855 5945-5948 6061 6149 6155 6182-6191 6243 6285 6287 6297-6298 6303-6307 6359-6362 6404 6443- 6444 6600-6601 6607 6629-6633 6663-6664 6715- 6716 6745-6746 6766-6767 6805-6809 6840 6846-

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thymus	Clontech	THMc02	8-9 14-19 38 45 86 91 105-107 111 121 144-145 193-195 213-215 233-237 277-278 283-284 286-287 330-340 342 366-369 380-382 388 402 407-408 416-418 432-433 459 476-477 480-482 530-531 533 555 576-578 580-581 588-591 603-606 633-634 659-665 676-680 688 707-708 712-715 723 759-760 822-829 831-833 905-908 930 941-942 945-947 960-961 979-980 982-985 988-989 991-994 1002 1005-1007 1015-1016 1055-1059 1072-1106 1110-1111 1148-1149 1177-1178 1200-1209 1227-1245 1297-1299 1334-1335 1341-1347 1359-1367 1413-1420 1439-1441 1455-1462 1466-1470 1478-1480 1488-1489 1495-1497 1505-1506 1511-1513 1542-1551 1562-1567 1602 1610 1616-1617 1622-1623 1637-1641 1655-1657 1659-1669 1680-1690 1702-1710 1718 1726-1727 1764 1784-1785 1824-1825 1839-1840 1857-1863 1876 1894-1895 1916-1927 1934-1935 1958-1963 1974-1978 1980-1984 1997 2001-2002 2011-2013 2037-2044 2063 2068-2075 2077-2078 2083-2085 2103-2107 2120-2121 2138-2141 2143-2146 2155 2165-2170 2174-2175 2223-2224 2237-2239 2241-2242 2276-2278 2290 2297-2299 2315-2322 2324-2327 2341-2343 2350-2352 2380 2382-2384 2389-2390 2408-2415 2420-2423 2442-2444 2453 2456 2458 2461 2464-2467 2495-2499 2502-2510 2522-2528 2536-2537 2543 2558 2585-2586 2592-2597 2625-2633 2658-2663 2665-2667 2689-2691 2722-2724 2731-2738 2744-2747 2758 2772-2775 2788-2793 2810-2811 2821-2822 2842-2848 2850-2851 2879 2916 2948-2950 2960-2971 2978-2979 3014-3023 3040-3042 3058-3063 3071 3080-3085 3102-3105 3122-3132 3138-3141 3161-3162 3165-3172 3175-3177 3218-3226 3274-3278 3280-3284 3287-3289 3311-3318 3334-3344 3346-3348 3361-3366 3375 3384-3385 3407-3408 3430 3438-3449 3481-3485 3517-3519 3521 3528-3535 3537-3554 3558-3559 3566-3567 3570 3591-3593 3605-3610 3612-3615 3633 3646-3652 3673-3674 3698-3701 3705 3717-3721 3733-3739 3743-3752 3767-3768 3791 3841-3849 3881-3882 3926 3931-3936 3938-3941 3966-3968 3983-3985 3988-3990 4009-4011 4015-4018 4020-4021 4027-4040 4043-4044 4048-4051 4067-4069 4080-4081 4097-4100 4102-4106 4128-4129 4157-4162 4203-4207 4266 4272-4273 4422-4424 4436-4438 4520-4528 4551-4552 4573-4602 4618 4622 4636-4639 4644-4645 4662 4695-4696 4752 4756 4780-4783 4817 4825 4840 4873-4876 4905-4906 4917-4918 4937-4939 4944-4945 4950-4953 4978 4984-4985 5008-5012 5022-5028 5032-5033 5060 5065-5072 5114 5129-5130 5134 5139-5140 5153-

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thyroid gland	Clontech	THR001	6-9 14-19 48 52-55 67 87 94 105 113 121 123- 126 150-151 161 195 201-209 212-215 231 253- 254 266-270 272 277-278 286-287 304 321 351- 352 373 384-385 407 416-418 426-428 430-431 454-455 468-473 495 513 527-529 533 537 539 556 559-560 579 588-591 603-606 608-609 645 650-651 670 706 712-713 733-737 753 757-758 765 774 788-789 803-804 828-829 866-867 884 887-891 921 923-927 941-942 952 971 974 982- 983 1022-1023 1037-1038 1160-1161 1185-1186 1206-1209 1227-1248 1287-1289 1297-1304 1309- 1313 1316-1317 1324-1335 1339-1340 1347 1349- 1353 1357-1370 1378-1379 1396-1414 1425-1431 1439-1441 1478-1480 1485-1491 1498-1500 1511- 1513 1518-1520 1531-1539 1542-1551 1557 1561- 1567 1571 1579-1580 1586-1595 1600-1602 1607- 1608 1610 1619-1620 1622-1628 1636 1655-1658 1660-1669 1671-1672 1694 1714-1715 1717-1721 1726-1728 1780-1785 1790-1795 1798-1800 1813- 1815 1819-1821 1824-1825 1839-1851 1853-1856 1864-1874 1876 1884-1889 1896 1907-1913 1916 1921 1944-1945 1947-1948 1950-1953 1958-1961 1964-1969 1980-1984 1986-1991 2001-2004 2014- 2017 2028 2032-2035 2037-2044 2050-2052 2059- 2060 2063 2067-2070 2080 2086 2112 2114-2119 2122 2138-2141 2155 2158-2162 2171-2173 2182- 2183 2186-2189 2195-2198 2204-2208 2240 2255- 2257 2266-2267 2276-2280 2282-2283 2285 2291- 2294 2302-2305 2315-2322 2329-2333 2341-2349 2353-2357 2361 2370-2372 2374-2378 2382-2386 2404-2415 2417-2423 2433-2434 2442-2444 2453- 2454 2458-2461 2464-2467 2469 2489-2490 2511- 2512 2515-2516 2543 2549-2550 2558 2573 2597 2603-2609 2623 2636-2641 2651-2652 2656-2660 2665-2667 2682-2683 2704-2711 2720 2722-2727 2729-2742 2748-2749 2778-2783 2794 2796 2806 2814-2815 2820 2826-2835 2842-2848 2850-2851 2857-2863 2867-2873 2875-2879 2902 2913-2915 2931-2946 2948-2971 2978-2979 3014-3016 3018- 3023 3033-3039 3043 3045-3048 3065-3067 3071

10760

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3475-3478	3486-	3488	3491-3493	3498-3499
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4166-4169	4177	4182-4183	4219-4220	4228
4241	4251	4253	4264	4271
4296-4297	4331-4333	4336	4353	4355-4359
4366-4367	4386-4387	4390	4392	4422-4424
4429	4436-4438	4441-4444	4484	4498-
4501	4512-4518	4529-4535	4544-4546	4554-4555
4561	4610	4613-4614	4622	4625
4644-4646	4662	4666-4671	4674-4675	4691
4710	4731-4733	4745-	4749	4765-4769
4771-4772	4774	4791-4792	4840-	4842
4873-4876	4889	4899	4909-4916	4920-4923
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6156	6165-6169	6174-6176	6178	6182-6191
6197	6213-6217	6243	6254-6256	6265
6272	6276-6278	6287	6289	6291-6292
6297-6298	6301	6305-6311	6316-6321	6338-6339
6343-6345	6348-6349	6353-6355	6378	6398
6418	6427-6431	6445	6462	6464-6466
6476-6479	6516	6552-6556	6598-6599	6613-6615
6618	6629-6633	6662-6676	6698	6703-6704
6718-6721	6734-6735	6742	6759-	6770
6776-6779	6784-6798	6828-6835	6839	6846-
6848	6858	6862	6896-6898	6922-6924
6927-6931	6937	6944-6945	6952	6954-6955
6957-6959	6990-	6992	7001-7002	7014-7027
7029-7033	7043-7044	7050-7053	7099-7102	7108-7110
7144	7155-7157			

			7169-7173 7196-7197 7225 7230 7270 7300 7308-7311 7321 7426 7428-7429 7439 7443 7505 7509-7510 7593-7594 7621 7630-7633 7662-7666 7693-7696 7729 7770-7772 7780-7790 7805 7852 7893 7904-7905 7907 7953-7954 7989 8031-8033 8043 8102-8113 8145 8162 8192-8196 8216-8218 8227-8229 8234-8235 8253 8277-8279 8329-8332 8372-8382 8397-8398 8403-8404 8413 8421 8430-8432 8443-8444 8466 8490-8495
trachea	Clontech	TRC001	55 69 161 230 241-243 264-265 293 397-398 411-413 416-418 491-494 533 549-551 753 759-760 857-859 945-947 1014 1049-1050 1160-1161 1216-1221 1334-1335 1339-1340 1415-1420 1446-1447 1465 1542-1548 1558-1560 1568-1574 1610 1616-1617 1626-1628 1694 1712-1713 1728 1778 1813-1815 1832-1834 1853 1884-1889 1922-1927 2018-2019 2037 2050-2052 2063-2066 2087-2094 2103-2107 2120-2121 2163-2164 2182-2183 2255-2257 2266-2267 2370-2372 2378 2382-2384 2387 2404-2405 2551-2553 2567-2568 2748-2749 2796 2805 2948-2952 3033 3049-3053 3065 3073-3074 3088-3091 3152-3155 3221-3226 3274-3275 3279 3290-3292 3361-3366 3409 3414-3415 3435-3437 3479-3480 3500-3503 3508-3511 3536 3555-3557 3597-3599 3616 3638 3678-3679 3707-3709 3742 3771-3774 3776-3778 3785-3787 3931-3936 3986-3987 4042 4044 4061-4062 4131 4205-4207 4255 4263 4272-4273 4415-4417 4444 4536-4537 4613 4662 4731 4750 4900 5043-5049 5062 5065-5072 5107-5109 5129-5130 5151 5156 5161 5167 5193 5206-5207 5284-5285 5290-5292 5431-5434 5452-5459 5526-5529 5546 5583-5584 5614-5615 5631 5660 5677 5693 6200-6202 6213-6217 6305-6307 6645 6662 6665-6668 6726-6728 6762-6763 6868 6979-6982 6997-6998 7014-7027 7046-7049 7465-7468 7555 7720-7721 7801 7989 8234-8235
uterus	Clontech	UTR001	6-7 10-13 114-115 121 144-145 201-209 213-215 246 345-349 441 527-529 537 814-821 845 982-983 1024 1067-1069 1192 1297-1302 1311-1313 1380-1390 1478-1480 1490-1491 1514-1515 1540-1551 1575-1577 1600-1602 1612-1615 1716 1780 1798-1800 1820-1821 1835-1840 1849 1854-1856 1870-1874 1916-1920 1967 1974-1978 2003-2008 2029 2046-2049 2063 2074-2075 2081 2113 2122 2131-2136 2148-2152 2241-2242 2266-2267 2315-2322 2353-2357 2381-2386 2388 2404-2405 2433-2434 2478 2511 2558 2587-2588 2592-2596 2619-2622 2636 2656-2657 2672-2678 2692-2696 2713-2715 2725-2727 2732-2738 2748-2749 2778-2783 2810-2811 2874 2931-2934 2948-2950 3014-3016 3065 3086-3087 3108-3110 3149-3150 3227-3228 3298-3300 3306-3307 3349-3352 3359-3360 3416-3418 3487-3488 3494-3496 3508-3511 3605 3638 3641 3707-3709 3717-3722 3730 3850-3854 4042 4173 4182-4183 4208 4269-4270 4286 4372 4422-4424 4448-4452 4480-4483 4491-4494 4508-4509 4614 4688-4690 4757-4758 4804 4885 4957-4958

			5073-5075 5098-5100 5184 5206-5207 5216-5220
			5284-5285 5302-5305 5331 5377 5392 5479-5482
			5515-5516 5561 5567-5568 5633 5678-5679 5731-
			5735 5769 5853-5855 5945-5948 5964-5966 6013
			6058-6060 6087-6090 6213-6217 6236-6241 6251
			6260-6262 6291-6292 6627-6628 6703-6704 6799-
			6804 6828-6832 6840 6949 7003-7004 7111-7112
			7151 7274-7275 7392-7393 7443 7480 7671 7853-
			7854 7937 7987 8052-8057 8086-8087 8110-8113
			8436 8459

Table 25

SEQ ID NO.	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	%IDENTITY
1	V00488	Homo sapiens alpha globin	776	90.141
2	V00488	Homo sapiens alpha globin	529	86.400
3	M60832	Homo sapiens alpha-2 type VIII collagen	96	31.343
5	M60832	Homo sapiens alpha-2 type VIII collagen	266	31.092
6	Z93394	Caenorhabditis elegans similar to Probable rabGAP domains	54	33.333
7	Z93394	Caenorhabditis elegans similar to Probable rabGAP domains	782	46.324
8	X55777	Homo sapiens put. ORF	56	32.432
9	X55777	Homo sapiens put. ORF	318	63.750
10	S72008	Homo sapiens CDC10 homolog=hCDC10	48	25.000
11	S72008	Homo sapiens CDC10 homolog=hCDC10	572	71.429
12	S72008	Homo sapiens CDC10 homolog=hCDC10	452	67.797
14	X76088	Mus musculus DNA binding protein RFX1	49	33.333
16	X76088	Mus musculus DNA binding protein RFX1	49	23.077
17	X76088	Mus musculus DNA binding protein RFX1	54	28.205
18	X76088	Mus musculus DNA binding protein RFX1	56	29.730
19	X76088	Mus musculus DNA binding protein RFX1	112	41.071
21	U25281	Rattus norvegicus SH3 domain binding protein	222	32.710
22	L24521	Homo sapiens transformation-related protein	47	33.333
23	L24521	Homo sapiens transformation-related protein	65	26.596
24	L24521	Homo sapiens transformation-related protein	297	63.855
26	AJ004810	Zea mays cytochrome P450 monooxygenase	105	49.091
27	AJ004810	Zea mays cytochrome P450 monooxygenase	54	36.111
28	AJ004810	Zea mays cytochrome P450 monooxygenase	442	56.477
29	X55777	Homo sapiens put. ORF	219	52.055
30	X74370	Homo sapiens mucin	130	38.554
31	AF189307	Homo sapiens unknown	136	45.000
32	X55777	Homo sapiens put. ORF	347	67.089
33	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	291	65.476
34	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	982	54.315
35	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	385	43.580
36	V00488	Homo sapiens alpha globin	776	90.141
38	AF182293	Homo sapiens U6 snRNA-associated Sm-like protein LSM7	213	67.857
40	D90041	Homo sapiens arylamine N-acetyltransferase	481	79.000
41	D90041	Homo sapiens arylamine N-acetyltransferase	1320	97.500
42	AL078468	Arabidopsis thaliana putative protein	194	26.425
43	AL078468	Arabidopsis thaliana putative protein	438	52.518
44	M15530	Homo sapiens B-cell growth factor	145	59.091

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47	X55777	Homo sapiens put. ORF	337	73.684
48	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	256	68.333
49	A31036	Nicotiana alata PRP2	101	28.037
50	A31036	Nicotiana alata PRP2	125	32.258
51	AL031177	Homo sapiens COL4A6 (Collagen Alpha 6(IV))	118	28.906
54	X55777	Homo sapiens put. ORF	377	76.316
55	AF084256	Homo sapiens beta glucuronidase isoform d	153	56.522
56	X65165	Volvox carteri extensin	276	31.925
57	X55777	Homo sapiens put. ORF	47	29.032
58	X55777	Homo sapiens put. ORF	48	28.261
59	X55777	Homo sapiens put. ORF	49	52.941
60	X55777	Homo sapiens put. ORF	48	31.429
61	X55777	Homo sapiens put. ORF	52	25.926
62	X55777	Homo sapiens put. ORF	44	40.000
63	X55777	Homo sapiens put. ORF	50	25.000
64	X55777	Homo sapiens put. ORF	47	30.357
65	X55777	Homo sapiens put. ORF	51	17.647
66	X55777	Homo sapiens put. ORF	281	54.945
68	X55777	Homo sapiens put. ORF	317	67.089
69	X55777	Homo sapiens put. ORF	318	69.444
71	M88700	Homo sapiens dopa decarboxylase	483	73.000
72	U79260	Homo sapiens unknown	118	39.394
73	M19301	Homo sapiens alpha-keto acid dehydrogenase precursor	468	75.352
74	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	368	50.633
75	X84692	Mus musculus spermatid perinuclear RNA binding protein	459	97.260
76	X84692	Mus musculus spermatid perinuclear RNA binding protein	483	95.122
78	AF196972	Homo sapiens JM24 protein	48	36.364
79	AF196972	Homo sapiens JM24 protein	347	55.769
81	L26953	Homo sapiens chromosomal protein	147	35.652
82	L26953	Homo sapiens chromosomal protein	224	34.225
83	U04627	Homo sapiens 78 kDa gastrin-binding protein	643	78.417
85	U41806	Homo sapiens p60	795	84.967
87	X55777	Homo sapiens put. ORF	243	56.000
89	U76992	Homo sapiens Tat-SF1	335	77.333
90	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	333	29.805
91	AF083501	Macaca mulatta rhadinovirus 17577 latent nuclear antigen	202	25.000
93	X71442	Rattus norvegicus ORF 1; putative	162	37.391
94	M30304	Rattus norvegicus cardiac myosin light chain 2	529	79.290
95	AB013606	Oryzias latipes elongation factor 1 alpha	2355	79.870
97	AB013606	Oryzias latipes elongation factor 1 alpha	1284	59.845
98	AB013606	Oryzias latipes elongation factor 1	982	81.818

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		alpha		
99	AB013606	Oryzias latipes elongation factor 1 alpha	1832	74.333
100	AC003027	Arabidopsis thaliana lcl prt_seq No definition line found	303	37.991
101	AC003027	Arabidopsis thaliana lcl prt_seq No definition line found	386	50.735
103	M81757	Homo sapiens S19 ribosomal protein	434	80.159
104	M34371	Nicotiana glauca extensin precursor	197	26.207
105	AF030001	Mus musculus unknown	102	28.713
107	AC006232	Arabidopsis thaliana putative proline-rich protein PRP2 precursor	344	26.837
108	X79802	Drosophila melanogaster WM6	244	54.255
109	U65092	Homo sapiens melanocyte-specific gene 1 nuclear protein	159	55.932
111	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	190	40.909
113	M83179	Gallus gallus alpha-3 type IX collagen	142	28.571
114	M68867	Homo sapiens retinoic acid binding protein II	35	50.000
115	M68867	Homo sapiens retinoic acid binding protein II	852	99.275
116	X55777	Homo sapiens put. ORF	102	73.684
117	X55777	Homo sapiens put. ORF	368	73.077
119	U58658	Homo sapiens unknown	209	49.485
121	AC006233	Arabidopsis thaliana unknown protein	436	28.288
123	AP000061	Aeropyrum pernix 114aa long hypothetical protein	73	31.707
125	AP000061	Aeropyrum pernix 114aa long hypothetical protein	42	40.000
126	AP000061	Aeropyrum pernix 114aa long hypothetical protein	128	46.429
127	X55777	Homo sapiens put. ORF	302	68.919
128	X55777	Homo sapiens put. ORF	256	61.039
130	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	147	45.763
131	Z71614	Saccharomyces cerevisiae ORF YNL338w	84	42.857
135	M12937	Homo sapiens ferritin heavy subunit	337	82.857
136	M12937	Homo sapiens ferritin heavy subunit	49	54.545
137	M12937	Homo sapiens ferritin heavy subunit	313	59.391
138	L24521	Homo sapiens transformation-related protein	239	58.889
139	S80905	Homo sapiens Con1=salivary concanavalin-A binding protein {exon 3}	290	27.594
140	M12937	Homo sapiens ferritin heavy subunit	337	82.857
141	M12937	Homo sapiens ferritin heavy subunit	252	42.442
142	M12937	Homo sapiens ferritin heavy subunit	298	55.941
143	X55777	Homo sapiens put. ORF	160	36.607
144	X68142	Oryctolagus cuniculus elongation factor 1 gamma	862	97.674
145	X68142	Oryctolagus cuniculus elongation factor 1 gamma	2265	87.557

146	X92098	Homo sapiens transmembrane protein	417	70.476
147	M86511	Homo sapiens monocyte antigen CD14	276	74.627
149	AB011169	Homo sapiens KIAA0597 protein	269	41.000
150	Z77132	Unknown Similarity to Worm protein C05C12.3; cDNA EST yk224b10.3 comes from this gene; cDNA EST yk2	460	44.382
151	Z77132	Unknown Similarity to Worm protein C05C12.3; cDNA EST yk224b10.3 comes from this gene; cDNA EST yk2	54	35.714
152	AF039694	Homo sapiens antigen NY-CO-16	369	81.818
153	U09823	Oryctolagus cuniculus elongation factor 1 alpha	871	48.866
154	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1520	69.895
155	U09823	Oryctolagus cuniculus elongation factor 1 alpha	349	90.000
156	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2923	98.681
157	AJ001019	Homo sapiens ring finger protein	53	36.000
158	AJ001019	Homo sapiens ring finger protein	380	46.667
159	AJ001019	Homo sapiens ring finger protein	143	62.222
160	S80119	Rattus sp. reverse transcriptase homolog	193	27.974
161	AF008551	Homo sapiens aurora-related kinase 1	236	35.602
162	U93569	Homo sapiens putative p150	1209	57.944
163	U93569	Homo sapiens putative p150	1346	61.877
164	X53581	Rattus norvegicus ORF3	43	22.222
165	X53581	Rattus norvegicus ORF3	58	57.143
166	X53581	Rattus norvegicus ORF3	58	57.143
167	X53581	Rattus norvegicus ORF3	53	32.500
168	X53581	Rattus norvegicus ORF3	50	33.333
170	U58658	Homo sapiens unknown	190	55.556
172	Y15173	Human papillomavirus type 75 E4 protein	133	35.955
173	Y15173	Human papillomavirus type 75 E4 protein	63	40.909
174	Y15173	Human papillomavirus type 75 E4 protein	44	28.125
175	Y15173	Human papillomavirus type 75 E4 protein	196	34.965
176	U49974	Homo sapiens mariner transposase	813	68.511
177	Z97628	Caenorhabditis elegans Similarity to Brugia peptidylprolyl isomerase (TR:G984562)	112	50.000
178	Z97628	Caenorhabditis elegans Similarity to Brugia peptidylprolyl isomerase (TR:G984562)	889	50.173
179	Z97628	Caenorhabditis elegans Similarity to Brugia peptidylprolyl isomerase (TR:G984562)	553	50.955
180	U23484	Caenorhabditis elegans weakly similar to serine/threonine protein kinase	58	27.619
181	U23484	Caenorhabditis elegans weakly similar to serine/threonine protein kinase	47	31.944

183	U23484	Caenorhabditis elegans weakly similar to serine/threonine protein kinase	219	35.294
185	X55777	Homo sapiens put. ORF	363	65.882
186	X98494	Homo sapiens M phase phosphoprotein 10	138	20.936
187	X98494	Homo sapiens M phase phosphoprotein 10	572	66.667
189	X98494	Homo sapiens M phase phosphoprotein 10	607	57.965
190	X55777	Homo sapiens put. ORF	306	65.000
191	L24521	Homo sapiens transformation-related protein	335	65.957
193	U79260	Homo sapiens unknown	189	43.421
194	U79260	Homo sapiens unknown	49	31.250
195	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	254	34.704
196	U79260	Homo sapiens unknown	164	53.226
199	X55777	Homo sapiens put. ORF	115	80.769
200	X55777	Homo sapiens put. ORF	310	68.354
201	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	59	23.729
202	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	80	23.200
203	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	57	29.167
204	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	52	29.630
205	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	55	29.032
206	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	56	20.588
207	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	55	29.032
208	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	57	29.167
209	U00001	Homo sapiens Human homologue of S. pombe nuc2+ and A. nidulans bima	91	28.099
210	AF145615	Drosophila melanogaster BcdNA.GH03377	577	38.542
211	AF145615	Drosophila melanogaster BcdNA.GH03377	337	56.452
212	M15530	Homo sapiens B-cell growth factor	140	77.143
213	L23646	Caenorhabditis elegans homology with dnaJ; putative	84	36.585
214	L23646	Caenorhabditis elegans homology with dnaJ; putative	247	29.224
215	L23646	Caenorhabditis elegans homology with dnaJ; putative	46	25.000
216	M15530	Homo sapiens B-cell growth factor	156	61.364
217	D90901	Synechocystis sp. hypothetical protein	219	39.456
218	L10908	Mus musculus Gcap1 gene product	126	33.333
219	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	351	81.333
220	U93569	Homo sapiens putative p150	195	37.288
221	L27428	Homo sapiens reverse transcriptase	35	50.000
222	L27428	Homo sapiens reverse transcriptase	498	45.525
225	U21603	Jembrana disease virus tat protein	116	38.462
226	X55777	Homo sapiens put. ORF	235	61.111
227	AL022120	Mycobacterium tuberculosis	183	25.869

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		hypothetical protein Rv3876		
228	L24521	Homo sapiens transformation-related protein	279	53.448
230	X51394	Xenopus laevis APEG precursor protein	132	25.789
231	L24521	Homo sapiens transformation-related protein	415	69.000
232	M22334	Homo sapiens unknown protein	349	44.944
233	X87212	Homo sapiens cathepsin C	63	100.000
234	X87212	Homo sapiens cathepsin C	503	98.667
235	X87212	Homo sapiens cathepsin C	1052	95.152
236	X87212	Homo sapiens cathepsin C	3084	99.352
237	X87212	Homo sapiens cathepsin C	466	94.340
238	L24521	Homo sapiens transformation-related protein	410	65.517
239	X61712	Homo sapiens HLA-A*6602 antigen	227	52.273
240	X61712	Homo sapiens HLA-A*6602 antigen	842	95.455
243	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	170	40.278
245	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	191	52.174
246	X53581	Rattus norvegicus ORF2	154	45.000
247	U82987	Homo sapiens Bcl-2 binding component 3	134	29.891
250	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	435	55.970
251	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	303	53.846
252	X55777	Homo sapiens put. ORF	286	69.697
253	M13043	Mus musculus alpha-1 (IV) collagen	74	30.612
254	M13043	Mus musculus alpha-1 (IV) collagen	149	39.080
256	X55777	Homo sapiens put. ORF	169	74.359
258	X55777	Homo sapiens put. ORF	281	66.667
259	M80344	Homo sapiens ORF1 codes for a 40 kDa product	151	26.471
260	X58523	Mus musculus MIPP	233	30.882
264	AF016448	Caenorhabditis elegans No definition line found	90	29.762
265	AF016448	Caenorhabditis elegans No definition line found	171	25.346
266	X65063	Giardia muris unknown	134	24.528
267	X65063	Giardia muris unknown	108	29.703
268	X65063	Giardia muris unknown	109	30.198
269	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	113	35.185
270	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	485	56.805
271	AF187988	Homo sapiens zinc finger protein ZNF222	595	76.552
272	U93572	Homo sapiens p40	286	32.338
273	X55777	Homo sapiens put. ORF	47	35.484
274	X55777	Homo sapiens put. ORF	317	65.789
276	M25282	Paracentrotus lividus alpha collagen type 1 precursor	212	27.624
277	AC003973	Homo sapiens ZNF91L	67	25.600
278	AC003973	Homo sapiens ZNF91L	1223	46.833

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279	X51394	Xenopus laevis APEG precursor protein	162	33.108
281	M64793	Rattus norvegicus salivary proline-rich protein	89	35.385
282	M64793	Rattus norvegicus salivary proline-rich protein	255	32.061
283	D86971	Homo sapiens no similarities to reported gene products	52	24.324
284	D86971	Homo sapiens no similarities to reported gene products	788	55.022
285	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	201	53.731
286	V01555	Human herpesvirus 4 BKRF1 encodes EBNA-1 protein, latent cycle gene.	80	35.556
287	V01555	Human herpesvirus 4 BKRF1 encodes EBNA-1 protein, latent cycle gene.	950	65.468
288	Z46242	Caenorhabditis elegans similar to WD domain, G-beta repeat; cDNA EST yk283e3.3 comes from this gene; cDNA EST yk238e2.3 comes from this gene; cDNA EST yk283e3.5 comes from this gene; cDNA EST yk238e2.5 comes from this gene	311	40.881
289	Z46242	Caenorhabditis elegans similar to WD domain, G-beta repeat; cDNA EST yk283e3.3 comes from this gene; cDNA EST yk238e2.3 comes from this gene; cDNA EST yk283e3.5 comes from this gene; cDNA EST yk238e2.5 comes from this gene	873	48.718
290	X73675	Human herpesvirus 6 ORF5	259	57.143
293	M15530	Homo sapiens B-cell growth factor	139	64.865
295	D13951	Nicotiana tabacum extensin precursor	183	34.677
297	X55777	Homo sapiens put. ORF	265	70.769
299	U00032	Caenorhabditis elegans No definition line found	336	43.243
301	L24521	Homo sapiens transformation-related protein	331	54.918
302	X55684	Lycopersicon esculentum extensin (class I)	83	37.879
303	M12099	Mus musculus proline-rich protein	180	34.320
304	U47856	Araneus diadematus fibroin-4	179	41.558
305	X88799	Oryza sativa DNA binding protein	129	41.791
307	Z25535	Homo sapiens nuclear pore complex protein hnup153	67	31.250
308	Z25535	Homo sapiens nuclear pore complex protein hnup153	98	32.184
309	Z25535	Homo sapiens nuclear pore complex protein hnup153	769	100.000
310	Z25535	Homo sapiens nuclear pore complex protein hnup153	65	31.731
311	Z25535	Homo sapiens nuclear pore complex protein hnup153	58	22.751
312	Z25535	Homo sapiens nuclear pore complex protein hnup153	65	37.931
313	Z25535	Homo sapiens nuclear pore complex	83	30.159

		protein hnup153		
314	Z25535	Homo sapiens nuclear pore complex protein hnup153	52	32.308
315	Z25535	Homo sapiens nuclear pore complex protein hnup153	233	100.000
316	Z25535	Homo sapiens nuclear pore complex protein hnup153	60	30.000
317	Z25535	Homo sapiens nuclear pore complex protein hnup153	70	22.111
318	Z25535	Homo sapiens nuclear pore complex protein hnup153	9658	100.000
319	Z25535	Homo sapiens nuclear pore complex protein hnup153	70	23.333
320	Z25535	Homo sapiens nuclear pore complex protein hnup153	1579	40.405
321	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	130	33.824
324	L76159	Homo sapiens FRG1 gene product	391	73.469
325	L76159	Homo sapiens FRG1 gene product	74	81.250
326	L76159	Homo sapiens FRG1 gene product	534	77.698
327	L76159	Homo sapiens FRG1 gene product	540	78.125
328	L76159	Homo sapiens FRG1 gene product	1029	79.565
329	X55777	Homo sapiens put. ORF	331	71.429
332	L19267	Homo sapiens putative	55	60.000
333	L19267	Homo sapiens putative	59	28.205
334	L19267	Homo sapiens putative	65	27.731
335	L19267	Homo sapiens putative	104	62.963
336	L19267	Homo sapiens putative	86	26.271
337	L19267	Homo sapiens putative	90	32.258
339	L19267	Homo sapiens putative	380	50.694
340	L19267	Homo sapiens putative	69	29.851
341	M11902	Mus musculus proline-rich salivary protein	192	37.209
342	M19537	Drosophila melanogaster RNA polymerase II largest subunit (, EC 2.7.7.6)	168	26.829
343	K03204	Homo sapiens salivary proline-rich protein precursor	755	95.413
344	K03204	Homo sapiens salivary proline-rich protein precursor	1223	84.865
345	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	56	41.667
346	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	56	41.667
347	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	53	34.884
348	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	126	56.250
349	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	342	46.445
350	X55777	Homo sapiens put. ORF	307	66.667
351	AF000195	Caenorhabditis elegans similar to oxysterol-binding proteins	68	39.286
352	AF000195	Caenorhabditis elegans similar to	1021	40.909

		oxysterol-binding proteins		
353	AF167320	Mus musculus zinc finger protein ZFP113	846	67.660
355	AF109402	Mus musculus neurotrophic factor artemin precursor	152	35.766
356	L27428	Homo sapiens reverse transcriptase	51	20.183
358	L27428	Homo sapiens reverse transcriptase	452	54.745
360	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	348	66.346
361	X55777	Homo sapiens put. ORF	388	75.000
362	A31800	Homo sapiens bile salt-stimulated lipase	4908	95.861
363	A31800	Homo sapiens bile salt-stimulated lipase	1998	73.585
364	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	381	52.151
365	V00148	Caenorhabditis elegans unnamed protein product	170	30.457
366	AF003540	Homo sapiens Krueppel family zinc finger protein	47	28.889
367	AF003540	Homo sapiens Krueppel family zinc finger protein	81	36.364
368	AF003540	Homo sapiens Krueppel family zinc finger protein	56	25.000
369	AF003540	Homo sapiens Krueppel family zinc finger protein	151	37.984
370	AJ010099	Homo sapiens NKp44RG1	171	27.411
371	AE001904	Deinococcus radiodurans hypothetical protein	170	23.011
372	AE001904	Deinococcus radiodurans hypothetical protein	165	33.333
373	AF008554	Rattus norvegicus implantation-associated protein	537	79.213
374	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	243	70.370
375	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	286	53.077
377	AF132177	Drosophila melanogaster unknown	94	61.905
378	AF132177	Drosophila melanogaster unknown	199	52.564
382	L24521	Homo sapiens transformation-related protein	334	58.462
383	U47856	Araneus diadematus fibroin-4	245	31.193
384	AJ004810	Zea mays cytochrome P450 monooxygenase	54	36.111
385	AJ004810	Zea mays cytochrome P450 monooxygenase	408	55.026
386	L23429	Canis familiaris beta-galactosides-binding lectin	160	34.783
387	X59289	Mus musculus ORF	150	32.061
388	AF177942	Xenopus laevis katanin p60	1185	53.864
389	M96232	Litomosoides carinii major microfilarial sheath protein	138	27.612
390	Z48045	Caenorhabditis elegans sre-2	432	48.175
391	Z48045	Caenorhabditis elegans sre-2	165	56.757
392	Z48045	Caenorhabditis elegans sre-2	202	29.437
393	Z48045	Caenorhabditis elegans sre-2	670	49.515

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394	Z48045	Caenorhabditis elegans sre-2	57	22.500
395	X55777	Homo sapiens put. ORF	328	60.920
396	AL133087	Homo sapiens hypothetical protein	124	23.203
397	Z82268	Unknown predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from	83	38.889
398	Z82268	Unknown predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from	116	30.435
399	U63542	Homo sapiens FAP protein	176	41.346
400	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	209	70.000
401	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	377	66.346
402	Z49209	Saccharomyces cerevisiae unknown	159	27.687
403	L24521	Homo sapiens transformation-related protein	434	38.416
405	L24521	Homo sapiens transformation-related protein	354	66.667
406	L24521	Homo sapiens transformation-related protein	369	59.524
407	X82200	Homo sapiens gpStaf50	606	57.988
408	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	221	28.918
409	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	307	48.322
410	M22332	Homo sapiens unknown protein	140	35.165
411	X55777	Homo sapiens put. ORF	47	30.000
412	X55777	Homo sapiens put. ORF	141	54.348
413	X55777	Homo sapiens put. ORF	157	54.545
414	K02550	Oncorhynchus mykiss 70-kilodalton heat shock protein	114	59.524
415	K02550	Oncorhynchus mykiss 70-kilodalton heat shock protein	552	67.421
416	D17554	Homo sapiens TAXREB107	43	31.818
417	D17554	Homo sapiens TAXREB107	1656	98.962
418	D17554	Homo sapiens TAXREB107	484	87.379
419	X14690	Homo sapiens lambda HuHITI-13	3406	96.514
420	X14690	Homo sapiens lambda HuHITI-13	409	35.740
421	X14690	Homo sapiens lambda HuHITI-13	355	100.000
422	X14690	Homo sapiens lambda HuHITI-13	387	79.070
423	X14690	Homo sapiens lambda HuHITI-13	3266	93.939
424	X14690	Homo sapiens lambda HuHITI-13	656	91.270
425	Z81038	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene	216	46.000
426	X57960	Mus musculus ribosomal protein L7	422	48.026
427	X57960	Mus musculus ribosomal protein L7	397	48.718
428	X57960	Mus musculus ribosomal protein L7	239	53.409
430	U96174	Onchocerca volvulus OvB8	153	35.135
431	U96174	Onchocerca volvulus OvB8	489	39.908
432	AP000399	Oryza sativa EST AU056133 (S20320) corresponds to a region of the predicted gene; similar to	126	63.636

		Caenorhabditis elegans cosmid D1054; hypothetical protein (Z74030)		
433	AP000399	Oryza sativa EST AU056133 (S20320) corresponds to a region of the predicted gene; similar to Caenorhabditis elegans cosmid D1054; hypothetical protein (Z74030)	414	52.239
434	L76159	Homo sapiens FRG1 gene product	361	74.725
435	L76159	Homo sapiens FRG1 gene product	1033	93.333
436	L76159	Homo sapiens FRG1 gene product	599	78.378
437	J03535	Mus musculus embigin precursor	242	53.750
439	M15386	Homo sapiens gamma-globin	897	93.421
440	M15386	Homo sapiens gamma-globin	631	77.640
441	L10110	Octopus dofleini alpha tubulin	358	73.333
442	U63840	Rattus norvegicus nucleoporin p54	701	67.039
443	U63840	Rattus norvegicus nucleoporin p54	192	51.852
444	U63840	Rattus norvegicus nucleoporin p54	1162	69.381
445	U63840	Rattus norvegicus nucleoporin p54	1155	88.835
447	AJ011118	Mus musculus skeletal muscle and cardiac protein	1408	85.714
448	AB033021	Homo sapiens KIAA1195 protein	3187	98.952
449	AL133204	Homo sapiens hypothetical protein	473	67.480
450	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	495	78.689
453	AC007842	Homo sapiens BC331191.1	649	50.192
454	AB033055	Homo sapiens KIAA1229 protein	4386	100.000
455	AB033055	Homo sapiens KIAA1229 protein	501	92.000
456	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	396	77.922
457	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	3580	99.628
458	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	384	100.000
459	AL031852	Schizosaccharomyces pombe conserved hypothetical protein	320	39.041
460	AB020499	Homo sapiens MD-1 homologue	43	34.783
461	AB020499	Homo sapiens MD-1 homologue	40	50.000
462	AB020499	Homo sapiens MD-1 homologue	120	43.333
464	AF109134	Homo sapiens 7-60	427	41.079
465	D25215	Homo sapiens KIAA0032	253	51.316
466	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	117	46.939
469	X96722	Saccharomyces cerevisiae ORF N0885	224	55.263
470	X96722	Saccharomyces cerevisiae ORF N0885	53	35.294
471	X96722	Saccharomyces cerevisiae ORF N0885	106	30.435
472	X96722	Saccharomyces cerevisiae ORF N0885	714	35.669
473	X96722	Saccharomyces cerevisiae ORF N0885	64	40.000
474	M11902	Mus musculus proline-rich salivary protein	157	42.857
475	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	329	70.652
476	AF036705	Unknown Similar to phytoene	90	60.000

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		desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el		
477	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	613	50.971
478	AB015630	Homo sapiens type II membrane protein	280	38.158
479	AF146793	Mus musculus H5AR	360	57.258
481	AF114816	Homo sapiens KRAB-zinc finger protein SZF1-1	2445	100.000
482	AF114816	Homo sapiens KRAB-zinc finger protein SZF1-1	703	95.455
483	AF021833	Mus musculus protein kinase A anchoring protein	2330	94.086
484	AF021833	Mus musculus protein kinase A anchoring protein	1828	69.933
485	AF021833	Mus musculus protein kinase A anchoring protein	434	48.454
486	AF021833	Mus musculus protein kinase A anchoring protein	570	86.275
488	M32334	Homo sapiens intercellular adhesion molecule 2 (ICAM-2)	404	87.640
489	M32334	Homo sapiens intercellular adhesion molecule 2 (ICAM-2)	571	88.000
490	M32334	Homo sapiens intercellular adhesion molecule 2 (ICAM-2)	1149	81.597
491	AF113251	Homo sapiens putative 2-hydroxyacid dehydrogenase	644	100.000
492	AF113251	Homo sapiens putative 2-hydroxyacid dehydrogenase	572	97.701
493	AF113251	Homo sapiens putative 2-hydroxyacid dehydrogenase	253	95.122
494	AF113251	Homo sapiens putative 2-hydroxyacid dehydrogenase	1321	94.378
495	X83413	Human herpesvirus 6 U88	527	54.872
496	AC004528	Homo sapiens R32184 3	933	60.357
497	AC004528	Homo sapiens R32184 3	624	91.176
498	U79260	Homo sapiens unknown	266	63.855
499	V00488	Homo sapiens alpha globin	925	100.000
500	V00488	Homo sapiens alpha globin	320	67.939
501	M15386	Homo sapiens gamma-globin	897	93.421
502	M15386	Homo sapiens gamma-globin	456	74.453
504	U93571	Homo sapiens p40	371	55.085
505	U93571	Homo sapiens p40	326	47.321
506	U93571	Homo sapiens p40	184	46.032
507	U93571	Homo sapiens p40	302	55.319
509	U93571	Homo sapiens p40	346	50.893
510	U93571	Homo sapiens p40	363	27.972
511	U93571	Homo sapiens p40	396	47.590
513	Z37139	Unknown similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; c	920	60.435
514	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	188	67.925
515	L19871	Homo sapiens activating transcription	242	72.881

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		factor 3		
516	L19871	Homo sapiens activating transcription factor 3	980	78.947
517	AL033514	Caenorhabditis elegans Y75B8A.12	244	35.455
519	U55376	Caenorhabditis elegans F16H11.2 gene product	301	83.929
520	U55376	Caenorhabditis elegans F16H11.2 gene product	142	78.571
521	U55376	Caenorhabditis elegans F16H11.2 gene product	31	36.842
522	U55376	Caenorhabditis elegans F16H11.2 gene product	174	83.333
523	U55376	Caenorhabditis elegans F16H11.2 gene product	54	35.714
524	AF003535	Homo sapiens ORF2-like protein	816	80.000
525	AF003535	Homo sapiens ORF2-like protein	96	42.000
526	AF003535	Homo sapiens ORF2-like protein	1161	74.793
527	Y12431	Mus musculus 5S ribosomal protein	353	100.000
528	Y12431	Mus musculus 5S ribosomal protein	231	94.444
530		Plasmodium falciparum 3' end., gene product	37	30.556
531		Plasmodium falciparum 3' end., gene product	206	28.636
532	X78933	Homo sapiens zinc finger protein	1627	60.574
533	L24521	Homo sapiens transformation-related protein	254	63.043
534	AL050321	Homo sapiens dJ717M23.1 (novel gene)	5126	100.000
535	AL050321	Homo sapiens dJ717M23.1 (novel gene)	352	96.386
536	X53581	Rattus norvegicus ORF2	139	54.000
537	X83413	Human herpesvirus 6 U88	446	30.000
539	X92485	Plasmodium vivax pval	144	56.863
541	AJ235271	Rickettsia prowazekii unknown	47	35.294
542	AJ235271	Rickettsia prowazekii unknown	265	41.284
543	AF061346	Mus musculus Edpl protein	195	35.211
544	AF061346	Mus musculus Edpl protein	153	30.464
545	AF061346	Mus musculus Edpl protein	50	26.471
546	M22463	Bos taurus ATP synthase gamma subunit precursor	39	26.087
547	M22463	Bos taurus ATP synthase gamma subunit precursor	1533	88.255
548	M22463	Bos taurus ATP synthase gamma subunit precursor	701	76.923
549	X57351	Homo sapiens 1-8D	527	90.909
550	X57351	Homo sapiens 1-8D	488	76.119
551	X57351	Homo sapiens 1-8D	383	76.984
552	AJ005870	Xenopus laevis RalB-binding protein	157	54.762
553	AJ005870	Xenopus laevis RalB-binding protein	2802	77.632
554	AJ005870	Xenopus laevis RalB-binding protein	1014	64.746
555	L24521	Homo sapiens transformation-related protein	388	58.120
556	AF045640	Caenorhabditis elegans No definition line found	201	42.353
557	U79260	Homo sapiens unknown	254	59.494
558	X57960	Mus musculus ribosomal protein L7	200	75.000

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559	AL033512	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:M88962 comes from this gene	118	55.556
560	AL033512	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:M88962 comes from this gene	370	31.716
562	Z83227	Caenorhabditis elegans predicted using Genefinder; Weak similarity to high-sulphur keratins.; cDNA EST yk663a1.3 comes from this gene	127	40.000
564	U79260	Homo sapiens unknown	253	61.429
565	M60177	Escherichia coli enterobactin	53	29.268
566	M60177	Escherichia coli enterobactin	67	26.087
567	M60177	Escherichia coli enterobactin	71	25.532
568	M60177	Escherichia coli enterobactin	55	40.741
569	M60177	Escherichia coli enterobactin	315	54.386
570	M60177	Escherichia coli enterobactin	877	95.035
571	M60177	Escherichia coli enterobactin	63	26.724
572	M60177	Escherichia coli enterobactin	56	31.818
573	M60177	Escherichia coli enterobactin	2057	94.627
574	M60177	Escherichia coli enterobactin	5030	97.564
575	M60177	Escherichia coli enterobactin	1825	78.426
576	Z74866	Saccharomyces cerevisiae ORF YOL124c	137	26.667
577	Z74866	Saccharomyces cerevisiae ORF YOL124c	530	37.553
578	Z74866	Saccharomyces cerevisiae ORF YOL124c	245	32.061
579	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	192	69.492
580	L21936	Homo sapiens succinate dehydrogenase flavoprotein subunit	681	92.381
581	L21936	Homo sapiens succinate dehydrogenase flavoprotein subunit	685	70.213
582	S73853	Homo sapiens NF2=neurofibromatosis type 2 {alternatively spliced, form A4}	108	65.625
584	AE000899	Methanobacterium thermoautotrophicum conserved protein	110	33.333
585	AL050024	Homo sapiens hypothetical protein	343	76.923
586	D86979	Homo sapiens KIAA0226	158	72.000
587	D86979	Homo sapiens KIAA0226	253	61.017
588	AC002045	Homo sapiens Unknown protein product CIT987SK-A-589H1 1 splice form 2	48	28.750
589	AC002045	Homo sapiens Unknown protein product CIT987SK-A-589H1 1 splice form 2	88	51.724
590	AC002045	Homo sapiens Unknown protein product CIT987SK-A-589H1 1 splice form 2	200	68.085
591	AC002045	Homo sapiens Unknown protein product CIT987SK-A-589H1 1 splice form 2	126	43.662
592	U60882	Rattus norvegicus protein arginine N-methyltransferase	1273	55.122
593	X55777	Homo sapiens put. ORF	310	67.442
594	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	111	31.250
595	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	332	70.732

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596	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	310	66.667
597	U79260	Homo sapiens unknown	46	37.037
599	M15386	Homo sapiens gamma-globin	897	93.421
600	M15386	Homo sapiens gamma-globin	528	76.812
601	M15386	Homo sapiens gamma-globin	897	93.421
602	M15386	Homo sapiens gamma-globin	633	90.647
604	U16031	Homo sapiens IL-4 Stat	47	44.444
605	U16031	Homo sapiens IL-4 Stat	42	25.714
608	M15530	Homo sapiens B-cell growth factor	121	75.000
609	M15530	Homo sapiens B-cell growth factor	188	61.702
610	M15386	Homo sapiens gamma-globin	897	93.421
611	M15386	Homo sapiens gamma-globin	531	71.429
612	X55777	Homo sapiens put. ORF	284	61.842
613	X55777	Homo sapiens put. ORF	173	59.574
616	X55777	Homo sapiens put. ORF	37	55.556
617	X55777	Homo sapiens put. ORF	239	55.556
621	AJ238096	Homo sapiens Lsm4 protein	134	28.030
623	M15386	Homo sapiens gamma-globin	897	93.421
624	M15386	Homo sapiens gamma-globin	627	81.132
625	U01317	Homo sapiens G-gamma globin	889	99.259
626	U01317	Homo sapiens G-gamma globin	695	92.647
627	Z98763	Schizosaccharomyces pombe hypothetical protein	116	37.255
628	Z98763	Schizosaccharomyces pombe hypothetical protein	255	33.571
632	X55777	Homo sapiens put. ORF	242	53.333
633	AC004557	Arabidopsis thaliana F17L21.21	87	45.455
634	AC004557	Arabidopsis thaliana F17L21.21	260	32.787
635	AF044953	Homo sapiens NADH:ubiquinone oxidoreductase PGIV subunit	217	67.925
638	M32865	Homo sapiens Ku protein subunit	150	100.000
639	M32865	Homo sapiens Ku protein subunit	742	94.355
640	D89150	Schizosaccharomyces pombe similar to Saccharomyces cerevisiae hypothetical 52.9KD protein in CDC26-YMR31 intergenic region, SWISS-PROT Accession Number P43616	327	62.162
641	X77689	Danio rerio translational elongation factor-1 alpha	2477	83.550
643	X77689	Danio rerio translational elongation factor-1 alpha	1018	81.818
644	X77689	Danio rerio translational elongation factor-1 alpha	1909	74.074
645	AL035259	Schizosaccharomyces pombe very hypothetical protein	96	37.037
648	U27842	Xenopus laevis insulin receptor substrate-1-like protein	122	26.891
650	X03342	Homo sapiens rpl32 (aa 1-135)	353	100.000
651	X03342	Homo sapiens rpl32 (aa 1-135)	783	97.015
652	J04765	Homo sapiens osteopontin	531	73.874
653	J04765	Homo sapiens osteopontin	1638	89.251
654	J04765	Homo sapiens osteopontin	1578	85.047
657	M99435	Homo sapiens transducin-like enhancer	964	85.870

		protein		
658	M99435	Homo sapiens transducin-like enhancer protein	501	88.750
660	D00570	Mus musculus open reading frame (251 AA)	109	25.342
661	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	47	50.000
662	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	41	29.630
663	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	44	34.211
664	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	160	39.394
665	Z81138	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D65543 comes from this gene	149	38.384
666	L24521	Homo sapiens transformation-related protein	344	65.476
668	V00488	Homo sapiens alpha globin	601	77.049
669	AF162270	Homo sapiens catalase interacting protein	117	77.273
670	X55777	Homo sapiens put. ORF	334	69.863
671	M15386	Homo sapiens gamma-globin	897	93.421
673	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2658	90.043
674	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1520	69.895
675	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1555	84.775
676	Y14040	Homo sapiens CASH beta protein	1297	94.521
677	Y14040	Homo sapiens CASH beta protein	1297	94.521
678	Y14040	Homo sapiens CASH beta protein	40	24.444
679	Y14040	Homo sapiens CASH beta protein	1376	99.548
680	Y14040	Homo sapiens CASH beta protein	1237	98.039
681	X81824	Dictyostelium discoideum putative RNA helicase	42	46.667
682	X81824	Dictyostelium discoideum putative RNA helicase	60	39.394
683	X81824	Dictyostelium discoideum putative RNA helicase	110	42.857
684	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	154	62.791
685	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2658	90.043
686	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2225	85.300
689	AC004537	Homo sapiens similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208)	599	74.101
690	AC004537	Homo sapiens similar to tumor suppressor p33ING1; similar to	939	93.902

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		AF044076 (PID:g2829208)		
692	U13066	Nicotiana alata arabinogalactan-protein precursor	133	38.542
696	X55777	Homo sapiens put. ORF	196	71.429
698	X55777	Homo sapiens put. ORF	292	59.459
699	U55376	Caenorhabditis elegans F16H11.2 gene product	119	51.515
700	U55376	Caenorhabditis elegans F16H11.2 gene product	207	50.000
701	U55376	Caenorhabditis elegans F16H11.2 gene product	178	53.061
702	U55376	Caenorhabditis elegans F16H11.2 gene product	124	44.444
703	U58658	Homo sapiens unknown	148	45.161
704	D00570	Mus musculus open reading frame (251 AA)	150	22.561
705	AL078579	Arabidopsis thaliana putative proline-rich protein	175	34.815
706	X55777	Homo sapiens put. ORF	276	63.514
708	AF048977	Homo sapiens Ser/Arg-related nuclear matrix protein	632	73.965
709	X55777	Homo sapiens put. ORF	277	64.615
712	M26708	Homo sapiens prothymosin alpha	152	96.000
713	M26708	Homo sapiens prothymosin alpha	374	62.281
714	AL050369	Homo sapiens hypothetical protein	3160	100.000
715	AL050369	Homo sapiens hypothetical protein	1887	68.657
716	X52164	Mus musculus Q300 protein (AA 1-77)	41	26.087
717	X52164	Mus musculus Q300 protein (AA 1-77)	125	65.217
718	X55777	Homo sapiens put. ORF	214	52.941
720	U24169	Homo sapiens JTV-1	545	78.333
721	U24169	Homo sapiens JTV-1	772	94.030
723	AF034636	Plasmodium falciparum merozoite surface protein 1	120	33.784
726	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2658	90.043
727	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2087	81.276
728	AJ133034	Chlamydia pneumoniae outer membrane protein 12	140	28.333
730	M15386	Homo sapiens gamma-globin	897	93.421
731	M15386	Homo sapiens gamma-globin	873	96.129
732	Y15913	Homo sapiens COL1A1 and PDGFB fusion transcript	95	34.524
733	AF079527	Mus musculus IER5	64	39.130
734	AF079527	Mus musculus IER5	209	34.807
735	M63279	Plasmodium falciparum malaria antigen	107	56.667
736	M17375	Gallus gallus type XII collagen	114	38.028
737	M17375	Gallus gallus type XII collagen	114	36.250
738	U79302	Homo sapiens unknown	145	31.210
739	M15530	Homo sapiens B-cell growth factor	135	76.923
740	L24521	Homo sapiens transformation-related protein	44	25.000
741	L24521	Homo sapiens transformation-related protein	170	45.161

743	AF170583	Homo sapiens ets homologous factor	581	73.043
744	U04609	Bradyrhizobium elkanii NodK	53	30.120
745	U04609	Bradyrhizobium elkanii NodK	56	33.333
746	U04609	Bradyrhizobium elkanii NodK	48	34.375
747	U04609	Bradyrhizobium elkanii NodK	123	25.510
748	AJ133273	Hylobates lar atrophin-1	115	36.082
749	AJ133273	Hylobates lar atrophin-1	81	29.630
750	AJ133273	Hylobates lar atrophin-1	138	32.143
753	AF175738	Abax parallelepipedus cytochrome c oxidase subunit II	123	28.440
754	L24521	Homo sapiens transformation-related protein	203	45.783
755	M15530	Homo sapiens B-cell growth factor	154	69.697
756	L24521	Homo sapiens transformation-related protein	196	46.667
757	AF077599	Homo sapiens hypothetical SBBI03 protein	223	60.656
758	AF077599	Homo sapiens hypothetical SBBI03 protein	2142	99.369
759	Z81490	Unknown similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene	1295	45.187
760	Z81490	Unknown similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene	779	64.706
763	AF045012	Hepatitis B virus surface antigen	102	34.722
764	AF148223	Plasmodium falciparum merozoite surface protein 2	135	35.514
765	M19419	Mus musculus proline-rich salivary protein	133	34.074
768	U79260	Homo sapiens unknown	150	64.103
771	L24521	Homo sapiens transformation-related protein	192	40.244
772	L24521	Homo sapiens transformation-related protein	192	40.244
773	X55777	Homo sapiens put. ORF	242	55.844
774	X92485	Plasmodium vivax pval	171	44.444
775	AB032916	Hylobates klossii dopamine receptor D4	143	36.364
777	X67703	Drosophila melanogaster Mst84Db	92	30.769
778	U03470	Rattus norvegicus ligand for Fas antigen	152	38.889
779	M84443	Homo sapiens galactokinase	281	100.000
780	M84443	Homo sapiens galactokinase	324	69.512
781	AB032910	Hylobates muelleri dopamine receptor D4	146	32.000
782	M15530	Homo sapiens B-cell growth factor	211	83.784
783	M15530	Homo sapiens B-cell growth factor	207	58.491
784	M15530	Homo sapiens B-cell growth factor	240	80.000
785	AF189307	Homo sapiens unknown	108	77.273
786	V00488	Homo sapiens alpha globin	776	90.141
787	V00488	Homo sapiens alpha globin	869	100.000
788	M15386	Homo sapiens gamma-globin	897	93.421
789	M15386	Homo sapiens gamma-globin	515	82.222
793	M15386	Homo sapiens gamma-globin	897	93.421

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794	M15386	Homo sapiens gamma-globin	492	86.525
795	M15386	Homo sapiens gamma-globin	159	88.462
796	M15386	Homo sapiens gamma-globin	460	64.122
797	M15386	Homo sapiens gamma-globin	896	92.763
798	M15386	Homo sapiens gamma-globin	724	81.646
799	M15386	Homo sapiens gamma-globin	669	81.250
800	M15386	Homo sapiens gamma-globin	938	88.889
801	M15386	Homo sapiens gamma-globin	954	100.000
802	X55777	Homo sapiens put. ORF	338	64.474
803	X55777	Homo sapiens put. ORF	123	80.000
804	X55777	Homo sapiens put. ORF	351	63.953
805	X55777	Homo sapiens put. ORF	304	63.889
806	D87453	Homo sapiens KIAA0264	40	35.000
807	D87453	Homo sapiens KIAA0264	172	23.214
809	D64005	Synechocystis sp. transposase	111	43.590
811	X01655	Homo sapiens type III procollagen (aa 892-1023)	42	37.500
812	X01655	Homo sapiens type III procollagen (aa 892-1023)	67	35.714
813	X01655	Homo sapiens type III procollagen (aa 892-1023)	135	35.514
814	X55777	Homo sapiens put. ORF	311	59.259
815	X55777	Homo sapiens put. ORF	302	63.636
816	X55777	Homo sapiens put. ORF	299	65.333
818	X55777	Homo sapiens put. ORF	252	51.190
819	X55777	Homo sapiens put. ORF	327	68.919
820	X55777	Homo sapiens put. ORF	204	70.732
821	X55777	Homo sapiens put. ORF	371	53.509
822	J02963	Homo sapiens platelet glycoprotein IIb precursor	55	55.556
823	J02963	Homo sapiens platelet glycoprotein IIb precursor	55	55.556
825	J02963	Homo sapiens platelet glycoprotein IIb precursor	42	24.000
826	J02963	Homo sapiens platelet glycoprotein IIb precursor	73	28.148
827	J02963	Homo sapiens platelet glycoprotein IIb precursor	176	29.902
828	M61870	Homo sapiens Krueppel-related DNA-binding protein	1242	92.821
829	M61870	Homo sapiens Krueppel-related DNA-binding protein	574	81.373
830	Z71178	Unknown cDNA EST EMBL:M88812 comes from this gene; cDNA EST EMBL:Z14521 comes from this gene; cDNA	176	32.847
831	AL031349	Schizosaccharomyces pombe hypothetical protein	221	60.000
832	AL031349	Schizosaccharomyces pombe hypothetical protein	169	58.000
833	AL031349	Schizosaccharomyces pombe hypothetical protein	69	36.923
835	AF062240	Homo sapiens immunoglobulin heavy chain variable region	550	84.211
836	D31767	Homo sapiens KIAA0058	53	28.947

837	D31767	Homo sapiens KIAA0058	328	97.778
838	D31767	Homo sapiens KIAA0058	1004	98.204
839	D87666	Homo sapiens heat shock protein 90	557	96.667
840	D87666	Homo sapiens heat shock protein 90	353	68.387
842	L01114	Klebsiella aerogenes unusual codon usage. ORF X	108	37.500
844	V00488	Homo sapiens alpha globin	270	73.333
845	Z93785	Unknown similar to ATPase; cDNA EST EMBL:D27734 comes from this gene; cDNA EST EMBL:D27733 comes fr	369	48.739
846	M15386	Homo sapiens gamma-globin	760	100.000
847	M15386	Homo sapiens gamma-globin	666	76.316
848	M15386	Homo sapiens gamma-globin	932	95.395
849	M15386	Homo sapiens gamma-globin	613	98.925
850	M15386	Homo sapiens gamma-globin	835	88.816
851	M15386	Homo sapiens gamma-globin	882	100.000
852	M15386	Homo sapiens gamma-globin	926	81.283
853	M15386	Homo sapiens gamma-globin	850	99.225
854	M15386	Homo sapiens gamma-globin	672	63.404
855	M15386	Homo sapiens gamma-globin	519	62.092
856	M15386	Homo sapiens gamma-globin	433	84.810
857	X79238	Homo sapiens ribosomal protein L30	323	100.000
858	X79238	Homo sapiens ribosomal protein L30	207	100.000
860	V00488	Homo sapiens alpha globin	776	90.141
861	V00488	Homo sapiens alpha globin	416	78.226
863	AL031670	Homo sapiens dJ681N20.2 (ferritin, light polypeptide-like 1)	317	98.039
864	AL031670	Homo sapiens dJ681N20.2 (ferritin, light polypeptide-like 1)	1062	95.977
865	AF123880	multiple sclerosis associated retrovirus element unknown protein U5/1	150	69.697
866	U09368	Homo sapiens zinc finger protein ZNF140	1232	45.498
867	U09368	Homo sapiens zinc finger protein ZNF140	296	62.500
868	J02963	Homo sapiens platelet glycoprotein IIb precursor	115	47.222
869	J02963	Homo sapiens platelet glycoprotein IIb precursor	166	75.000
870	J02963	Homo sapiens platelet glycoprotein IIb precursor	118	76.190
871	J02963	Homo sapiens platelet glycoprotein IIb precursor	192	33.987
872	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	128	35.185
875	AC004973	Homo sapiens carrier protein-like; similar to Q01888 (PID:g266574)	1520	100.000
876	AC004973	Homo sapiens carrier protein-like; similar to Q01888 (PID:g266574)	169	100.000
877	U29488	Caenorhabditis elegans No definition line found	455	42.593
878	U29488	Caenorhabditis elegans No definition line found	551	45.205

881	AF062385	Homo sapiens unknown	925	82.584
882	AF062385	Homo sapiens unknown	1117	81.641
883	AF132984	Homo sapiens nuclear pore complex interacting protein NP1P	510	73.874
885	X14332	Homo sapiens ventricular myosin light chain 2 (AA 1-165)	661	85.039
886	X14332	Homo sapiens ventricular myosin light chain 2 (AA 1-165)	781	83.140
887	AP000616	Oryza sativa similar to RING-H2 finger protein RHAla (AF078683)	44	60.000
889	AP000616	Oryza sativa similar to RING-H2 finger protein RHAla (AF078683)	90	30.909
890	AP000616	Oryza sativa similar to RING-H2 finger protein RHAla (AF078683)	60	32.500
891	AP000616	Oryza sativa similar to RING-H2 finger protein RHAla (AF078683)	62	32.353
893	U57092	Homo sapiens Rab30	44	30.303
894	U57092	Homo sapiens Rab30	42	26.415
895	U57092	Homo sapiens Rab30	40	36.364
896	U57092	Homo sapiens Rab30	48	43.750
897	U57092	Homo sapiens Rab30	49	50.000
898	U57092	Homo sapiens Rab30	127	95.455
899	D67035	Homo sapiens SCP-1	189	22.000
900	U70214	Escherichia coli glutamate 5-kinase	41	41.176
902	U70214	Escherichia coli glutamate 5-kinase	41	39.286
903	U70214	Escherichia coli glutamate 5-kinase	914	100.000
904	U39317	Homo sapiens UbCH5B	130	100.000
905	U12089	Human immunodeficiency virus type 1 envelope glycoprotein	41	40.000
906	U12089	Human immunodeficiency virus type 1 envelope glycoprotein	39	45.455
907	U12089	Human immunodeficiency virus type 1 envelope glycoprotein	70	42.308
908	U12089	Human immunodeficiency virus type 1 envelope glycoprotein	46	21.277
909	D49387	Homo sapiens NADP dependent leukotriene b4 12-hydroxydehydrogenase	281	77.612
910	D49387	Homo sapiens NADP dependent leukotriene b4 12-hydroxydehydrogenase	682	85.185
911	D49387	Homo sapiens NADP dependent leukotriene b4 12-hydroxydehydrogenase	1092	92.708
912	D49387	Homo sapiens NADP dependent leukotriene b4 12-hydroxydehydrogenase	443	93.151
913	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	51.613
914	U93571	Homo sapiens p40	258	55.422
915	U93571	Homo sapiens p40	497	57.554
916	U93571	Homo sapiens p40	471	58.915
920	M14549	Drosophila melanogaster segmentation protein PRD 4	117	61.905
921	AF169035	Homo sapiens protein kinase	164	41.667
923	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2684	90.217
924	U09823	Oryctolagus cuniculus elongation	2658	90.043

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		factor 1 alpha		
925	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1021	100.000
927	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2182	83.093
929	AF159055	Homo sapiens leucine zipper-like protein	115	75.000
930	L24521	Homo sapiens transformation-related protein	228	91.176
931	AF121360	Drosophila melanogaster DNZDHC/NEW1 zinc finger protein 11	59	26.415
932	AF121360	Drosophila melanogaster DNZDHC/NEW1 zinc finger protein 11	357	32.692
934	J00314	Homo sapiens beta-tubulin	640	95.833
936	X16134	Drosophila melanogaster Abd-B protein (AA 1-491)	160	29.752
937	AL117434	Homo sapiens hypothetical protein	161	96.296
938	AL117434	Homo sapiens hypothetical protein	4186	100.000
939	AL117434	Homo sapiens hypothetical protein	49	21.168
940	AL117434	Homo sapiens hypothetical protein	698	99.107
941	D45834	Size marker plasmid pKF339 protein responsible for tetracycline resistance	47	22.581
942	D45834	Size marker plasmid pKF339 protein responsible for tetracycline resistance	561	94.624
943	U05237	Homo sapiens FAC1 gene product	5415	100.000
944	U05237	Homo sapiens FAC1 gene product	455	78.022
945	U48248	Rattus norvegicus protein kinase C-binding protein Beta 15; RBCK1	69	36.066
946	U48248	Rattus norvegicus protein kinase C-binding protein Beta 15; RBCK1	48	25.806
947	U48248	Rattus norvegicus protein kinase C-binding protein Beta 15; RBCK1	180	25.581
949	AF151857	Homo sapiens CGI-99 protein	778	92.437
950	AF151857	Homo sapiens CGI-99 protein	437	100.000
951	AF151857	Homo sapiens CGI-99 protein	1040	80.000
952	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	150	80.769
953	X52332	Homo sapiens zinc finger protein 10	129	53.846
954	X52332	Homo sapiens zinc finger protein 10	1038	41.737
955	AB022277	Homo sapiens tubulointerstitial nephritis antigen	492	66.087
956	AB022277	Homo sapiens tubulointerstitial nephritis antigen	1999	68.067
957	AB022277	Homo sapiens tubulointerstitial nephritis antigen	3332	99.580
960	X99699	Homo sapiens XIAP associated factor-1 (ZAP-1)	2204	98.738
961	X99699	Homo sapiens XIAP associated factor-1 (ZAP-1)	406	98.214
962	AL009147	Unknown /prediction=(method:"genscan", version:"1.0", score:"184.75"); /prediction=(method:	158	41.538
964	AL009147	Unknown	458	55.147

		/prediction=(method:"genscan", version:"1.0", score:"184.75"); /prediction=(method:		
965	AL009147	Unknown /prediction=(method:"genscan", version:"1.0", score:"184.75"); /prediction=(method:	53	21.978
966	AL009147	Unknown /prediction=(method:"genscan", version:"1.0", score:"184.75"); /prediction=(method:	747	39.031
967	L34291	Pisum sativum ribulose-1,5 biphosphate carboxylase large subunit N-methyltransferase	45	25.000
968	L34291	Pisum sativum ribulose-1,5 biphosphate carboxylase large subunit N-methyltransferase	53	29.268
969	L34291	Pisum sativum ribulose-1,5 biphosphate carboxylase large subunit N-methyltransferase	159	27.184
971	AF031903	Mus musculus ADP-ribosylation-like factor homolog ARL6	366	93.651
974	U79260	Homo sapiens unknown	273	61.333
979	X78925	Homo sapiens zinc finger protein	173	71.429
980	X78925	Homo sapiens zinc finger protein	162	60.870
982	U89415	Mus musculus elongation factor 2	1488	95.367
983	U89415	Mus musculus elongation factor 2	134	95.455
984	AF151824	Homo sapiens CGI-66 protein	43	44.000
985	AF151824	Homo sapiens CGI-66 protein	190	66.038
986	U58658	Homo sapiens unknown	170	68.571
988	Z78542	Unknown cDNA EST EMBL:D72182 comes from this gene; cDNA EST EMBL:D72353 comes from this gene; cDNA	149	29.000
989	X67703	Drosophila melanogaster Mst84Dd	97	38.095
991	U44731	Mus musculus purine nucleotide binding protein	576	76.271
992	U70063	Homo sapiens acid ceramidase	54	20.000
993	U70063	Homo sapiens acid ceramidase	47	42.857
994	U70063	Homo sapiens acid ceramidase	50	26.923
995	U70063	Homo sapiens acid ceramidase	44	21.212
996	U70063	Homo sapiens acid ceramidase	47	33.333
997	U70063	Homo sapiens acid ceramidase	740	84.496
999	U70063	Homo sapiens acid ceramidase	2260	94.710
1000	Z99260	Schizosaccharomyces pombe putative microsomal dipeptidase precursor	45	23.762
1001	Z99260	Schizosaccharomyces pombe putative microsomal dipeptidase precursor	171	44.068
1002	M68864	Homo sapiens ORF	152	47.826
1004	S79410	Mus sp. nuclear localization signals (NLS)-binding protein-spot-1	139	85.714
1005	Z37166	Homo sapiens nuclear RNA helicase (DEAD family)	716	90.769
1006	Z37166	Homo sapiens nuclear RNA helicase (DEAD family)	445	100.000
1007	Z37166	Homo sapiens nuclear RNA helicase	2459	93.533

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		(DEAD family)		
1011	AF016448	Caenorhabditis elegans No definition line found	48	26.190
1012	AF016448	Caenorhabditis elegans No definition line found	901	35.561
1013	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	112	73.684
1017	D79988	Homo sapiens There are three putative hydrophobic domains in the central region.	586	100.000
1018	D79988	Homo sapiens There are three putative hydrophobic domains in the central region.	169	81.250
1019	AL132896	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	192	28.148
1021	U82303	Homo sapiens unknown	109	80.952
1022	M10119	Homo sapiens ferritin light subunit	353	62.295
1023	M10119	Homo sapiens ferritin light subunit	1080	98.857
1024	U79260	Homo sapiens unknown	170	56.000
1025	AF125462	Caenorhabditis elegans No definition line found	138	38.710
1026	AF125462	Caenorhabditis elegans No definition line found	107	40.476
1027	AF125462	Caenorhabditis elegans No definition line found	88	45.238
1028	U89439	Bos taurus ubiquitin-like protein	578	98.851
1029	U89439	Bos taurus ubiquitin-like protein	539	86.316
1030	U89439	Bos taurus ubiquitin-like protein	381	80.412
1031	AF084530	Homo sapiens cyclin-D binding Myb-like protein	218	94.444
1032	X55777	Homo sapiens put. ORF	335	66.667
1033	Y17454	Homo sapiens LSFR1 protein	585	100.000
1035	Y17454	Homo sapiens LSFR1 protein	602	100.000
1036	AF107406	Homo sapiens GW128	124	73.913
1037	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	241	60.938
1039	U93564	Homo sapiens putative p150	1882	84.330
1040	U93564	Homo sapiens putative p150	2284	93.931
1041	AF186469	Rattus norvegicus TM6P1	391	54.422
1042	AF186469	Rattus norvegicus TM6P1	1482	90.336
1043	AF186469	Rattus norvegicus TM6P1	1052	91.975
1044	AL117629	Homo sapiens hypothetical protein	1253	100.000
1045	AL117629	Homo sapiens hypothetical protein	771	73.016
1046	AL117629	Homo sapiens hypothetical protein	471	53.191
1048	AF025664	Bos taurus Na-Ca+K exchanger	157	71.429
1049	Z34278	Homo sapiens mucin	144	29.126
1050	AF151831	Homo sapiens CGI-73 protein	413	33.696
1052	U43585	Mus musculus protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	348	76.623
1053	U43585	Mus musculus protein kinase related to Raf protein kinases; Method: conceptual translation supplied by	351	74.684

		author		
1055	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	302	84.906
1056	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	49	57.143
1057	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	49	57.143
1058	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	498	75.000
1059	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	193	78.788
1060	U43701	Homo sapiens ribosomal protein L23a	315	84.483
1061	AL035309	Homo sapiens hypothetical protein	152	88.462
1062	M83248	Homo sapiens nephropontin	1111	92.670
1063	M83248	Homo sapiens nephropontin	1072	100.000
1064	J04765	Homo sapiens osteopontin	1414	84.516
1065	J04765	Homo sapiens osteopontin	1627	84.424
1066	U05812	Herpetomonas muscarum 3'-end	56	70.000
1067	AF084256	Homo sapiens beta glucuronidase isoform d	69	70.588
1068	AF084256	Homo sapiens beta glucuronidase isoform d	235	72.549
1069	AF084256	Homo sapiens beta glucuronidase isoform d	250	74.510
1070	AF114430	Homo sapiens phosphatidylcholine transfer protein	198	90.000
1071	AF114430	Homo sapiens phosphatidylcholine transfer protein	1405	100.000
1072	AF151794	Phascolarctos cinereus pol protein	628	49.495
1088	AF151794	Phascolarctos cinereus pol protein	523	50.641
1105	AF151794	Phascolarctos cinereus pol protein	1214	41.762
1106	U53366	Oncorhynchus mykiss terminal deoxynucleotidyl transferase	473	43.333
1107	Y14486	Homo sapiens cytosolic serine hydroxymethyltransferase	1926	97.068
1109	Y14486	Homo sapiens cytosolic serine hydroxymethyltransferase	1882	98.714
1110	L36342	Morone saxatilis beta-actin	253	92.105
1114	AB024366	TT virus ORF1	113	57.895
1115	AB024366	TT virus ORF1	107	64.000
1116	AB024366	TT virus ORF1	35	50.000
1117	AB024366	TT virus ORF1	109	64.000
1118	AL022157	Homo sapiens SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	153	65.714
1119	AL022157	Homo sapiens SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1291	77.586
1120	AL022157	Homo sapiens SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	274	72.000
1148	AF003151	Caenorhabditis elegans No definition line found	46	54.545
1149	AF003151	Caenorhabditis elegans No definition line found	156	29.508
1151	U96721	Homo sapiens alternative Hermansky-Pudlak syndrome associated protein	245	62.500

1152	U96721	Homo sapiens alternative Hermansky-Pudlak syndrome associated protein	614	98.958
1153	U93571	Homo sapiens p40	647	68.667
1154	U93571	Homo sapiens p40	250	55.263
1155	U93571	Homo sapiens p40	194	61.111
1156	U93571	Homo sapiens p40	1054	92.000
1157	U93571	Homo sapiens p40	43	31.818
1158	U93571	Homo sapiens p40	770	71.667
1160	D14531	Homo sapiens 'human homologue of rat ribosomal protein L9'	910	78.646
1161	D14531	Homo sapiens 'human homologue of rat ribosomal protein L9'	442	65.366
1163	AC002535	Arabidopsis thaliana putative G-beta-repeat containing protein, 5' partial	60	47.059
1164	AC002535	Arabidopsis thaliana putative G-beta-repeat containing protein, 5' partial	44	24.211
1165	AC002535	Arabidopsis thaliana putative G-beta-repeat containing protein, 5' partial	409	36.744
1166	X55777	Homo sapiens put. ORF	195	47.674
1167	X55777	Homo sapiens put. ORF	315	63.095
1168	X55777	Homo sapiens put. ORF	57	47.619
1169	X55777	Homo sapiens put. ORF	276	66.234
1170	X55777	Homo sapiens put. ORF	383	64.444
1171	X55777	Homo sapiens put. ORF	310	58.537
1172	D37786	Felis catus Max	135	100.000
1173	U34973	Mus musculus protein tyrosine phosphatase-like	240	65.000
1174	U34973	Mus musculus protein tyrosine phosphatase-like	458	47.826
1175	AL032657	Unknown predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 come	262	58.571
1176	AL032657	Unknown predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 come	183	41.791
1177	AF140227	Streptococcus pyogenes M protein	120	28.125
1178	AF140227	Streptococcus pyogenes M protein	145	30.612
1180	X55777	Homo sapiens put. ORF	159	53.846
1181	X99099	Medicago sativa auxin induced proline rich protein	94	40.541
1182	D89667	Homo sapiens c-myc binding protein	191	80.556
1183	D89667	Homo sapiens c-myc binding protein	734	93.671
1184	U79260	Homo sapiens unknown	146	52.941
1185	D49382	Mus musculus septin	260	75.439
1186	D49382	Mus musculus septin	1911	87.366
1187	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	138	45.614
1189	AL080206	Homo sapiens hypothetical protein	128	74.074
1191	AC006234	Arabidopsis thaliana unknown protein	141	24.476
1192	X99518	Saimiriine herpesvirus 2 StpCl39	111	51.163
1193	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	109	59.259
1194	AF125053	Homo sapiens pyruvate dehydrogenase E1 alpha subunit	700	99.074

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1195	AF125053	Homo sapiens pyruvate dehydrogenase E1 alpha subunit	131	85.714
1196	AF125053	Homo sapiens pyruvate dehydrogenase E1 alpha subunit	821	97.037
1197	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	917	82.738
1198	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	1420	74.754
1199	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	168	71.053
1201	Z26248	Homo sapiens eosinophil granule major basic pre-proprotein	45	36.364
1202	Z26248	Homo sapiens eosinophil granule major basic pre-proprotein	45	55.556
1203	Z26248	Homo sapiens eosinophil granule major basic pre-proprotein	1423	99.507
1204	Z26248	Homo sapiens eosinophil granule major basic pre-proprotein	1310	99.457
1205	Z26248	Homo sapiens eosinophil granule major basic pre-proprotein	584	67.647
1206	AF070664	Homo sapiens HSPC008	681	74.648
1207	AF070664	Homo sapiens HSPC008	584	69.853
1208	AF070664	Homo sapiens HSPC008	182	100.000
1209	AF070664	Homo sapiens HSPC008	1610	94.479
1210	A14829	Homo sapiens preproapolipoprotein	601	61.644
1211	V00488	Homo sapiens alpha globin	905	100.000
1212	V00488	Homo sapiens alpha globin	321	75.833
1213	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	690	24.878
1214	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	551	95.604
1215	AF128406	Homo sapiens prenyl-dependent prelamin A binding protein Narf	1663	80.819
1216	AL110239	Homo sapiens hypothetical protein	470	98.507
1217	AL110239	Homo sapiens hypothetical protein	510	100.000
1218	AL110239	Homo sapiens hypothetical protein	157	96.552
1219	AL110239	Homo sapiens hypothetical protein	881	71.233
1220	AL110239	Homo sapiens hypothetical protein	44	35.000
1221	AL110239	Homo sapiens hypothetical protein	727	72.691
1222	AJ242797	Bos taurus hemoglobin alpha chain	759	86.620
1223	AJ242797	Bos taurus hemoglobin alpha chain	551	75.410
1224	AJ242797	Bos taurus hemoglobin alpha chain	278	66.071
1225	J00044	Capra hircus alpha-ii globin	797	85.915
1226	J00044	Capra hircus alpha-ii globin	348	66.923
1228	AL117237	Homo sapiens hypothetical protein	822	74.586
1230	AL117237	Homo sapiens hypothetical protein	198	96.667
1232	AL117237	Homo sapiens hypothetical protein	105	100.000
1233	AL117237	Homo sapiens hypothetical protein	1592	89.085
1236	AL117237	Homo sapiens hypothetical protein	1122	54.722
1237	AL117237	Homo sapiens hypothetical protein	707	45.161
1239	AL117237	Homo sapiens hypothetical protein	218	64.286
1240	AL117237	Homo sapiens hypothetical protein	2069	81.546
1241	AL117237	Homo sapiens hypothetical protein	1907	64.151
1242	AL117237	Homo sapiens hypothetical protein	4888	80.164

1243	AL117237	Homo sapiens hypothetical protein	5468	94.673
1244	U27112	Homo sapiens HT-1080 protein	67	71.429
1245	U27112	Homo sapiens HT-1080 protein	1649	86.550
1246	X13794	Homo sapiens lactate dehydrogenase B	542	67.361
1247	X13794	Homo sapiens lactate dehydrogenase B	907	75.783
1248	AJ225898	Oryctolagus cuniculus translationally controlled tumor protein	349	67.630
1249	M60618	Homo sapiens nuclear autoantigen	218	41.379
1250	M60618	Homo sapiens nuclear autoantigen	263	50.943
1251	M60618	Homo sapiens nuclear autoantigen	328	75.641
1252	M60618	Homo sapiens nuclear autoantigen	3195	99.582
1253	M60618	Homo sapiens nuclear autoantigen	2121	82.258
1254	X06749	Gallus gallus metallthionein (AA 1 - 63)	321	59.211
1255	X06749	Gallus gallus metallthionein (AA 1 - 63)	263	71.795
1256	X06749	Gallus gallus metallthionein (AA 1 - 63)	147	60.526
1258	X05289	Papio hamadryas anubis alpha-1 globin	848	92.254
1259	X05289	Papio hamadryas anubis alpha-1 globin	307	74.603
1260	A78803	unidentified unnamed protein product	359	74.242
1261	M28583	Homo sapiens MHC class II DR-beta	1539	80.519
1262	M28583	Homo sapiens MHC class II DR-beta	1445	87.640
1263	M28583	Homo sapiens MHC class II DR-beta	1373	92.135
1264	A78803	unidentified unnamed protein product	286	68.939
1265	X73460	Homo sapiens ribosomal protein L3	1209	80.972
1266	X73460	Homo sapiens ribosomal protein L3	1909	79.167
1267	X73460	Homo sapiens ribosomal protein L3	1710	83.019
1268	X73460	Homo sapiens ribosomal protein L3	2265	87.841
1269	X73460	Homo sapiens ribosomal protein L3	1882	88.321
1270	X05289	Papio hamadryas anubis alpha-1 globin	848	92.254
1271	X05289	Papio hamadryas anubis alpha-1 globin	265	64.655
1272	X51706	Rattus rattus ribosomal protein L9 (AA 1-192)	295	54.500
1274	J03048	Homo sapiens hemopexin precursor	1484	72.967
1275	M74220	Homo sapiens plasminogen	4801	95.007
1276	M74220	Homo sapiens plasminogen	3096	74.590
1277	M16961	Homo sapiens alpha-2-HS-glycoprotein	826	68.812
1278	M16961	Homo sapiens alpha-2-HS-glycoprotein	979	80.628
1279	M16961	Homo sapiens alpha-2-HS-glycoprotein	1425	77.344
1280	X52977	Xenopus laevis elongation factor 1-alpha (454 AA)	2420	82.119
1281	X52977	Xenopus laevis elongation factor 1-alpha (454 AA)	1386	62.827
1283	X52977	Xenopus laevis elongation factor 1-alpha (454 AA)	1782	74.586
1284	X52977	Xenopus laevis elongation factor 1-alpha (454 AA)	2433	81.236
1285	X52977	Xenopus laevis elongation factor 1-alpha (454 AA)	1461	68.790
1286	M15386	Homo sapiens gamma-globin	214	60.927
1287	Z83110	Unknown cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST	218	38.462

1288	Z83110	Unknown cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST	145	41.509
1289	Z83110	Unknown cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST	211	29.932
1290	AJ243310	Homo sapiens C14orf3 protein	103	28.889
1291	AJ243310	Homo sapiens C14orf3 protein	528	30.667
1292	AJ243310	Homo sapiens C14orf3 protein	87	29.310
1293	AJ243310	Homo sapiens C14orf3 protein	312	33.535
1295	AF078819	Spalax ehrenbergi high mobility group protein	379	100.000
1296	AF078819	Spalax ehrenbergi high mobility group protein	889	81.818
1297	X53777	Homo sapiens putative ribosomal protein (AA 1-184)	939	87.059
1298	X53777	Homo sapiens putative ribosomal protein (AA 1-184)	975	94.268
1299	X53777	Homo sapiens putative ribosomal protein (AA 1-184)	609	78.495
1300	U43918	Mus musculus proliferation-associated protein 1	196	78.947
1301	U43918	Mus musculus proliferation-associated protein 1	1244	89.671
1302	U43918	Mus musculus proliferation-associated protein 1	1576	85.354
1304	S56599	Mus sp. AP56=acetaminophen-binding protein	1543	65.051
1305	J03037	Homo sapiens carbonic anhydrase II	1298	87.925
1307	AF013214	Bos taurus acidic ribosomal phosphoprotein PO	1178	74.744
1308	AF013214	Bos taurus acidic ribosomal phosphoprotein PO	670	60.185
1309	AL031778	Homo sapiens dJ34B21.2 (PUTATIVE novel protein similar to part of APOBEC1 (Phorbolin 1, Apolipoprotein B mRNA editing protein))	886	86.747
1310	AL031778	Homo sapiens dJ34B21.2 (PUTATIVE novel protein similar to part of APOBEC1 (Phorbolin 1, Apolipoprotein B mRNA editing protein))	1001	86.580
1311	M21142	Homo sapiens guanine nucleotide-binding protein G-s-alpha-2	1374	90.980
1312	M21142	Homo sapiens guanine nucleotide-binding protein G-s-alpha-2	2108	98.576
1313	M21142	Homo sapiens guanine nucleotide-binding protein G-s-alpha-2	1691	86.047
1314	AF151825	Homo sapiens CGI-67 protein	659	50.000
1315	AF151825	Homo sapiens CGI-67 protein	732	62.983
1316	S85655	Homo sapiens prohibitin	347	87.324
1317	S85655	Homo sapiens prohibitin	829	79.505
1318	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	54	58.333
1319	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	538	68.852

1320	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	2830	74.765
1321	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	777	72.222
1322	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	57	17.857
1323	L10391	Oryctolagus cuniculus flavin-containing monooxygenase FMO3	652	82.759
1326	X99920	Homo sapiens S100 calcium-binding protein A13 (S100A13)	216	65.714
1327	AF150089	Homo sapiens small zinc finger-like protein	37	29.167
1328	AF150089	Homo sapiens small zinc finger-like protein	42	36.000
1329	AF150089	Homo sapiens small zinc finger-like protein	36	19.149
1330	AF150089	Homo sapiens small zinc finger-like protein	46	25.000
1332	AF150089	Homo sapiens small zinc finger-like protein	560	97.619
1333	AF150089	Homo sapiens small zinc finger-like protein	338	84.000
1334	D63480	Homo sapiens The KIAA0146 gene product is novel.	757	72.067
1335	D63480	Homo sapiens The KIAA0146 gene product is novel.	4971	95.022
1336	U01317	Homo sapiens A-gamma globin	242	61.594
1337	A78803	unidentified unnamed protein product	750	88.652
1338	A78803	unidentified unnamed protein product	313	73.134
1339	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	222	50.000
1340	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	717	46.524
1341	AB002310	Homo sapiens KIAA0312	949	98.773
1342	AB002310	Homo sapiens KIAA0312	928	67.829
1343	AB002310	Homo sapiens KIAA0312	567	100.000
1344	AB002310	Homo sapiens KIAA0312	1677	87.781
1345	AB002310	Homo sapiens KIAA0312	4324	84.217
1346	AB002310	Homo sapiens KIAA0312	10980	96.025
1347	U47101	Homo sapiens NifU-like protein	327	72.868
1348	AC011560	Arabidopsis thaliana hypothetical protein	351	41.935
1350	M11791	Homo sapiens proapo-A-I protein	1065	95.402
1351	M11791	Homo sapiens proapo-A-I protein	232	100.000
1353	M11791	Homo sapiens proapo-A-I protein	790	70.175
1354	S62928	Homo sapiens PRB1M precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor(Ps 1=basic proline-rich protein) {C-terminal}	105	32.394
1355	S62928	Homo sapiens PRB1M precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor(Ps 1=basic proline-rich protein) {C-terminal}	137	29.605

1356	AJ005562	Mus musculus SPR2D protein	134	43.750
1357	X17042	Homo sapiens hematopoietic proteoglycan core protein (AA 1 - 158)	554	98.810
1358	X17042	Homo sapiens hematopoietic proteoglycan core protein (AA 1 - 158)	712	86.875
1359	AJ242910	Homo sapiens N-Acetylglucosamine kinase	107	100.000
1360	AJ242910	Homo sapiens N-Acetylglucosamine kinase	623	68.590
1361	AJ242910	Homo sapiens N-Acetylglucosamine kinase	289	82.812
1362	AJ242910	Homo sapiens N-Acetylglucosamine kinase	65	100.000
1363	AJ242910	Homo sapiens N-Acetylglucosamine kinase	39	44.444
1364	AJ242910	Homo sapiens N-Acetylglucosamine kinase	56	52.941
1365	AJ242910	Homo sapiens N-Acetylglucosamine kinase	56	52.941
1366	AJ242910	Homo sapiens N-Acetylglucosamine kinase	53	47.059
1367	AJ242910	Homo sapiens N-Acetylglucosamine kinase	1743	91.453
1368	AJ003023	Oryctolagus cuniculus hnRNP-E1 protein	1272	78.378
1369	X76488	Homo sapiens sterol esterase	246	92.308
1370	X76488	Homo sapiens sterol esterase	2349	93.000
1373	X12525	Xenopus laevis alpha 3-actin	1275	81.818
1376	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	70	26.316
1377	AF121009	Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534	248	30.263
1378	X70476	Homo sapiens subunit of coatomer complex	339	78.161
1379	X70476	Homo sapiens subunit of coatomer complex	5128	91.338
1381	S80864	Homo sapiens cytochrome c-like polypeptide	39	37.500
1383	S80864	Homo sapiens cytochrome c-like polypeptide	254	84.444
1384	S80864	Homo sapiens cytochrome c-like polypeptide	135	82.609
1387	S80864	Homo sapiens cytochrome c-like polypeptide	310	72.000
1388	S80864	Homo sapiens cytochrome c-like polypeptide	397	60.305
1389	S80864	Homo sapiens cytochrome c-like polypeptide	146	76.316
1390	S80864	Homo sapiens cytochrome c-like polypeptide	818	83.077
1391	Z69720	Homo sapiens 3-methyl-adenine DNA glycosylase	1177	82.895
1392	X05289	Papio hamadryas anubis alpha-1 globin	848	92.254
1393	X05289	Papio hamadryas anubis alpha-1 globin	257	56.391
1394	D31767	Homo sapiens KIAA0058	739	98.165
1395	D31767	Homo sapiens KIAA0058	704	89.881

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1396	L10678	Homo sapiens profilin II	751	86.131
1397	L10678	Homo sapiens profilin II	752	100.000
1398	L10678	Homo sapiens profilin II	582	86.331
1399	M24842	Homo sapiens keratin 18	243	95.122
1400	M24842	Homo sapiens keratin 18	1931	88.950
1401	M24842	Homo sapiens keratin 18	1334	78.396
1402	U50733	Homo sapiens dynamitin	645	93.578
1403	U50733	Homo sapiens dynamitin	421	98.551
1404	U50733	Homo sapiens dynamitin	654	93.694
1405	U50733	Homo sapiens dynamitin	2285	95.431
1406	U50733	Homo sapiens dynamitin	252	97.368
1407	U50733	Homo sapiens dynamitin	1372	77.412
1408	U19718	Homo sapiens microfibril-associated glycoprotein	1067	100.000
1409	U19718	Homo sapiens microfibril-associated glycoprotein	837	90.217
1410	Z11694	Homo sapiens 41kD protein kinase	236	97.436
1411	Z11694	Homo sapiens 41kD protein kinase	41	21.000
1412	Z11694	Homo sapiens 41kD protein kinase	1269	79.784
1413	AF047439	Homo sapiens unknown	251	100.000
1414	AF047439	Homo sapiens unknown	1096	75.719
1416	L13635	Rattus rattus growth response protein	420	92.000
1417	L13635	Rattus rattus growth response protein	791	99.180
1418	L13635	Rattus rattus growth response protein	662	87.582
1419	L13635	Rattus rattus growth response protein	1267	68.320
1420	L13635	Rattus rattus growth response protein	989	72.763
1421	AF071491	Homo sapiens potassium channel	1893	99.648
1422	AF071491	Homo sapiens potassium channel	957	97.987
1423	AF071491	Homo sapiens potassium channel	5435	96.693
1424	V00488	Homo sapiens alpha globin	328	75.676
1426	D12618	Mus musculus nucleosome assembly protein-1	777	95.238
1427	D12618	Mus musculus nucleosome assembly protein-1	277	67.692
1428	D12618	Mus musculus nucleosome assembly protein-1	277	67.692
1429	D12618	Mus musculus nucleosome assembly protein-1	788	96.183
1430	D12618	Mus musculus nucleosome assembly protein-1	45	26.389
1431	D12618	Mus musculus nucleosome assembly protein-1	1871	88.101
1432	M25660	Homo sapiens beta-hemoglobin	200	70.175
1433	X54101	Homo sapiens NKG5 product	495	100.000
1434	X54101	Homo sapiens NKG5 product	150	100.000
1435	X54101	Homo sapiens NKG5 product	402	77.108
1436	X54101	Homo sapiens NKG5 product	526	87.023
1437	A78803	unidentified unnamed protein product	918	100.000
1438	A78803	unidentified unnamed protein product	336	71.429
1439	AF000381	Homo sapiens non-functional folate binding protein	57	20.588
1440	AF000381	Homo sapiens non-functional folate binding protein	57	28.889
1441	AF000381	Homo sapiens non-functional folate	1042	84.942

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		binding protein		
1442	L76200	Homo sapiens guanylate kinase	38	35.000
1443	L76200	Homo sapiens guanylate kinase	208	78.049
1444	L76200	Homo sapiens guanylate kinase	511	67.431
1445	L38941	Homo sapiens ribosomal protein L34	242	71.717
1447	AF108225	Monodelphis domestica immunoglobulin alpha heavy chain precursor	1084	42.938
1449	X00318	Homo sapiens apoferritin H chain	42	19.540
1450	X00318	Homo sapiens apoferritin H chain	467	71.220
1451	M15386	Homo sapiens gamma-globin	897	93.421
1452	M15386	Homo sapiens gamma-globin	403	77.019
1453	X61123	Homo sapiens BTG1	962	67.589
1454	X61123	Homo sapiens BTG1	425	65.193
1455	U39412	Homo sapiens alpha SNAP	36	66.667
1456	U39412	Homo sapiens alpha SNAP	267	100.000
1457	U39412	Homo sapiens alpha SNAP	400	100.000
1458	U39412	Homo sapiens alpha SNAP	42	39.130
1459	U39412	Homo sapiens alpha SNAP	871	74.671
1460	AB012918	Canis familiaris Catalase	2807	80.000
1462	AB012918	Canis familiaris Catalase	1758	71.619
1463	A78803	unidentified unnamed protein product	918	100.000
1464	A78803	unidentified unnamed protein product	341	67.969
1465	D88010	Homo sapiens ribosomal protein S13	386	83.562
1466	M23613	Homo sapiens nucleophosmin	534	59.639
1467	M23613	Homo sapiens nucleophosmin	1029	88.780
1468	M23613	Homo sapiens nucleophosmin	877	100.000
1469	M23613	Homo sapiens nucleophosmin	789	85.517
1470	M23613	Homo sapiens nucleophosmin	1174	78.710
1471	M14567	Dasyurus viverrinus alpha globin	306	58.974
1472	D86850	Homo sapiens HADHB	2742	100.000
1473	D86850	Homo sapiens HADHB	1877	78.537
1474	D86850	Homo sapiens HADHB	173	76.190
1475	D86850	Homo sapiens HADHB	48	30.189
1476	D86850	Homo sapiens HADHB	260	100.000
1477	D86850	Homo sapiens HADHB	1909	80.042
1478	S73591	Homo sapiens VDUP1=1,25-dihydroxyvitamin D-3 up-regulated	758	98.214
1479	S73591	Homo sapiens VDUP1=1,25-dihydroxyvitamin D-3 up-regulated	1074	94.022
1480	S73591	Homo sapiens VDUP1=1,25-dihydroxyvitamin D-3 up-regulated	1664	87.121
1482	M60854	Homo sapiens RPS16	338	53.472
1483	M60854	Homo sapiens RPS16	367	56.173
1484	M60854	Homo sapiens RPS16	237	67.066
1486	M17885	Homo sapiens acidic ribosomal phosphoprotein (P0)	1209	76.027
1487	M17885	Homo sapiens acidic ribosomal phosphoprotein (P0)	785	63.205
1489	AJ012008	Homo sapiens RNCC protein	741	66.792
1490	U08291	Cercopithecus aethiops prion protein	1731	95.918
1491	U08291	Cercopithecus aethiops prion protein	1614	90.514
1492	X55656	Homo sapiens gamma-G globin	958	97.333
1493	X55656	Homo sapiens gamma-G globin	256	62.424

1494	M15386	Homo sapiens gamma-globin	275	65.714
1495	AF042746	Homo sapiens cytochrome c oxidase subunit IV	676	79.167
1496	AF042746	Homo sapiens cytochrome c oxidase subunit IV	356	100.000
1497	AF042746	Homo sapiens cytochrome c oxidase subunit IV	200	47.239
1499	AF010494	Callithrix sp. sorbitol dehydrogenase	310	75.862
1500	AF010494	Callithrix sp. sorbitol dehydrogenase	1547	82.477
1501	AB025357	Anguilla japonica proliferating cell nuclear antigen	751	88.372
1502	AB025357	Anguilla japonica proliferating cell nuclear antigen	557	64.207
1503	X55656	Homo sapiens gamma-G globin	958	97.333
1504	X55656	Homo sapiens gamma-G globin	390	64.072
1505	L20688	Homo sapiens GDP dissociation inhibitor	401	100.000
1506	L20688	Homo sapiens GDP dissociation inhibitor	744	78.365
1507	K03020	Homo sapiens phenylalanine hydroxylase	542	95.699
1508	K03020	Homo sapiens phenylalanine hydroxylase	35	42.105
1509	K03020	Homo sapiens phenylalanine hydroxylase	995	90.698
1510	K03020	Homo sapiens phenylalanine hydroxylase	2149	87.905
1511	AF076191	Trichosurus vulpecula gamma-actin	347	87.302
1512	AF076191	Trichosurus vulpecula gamma-actin	466	82.456
1513	AF076191	Trichosurus vulpecula gamma-actin	1556	82.429
1515	X83218	Homo sapiens ATP synthase, oligomycin sensitivity conferring protein	492	67.982
1516	D29832	Homo sapiens antithrombin III (AT-III) variant	2827	91.057
1517	D29832	Homo sapiens antithrombin III (AT-III) variant	1562	78.395
1518	D13748	Homo sapiens eukaryotic initiation factor 4AI	612	75.676
1519	D13748	Homo sapiens eukaryotic initiation factor 4AI	394	56.757
1520	D13748	Homo sapiens eukaryotic initiation factor 4AI	806	51.937
1521	X55656	Homo sapiens gamma-G globin	141	44.253
1522	M32723	Homo sapiens G-gamma-hemoglobin	298	87.671
1523	M32723	Homo sapiens G-gamma-hemoglobin	567	96.809
1524	M32723	Homo sapiens G-gamma-hemoglobin	113	50.467
1525	AF078848	Homo sapiens BUP	677	67.179
1526	AF078848	Homo sapiens BUP	791	72.340
1527	AF078848	Homo sapiens BUP	293	95.918
1528	AF078848	Homo sapiens BUP	532	77.295
1529	D11428	Homo sapiens PMP-22 (PAS-II/SR13/Gas-3)	255	83.333
1530	D11428	Homo sapiens PMP-22 (PAS-II/SR13/Gas-3)	761	88.889
1531	AF015913	Homo sapiens Skb1Hs	691	88.496
1532	AF015913	Homo sapiens Skb1Hs	926	76.963
1534	AF015913	Homo sapiens Skb1Hs	1021	56.250
1535	AF015913	Homo sapiens Skb1Hs	486	97.101
1536	AF015913	Homo sapiens Skb1Hs	890	90.789
1537	AF015913	Homo sapiens Skb1Hs	3255	89.325

1538	X55687	Lycopersicon esculentum extensin (class II)	43	31.250
1539	X55687	Lycopersicon esculentum extensin (class II)	95	30.000
1541	U94855	Homo sapiens translation initiation factor 3 47 kDa subunit	1292	80.688
1542	U91318	Homo sapiens pM5 (3' partial)	6449	85.726
1543	U91318	Homo sapiens pM5 (3' partial)	2232	88.725
1544	U91318	Homo sapiens pM5 (3' partial)	246	70.968
1545	U91318	Homo sapiens pM5 (3' partial)	284	88.000
1546	U91318	Homo sapiens pM5 (3' partial)	214	100.000
1547	U91318	Homo sapiens pM5 (3' partial)	1561	87.197
1548	U91318	Homo sapiens pM5 (3' partial)	5972	91.810
1549	AJ011915	Homo sapiens synaptosome associated protein of 23 kilodaltons, isoform A	889	74.408
1550	AJ011915	Homo sapiens synaptosome associated protein of 23 kilodaltons, isoform A	1064	92.398
1551	AJ011915	Homo sapiens synaptosome associated protein of 23 kilodaltons, isoform A	945	88.557
1552	U77665	Homo sapiens RNaseP protein P30	497	98.684
1553	U77665	Homo sapiens RNaseP protein P30	243	100.000
1554	U77665	Homo sapiens RNaseP protein P30	613	100.000
1555	U77665	Homo sapiens RNaseP protein P30	1076	78.417
1556	AF110493	Homo sapiens hemoglobin gamma-G	316	62.698
1557	U58658	Homo sapiens unknown	231	70.149
1558	X74776	Drosophila melanogaster ribosomal protein L19	658	58.031
1560	X74776	Drosophila melanogaster ribosomal protein L19	331	53.333
1562	M87503	Homo sapiens IFN-alpha responsive transcription factor	880	87.013
1563	M87503	Homo sapiens IFN-alpha responsive transcription factor	826	98.400
1564	M87503	Homo sapiens IFN-alpha responsive transcription factor	345	77.143
1565	M87503	Homo sapiens IFN-alpha responsive transcription factor	55	31.429
1566	M87503	Homo sapiens IFN-alpha responsive transcription factor	57	39.474
1567	M87503	Homo sapiens IFN-alpha responsive transcription factor	2148	93.687
1569	D16111	Homo sapiens human homologue of rat phosphatidylethanolamine binding protein	48	28.000
1570	D16111	Homo sapiens human homologue of rat phosphatidylethanolamine binding protein	536	75.978
1571	Z83838	Homo sapiens GTPASE-ACTIVATING PROTEIN	564	62.069
1572	Z14136	Homo sapiens spermidine/spermine N1-acetyltransferase	396	39.286
1573	Z14136	Homo sapiens spermidine/spermine N1-acetyltransferase	285	30.769
1574	Z14136	Homo sapiens spermidine/spermine N1-acetyltransferase	206	36.872

1575	S79980	Bos taurus ribosomal protein L37	540	97.468
1576	S79980	Bos taurus ribosomal protein L37	628	97.849
1577	S79980	Bos taurus ribosomal protein L37	423	86.364
1578	M15386	Homo sapiens gamma-globin	328	69.939
1579	X52882	Homo sapiens t-complex polypeptide 1 (AA 1-556)	50	72.727
1580	X52882	Homo sapiens t-complex polypeptide 1 (AA 1-556)	2908	94.118
1581	M23984	Rattus norvegicus mitochondrial phosphate transporter precursor	595	74.497
1582	M23984	Rattus norvegicus mitochondrial phosphate transporter precursor	1206	72.776
1583	M83654	Homo sapiens cytoplasmic phosphotyrosyl protein phosphatase	390	61.261
1584	M83654	Homo sapiens cytoplasmic phosphotyrosyl protein phosphatase	1065	100.000
1585	M83654	Homo sapiens cytoplasmic phosphotyrosyl protein phosphatase	686	82.738
1586	AB007922	Homo sapiens KIAA0453 protein	1078	80.258
1587	AB007922	Homo sapiens KIAA0453 protein	52	71.429
1589	AB007922	Homo sapiens KIAA0453 protein	47	22.222
1590	AB007922	Homo sapiens KIAA0453 protein	613	73.026
1591	AB007922	Homo sapiens KIAA0453 protein	6686	98.769
1593	X87176	Homo sapiens 17beta-hydroxysteroid dehydrogenase	300	80.357
1594	X87176	Homo sapiens 17beta-hydroxysteroid dehydrogenase	120	95.000
1595	X87176	Homo sapiens 17beta-hydroxysteroid dehydrogenase	3682	87.071
1596	M62839	Homo sapiens apolipoprotein H	640	100.000
1597	M62839	Homo sapiens apolipoprotein H	882	99.180
1598	M62839	Homo sapiens apolipoprotein H	651	82.836
1599	M62839	Homo sapiens apolipoprotein H	903	64.644
1600	J02621	Homo sapiens high mobility group protein 14	262	100.000
1601	J02621	Homo sapiens high mobility group protein 14	526	95.000
1602	L08048	Homo sapiens HMG-1	931	86.364
1603	M10014	Homo sapiens fibrinogen gamma chain	387	98.276
1604	M10014	Homo sapiens fibrinogen gamma chain	753	96.460
1605	M10014	Homo sapiens fibrinogen gamma chain	47	19.802
1606	M10014	Homo sapiens fibrinogen gamma chain	1687	77.655
1607	Y11435	Homo sapiens b4 integrin interactor	897	73.059
1608	Y11435	Homo sapiens b4 integrin interactor	527	61.049
1610	S70290	Homo sapiens glutamine synthetase, GS {EC 6.3.1.2}	1802	88.398
1611	AJ005894	Homo sapiens JM27	384	80.612
1612	D84108	Homo sapiens RBP-MS/type 2	1370	100.000
1613	D84108	Homo sapiens RBP-MS/type 2	726	98.230
1614	D84108	Homo sapiens RBP-MS/type 2	980	86.070
1615	D84108	Homo sapiens RBP-MS/type 2	946	92.973
1616	Z81038	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene	63	32.500

1617	Z81038	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene	201	33.929
1618	X55656	Homo sapiens gamma-G globin	413	70.186
1619	U27315	Mus musculus adenine nucleotide translocase-1	369	94.545
1620	U27315	Mus musculus adenine nucleotide translocase-1	696	61.589
1622	AC003973	Homo sapiens ZNF91L	1256	43.371
1623	AC003973	Homo sapiens ZNF91L	3211	43.592
1624	AL050373	Homo sapiens hypothetical protein	744	81.915
1625	AL050373	Homo sapiens hypothetical protein	2078	87.047
1626	X55683	Lycopersicon esculentum extensin (class I)	85	34.783
1627	X55683	Lycopersicon esculentum extensin (class I)	48	25.714
1628	X55683	Lycopersicon esculentum extensin (class I)	120	45.652
1629	X69151	Homo sapiens vacuolar proton-ATPase	1684	85.166
1630	L35546	Homo sapiens gamma-glutamylcysteine synthetase light subunit	51	17.143
1631	L35546	Homo sapiens gamma-glutamylcysteine synthetase light subunit	1274	90.826
1632	L35546	Homo sapiens gamma-glutamylcysteine synthetase light subunit	1242	80.488
1634	AF039698	Homo sapiens antigen NY-CO-33	4175	97.678
1635	X55777	Homo sapiens put. ORF	303	68.966
1637	AC004401	Arabidopsis thaliana putative casein kinase II catalytic subunit	37	44.444
1638	AC004401	Arabidopsis thaliana putative casein kinase II catalytic subunit	789	69.512
1639	AC004401	Arabidopsis thaliana putative casein kinase II catalytic subunit	1458	69.967
1640	AC004401	Arabidopsis thaliana putative casein kinase II catalytic subunit	44	39.130
1641	AC004401	Arabidopsis thaliana putative casein kinase II catalytic subunit	1363	67.705
1642	U58658	Homo sapiens unknown	271	65.789
1643	M32724	Homo sapiens A-gamma-hemoglobin	815	100.000
1644	M32724	Homo sapiens A-gamma-hemoglobin	202	54.861
1645	X17459	Mus musculus J kappa RS-binding protein	525	90.805
1647	X17459	Mus musculus J kappa RS-binding protein	380	78.313
1648	X17459	Mus musculus J kappa RS-binding protein	974	93.631
1649	X17459	Mus musculus J kappa RS-binding protein	1035	98.851
1650	X17459	Mus musculus J kappa RS-binding protein	892	95.322
1651	X17459	Mus musculus J kappa RS-binding protein	2483	83.778
1652	X92485	Plasmodium vivax pva1	175	50.000
1653	Z75331	Homo sapiens nuclear protein SA-2	52	48.000

1654	Z75331	Homo sapiens nuclear protein SA-2	7303	98.883
1655	AF126736	Homo sapiens ubiquitin processing protease	5044	94.168
1656	AF126736	Homo sapiens ubiquitin processing protease	46	25.000
1657	AF126736	Homo sapiens ubiquitin processing protease	4893	95.995
1658	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	634	65.217
1659	M76979	Homo sapiens pigment epithelial-differentiating factor	1276	73.258
1660	AF093673	Cricetulus griseus layilin	606	85.437
1661	AF093673	Cricetulus griseus layilin	496	69.231
1662	AF093673	Cricetulus griseus layilin	97	100.000
1664	AF093673	Cricetulus griseus layilin	45	29.545
1665	AF093673	Cricetulus griseus layilin	41	27.273
1666	AF093673	Cricetulus griseus layilin	44	27.273
1667	AF093673	Cricetulus griseus layilin	43	83.333
1668	AF093673	Cricetulus griseus layilin	51	27.660
1669	AF093673	Cricetulus griseus layilin	1928	81.948
1670	AF174599	Homo sapiens F-box protein Fbx11	1279	95.431
1672	X80638	Mus musculus p21RhoC	545	61.722
1673	AB000407	Gallus gallus DNA topoisomerase I	477	46.396
1674	AB000407	Gallus gallus DNA topoisomerase I	2736	70.536
1675	L10908	Mus musculus Gcap1 gene product	83	47.059
1676	Z48166	Schizosaccharomyces pombe gar2	53	18.248
1677	Z48166	Schizosaccharomyces pombe gar2	140	25.287
1678	L24521	Homo sapiens transformation-related protein	334	62.766
1679	U17332	Mus musculus ribosomal protein L9	245	52.356
1681	X92485	Plasmodium vivax pval	68	37.931
1683	X92485	Plasmodium vivax pval	68	41.176
1684	X92485	Plasmodium vivax pval	94	59.091
1685	X92485	Plasmodium vivax pval	67	30.882
1686	X92485	Plasmodium vivax pval	76	28.873
1687	X92485	Plasmodium vivax pval	65	31.343
1689	X92485	Plasmodium vivax pval	58	26.667
1690	X92485	Plasmodium vivax pval	284	47.059
1691	X55777	Homo sapiens put. ORF	51	32.143
1692	X55777	Homo sapiens put. ORF	360	57.426
1693	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	695	62.842
1694	X51754	Homo sapiens lambda-immunoglobulin light chain	925	77.366
1695	X99699	Homo sapiens XIAP associated factor-1 (ZAP-1)	406	98.214
1696	X99699	Homo sapiens XIAP associated factor-1 (ZAP-1)	2184	98.738
1697	Z47547	Chondrus crispus unique orf	79	38.298
1698	AL117608	Homo sapiens hypothetical protein	39	47.059
1699	AL117608	Homo sapiens hypothetical protein	800	100.000
1700	AL117608	Homo sapiens hypothetical protein	344	84.783
1701	AL031910	Leishmania major hypothetical protein L2743.10	114	42.857

1702	X90857	Homo sapiens -14	717	84.138
1703	X90857	Homo sapiens -14	861	98.630
1704	X90857	Homo sapiens -14	957	82.979
1705	X90857	Homo sapiens -14	239	100.000
1706	X90857	Homo sapiens -14	900	30.323
1707	X90857	Homo sapiens -14	43	35.484
1708	X90857	Homo sapiens -14	250	88.636
1709	X90857	Homo sapiens -14	188	80.000
1710	X90857	Homo sapiens -14	2759	91.379
1711	X02345	Pan troglodytes beta-globin	138	54.545
1712	X02490	Homo sapiens longest open reading frame	558	81.132
1713	X02490	Homo sapiens longest open reading frame	389	62.500
1714	X55777	Homo sapiens put. ORF	349	62.921
1715	X17576	Homo sapiens nck protein (AA 1-377)	2018	90.237
1716	X88799	Oryza sativa DNA binding protein	115	34.409
1717	L10908	Mus musculus Gcap1 gene product	132	33.846
1718	J04973	Homo sapiens core protein II precursor	1292	72.708
1719	AB008164	Homo sapiens ST1C2	657	86.667
1720	AB008164	Homo sapiens ST1C2	1799	70.476
1721	AB008164	Homo sapiens ST1C2	1337	91.030
1722	Z70290	Sordaria macrospora alpha-tubulin	807	59.000
1723	Z70290	Sordaria macrospora alpha-tubulin	1594	64.333
1724	Z70290	Sordaria macrospora alpha-tubulin	1700	66.524
1725	AF084256	Homo sapiens beta glucuronidase isoform d	176	59.615
1726	U07973	Gallus gallus alpha-1 collagen type III	77	37.778
1727	U07973	Gallus gallus alpha-1 collagen type III	265	28.405
1728	L77967	Ovis aries small proline-rich protein with paired repeat	84	31.250
1729	U79260	Homo sapiens unknown	268	44.203
1730	U58658	Homo sapiens unknown	232	67.213
1759	U53831	Homo sapiens putative collagen homolog protein-b	58	46.154
1760	U53831	Homo sapiens putative collagen homolog protein-b	133	41.270
1762	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	37	37.500
1764	U14009	Pyrus communis arabinogalactan-protein	138	35.156
1766	D50579	Homo sapiens carboxylesterase precursor	1286	91.038
1767	D50579	Homo sapiens carboxylesterase precursor	2704	89.860
1768	L33989	Homo sapiens ORF; putative	67	31.081
1769	L33989	Homo sapiens ORF; putative	113	32.456
1770	AJ243460	Leishmania major proteophosphoglycan	72	23.622
1771	AJ243460	Leishmania major proteophosphoglycan	58	26.786
1772	AJ243460	Leishmania major proteophosphoglycan	178	26.104
1773	AJ243460	Leishmania major proteophosphoglycan	178	26.697
1774	U07974	Gallus gallus unknown	71	28.846
1775	U07974	Gallus gallus unknown	100	30.435

1776	U07974	Gallus gallus unknown	124	27.211
1777	K02576	Homo sapiens salivary proline-rich protein 1	172	37.748
1778	X55687	Lycopersicon esculentum extensin (class II)	87	31.579
1779	M15530	Homo sapiens B-cell growth factor	169	39.167
1780	L17318	Rattus norvegicus proline-rich proteoglycan	185	30.542
1782	Z28396	Sus scrofa glucosephosphate isomerase	1444	83.582
1783	Z28396	Sus scrofa glucosephosphate isomerase	2091	78.191
1785	M17885	Homo sapiens acidic ribosomal phosphoprotein (P0)	839	60.641
1786	AC002073	Homo sapiens Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111)	741	100.000
1787	AC002073	Homo sapiens Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111)	1683	97.338
1788	AC002073	Homo sapiens Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111)	38	20.312
1789	AC002073	Homo sapiens Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111)	1527	94.697
1790	U90446	Mus musculus RNase L inhibitor	3265	92.257
1791	X71129	Homo sapiens electron transfer flavoprotein beta subunit	465	73.729
1792	X71129	Homo sapiens electron transfer flavoprotein beta subunit	656	64.878
1793	X71129	Homo sapiens electron transfer flavoprotein beta subunit	336	45.509
1794	X71129	Homo sapiens electron transfer flavoprotein beta subunit	48	19.588
1795	X71129	Homo sapiens electron transfer flavoprotein beta subunit	973	79.921
1796	X78992	Homo sapiens ERF-2	2655	86.032
1797	X78992	Homo sapiens ERF-2	2815	94.366
1798	AB020724	Homo sapiens KIAA0917 protein	447	75.000
1800	AB020724	Homo sapiens KIAA0917 protein	2983	87.500

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1801	D13286	Homo sapiens glucocerebrosidase	428	100.000
1802	D13286	Homo sapiens glucocerebrosidase	892	98.561
1803	D13286	Homo sapiens glucocerebrosidase	3227	95.379
1804	D13286	Homo sapiens glucocerebrosidase	2728	86.989
1805	L24521	Homo sapiens transformation-related protein	376	62.385
1806	AF107406	Homo sapiens GW128	42	38.462
1807	AF107406	Homo sapiens GW128	46	83.333
1808	AF107406	Homo sapiens GW128	185	48.980
1809	L22253	Homo sapiens 9G8 splicing factor	1200	57.664
1810	L22253	Homo sapiens 9G8 splicing factor	1203	90.909
1811	J04765	Homo sapiens osteopontin	907	90.476
1812	J04765	Homo sapiens osteopontin	1090	81.481
1813	J04794	Homo sapiens aldehyde reductase (EC 1.1.1.2)	471	98.592
1814	J04794	Homo sapiens aldehyde reductase (EC 1.1.1.2)	318	87.719
1815	J04794	Homo sapiens aldehyde reductase (EC 1.1.1.2)	890	71.637
1817	AF151874	Homo sapiens CGI-116 protein	177	93.103
1818	AF151874	Homo sapiens CGI-116 protein	618	85.500
1819	L10908	Mus musculus Gcap1 gene product	116	28.571
1820	AF110763	Homo sapiens skeletal muscle LIM-protein 1	1863	78.386
1821	AF110763	Homo sapiens skeletal muscle LIM-protein 1	1735	93.262
1822	M69297	Homo sapiens ORF 3	224	37.121
1823	AF088982	Homo sapiens heat shock protein hsp40-3	1872	92.045
1824	U27460	Homo sapiens uridine diphosphoglucose pyrophosphorylase	277	100.000
1825	U27460	Homo sapiens uridine diphosphoglucose pyrophosphorylase	2122	85.575
1826	X79855	Homo sapiens troponin T	341	72.477
1827	L49470	Mus musculus troponin T fast skeletal muscle isoform	301	77.612
1828	L49470	Mus musculus troponin T fast skeletal muscle isoform	481	95.062
1829	L49470	Mus musculus troponin T fast skeletal muscle isoform	533	88.889
1830	L49470	Mus musculus troponin T fast skeletal muscle isoform	970	78.810
1831	A75737	Homo sapiens unnamed protein product	1642	71.498
1832	U46756	Gallus gallus CLE7	511	87.619
1833	U46756	Gallus gallus CLE7	793	73.626
1834	U46756	Gallus gallus CLE7	527	59.922
1835	AF174429	Arabidopsis thaliana FH protein interacting protein FIP2	206	34.043
1836	AF174429	Arabidopsis thaliana FH protein interacting protein FIP2	170	41.250
1837	AF174429	Arabidopsis thaliana FH protein interacting protein FIP2	206	34.043
1838	AF174429	Arabidopsis thaliana FH protein interacting protein FIP2	430	31.683

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1839	U60882	Rattus norvegicus protein arginine N-methyltransferase	195	80.000
1840	U60882	Rattus norvegicus protein arginine N-methyltransferase	965	70.732
1841	M37984	Homo sapiens slow twitch skeletal/cardiac muscle troponin C	101	100.000
1842	M37984	Homo sapiens slow twitch skeletal/cardiac muscle troponin C	414	71.765
1843	AL049483	Arabidopsis thaliana putative leucine-rich-repeat protein	349	30.464
1844	M14156	Homo sapiens insulin-like growth factor IB	421	63.303
1845	M14156	Homo sapiens insulin-like growth factor IB	599	71.223
1846	M14156	Homo sapiens insulin-like growth factor IB	599	71.223
1847	M14156	Homo sapiens insulin-like growth factor IB	1356	100.000
1848	M14156	Homo sapiens insulin-like growth factor IB	560	71.006
1849	Z50109	Unknown similar to 60S ribosomal protein; cDNA EST EMBL:T01767 comes from this gene; cDNA EST EMBL:	292	60.000
1850	Z74167	Saccharomyces cerevisiae ORF YDL119c	102	37.736
1852	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	304	62.821
1853	U01849	Trypanosoma brucei ORF2	148	27.559
1854	L19783	Homo sapiens GPI-H	806	82.927
1855	L19783	Homo sapiens GPI-H	309	97.778
1856	L19783	Homo sapiens GPI-H	841	84.694
1857	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	1000	73.333
1858	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	827	83.529
1859	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	107	100.000
1860	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	1028	82.101
1861	D21235	Homo sapiens HHR23A protein	586	90.000
1862	D21235	Homo sapiens HHR23A protein	634	97.115
1863	D21235	Homo sapiens HHR23A protein	1167	78.364
1864	AB028956	Homo sapiens KIAA1033 protein	629	91.129
1865	AB028956	Homo sapiens KIAA1033 protein	1170	80.658
1866	AB028956	Homo sapiens KIAA1033 protein	276	79.630
1867	AB028956	Homo sapiens KIAA1033 protein	175	90.909
1868	AB028956	Homo sapiens KIAA1033 protein	889	86.624
1869	AB028956	Homo sapiens KIAA1033 protein	7118	96.669
1871	L01131	Homo sapiens decorin	849	91.083
1872	L01131	Homo sapiens decorin	1017	55.710
1873	L01131	Homo sapiens decorin	1699	92.113
1874	L01131	Homo sapiens decorin	1206	78.706
1875	U50545	Cavia porcellus cytosolic beta-glucosidase	2621	80.810
1876	AF038953	Homo sapiens E25 protein	949	77.978

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1877	U79260	Homo sapiens unknown	189	49.485
1878	AJ005559	Mus musculus SPR2A protein	113	29.762
1880	X71355	Homo sapiens Sodium-Phosphate Transport System 1	2564	91.755
1881	AJ223980	Homo sapiens BCL7C	305	70.588
1882	AJ223980	Homo sapiens BCL7C	978	85.068
1883	M15530	Homo sapiens B-cell growth factor	186	45.570
1884	X66285	Mus musculus HC1 ORF	157	33.846
1885	AF053233	Homo sapiens endobrevin	330	94.643
1886	AF053233	Homo sapiens endobrevin	348	92.424
1887	AF053233	Homo sapiens endobrevin	373	100.000
1888	AF053233	Homo sapiens endobrevin	334	84.615
1889	AF053233	Homo sapiens endobrevin	329	79.048
1890	D21820	Lilium longiflorum ORF	172	37.681
1893	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	353	29.579
1894	X71980	Torpedo marmorata alpha-tubulin	1010	89.362
1895	X71980	Torpedo marmorata alpha-tubulin	1689	84.096
1896	M11147	Homo sapiens ferritin light chain	316	65.241
1897	M20472	Homo sapiens clathrin light-chain A	525	78.761
1898	M20472	Homo sapiens clathrin light-chain A	374	98.276
1899	M20472	Homo sapiens clathrin light-chain A	861	74.000
1900	M20472	Homo sapiens clathrin light-chain A	919	77.533
1901	D14531	Homo sapiens 'human homologue of rat ribosomal protein L9'	865	78.836
1902	D14531	Homo sapiens 'human homologue of rat ribosomal protein L9'	371	63.473
1903	U79260	Homo sapiens unknown	376	66.337
1905	X97276	Sparus aurata metallothionein A	86	43.750
1906	AC006592	Arabidopsis thaliana unknown protein	134	33.333
1907	AF115850	Homo sapiens PAR protein	523	87.640
1908	AF115850	Homo sapiens PAR protein	53	25.600
1909	AF115850	Homo sapiens PAR protein	1418	100.000
1910	AF115850	Homo sapiens PAR protein	212	89.583
1911	AF115850	Homo sapiens PAR protein	756	68.966
1912	D00682	Homo sapiens cofilin	414	68.605
1913	M20372	Homo sapiens ornithine decarboxylase (EC 4.1.1.17)	1307	81.766
1914	X92485	Plasmodium vivax pval	359	62.000
1915	AF026689	Homo sapiens prostate-specific transglutaminase	98	55.000
1916	X69392	Homo sapiens ribosomal protein L26	314	64.706
1917	L48937	Homo sapiens ptp-IV1b, PTP-IV1 gene product	923	83.234
1918	L48937	Homo sapiens ptp-IV1b, PTP-IV1 gene product	406	98.413
1919	L48937	Homo sapiens ptp-IV1b, PTP-IV1 gene product	41	20.370
1920	L48937	Homo sapiens ptp-IV1b, PTP-IV1 gene product	580	71.910
1921	Z81029	Unknown Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes	281	34.343

1922	AL021366	Homo sapiens cICK0721Q.5 (polypeptide from patented cDNA EMBL:E06811)	298	100.000
1924	AL021366	Homo sapiens cICK0721Q.5 (polypeptide from patented cDNA EMBL:E06811)	668	86.466
1925	AL021366	Homo sapiens cICK0721Q.5 (polypeptide from patented cDNA EMBL:E06811)	407	100.000
1927	AL021366	Homo sapiens cICK0721Q.5 (polypeptide from patented cDNA EMBL:E06811)	348	67.857
1928	M15530	Homo sapiens B-cell growth factor	166	69.048
1929	X55777	Homo sapiens put. ORF	324	56.989
1930	Z32554	Cricetulus griseus epsilon-COP; ldlFp	970	64.961
1931	Z32554	Cricetulus griseus epsilon-COP; ldlFp	485	54.974
1932	Z32554	Cricetulus griseus epsilon-COP; ldlFp	693	65.741
1934	X65550	Homo sapiens antigen of the monoclonal antibody Ki-67	21240	99.908
1935	X65550	Homo sapiens antigen of the monoclonal antibody Ki-67	17404	8.946
1936	U97553	murine herpesvirus 68 unknown	120	37.931
1937	AB030905	Homo sapiens Heterochromatin protein 1 gamma	1157	99.422
1938	AB030905	Homo sapiens Heterochromatin protein 1 gamma	42	25.926
1939	AB030905	Homo sapiens Heterochromatin protein 1 gamma	36	24.324
1940	AB030905	Homo sapiens Heterochromatin protein 1 gamma	297	97.826
1941	AB030905	Homo sapiens Heterochromatin protein 1 gamma	44	35.714
1942	AB030905	Homo sapiens Heterochromatin protein 1 gamma	542	79.775
1943	AF084256	Homo sapiens beta glucuronidase isoform d	237	66.667
1944	D88378	Homo sapiens proteasome inhibitor hPI31 subunit	756	81.818
1945	D88378	Homo sapiens proteasome inhibitor hPI31 subunit	1277	83.154
1946	Y07566	Homo sapiens RIT (Ric-related gene expressed in many tissues)	744	77.729
1947	M15530	Homo sapiens B-cell growth factor	49	39.130
1948	M15530	Homo sapiens B-cell growth factor	152	68.421
1949	U79260	Homo sapiens unknown	207	37.398
1950	AF119297	Homo sapiens neuroendocrine-specific protein-like protein 1	327	96.078
1952	AF119297	Homo sapiens neuroendocrine-specific protein-like protein 1	486	78.846
1953	AF119297	Homo sapiens neuroendocrine-specific protein-like protein 1	1074	87.866
1954	M92296	Pongo pygmaeus gamma-1 globin	219	59.712
1955	AB020981	Homo sapiens cyclin B2	254	100.000
1956	AB020981	Homo sapiens cyclin B2	638	98.039
1957	AB020981	Homo sapiens cyclin B2	1643	81.509
1958	D90861	Escherichia coli similar to	141	36.905
1959	D90861	Escherichia coli similar to	65	30.357
1960	D90861	Escherichia coli similar to	321	34.528

1961	D90861	Escherichia coli similar to	196	42.241
1962	M64716	Homo sapiens ribosomal protein	587	97.872
1963	M64716	Homo sapiens ribosomal protein	126	38.060
1964	AC004382	Homo sapiens Unknown gene product	947	98.052
1965	AC004382	Homo sapiens Unknown gene product	834	68.376
1966	AC004382	Homo sapiens Unknown gene product	1653	81.013
1967	X54941	Homo sapiens Cks1 protein homologue	304	62.393
1968	X56932	Homo sapiens 23 kD highly basic protein	469	75.829
1969	M14820	Trypanosoma brucei ORF2 bases 1807-2850; first start codon at 2032; putative	119	29.167
1971	AL035064	Schizosaccharomyces pombe queuine trna-ribosyltransferase	1057	43.867
1972	S62936	Homo sapiens PRB1S precursor protein-basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor {C-terminal}	222	28.241
1973	M25660	Homo sapiens beta-hemoglobin	209	71.930
1974	D28482	Homo sapiens SCR2	327	100.000
1975	D28482	Homo sapiens SCR2	287	100.000
1976	D28482	Homo sapiens SCR2	1183	62.147
1977	D28482	Homo sapiens SCR2	1785	84.412
1978	D28482	Homo sapiens SCR2	2033	76.221
1979	U79260	Homo sapiens unknown	168	57.377
1980	D16217	Homo sapiens calpastatin	621	98.980
1981	D16217	Homo sapiens calpastatin	61	19.780
1982	D16217	Homo sapiens calpastatin	4082	93.723
1983	D16217	Homo sapiens calpastatin	2485	94.444
1984	D16217	Homo sapiens calpastatin	3586	93.287
1985	X57801	Homo sapiens immunoglobulin lambda light chain	538	54.878
1986	AF155114	Homo sapiens NY-REN-57 antigen	107	58.065
1988	AF155114	Homo sapiens NY-REN-57 antigen	43	28.000
1989	AF155114	Homo sapiens NY-REN-57 antigen	39	29.268
1990	AF155114	Homo sapiens NY-REN-57 antigen	503	100.000
1991	AF155114	Homo sapiens NY-REN-57 antigen	2284	89.796
1992	X79417	Sus scrofa 40S ribosomal protein S12	240	97.222
1993	X79417	Sus scrofa 40S ribosomal protein S12	147	70.270
1994	X79417	Sus scrofa 40S ribosomal protein S12	263	68.696
1995	J04495	Macaca mulatta alpha-globin	895	96.479
1996	J04495	Macaca mulatta alpha-globin	290	63.281
1997	AF044958	Homo sapiens NADH:ubiquinone oxidoreductase ASH1 subunit	216	60.000
1998	S85655	Homo sapiens prohibitin	1224	82.288
1999	S85655	Homo sapiens prohibitin	680	93.333
2000	AF083929	Mus musculus ES18	187	39.216
2001	AL023286	Schizosaccharomyces pombe hypothetical protein	270	57.333
2002	AL023286	Schizosaccharomyces pombe hypothetical protein	259	43.094
2003	AF051137	Monodelphis domestica ribosomal protein S4 Y isoform	676	68.966
2004	AF051137	Monodelphis domestica ribosomal	675	67.491

		protein S4 Y isoform		
2005	L05092	Homo sapiens ribosomal protein L11	756	77.914
2006	L05092	Homo sapiens ribosomal protein L11	38	66.667
2007	L05092	Homo sapiens ribosomal protein L11	320	100.000
2008	L05092	Homo sapiens ribosomal protein L11	406	62.694
2009	M15530	Homo sapiens B-cell growth factor	205	57.407
2010	L41558	Rattus rattus rBB1 gene product	122	58.333
2011	AF043183	Homo sapiens T cell receptor beta chain	245	66.667
2012	AF043183	Homo sapiens T cell receptor beta chain	1196	94.924
2013	AF043183	Homo sapiens T cell receptor beta chain	1772	92.038
2014	D83489	Tokudaia osimensis part of Zfy containing 11 zinc finger motifs	48	44.444
2015	D83489	Tokudaia osimensis part of Zfy containing 11 zinc finger motifs	192	25.263
2016	AF047659	Caenorhabditis elegans No definition line found	331	47.748
2017	AF047659	Caenorhabditis elegans No definition line found	875	42.998
2018	X73974	Homo sapiens ribosomal protein L4	784	93.130
2019	X73974	Homo sapiens ribosomal protein L4	1155	77.852
2020	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	4620	92.468
2021	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	298	98.039
2022	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	855	92.958
2023	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	61	30.000
2024	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	348	91.525
2026	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	66	19.565
2027	AF085693	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein	2624	87.928
2028	U22376	Homo sapiens alternatively spliced product using exon 13A	366	40.175
2029	M15530	Homo sapiens B-cell growth factor	197	43.689
2030	S47413	Arabidopsis thaliana, C24, Peptide	43	37.500

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		Partial, 112 aa glycine-rich protein, atGRP {clone atGRP-4}		
2031	S47413	Arabidopsis thaliana, C24, Peptide Partial, 112 aa glycine-rich protein, atGRP {clone atGRP-4}	111	31.776
2032	U83176	Mus musculus ROSA26AS	43	40.000
2033	U83176	Mus musculus ROSA26AS	52	22.727
2034	U83176	Mus musculus ROSA26AS	2049	82.500
2035	U83176	Mus musculus ROSA26AS	1952	79.419
2036	U41654	Homo sapiens adenovirus E3-14.7K interacting protein 1	925	75.767
2037	X91911	Homo sapiens rtvp-1	992	86.131
2038	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	147	68.571
2039	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	29.412
2040	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	23.932
2041	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	36.000
2042	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	42	30.612
2043	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	74	31.783
2044	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	397	32.500
2045	X61109	Gorilla gorilla beta-globin	501	80.952
2046	X87212	Homo sapiens cathepsin C	503	98.667
2047	X87212	Homo sapiens cathepsin C	1052	95.152
2048	X87212	Homo sapiens cathepsin C	734	73.885
2049	X87212	Homo sapiens cathepsin C	1746	87.703
2051	M74090	Homo sapiens TB2	212	96.970
2052	M74090	Homo sapiens TB2	683	70.388
2054	M19419	Mus musculus proline-rich salivary protein	105	32.394
2055	M19419	Mus musculus proline-rich salivary protein	105	37.778
2056	M19419	Mus musculus proline-rich salivary protein	141	29.167
2057	M19419	Mus musculus proline-rich salivary protein	141	29.050
2058	M19419	Mus musculus proline-rich salivary protein	165	35.417
2059	AL050019	Homo sapiens hypothetical protein	733	65.455
2060	AL050019	Homo sapiens hypothetical protein	4704	98.143
2061	X15606	Homo sapiens ICAM-2 preprotein (AA -21 to 254)	623	72.759
2062	X73541	Saccharomyces cerevisiae ORF YKR412	165	21.394
2063	AB021288	Homo sapiens beta 2-microglobulin	539	85.833
2064	M69043	Homo sapiens MAD3	310	95.918
2065	M69043	Homo sapiens MAD3	606	50.730
2066	M69043	Homo sapiens MAD3	1164	75.301
2068	U46690	Mus musculus ATP-dependent RNA helicase	663	90.909

2069	U46690	Mus musculus ATP-dependent RNA helicase	342	66.667
2070	U46690	Mus musculus ATP-dependent RNA helicase	1134	63.690
2071	D80010	Homo sapiens KIAA0188	621	89.381
2072	D80010	Homo sapiens KIAA0188	51	37.931
2073	D80010	Homo sapiens KIAA0188	5542	98.554
2074	L20868	Homo sapiens ribosomal protein L4	784	93.130
2075	L20868	Homo sapiens ribosomal protein L4	1206	70.732
2076	L28677	Tetrahymena pyriformis ORF3	80	25.714
2077	AF151876	Homo sapiens CGI-118 protein	414	97.333
2078	AF151876	Homo sapiens CGI-118 protein	751	72.685
2079	X02490	Homo sapiens longest open reading frame	313	55.689
2080	L24521	Homo sapiens transformation-related protein	262	67.857
2081	D23661	Homo sapiens ribosomal protein L37	363	78.652
2082	AF060228	Homo sapiens retinoic acid receptor responder 3	570	76.471
2083	AF043181	Homo sapiens T cell receptor beta chain	272	38.095
2084	AF043181	Homo sapiens T cell receptor beta chain	729	88.000
2085	AF043181	Homo sapiens T cell receptor beta chain	1755	89.441
2086	U30221	Crithidia fasciculata NADH dehydrogenase subunit 5	105	29.630
2088	X94335	Saccharomyces cerevisiae YOR3160w	38	37.500
2089	X94335	Saccharomyces cerevisiae YOR3160w	49	28.571
2090	X94335	Saccharomyces cerevisiae YOR3160w	49	45.455
2092	X94335	Saccharomyces cerevisiae YOR3160w	267	60.000
2093	X94335	Saccharomyces cerevisiae YOR3160w	61	23.762
2094	X94335	Saccharomyces cerevisiae YOR3160w	658	48.819
2095	AF031079	Camptotheca acuminata isopentenyl diphosphate isomerase I	197	49.231
2096	AF031079	Camptotheca acuminata isopentenyl diphosphate isomerase I	147	47.727
2097	AF031079	Camptotheca acuminata isopentenyl diphosphate isomerase I	607	50.000
2098	U80744	Homo sapiens CTG4a	403	76.842
2099	U80744	Homo sapiens CTG4a	796	68.421
2100	U80744	Homo sapiens CTG4a	921	100.000
2101	U80744	Homo sapiens CTG4a	701	80.690
2102	AB004316	Bos taurus mitochondrial methionyl-tRNA transformylase	1915	83.967
2103	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	407	96.970
2104	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	682	98.230
2105	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	222	100.000
2106	D50918	Homo sapiens The KIAA0128 gene is related to cdc10.	1973	94.277
2107	D50918	Homo sapiens The KIAA0128 gene is	2413	95.305

		related to cdc10.		
2108	AJ011916	Homo sapiens hypothetical protein	1170	79.098
2109	AJ011916	Homo sapiens hypothetical protein	901	97.887
2110	AJ011916	Homo sapiens hypothetical protein	1179	90.909
2111	U28917	Mus musculus 60S ribosomal protein	548	67.453
2112	X64707	Homo sapiens BBC1	644	69.091
2114	AF098798	Homo sapiens unknown	363	62.931
2115	AF098798	Homo sapiens unknown	987	99.342
2116	AF098798	Homo sapiens unknown	701	61.395
2117	AF098798	Homo sapiens unknown	469	98.551
2118	AF098798	Homo sapiens unknown	304	92.453
2119	AF098798	Homo sapiens unknown	1780	88.301
2120	M32865	Homo sapiens Ku protein subunit	402	96.970
2121	M32865	Homo sapiens Ku protein subunit	1747	59.744
2122	X92485	Plasmodium vivax pval	284	42.857
2123	AF172066	Homo sapiens retinoic acid repressible protein	886	85.484
2124	U10414	Caenorhabditis elegans Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2	326	60.526
2125	U10414	Caenorhabditis elegans Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2	433	46.522
2126	U10414	Caenorhabditis elegans Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2	1865	48.378
2128	AF071317	Mus musculus COP9 complex subunit 7b	1318	72.836
2129	AC002388	Arabidopsis thaliana hypothetical protein, 5' partial	54	53.333
2130	AC002388	Arabidopsis thaliana hypothetical protein, 5' partial	177	37.415
2131	X69556	Bos taurus cpn10 protein	418	100.000
2132	X69556	Bos taurus cpn10 protein	418	100.000
2133	X69556	Bos taurus cpn10 protein	303	97.826
2134	X69556	Bos taurus cpn10 protein	569	78.571
2135	X69556	Bos taurus cpn10 protein	207	63.514
2137	U62673	Mus musculus histone H2a(B)-613	427	77.612
2138	X94335	Saccharomyces cerevisiae YOR3513c	38	22.857
2139	X94335	Saccharomyces cerevisiae YOR3513c	35	25.000
2140	X94335	Saccharomyces cerevisiae YOR3513c	56	28.205
2141	X94335	Saccharomyces cerevisiae YOR3513c	530	57.297
2142	U05313	Trypanosoma brucei CR3	84	37.143
2143	X73434	Ovis aries KAP5.4 keratin protein	97	40.698
2145	X73434	Ovis aries KAP5.4 keratin protein	201	32.022
2146	X73434	Ovis aries KAP5.4 keratin protein	197	36.571
2147	X91809	Homo sapiens GAIP	1312	93.839
2148	AF045244	Klebsiella pneumoniae ribitol kinase	213	36.567
2149	AF045244	Klebsiella pneumoniae ribitol kinase	314	47.000
2150	AF045244	Klebsiella pneumoniae ribitol kinase	175	71.875
2151	AF045244	Klebsiella pneumoniae ribitol kinase	154	34.021
2152	AF045244	Klebsiella pneumoniae ribitol kinase	1248	44.358

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2153	Z71261	Caenorhabditis elegans Similarity to Bovine protein kinase C inhibitor 1 (SW:IPK1 BOVIN)	350	40.523
2154	Z71261	Caenorhabditis elegans Similarity to Bovine protein kinase C inhibitor 1 (SW:IPK1 BOVIN)	215	44.048
2155	X15081	Crithidia fasciculata MURF2 protein (AA 1-348)	197	25.714
2157	U15174	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 3	969	86.500
2158	AJ007418	Homo sapiens phenol sulfotransferase	623	94.898
2159	AJ007418	Homo sapiens phenol sulfotransferase	604	100.000
2160	AJ007418	Homo sapiens phenol sulfotransferase	822	97.600
2161	AJ007418	Homo sapiens phenol sulfotransferase	331	60.638
2162	AJ007418	Homo sapiens phenol sulfotransferase	1095	82.237
2163	Y00144	Lycopersicon esculentum biotin-binding protein	131	36.923
2164	Y00144	Lycopersicon esculentum biotin-binding protein	122	45.283
2166	U43701	Homo sapiens ribosomal protein L23a	297	80.702
2167	U43701	Homo sapiens ribosomal protein L23a	513	62.238
2168	U43701	Homo sapiens ribosomal protein L23a	436	100.000
2169	U43701	Homo sapiens ribosomal protein L23a	425	88.095
2170	U43701	Homo sapiens ribosomal protein L23a	640	78.981
2171	AF172095	Picea rubens unknown	154	27.206
2172	AF172095	Picea rubens unknown	68	27.119
2173	AF172095	Picea rubens unknown	147	28.947
2175	AF115345	Homo sapiens calcium-regulated heat stable protein CRHSP-24	456	71.875
2176	Z30423	Caenorhabditis elegans T20G5.9	51	25.000
2177	Z30423	Caenorhabditis elegans T20G5.9	136	28.169
2178	X54162	Homo sapiens 64 Kd autoantigen	152	31.522
2179	X54162	Homo sapiens 64 Kd autoantigen	151	32.967
2180	X54162	Homo sapiens 64 Kd autoantigen	95	44.118
2181	X54162	Homo sapiens 64 Kd autoantigen	952	38.447
2182	AB007941	Homo sapiens KIAA0472 protein	221	100.000
2183	AB007941	Homo sapiens KIAA0472 protein	2296	97.820
2184	M16715	Gallus gallus collagen type IX	104	40.541
2185	X83703	Homo sapiens nuclear protein	1686	90.123
2186	AL132880	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	90	41.667
2187	AL132880	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	46	26.190
2189	AL132880	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	167	27.083
2190	AF039568	Homo sapiens vesicle trafficking protein	641	67.836
2191	AF039568	Homo sapiens vesicle trafficking protein	1304	89.167
2192	X79444	Homo sapiens endonuclease	1884	88.288
2193	X79444	Homo sapiens endonuclease	466	84.211
2194	X79444	Homo sapiens endonuclease	1758	97.315
2195	AF000412	Plasmodium berghei merozoite surface protein-1	151	36.364

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2196	AC004955	Homo sapiens supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan	693	87.500
2197	AC004955	Homo sapiens supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan	159	100.000
2198	AC004955	Homo sapiens supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan	3159	84.992
2199	X92485	Plasmodium vivax pval	50	43.333
2200	X92485	Plasmodium vivax pval	174	42.708
2202	AF103731	Homo sapiens putative glycolipid transfer protein	2529	100.000
2203	AF103731	Homo sapiens putative glycolipid transfer protein	852	46.835
2204	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST E	58	22.222
2205	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST B	58	22.222
2206	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST E	53	34.615
2207	Z75550	Unknown limited similarity with some myosins; cDNA EST EMBL:C08402 comes from this gene; cDNA EST E	374	27.419
2208	AJ243938	Homo sapiens G18.2 protein	111	33.333
2209	AF053368	Mus musculus lysyl oxidase-related protein 2	356	61.000
2210	AF053368	Mus musculus lysyl oxidase-related protein 2	268	71.429
2211	AF053368	Mus musculus lysyl oxidase-related protein 2	341	80.303
2212	AF053368	Mus musculus lysyl oxidase-related protein 2	329	78.788
2214	AF053368	Mus musculus lysyl oxidase-related protein 2	849	81.879
2215	AF053368	Mus musculus lysyl oxidase-related protein 2	1113	59.365
2216	AF053368	Mus musculus lysyl oxidase-related protein 2	1966	84.503
2217	AF053368	Mus musculus lysyl oxidase-related protein 2	4677	88.173
2218	J03191	Homo sapiens profilin	412	100.000
2219	J03191	Homo sapiens profilin	300	58.503
2220	AL031009	Homo sapiens c431H6.1.2 (PUTATIVE novel protein) (PUTATIVE isoform 2)	594	94.898
2221	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	395	48.372
2222	U79260	Homo sapiens unknown	243	59.155
2223	V00599	Homo sapiens beta-tubulin	757	98.261
2224	V00599	Homo sapiens beta-tubulin	1512	82.183
2225	L13291	Homo sapiens ADP-ribosylarginine hydrolase	962	44.789

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2226	AF000944	Rattus norvegicus TFIIA small subunit	376	67.890
2227	AF000944	Rattus norvegicus TFIIA small subunit	195	64.220
2228	U05313	Trypanosoma brucei CR3	88	45.455
2229	X83218	Homo sapiens ATP synthase, oligomycin sensitivity conferring protein	399	100.000
2230	X83218	Homo sapiens ATP synthase, oligomycin sensitivity conferring protein	381	66.957
2231	AC002398	pir B53814 Homo sapiens p20 protein	121	30.097
2232	AC002398	pir B53814 Homo sapiens p20 protein	175	37.956
2233	AC002398	pir B53814 Homo sapiens p20 protein	180	33.858
2234	M37275	Drosophila melanogaster ND4-L gene product	56	15.385
2235	M37275	Drosophila melanogaster ND4-L gene product	49	36.842
2236	M37275	Drosophila melanogaster ND4-L gene product	108	28.947
2238	AF047181	Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH	852	80.435
2239	AF047181	Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH	599	69.849
2240	U79260	Homo sapiens unknown	148	52.083
2242	AF153612	Homo sapiens peroxisomal D3,D2-enoyl-CoA isomerase	1253	76.862
2245	Y11739	Homo sapiens transcription factor	59	35.556
2246	Y11739	Homo sapiens transcription factor	92	23.177
2247	Y11739	Homo sapiens transcription factor	150	32.086
2248	Y11739	Homo sapiens transcription factor	97	39.394
2249	A27282	Homo sapiens TGR-CL3C	85	31.193
2250	A27282	Homo sapiens TGR-CL3C	86	35.897
2251	M69297	Homo sapiens ORF 3	297	51.111
2252	M22332	Homo sapiens unknown protein	159	80.645
2253	M22332	Homo sapiens unknown protein	158	77.419
2254	M22332	Homo sapiens unknown protein	203	60.000
2255	D61391	Homo sapiens phosphoribosypyrophosphate synthetase-associated protein 39	577	100.000
2256	D61391	Homo sapiens phosphoribosypyrophosphate synthetase-associated protein 39	477	100.000
2257	D61391	Homo sapiens phosphoribosypyrophosphate synthetase-associated protein 39	1647	87.123
2260	M83248	Homo sapiens nephropontin	983	88.235
2261	M83248	Homo sapiens nephropontin	1482	89.809
2262	X53778	Homo sapiens uracil DNA glycosylase	870	61.039
2263	X53778	Homo sapiens uracil DNA glycosylase	59	26.000
2264	X53778	Homo sapiens uracil DNA glycosylase	976	77.971
2265	U62326	Rattus norvegicus macrophage migration inhibitory factor	244	61.864
2266	AB024935	Mus musculus Sid3177p	316	56.757
2267	AB024935	Mus musculus Sid3177p	460	72.941
2268	Y13374	Homo sapiens putative prenylated protein	446	96.774
2269	Y13374	Homo sapiens putative prenylated	514	98.529

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		protein		
2270	Y13374	Homo sapiens putative prenylated protein	123	65.714
2271	Y13374	Homo sapiens putative prenylated protein	1106	88.679
2272	AB001993	Homo sapiens glia maturation factor homologous protein	221	100.000
2274	AB001993	Homo sapiens glia maturation factor homologous protein	611	78.195
2275	AB001993	Homo sapiens glia maturation factor homologous protein	445	76.871
2276	AF110812	Mus musculus 25 kDa FK506-binding protein	451	89.041
2277	AF110812	Mus musculus 25 kDa FK506-binding protein	233	97.222
2278	AF110812	Mus musculus 25 kDa FK506-binding protein	685	74.249
2279	Z49148	Homo sapiens ribosomal protein L29	770	77.987
2280	Z49148	Homo sapiens ribosomal protein L29	315	61.453
2281	S71129	Homo sapiens acetylcholinesterase, acetylcholine acetylhydrolase, AChE {I4-E5 domain, alternatively spliced} {EC 3.1.1.7}	80	42.188
2282	L03814	Mus musculus regulatory protein	388	80.000
2283	L03814	Mus musculus regulatory protein	1383	68.263
2284	AJ224997	Rattus norvegicus huntingtin	91	42.308
2285	M15530	Homo sapiens B-cell growth factor	129	36.458
2286	AF007170	Homo sapiens unknown	154	85.714
2287	AF007170	Homo sapiens unknown	1781	58.176
2288	AF007170	Homo sapiens unknown	3584	99.290
2289	U79260	Homo sapiens unknown	245	43.103
2290	AB020725	Homo sapiens KIAA0918 protein	2558	47.707
2291	AF200715	Homo sapiens PTB domain adaptor protein CED-6	1606	84.539
2293	AF200715	Homo sapiens PTB domain adaptor protein CED-6	392	98.333
2294	AF200715	Homo sapiens PTB domain adaptor protein CED-6	1862	96.440
2295	AB032917	Hylobates muelleri dopamine receptor D4	135	30.508
2296	AB032917	Hylobates muelleri dopamine receptor D4	123	31.452
2297	U70734	Homo sapiens 38 kDa Mov34 homolog	728	100.000
2298	U70734	Homo sapiens 38 kDa Mov34 homolog	176	100.000
2299	U70734	Homo sapiens 38 kDa Mov34 homolog	1080	80.229
2300	AF056184	Homo sapiens WS basic-helix-loop-helix leucine zipper protein	615	83.200
2301	AF056184	Homo sapiens WS basic-helix-loop-helix leucine zipper protein	1171	84.307
2302	Y08319	Homo sapiens kinesin-2	1137	89.848
2303	Y08319	Homo sapiens kinesin-2	179	93.333
2304	Y08319	Homo sapiens kinesin-2	285	93.750
2305	Y08319	Homo sapiens kinesin-2	4002	96.916
2306	M15530	Homo sapiens B-cell growth factor	140	54.717

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2308	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	53	46.667
2309	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	49	38.462
2310	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	41	40.000
2311	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	70	37.500
2312	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	51	30.303
2313	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	66	30.645
2314	A32622	synthetic construct HBsAg ayw Pre-S1 sequence	106	30.120
2315	X73460	Homo sapiens ribosomal protein L3	949	74.545
2316	X73460	Homo sapiens ribosomal protein L3	676	71.667
2317	X73460	Homo sapiens ribosomal protein L3	1209	80.972
2318	X73460	Homo sapiens ribosomal protein L3	1909	79.167
2319	X73460	Homo sapiens ribosomal protein L3	1710	83.019
2320	X73460	Homo sapiens ribosomal protein L3	2210	85.750
2321	X73460	Homo sapiens ribosomal protein L3	2265	87.841
2322	X73460	Homo sapiens ribosomal protein L3	1519	80.288
2323	D14688	Rattus norvegicus myosin regulatory light chain	371	59.474
2324	X81109	Homo sapiens tumor-associated antigen	371	93.548
2325	X81109	Homo sapiens tumor-associated antigen	437	100.000
2326	X81109	Homo sapiens tumor-associated antigen	402	100.000
2327	X81109	Homo sapiens tumor-associated antigen	602	66.540
2328	Y15061	Homo sapiens GalT4 protein	2204	92.913
2329	U64444	Homo sapiens ubiquitin fusion-degradation 1 like protein	749	87.248
2330	U64444	Homo sapiens ubiquitin fusion-degradation 1 like protein	2162	99.688
2331	U64444	Homo sapiens ubiquitin fusion-degradation 1 like protein	888	69.081
2332	X58833	Streptomyces coelicolor actVA 4	44	24.324
2333	X58833	Streptomyces coelicolor actVA 4	169	27.987
2334	U10903	Mus musculus zinc finger protein	196	31.366
2335	AL050300	Arabidopsis thaliana putative protein	199	53.030
2336	AL050300	Arabidopsis thaliana putative protein	481	43.243
2338	X83617	Homo sapiens RanBP1	328	100.000
2339	X83617	Homo sapiens RanBP1	494	69.378
2341	AB012190	Homo sapiens Nedd8-activating enzyme hUba3	182	100.000
2342	AB012190	Homo sapiens Nedd8-activating enzyme hUba3	531	92.683
2343	AB012190	Homo sapiens Nedd8-activating enzyme hUba3	1839	86.801
2346	U58658	Homo sapiens unknown	187	50.602
2348	AB033105	Homo sapiens KIAA1279 protein	2047	93.732
2349	AB033105	Homo sapiens KIAA1279 protein	3199	95.138
2350	D50930	Homo sapiens The KIAA0140 gene product is novel.	60	26.957
2352	D50930	Homo sapiens The KIAA0140 gene product	368	36.889

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		is novel.		
2353	AB017018	Homo sapiens JKTBP2	502	60.811
2354	AB017018	Homo sapiens JKTBP2	1178	60.054
2355	AB017018	Homo sapiens JKTBP2	71	35.849
2356	AB017018	Homo sapiens JKTBP2	1930	92.962
2357	AB017018	Homo sapiens JKTBP2	2436	94.104
2358	AF026977	Homo sapiens microsomal glutathione S-transferase 3	242	52.695
2359	M13100	Rattus norvegicus unknown protein	221	40.000
2361	U40766	Meloidogyne incognita COL-1	129	31.515
2362	A78803	unidentified unnamed protein product	769	90.071
2363	A78803	unidentified unnamed protein product	918	100.000
2364	A78803	unidentified unnamed protein product	337	66.418
2365	A27282	Homo sapiens TGR-CL3C	67	30.909
2366	A27282	Homo sapiens TGR-CL3C	72	30.508
2367	AB000584	Homo sapiens TGF-beta superfamily protein	1090	77.116
2368	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	101	29.703
2369	AF181640	Drosophila melanogaster BcDNA.GH09817	704	41.566
2370	AB007141	Mus musculus AZ2	404	82.432
2371	AB007141	Mus musculus AZ2	522	82.653
2372	AB007141	Mus musculus AZ2	1450	72.596
2374	U79260	Homo sapiens unknown	328	67.532
2375	AF151877	Homo sapiens CGI-119 protein	499	98.810
2376	AF151877	Homo sapiens CGI-119 protein	256	67.442
2377	AF151877	Homo sapiens CGI-119 protein	905	87.554
2378	U09368	Homo sapiens zinc finger protein ZNF140	2803	93.506
2379	U58658	Homo sapiens unknown	212	51.111
2380	AP000061	Aeropyrum pernix 175aa long hypothetical protein	101	28.788
2381	AL080092	Homo sapiens hypothetical protein	261	61.654
2382	M77693	Homo sapiens spermidine/spermine N1-acetyltransferase	140	100.000
2383	M77693	Homo sapiens spermidine/spermine N1-acetyltransferase	466	98.551
2384	M77693	Homo sapiens spermidine/spermine N1-acetyltransferase	551	62.755
2385	AB011145	Homo sapiens KIAA0573 protein	684	97.059
2386	AB011145	Homo sapiens KIAA0573 protein	1817	77.662
2387	AF004561	Homo sapiens p21-Arc	570	74.211
2388	AF060087	Mus musculus proteasome subunit iota	555	64.885
2389	AF127761	Homo sapiens ribonucleoprotein RBM8	444	64.844
2390	AF127761	Homo sapiens ribonucleoprotein RBM8	876	87.006
2392	L17318	Rattus norvegicus proline-rich proteoglycan	142	34.932
2393	L17318	Rattus norvegicus proline-rich proteoglycan	142	29.891
2394	L17318	Rattus norvegicus proline-rich proteoglycan	52	33.333
2395	L17318	Rattus norvegicus proline-rich proteoglycan	136	31.915
2396	L17318	Rattus norvegicus proline-rich	135	32.292

		proteoglycan		
2397	L17318	Rattus norvegicus proline-rich proteoglycan	239	31.553
2398	AF106941	Homo sapiens beta-arrestin 2	560	77.099
2399	AF106941	Homo sapiens beta-arrestin 2	783	80.240
2400	AF106941	Homo sapiens beta-arrestin 2	37	44.444
2401	AF106941	Homo sapiens beta-arrestin 2	320	97.917
2402	AF106941	Homo sapiens beta-arrestin 2	709	100.000
2403	AF106941	Homo sapiens beta-arrestin 2	2171	93.253
2404	AF056035	Rattus norvegicus s-nexilin	476	94.203
2405	AF056035	Rattus norvegicus s-nexilin	2991	84.072
2407	A01769	synthetic construct vascular anticoagulating protein	975	79.819
2408	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	56	40.000
2410	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	56	40.000
2411	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	635	69.461
2412	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	40	54.545
2413	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	51	33.333
2414	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	56	20.000
2415	AL034428	Homo sapiens dJ705D16.1 (U2 small nuclear RNA-associated B'' antigen)	1000	84.556
2416	U58658	Homo sapiens unknown	183	46.988
2417	D63486	Homo sapiens The KIAA0152 gene product is related to a putative C.elegans gene encoded in cosmid F44E2.	621	91.346
2418	D63486	Homo sapiens The KIAA0152 gene product is related to a putative C.elegans gene encoded in cosmid F44E2.	38	30.556
2419	D63486	Homo sapiens The KIAA0152 gene product is related to a putative C.elegans gene encoded in cosmid F44E2.	1376	86.242
2420	AF180920	Homo sapiens cyclin L ania-6a	845	80.000
2421	AF180920	Homo sapiens cyclin L ania-6a	597	80.315
2422	AF180920	Homo sapiens cyclin L ania-6a	491	95.000
2423	AF180920	Homo sapiens cyclin L ania-6a	2694	91.902
2424	U68105	Homo sapiens poly(A)-binding protein	3245	85.270
2425	U68105	Homo sapiens poly(A)-binding protein	669	68.902
2426	U68105	Homo sapiens poly(A)-binding protein	3871	94.182
2427	U68105	Homo sapiens poly(A)-binding protein	4101	99.371
2428	D84316	Drosophila melanogaster rab14	406	72.340
2429	D84316	Drosophila melanogaster rab14	564	69.271
2430	U82303	Homo sapiens unknown	117	80.769
2431	U82303	Homo sapiens unknown	45	28.571
2432	U82303	Homo sapiens unknown	169	56.897
2433	AJ238094	Homo sapiens Lsm1 protein	713	98.261
2434	AJ238094	Homo sapiens Lsm1 protein	465	88.889
2435	J04564	Homo sapiens snRNP polypeptide B	160	28.736
2436	AL080159	Homo sapiens hypothetical protein	86	30.337

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2437	AL080159	Homo sapiens hypothetical protein	101	33.333
2438	AL080159	Homo sapiens hypothetical protein	389	40.230
2440	X61046	Hydra sp. mini-collagen	177	38.462
2441	X61046	Hydra sp. mini-collagen	154	35.185
2442	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	496	78.899
2443	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	679	100.000
2444	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	3877	91.742
2445	AB029022	Homo sapiens KIAA1099 protein	52	36.364
2446	AB029022	Homo sapiens KIAA1099 protein	266	67.797
2447	AB029022	Homo sapiens KIAA1099 protein	249	80.851
2448	AB029022	Homo sapiens KIAA1099 protein	71	24.561
2449	AB029022	Homo sapiens KIAA1099 protein	57	60.000
2450	AB029022	Homo sapiens KIAA1099 protein	1894	55.609
2451	AB029022	Homo sapiens KIAA1099 protein	2364	50.932
2452	U79260	Homo sapiens unknown	338	68.817
2453	U31118	Xenopus laevis cytoplasmic myosin II regulatory light chain	485	70.000
2454	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	620	48.197
2455	AC005328	Homo sapiens R26660 1, partial CDS	201	78.462
2456	X06026	Homo sapiens T-cell receptor T3 gamma chain	589	74.346
2457	AF159055	Homo sapiens leucine zipper-like protein	154	61.224
2458	X16064	Homo sapiens tumor protein (AA 1 - 172)	617	98.969
2460	X16064	Homo sapiens tumor protein (AA 1 - 172)	41	24.000
2461	X16064	Homo sapiens tumor protein (AA 1 - 172)	366	59.887
2462	U66372	Bos taurus ribosomal protein S29	215	67.308
2463	U66372	Bos taurus ribosomal protein S29	184	96.875
2464	X56389	Canis familiaris rab4b	914	97.973
2465	X56389	Canis familiaris rab4b	775	83.051
2466	X56389	Canis familiaris rab4b	874	88.199
2467	X56389	Canis familiaris rab4b	1084	90.741
2468	Z25820	Homo sapiens dodecenoyl-CoA delta-isomerase	1254	80.769
2470	AF047183	Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-B12	266	66.981
2471	Y14586	Cricetulus griseus kinesin light chain isoform D	97	64.000

2472	Y14586	Cricetulus griseus kinesin light chain isoform D	115	42.857
2475	X14968	Homo sapiens RII-alpha subunit (AA 1-404)	2365	95.556
2476	U67934	Homo sapiens 44.9 kDa protein C18B11 homolog	56	28.235
2477	U67934	Homo sapiens 44.9 kDa protein C18B11 homolog	963	90.052
2478	U43360	Peromyscus maniculatus reverse transcriptase	300	34.021
2479	U97553	murine herpesvirus 68 unknown	112	30.000
2480	U58658	Homo sapiens unknown	179	51.351
2481	U79260	Homo sapiens unknown	253	50.467
2482	AF151826	Homo sapiens CGI-68 protein	320	65.385
2483	AF151826	Homo sapiens CGI-68 protein	269	86.667
2484	AF151826	Homo sapiens CGI-68 protein	494	95.000
2485	AF151826	Homo sapiens CGI-68 protein	52	37.500
2486	AF151826	Homo sapiens CGI-68 protein	1244	80.571
2487	D10699	Rattus norvegicus ubiquitin carboxyl-terminal hydrolase PGP9.5	446	97.015
2488	D10699	Rattus norvegicus ubiquitin carboxyl-terminal hydrolase PGP9.5	672	70.192
2489	U96915	Homo sapiens sin3 associated polypeptide p18	47	32.353
2490	U96915	Homo sapiens sin3 associated polypeptide p18	600	83.436
2491	L47668	Homo sapiens alpha-2 collagen type I	134	44.737
2492	U01317	Homo sapiens beta-globin	343	60.736
2494	AF004561	Homo sapiens p21-Arc	498	73.684
2495	D50840	Homo sapiens ceramide glucosyltransferase	816	62.500
2496	D50840	Homo sapiens ceramide glucosyltransferase	848	96.269
2497	D50840	Homo sapiens ceramide glucosyltransferase	939	85.057
2498	D50840	Homo sapiens ceramide glucosyltransferase	389	100.000
2499	D50840	Homo sapiens ceramide glucosyltransferase	1957	88.509
2500	L24521	Homo sapiens transformation-related protein	143	35.644
2501	L24521	Homo sapiens transformation-related protein	278	62.791
2502	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	768	69.058
2503	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	454	68.254
2504	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	905	76.119
2505	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	93	22.909
2506	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	661	87.903
2507	AL031588	Homo sapiens dJ1163J1.3 (novel protein	3198	73.684

		similar to mouse B99)		
2508	AL031588	Homo sapiens dJ1163J1.3 (novel protein similar to mouse B99)	4125	96.639
2509	Y11651	Homo sapiens phosphate cyclase	497	55.897
2510	Y11651	Homo sapiens phosphate cyclase	1999	92.000
2511	X51706	Rattus rattus ribosomal protein L9 (AA 1-192)	400	63.317
2512	X55777	Homo sapiens put. ORF	351	69.048
2513	X96713	Globodera pallida collagen	174	39.167
2514	X67703	Drosophila melanogaster Mst84Db	84	35.000
2515	AF160728	Homo sapiens sex comb on midleg-like-1 protein	1027	79.048
2516	AF160728	Homo sapiens sex comb on midleg-like-1 protein	1001	89.573
2517	AC004539	Homo sapiens unknown function; similar to Y09105 (PID:g1666171)	40	42.857
2519	AC004539	Homo sapiens unknown function; similar to Y09105 (PID:g1666171)	46	22.581
2520	AC004539	Homo sapiens unknown function; similar to Y09105 (PID:g1666171)	820	90.909
2521	X59720	Saccharomyces cerevisiae YCR053w, len:514	878	37.472
2522	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	57	43.478
2523	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	74	32.143
2524	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	175	45.614
2525	AL117204	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk381b7.5 comes from this gene	1082	34.412
2526	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
2527	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
2528	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	268	52.294
2530	U80559	Human immunodeficiency virus type 1 tat protein	100	38.710
2532	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	245	64.062
2533	AP000060	Aeropyrum pernix 100aa long hypothetical protein	109	34.066
2534	X55656	Homo sapiens gamma-G globin	843	89.542
2535	X55656	Homo sapiens gamma-G globin	421	81.699
2536	AJ223953	Homo sapiens hPTTG	469	100.000
2537	AJ223953	Homo sapiens hPTTG	469	63.514
2538	X69532	Homo sapiens inter-alpha-trypsin inhibitor heavy chain H1	494	62.143
2539	X69532	Homo sapiens inter-alpha-trypsin inhibitor heavy chain H1	1070	94.118
2540	X69532	Homo sapiens inter-alpha-trypsin	554	83.178

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		inhibitor heavy chain H1		
2541	X69532	Homo sapiens inter-alpha-trypsin inhibitor heavy chain H1	728	54.110
2542	X69532	Homo sapiens inter-alpha-trypsin inhibitor heavy chain H1	4793	89.915
2543	AJ243721	Homo sapiens dTDP-4-keto-6-deoxy-D-glucose 4-reductase	1093	74.419
2544	D13892	Homo sapiens carboxyl methyltransferase	509	93.103
2545	D13892	Homo sapiens carboxyl methyltransferase	38	30.000
2546	D13892	Homo sapiens carboxyl methyltransferase	41	33.333
2548	D13892	Homo sapiens carboxyl methyltransferase	785	80.085
2549	M16447	Homo sapiens dihydropteridine reductase (EC 1.6.99.7)	713	92.500
2550	M16447	Homo sapiens dihydropteridine reductase (EC 1.6.99.7)	1022	89.474
2552	U35376	Homo sapiens repressor transcriptional factor	534	60.526
2553	U35376	Homo sapiens repressor transcriptional factor	1868	50.000
2554	S42658	Homo sapiens S3 ribosomal protein	1032	87.500
2555	S42658	Homo sapiens S3 ribosomal protein	847	65.021
2556	S42658	Homo sapiens S3 ribosomal protein	689	77.647
2557	AF041330	Bodo saltans NADH dehydrogenase subunit 5	166	28.671
2558	AF030162	Homo sapiens inner mitochondrial membrane translocase Tim23	750	79.535
2559	U27488	Pseudorabies virus glycoprotein gX	57	44.000
2560	U27488	Pseudorabies virus glycoprotein gX	148	39.326
2561	AF034580	Mus musculus TSG118.1	64	34.375
2562	AF034580	Mus musculus TSG118.1	270	43.796
2563	AF034580	Mus musculus TSG118.1	294	75.410
2564	AF034580	Mus musculus TSG118.1	64	34.375
2565	AF034580	Mus musculus TSG118.1	1622	58.378
2566	X61046	Hydra sp. mini-collagen	160	44.156
2567	AF126062	Homo sapiens Arf-like 2 binding protein BART1	624	97.030
2568	AF126062	Homo sapiens Arf-like 2 binding protein BART1	673	89.222
2569	U26162	Homo sapiens myosin regulatory light chain	269	61.622
2570	U79260	Homo sapiens unknown	195	52.381
2571	U05313	Trypanosoma brucei CR3	78	36.364
2572	Z14134	Dictyostelium discoideum ras-related protein	247	29.648
2573	U79260	Homo sapiens unknown	309	64.894
2574	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	385	98.361
2575	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	1359	90.837
2576	AF044127	Homo sapiens peroxisomal short-chain	46	30.303

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		alcohol dehydrogenase		
2577	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	162	92.593
2578	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	153	100.000
2579	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	706	61.450
2580	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	1286	92.490
2581	AB030236	Canis familiaris D4 dopamine receptor	147	41.270
2582	AB030236	Canis familiaris D4 dopamine receptor	105	42.424
2583	M19419	Mus musculus proline-rich salivary protein	189	30.682
2584	M19419	Mus musculus proline-rich salivary protein	205	38.583
2585	Z81039	Unknown predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3	300	33.803
2586	Z81039	Unknown predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3	208	28.994
2587	AF151875	Homo sapiens CGI-117 protein	276	62.921
2588	AF151875	Homo sapiens CGI-117 protein	660	85.165
2589	M27444	Bos taurus phosphoprotein	511	78.846
2590	M27444	Bos taurus phosphoprotein	923	81.053
2591	S54563	Mus sp. alpha 2(XI) collagen	111	40.000
2592	X73608	Homo sapiens testican	42	27.586
2593	X73608	Homo sapiens testican	42	27.586
2594	X73608	Homo sapiens testican	46	35.897
2595	X73608	Homo sapiens testican	1481	87.747
2596	X73608	Homo sapiens testican	2423	90.265
2597	M57290	Gallus gallus non-tyrosine protein kinase	155	28.761
2599	D78255	Mus musculus PAP-1	45	27.273
2600	D78255	Mus musculus PAP-1	1240	92.821
2601	D78255	Mus musculus PAP-1	770	51.125
2603	AF173378	Homo sapiens 60S acidic ribosomal protein PO	47	28.571
2604	AF173378	Homo sapiens 60S acidic ribosomal protein PO	44	77.778
2605	AF173378	Homo sapiens 60S acidic ribosomal protein PO	44	77.778
2606	AF173378	Homo sapiens 60S acidic ribosomal protein PO	364	100.000
2607	AF173378	Homo sapiens 60S acidic ribosomal protein PO	51	23.684
2608	AF173378	Homo sapiens 60S acidic ribosomal protein PO	545	100.000
2609	AF173378	Homo sapiens 60S acidic ribosomal protein PO	1082	87.288
2610	X67703	Drosophila melanogaster Mst84Db	79	38.889
2611	X67703	Drosophila melanogaster Mst84Db	152	45.455
2612	M13974	Bos taurus beta type protein kinase C	517	81.928
2613	M13974	Bos taurus beta type protein kinase C	991	58.983

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2614	M13974	Bos taurus beta type protein kinase C	791	38.095
2615	M13974	Bos taurus beta type protein kinase C	3455	77.581
2616	U03886	Homo sapiens a gene isolated from a CpG island between STS and KAL	1574	97.610
2617	U03886	Homo sapiens a gene isolated from a CpG island between STS and KAL	1099	89.961
2618	AJ005894	Homo sapiens JM27	158	44.304
2619	X03145	Homo sapiens pot. ORF IIII	45	44.444
2620	X03145	Homo sapiens pot. ORF IIII	44	30.000
2621	X03145	Homo sapiens pot. ORF IIII	130	37.168
2622	X03145	Homo sapiens pot. ORF IIII	162	34.400
2623	X55683	Lycopersicon esculentum extensin (class I)	159	36.111
2624	Z98204	Hordeum vulgare extensin	354	29.499
2625	S76877	Danio rerio=zebrafish embryos, Peptide, 215 aa casein kinase 2 beta subunit, CK2 beta=protein kinase	434	64.348
2627	AF135421	Homo sapiens GDP-mannose pyrophosphorylase B	50	23.529
2628	AF135421	Homo sapiens GDP-mannose pyrophosphorylase B	2150	82.394
2629	AF135421	Homo sapiens GDP-mannose pyrophosphorylase B	2279	98.333
2631	Y16610	Homo sapiens paraplegin	528	98.795
2632	Y16610	Homo sapiens paraplegin	1781	56.792
2633	Y16610	Homo sapiens paraplegin	4874	98.996
2634	D86864	Homo sapiens acetyl LDL receptor	733	59.091
2635	D86864	Homo sapiens acetyl LDL receptor	2083	37.377
2636	Z21507	Homo sapiens human elongation factor-1-delta	1095	82.353
2637	AF151863	Homo sapiens CGI-105 protein	621	91.589
2638	AF151863	Homo sapiens CGI-105 protein	1812	89.172
2639	AF151863	Homo sapiens CGI-105 protein	696	53.571
2640	AF151863	Homo sapiens CGI-105 protein	356	47.191
2641	AF151863	Homo sapiens CGI-105 protein	683	67.000
2642	AF132181	Drosophila melanogaster unknown	730	46.209
2643	AF132181	Drosophila melanogaster unknown	1478	35.006
2644	AB029029	Homo sapiens KIAA1106 protein	304	94.118
2645	AB029029	Homo sapiens KIAA1106 protein	293	97.959
2646	AB029029	Homo sapiens KIAA1106 protein	4806	97.305
2647	AB029029	Homo sapiens KIAA1106 protein	6761	99.113
2648	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	100	25.000
2649	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	204	55.357
2650	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1604	40.859
2651	L39874	Homo sapiens deoxycytidylate deaminase	38	26.154
2652	L39874	Homo sapiens deoxycytidylate deaminase	605	69.149
2653	U77381	Arabidopsis thaliana WD-40 repeat protein	296	58.333
2654	U77381	Arabidopsis thaliana WD-40 repeat protein	524	46.041
2655	AP000060	Aeropyrum pernix 128aa long	137	39.623

		hypothetical protein		
2656	S57432	Xenopus laevis, splenocytes, Peptide, 165 aa 40S ribosomal small subunit protein S10	694	90.090
2657	S57432	Xenopus laevis, splenocytes, Peptide, 165 aa 40S ribosomal small subunit protein S10	279	58.915
2658	AJ005962	Drosophila melanogaster clathrin-associated protein	746	78.873
2660	AJ005962	Drosophila melanogaster clathrin-associated protein	1849	78.378
2661	Z93241	Homo sapiens dJ222E13.1a.1 (C-terminal part of novel protein dJ222E13.1) (partial isoform 1)	120	57.576
2662	Z93241	Homo sapiens dJ222E13.1a.1 (C-terminal part of novel protein dJ222E13.1) (partial isoform 1)	796	89.510
2663	Z93241	Homo sapiens dJ222E13.1a.1 (C-terminal part of novel protein dJ222E13.1) (partial isoform 1)	186	61.538
2665	M27024	Homo sapiens heat shock protein	473	49.167
2666	M27024	Homo sapiens heat shock protein	458	98.649
2667	M27024	Homo sapiens heat shock protein	3109	87.919
2668	U58658	Homo sapiens unknown	301	64.286
2670	AP000060	Aeropyrum pernix 143aa long hypothetical protein	111	30.894
2671	D10653	Homo sapiens cell surface glycoprotein	1226	93.305
2672	L48546	Homo sapiens tuberin	956	95.455
2673	L48546	Homo sapiens tuberin	283	97.727
2674	L48546	Homo sapiens tuberin	258	97.500
2675	L48546	Homo sapiens tuberin	452	97.222
2676	L48546	Homo sapiens tuberin	11312	88.681
2677	L48546	Homo sapiens tuberin	10891	96.152
2678	L48546	Homo sapiens tuberin	11286	97.573
2679	AJ005564	Mus musculus SPR2F protein	48	58.824
2680	AJ005564	Mus musculus SPR2F protein	105	31.169
2681	L43361	Mycoplasma gallisepticum haemagglutinin	109	35.556
2682	Z69637	Caenorhabditis elegans predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene	309	63.291
2683	Z69637	Caenorhabditis elegans predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene	476	48.131
2686	AB023185	Homo sapiens KIAA0968 protein	278	56.098
2687	AB023185	Homo sapiens KIAA0968 protein	3181	97.546
2688	AB023185	Homo sapiens KIAA0968 protein	3273	96.947
2690	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	181	59.701
2691	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	219	59.701

2692	AF151886	Homo sapiens CGI-128 protein	630	96.040
2693	AF151886	Homo sapiens CGI-128 protein	352	91.525
2694	AF151886	Homo sapiens CGI-128 protein	854	76.923
2695	AF151886	Homo sapiens CGI-128 protein	678	69.945
2696	AF151886	Homo sapiens CGI-128 protein	472	70.349
2697	AF132970	Homo sapiens CGI-36 protein	543	71.176
2698	U54638	Mus musculus rhotekin	726	66.292
2699	U54638	Mus musculus rhotekin	2192	76.821
2700	U54638	Mus musculus rhotekin	339	60.396
2701	U54638	Mus musculus rhotekin	55	28.767
2702	U54638	Mus musculus rhotekin	756	62.755
2703	U54638	Mus musculus rhotekin	2257	79.667
2704	U97006	Caenorhabditis elegans No definition line found	214	43.000
2705	U97006	Caenorhabditis elegans No definition line found	131	39.130
2706	U97006	Caenorhabditis elegans No definition line found	120	36.957
2707	U97006	Caenorhabditis elegans No definition line found	122	36.207
2708	U97006	Caenorhabditis elegans No definition line found	142	29.600
2709	U97006	Caenorhabditis elegans No definition line found	327	44.737
2710	U97006	Caenorhabditis elegans No definition line found	2671	29.978
2711	AJ238629	Chlorella protothecoides putative extensin-like protein	66	31.111
2712	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	185	61.818
2713	Z49199	Homo sapiens RNA polymerase II subunit hRPB17	427	72.277
2714	Z49199	Homo sapiens RNA polymerase II subunit hRPB17	210	82.500
2715	Z49199	Homo sapiens RNA polymerase II subunit hRPB17	701	88.816
2716	D50926	Homo sapiens The KIAA0136 gene product is novel.	4748	84.701
2717	D50926	Homo sapiens The KIAA0136 gene product is novel.	1947	81.888
2718	D50926	Homo sapiens The KIAA0136 gene product is novel.	328	94.340
2719	D50926	Homo sapiens The KIAA0136 gene product is novel.	5808	97.275
2720	L24521	Homo sapiens transformation-related protein	176	58.108
2721	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	283	42.442
2722	AJ000644	Homo sapiens SPOP	780	92.424
2723	AJ000644	Homo sapiens SPOP	90	100.000
2724	AJ000644	Homo sapiens SPOP	1837	92.308
2726	J04196	Bos taurus GTP-binding protein	1026	100.000
2727	J04196	Bos taurus GTP-binding protein	763	80.214
2728	M15530	Homo sapiens B-cell growth factor	219	66.038

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2730	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	465	52.308
2731	M34671	Homo sapiens antigen CD59 precursor (CD59)	299	66.667
2732	M86667	Homo sapiens NAP	658	99.020
2734	M86667	Homo sapiens NAP	263	90.000
2735	M86667	Homo sapiens NAP	783	99.194
2736	M86667	Homo sapiens NAP	277	67.692
2737	M86667	Homo sapiens NAP	291	70.769
2738	M86667	Homo sapiens NAP	1638	85.600
2739	AL080155	Homo sapiens hypothetical protein	804	75.132
2740	AL080155	Homo sapiens hypothetical protein	832	88.312
2741	AL080155	Homo sapiens hypothetical protein	2026	94.805
2742	AL080155	Homo sapiens hypothetical protein	2339	95.852
2743	AF020261	Santalum album proline rich protein	245	31.270
2744	M94383	Drosophila melanogaster suppressor of hairless protein	209	61.224
2745	M94383	Drosophila melanogaster suppressor of hairless protein	322	90.385
2746	M94383	Drosophila melanogaster suppressor of hairless protein	681	85.345
2747	M94383	Drosophila melanogaster suppressor of hairless protein	1699	67.086
2748	X01655	Homo sapiens type III procollagen (aa 892-1023)	43	39.130
2749	X01655	Homo sapiens type III procollagen (aa 892-1023)	106	38.596
2750	AB025008	Homo sapiens novel member of chitinase family	144	58.537
2751	AB025008	Homo sapiens novel member of chitinase family	44	22.772
2752	AB025008	Homo sapiens novel member of chitinase family	861	47.703
2753	AB025008	Homo sapiens novel member of chitinase family	44	36.364
2754	AB025008	Homo sapiens novel member of chitinase family	508	34.225
2756	S74659	Homo sapiens aggrecan keratan sulfate domain {hexapeptide repeats}	110	35.870
2757	X85785	Homo sapiens duffy antigen/cherokine receptor	1539	86.350
2758	AF120155	Sus scrofa FOSB protein	99	43.860
2761	M22334	Homo sapiens unknown protein	1528	87.589
2763	M22334	Homo sapiens unknown protein	897	94.000
2767	M22334	Homo sapiens unknown protein	714	90.625
2768	M22334	Homo sapiens unknown protein	49	37.500
2769	M22334	Homo sapiens unknown protein	1181	94.898
2770	M22334	Homo sapiens unknown protein	925	90.854
2771	M22334	Homo sapiens unknown protein	2804	88.690
2772	AL031427	Homo sapiens dJ167A19.3 (novel protein)	506	78.505
2773	AL031427	Homo sapiens dJ167A19.3 (novel protein)	385	59.028
2774	AL031427	Homo sapiens dJ167A19.3 (novel	236	97.500

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		protein)		
2775	AL031427	Homo sapiens dJ167A19.3 (novel protein)	576	85.714
2776	Y17328	Rattus norvegicus mu crystallin	121	91.667
2777	Y17328	Rattus norvegicus mu crystallin	1339	76.398
2778	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	4141	95.008
2779	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	289	95.000
2780	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	450	92.958
2781	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	385	90.000
2782	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	423	98.507
2783	X71440	Homo sapiens peroxisomal acyl-CoA oxidase	3736	95.152
2784	S54563	Mus sp. alpha 2(XI) collagen	70	30.769
2785	S54563	Mus sp. alpha 2(XI) collagen	70	30.769
2786	S54563	Mus sp. alpha 2(XI) collagen	112	33.663
2787	AF189307	Homo sapiens unknown	133	44.828
2788	AF132961	Homo sapiens CGI-27 protein	220	91.892
2790	AF132961	Homo sapiens CGI-27 protein	597	77.311
2791	AF132961	Homo sapiens CGI-27 protein	1386	72.121
2792	AF132961	Homo sapiens CGI-27 protein	416	52.023
2793	AF132961	Homo sapiens CGI-27 protein	1838	98.969
2794	Z47087	Homo sapiens RNA polymerase II elongation factor-like protein	506	70.760
2795	J04655	Ascaris suum collagen	125	38.235
2796	X77337	Homo sapiens phosphate carrier	1404	82.703
2797	Z79694	Unknown predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65535 comes from this gene;	154	33.333
2798	AF022985	Caenorhabditis elegans Similar to collagen	175	30.070
2799	U44111	Homo sapiens histamine N-methyltransferase	1448	85.502
2800	U44111	Homo sapiens histamine N-methyltransferase	1355	90.236
2801	AB011084	Homo sapiens KIAA0512 protein	626	34.106
2802	AB011084	Homo sapiens KIAA0512 protein	39	22.222
2803	AB011084	Homo sapiens KIAA0512 protein	644	27.087
2804	AB011084	Homo sapiens KIAA0512 protein	445	32.787
2805	X73435	Ovis aries KAP5.5 keratin protein	115	33.708
2806	M90657	Homo sapiens L6	386	41.053
2807	X60957	Homo sapiens receptor tyrosine kinase	7394	95.958
2808	X60957	Homo sapiens receptor tyrosine kinase	406	95.588
2809	X60957	Homo sapiens receptor tyrosine kinase	7014	94.952
2811	X56468	Homo sapiens 14.3.3 protein	787	85.214
2812	X59244	Homo sapiens ZNF43	38	50.000
2813	X59244	Homo sapiens ZNF43	1918	41.124
2814	AC004544	Homo sapiens cytochrome C oxidase; match to P14406 (PID:g117121)	324	64.486
2815	AC004544	Homo sapiens cytochrome C oxidase;	154	59.140

		match to P14406 (PID:g117121)		
2816	X02490	Homo sapiens longest open reading frame	446	70.807
2817	U08021	Homo sapiens nicotinamide N-methyltransferase	671	63.793
2818	AF161181	Mus musculus P55T protein	3284	97.461
2819	AF161181	Mus musculus P55T protein	2980	89.908
2820	AJ005564	Mus musculus SPR2F protein	77	40.816
2821	X67703	Drosophila melanogaster Mst84Da	103	34.043
2822	X67703	Drosophila melanogaster Mst84Da	93	29.787
2824	M86564	Rattus norvegicus alpha-prothymosin	431	91.781
2825	M86564	Rattus norvegicus alpha-prothymosin	246	65.289
2826	U18385	Caenorhabditis elegans collagen	43	42.857
2828	U18385	Caenorhabditis elegans collagen	73	23.611
2829	U18385	Caenorhabditis elegans collagen	33	66.667
2830	U18385	Caenorhabditis elegans collagen	93	22.632
2831	U18385	Caenorhabditis elegans collagen	46	28.571
2832	U18385	Caenorhabditis elegans collagen	117	20.904
2834	U18385	Caenorhabditis elegans collagen	114	20.690
2835	U26162	Homo sapiens myosin regulatory light chain	326	65.169
2836	AL050179	Homo sapiens hypothetical protein	455	77.586
2837	AL050179	Homo sapiens hypothetical protein	905	75.820
2838	AL050179	Homo sapiens hypothetical protein	871	67.541
2839	X57432	Rattus rattus ribosomal protein S2	84	58.824
2840	X57432	Rattus rattus ribosomal protein S2	50	34.483
2841	X57432	Rattus rattus ribosomal protein S2	311	70.000
2842	AL050101	Homo sapiens hypothetical protein	52	22.308
2843	AL050101	Homo sapiens hypothetical protein	49	34.286
2844	AL050101	Homo sapiens hypothetical protein	59	26.000
2845	AL050101	Homo sapiens hypothetical protein	447	98.611
2846	AL050101	Homo sapiens hypothetical protein	47	29.787
2847	AL050101	Homo sapiens hypothetical protein	46	34.483
2848	AL050101	Homo sapiens hypothetical protein	3185	97.253
2849	AF041330	Bodo saltans NADH dehydrogenase subunit 5	158	28.333
2850	X15389	Paracentrotus lividus beta-tubulin (AA 1 - 447)	677	99.029
2851	X15389	Paracentrotus lividus beta-tubulin (AA 1 - 447)	1737	77.007
2853	AF064603	Homo sapiens GA17 protein	266	92.857
2854	AF064603	Homo sapiens GA17 protein	144	95.652
2855	AF064603	Homo sapiens GA17 protein	925	66.583
2856	X52235	Homo sapiens ORFII	745	31.960
2857	V01184	Mus musculus reading frame v-fos (p55)	748	70.718
2858	V01184	Mus musculus reading frame v-fos (p55)	628	44.266
2859	V01184	Mus musculus reading frame v-fos (p55)	1140	69.159
2861	A48861	Homo sapiens unnamed protein product	2066	93.294
2862	A48861	Homo sapiens unnamed protein product	1478	91.103
2863	A48861	Homo sapiens unnamed protein product	1277	77.273
2864	AJ005564	Mus musculus SPR2F protein	67	32.203
2865	AJ005564	Mus musculus SPR2F protein	105	37.313
2866	M15530	Homo sapiens B-cell growth factor	155	56.522

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2867	AL080080	Homo sapiens hypothetical protein	1746	96.864
2868	AF128625	Homo sapiens CDC42-binding protein kinase beta	905	83.432
2869	AF128625	Homo sapiens CDC42-binding protein kinase beta	842	97.163
2870	AF128625	Homo sapiens CDC42-binding protein kinase beta	9242	87.909
2871	AF128625	Homo sapiens CDC42-binding protein kinase beta	302	100.000
2872	AF128625	Homo sapiens CDC42-binding protein kinase beta	795	97.458
2873	AF128625	Homo sapiens CDC42-binding protein kinase beta	10874	98.660
2874	J04657	Ascaris suum collagen	230	36.287
2875	AF042386	Homo sapiens cyclophilin-33B	580	72.441
2876	AF042386	Homo sapiens cyclophilin-33B	2000	100.000
2877	AF042386	Homo sapiens cyclophilin-33B	103	88.889
2878	AF042386	Homo sapiens cyclophilin-33B	434	56.213
2879	AF101074	Homo sapiens step II splicing factor SLU7	3499	97.952
2880	AP000060	Aeropyrum pernix 101aa long hypothetical protein	132	41.250
2881	AF125101	Homo sapiens HSPC040 protein	415	82.143
2882	AF125101	Homo sapiens HSPC040 protein	158	100.000
2883	AF125101	Homo sapiens HSPC040 protein	323	81.905
2884	X98126	Homo sapiens enoyl-CoA hydratase	241	71.642
2885	X98126	Homo sapiens enoyl-CoA hydratase	383	94.737
2886	X98126	Homo sapiens enoyl-CoA hydratase	421	75.248
2887	X98126	Homo sapiens enoyl-CoA hydratase	1235	85.441
2888	X98126	Homo sapiens enoyl-CoA hydratase	1048	77.888
2889	AF098499	Caenorhabditis elegans No definition line found	181	32.026
2890	AF098499	Caenorhabditis elegans No definition line found	242	41.111
2891	AF098499	Caenorhabditis elegans No definition line found	315	40.000
2892	AF098499	Caenorhabditis elegans No definition line found	291	37.500
2893	AF098499	Caenorhabditis elegans No definition line found	221	32.353
2894	M28297	Rattus norvegicus alpha-1-inhibitor 3	36	46.154
2895	M28297	Rattus norvegicus alpha-1-inhibitor 3	231	43.689
2896	M28297	Rattus norvegicus alpha-1-inhibitor 3	212	39.362
2897	M28297	Rattus norvegicus alpha-1-inhibitor 3	350	37.696
2898	M28297	Rattus norvegicus alpha-1-inhibitor 3	93	55.556
2899	M28297	Rattus norvegicus alpha-1-inhibitor 3	146	36.111
2900	M28297	Rattus norvegicus alpha-1-inhibitor 3	43	23.214
2901	M28297	Rattus norvegicus alpha-1-inhibitor 3	247	34.951
2902	AJ005560	Mus musculus SPR2B protein	133	32.292
2903	S83341	Homo sapiens prion protein {intervening sequence, repetitive element}	125	38.372
2904	X80035	Oryctolagus cuniculus cysteine rich hair keratin associated protein	183	32.117

2905	AB025186	Homo sapiens EB3 protein	1009	84.492
2906	AB025186	Homo sapiens EB3 protein	617	92.188
2907	AB025186	Homo sapiens EB3 protein	1275	79.567
2908	AF168008	Danio rerio PEA3	52	24.000
2909	AF168008	Danio rerio PEA3	334	81.356
2910	AF168008	Danio rerio PEA3	134	90.476
2911	AF168008	Danio rerio PEA3	1722	60.163
2912	X53064	Homo sapiens small proline-rich protein	110	39.344
2913	AF060862	Homo sapiens unknown	749	88.235
2914	AF060862	Homo sapiens unknown	401	50.000
2915	U68729	Meloidogyne incognita cuticle preprocollagen	186	30.808
2916	AF026689	Homo sapiens prostate-specific transglutaminase	111	52.083
2917	X55777	Homo sapiens put. ORF	277	51.807
2919	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	417	67.961
2920	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	51	50.000
2921	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	48	35.088
2922	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	32	100.000
2923	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	63	29.167
2924	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	46	47.059
2925	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	46	29.630
2926	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	48	22.222
2927	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	47	32.000
2928	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	59	20.833
2929	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	48	43.750
2930	AF044670	Homo sapiens 33 kDa Vamp-associated protein; VAP-33	1255	88.235
2931	U47686	Homo sapiens signal transducer and activator of transcription Stat5B	762	70.899
2932	U47686	Homo sapiens signal transducer and activator of transcription Stat5B	1006	91.875
2933	U47686	Homo sapiens signal transducer and activator of transcription Stat5B	430	73.684
2934	U47686	Homo sapiens signal transducer and activator of transcription Stat5B	4969	98.861
2936	X57346	Homo sapiens HS1	481	84.000
2937	X57346	Homo sapiens HS1	202	100.000
2938	X57346	Homo sapiens HS1	1040	80.784
2939	X57346	Homo sapiens HS1	795	71.698
2940	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	477	60.741

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2941	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	521	69.565
2942	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	175	80.645
2943	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	268	53.165
2945	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	219	86.842
2946	D10026	Rattus norvegicus glutathione S-transferase Yrs-Yrs	742	68.016
2947	M15530	Homo sapiens B-cell growth factor	156	54.717
2948	X63563	Homo sapiens RNA polymerase II 140 kDa subunit	49	31.034
2949	X63563	Homo sapiens RNA polymerase II 140 kDa subunit	48	29.268
2950	X63563	Homo sapiens RNA polymerase II 140 kDa subunit	6745	93.361
2952	U23452	Caenorhabditis elegans No definition line found	367	31.410
2953	X54977	Bos taurus 17,000 dalton myosin light chain	777	84.106
2954	X54977	Bos taurus 17,000 dalton myosin light chain	652	75.839
2955	X54977	Bos taurus 17,000 dalton myosin light chain	582	91.667
2956	X54977	Bos taurus 17,000 dalton myosin light chain	55	100.000
2957	X54977	Bos taurus 17,000 dalton myosin light chain	444	86.076
2958	X54977	Bos taurus 17,000 dalton myosin light chain	605	86.986
2959	X54977	Bos taurus 17,000 dalton myosin light chain	454	74.684
2960	AL050272	Homo sapiens hypothetical protein	48	37.500
2961	AL050272	Homo sapiens hypothetical protein	151	100.000
2962	AL050272	Homo sapiens hypothetical protein	704	94.776
2963	Y14040	Homo sapiens CASH beta protein	259	100.000
2964	Y14040	Homo sapiens CASH beta protein	669	100.000
2965	Y14040	Homo sapiens CASH beta protein	1297	94.521
2966	Y14040	Homo sapiens CASH beta protein	1107	97.778
2967	Y14040	Homo sapiens CASH beta protein	1285	99.507
2968	Y14040	Homo sapiens CASH beta protein	1424	100.000
2969	Y14040	Homo sapiens CASH beta protein	1297	94.521
2970	Y14040	Homo sapiens CASH beta protein	1192	98.522
2971	Y14040	Homo sapiens CASH beta protein	1076	92.825
2972	U79260	Homo sapiens unknown	166	47.059
2973	X16660	Homo sapiens p25 protein	140	37.500
2974	X55687	Lycopersicon esculentum extensin (class II)	39	37.500
2976	X55687	Lycopersicon esculentum extensin (class II)	39	37.500
2977	X55687	Lycopersicon esculentum extensin (class II)	87	33.803
2978	D25542	Homo sapiens human gcp372	53	40.000

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2979	D25542	Homo sapiens human gcp372	19354	98.299
2980	U92819	Homo sapiens unnamed HERV-H protein	480	100.000
2988	U92819	Homo sapiens unnamed HERV-H protein	263	63.235
2989	U92819	Homo sapiens unnamed HERV-H protein	242	81.395
2993	U92819	Homo sapiens unnamed HERV-H protein	221	78.049
3000	U92819	Homo sapiens unnamed HERV-H protein	259	73.214
3012	U92819	Homo sapiens unnamed HERV-H protein	247	83.721
3015	AJ130978	Homo sapiens Ariadne-2 protein (ARI2)	40	23.333
3016	AJ130978	Homo sapiens Ariadne-2 protein (ARI2)	2249	89.084
3017	AF151905	Homo sapiens CGI-147 protein	663	78.610
3018	AF132947	Homo sapiens CGI-13 protein	606	83.471
3019	AF132947	Homo sapiens CGI-13 protein	142	91.304
3020	AF132947	Homo sapiens CGI-13 protein	140	88.889
3021	AF132947	Homo sapiens CGI-13 protein	1471	75.516
3022	AF132947	Homo sapiens CGI-13 protein	453	98.592
3023	AF132947	Homo sapiens CGI-13 protein	2508	94.433
3024	D42073	Homo sapiens reticulocalbin	194	54.000
3025	D42073	Homo sapiens reticulocalbin	1176	58.446
3026	U46188	Homo sapiens KRAB A domain	28	26.316
3027	U46188	Homo sapiens KRAB A domain	149	72.500
3028	X52949	Giardia intestinalis unidentified reading frame; alternative codon use	145	27.604
3029	Z38112	Unknown cDNA EST EMBL:D35592 comes from this gene; cDNA EST EMBL:D68073 comes from this gene; cDNA	308	38.462
3030	Z38112	Unknown cDNA EST EMBL:D35592 comes from this gene; cDNA EST EMBL:D68073 comes from this gene; cDNA	630	39.589
3031	Z38112	Unknown cDNA EST EMBL:D35592 comes from this gene; cDNA EST EMBL:D68073 comes from this gene; cDNA	476	26.571
3032	M68864	Homo sapiens ORF	1078	85.959
3033	AB016592	Mus musculus GOB-4	563	60.714
3034	AJ001810	Homo sapiens mRNA cleavage factor I 25 kDa subunit	265	100.000
3035	AJ001810	Homo sapiens mRNA cleavage factor I 25 kDa subunit	698	72.840
3036	Y17394	Homo sapiens prefoldin subunit 3	687	76.777
3037	L11566	Homo sapiens ribosomal protein L18	755	78.035
3038	L11566	Homo sapiens ribosomal protein L18	1135	81.385
3039	L11566	Homo sapiens ribosomal protein L18	417	62.694
3040	AF107727	Rattus norvegicus sertolin	92	68.182
3041	AF107727	Rattus norvegicus sertolin	72	30.588
3042	AF107727	Rattus norvegicus sertolin	291	47.482
3043	U36598	synthetic construct HSOD-GlyProGly-A+	419	68.391
3044	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	484	59.172
3045	AC009322	Arabidopsis thaliana Unknown protein	35	33.333
3047	AC009322	Arabidopsis thaliana Unknown protein	47	57.143
3048	AC009322	Arabidopsis thaliana Unknown protein	199	34.211
3050	X80038	Homo sapiens Polio virus receptor protein	71	50.000
3051	X80038	Homo sapiens Polio virus receptor protein	2251	76.531

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3052	X80038	Homo sapiens Polio virus receptor protein	3457	98.513
3053	X80038	Homo sapiens Polio virus receptor protein	2715	70.856
3054	D78152	Homo sapiens annexin IV (carbohydrate-binding protein p33/41)	647	97.170
3055	D78152	Homo sapiens annexin IV (carbohydrate-binding protein p33/41)	218	97.297
3056	D78152	Homo sapiens annexin IV (carbohydrate-binding protein p33/41)	676	85.135
3057	D78152	Homo sapiens annexin IV (carbohydrate-binding protein p33/41)	1218	85.061
3058	AB028966	Homo sapiens KIAA1043 protein	6924	78.369
3059	AB028966	Homo sapiens KIAA1043 protein	316	54.808
3061	AB028966	Homo sapiens KIAA1043 protein	587	100.000
3062	AB028966	Homo sapiens KIAA1043 protein	6707	90.262
3063	AB028966	Homo sapiens KIAA1043 protein	8008	98.420
3064	A01592	Homo sapiens haemoglobin A beta chain	267	54.375
3065	L48932	Homo sapiens beta-globin	323	69.173
3066	U28917	Mus musculus 60S ribosomal protein	549	60.930
3067	AF067619	Caenorhabditis elegans contains similarity to CUB domains (Pfam; CUB, score; 101.9 and 42.78)	390	33.597
3068	Y18206	Homo sapiens serine-threonine specific protein phosphatase	60	44.737
3069	Y18206	Homo sapiens serine-threonine specific protein phosphatase	58	42.857
3070	Y18206	Homo sapiens serine-threonine specific protein phosphatase	429	37.676
3071	AF006636	Homo sapiens melanoma differentiation associated protein-9	1310	85.526
3072	AF113944	Muntiacus muntjak prion protein	108	40.244
3073	AP000006	Pyrococcus horikoshii 249aa long hypothetical protein	202	52.727
3074	AP000006	Pyrococcus horikoshii 249aa long hypothetical protein	331	38.350
3075	AC005031	Homo sapiens neuronal apoptosis inhibitory protein	126	24.324
3076	AC005031	Homo sapiens neuronal apoptosis inhibitory protein	77	26.667
3077	AC005031	Homo sapiens neuronal apoptosis inhibitory protein	612	30.490
3078	AC005031	Homo sapiens neuronal apoptosis inhibitory protein	383	25.664
3079	M26312	Oryctolagus cuniculus unknown protein	174	36.170
3080	X75756	Homo sapiens protein kinase C mu	62	30.435
3081	X75756	Homo sapiens protein kinase C mu	574	58.084
3082	X75756	Homo sapiens protein kinase C mu	46	46.667
3083	X75756	Homo sapiens protein kinase C mu	496	64.602
3084	X75756	Homo sapiens protein kinase C mu	53	33.333
3085	X75756	Homo sapiens protein kinase C mu	3208	62.891
3086	AF033566	Mus musculus cdc2/CDC28-like protein kinase 4	673	77.419
3087	AF033566	Mus musculus cdc2/CDC28-like protein	2680	84.742

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		kinase 4		
3088	AL035071	Homo sapiens dJ1085F17.2 (EB1 (APC binding protein))	361	100.000
3089	AL035071	Homo sapiens dJ1085F17.2 (EB1 (APC binding protein))	511	92.683
3090	AL035071	Homo sapiens dJ1085F17.2 (EB1 (APC binding protein))	350	98.305
3091	AL035071	Homo sapiens dJ1085F17.2 (EB1 (APC binding protein))	1366	93.727
3092	U49973	Homo sapiens ORF2: function unknown	537	72.868
3093	X92485	Plasmodium vivax pva1	171	40.496
3095	AC005521	Homo sapiens similar to yeast SSU72; similar to P53538 (PID:g1711532)	364	72.973
3096	AC005521	Homo sapiens similar to yeast SSU72; similar to P53538 (PID:g1711532)	477	62.755
3098	AB032953	Homo sapiens KIAA1127 protein	558	93.407
3099	AB032953	Homo sapiens KIAA1127 protein	843	100.000
3100	AB032953	Homo sapiens KIAA1127 protein	783	96.800
3101	AB032953	Homo sapiens KIAA1127 protein	10807	97.589
3102	AF007548	Homo sapiens golgi SNARE	40	42.857
3103	AF007548	Homo sapiens golgi SNARE	215	100.000
3104	AF007548	Homo sapiens golgi SNARE	838	82.075
3105	AF007548	Homo sapiens golgi SNARE	690	67.907
3106	M84237	Homo sapiens integrin beta-1 subunit	29	33.333
3107	M84237	Homo sapiens integrin beta-1 subunit	114	56.098
3108	Z11922	Canis familiaris Ran	1269	94.737
3109	Z11922	Canis familiaris Ran	1109	81.019
3110	Z11922	Canis familiaris Ran	706	74.123
3111	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit	250	68.571
3112	D31769	Mus musculus amelogenin precursor	63	28.571
3113	D31769	Mus musculus amelogenin precursor	93	30.488
3114	D31769	Mus musculus amelogenin precursor	135	32.000
3115	D44497	Homo sapiens human p57	455	100.000
3116	D44497	Homo sapiens human p57	2059	86.596
3117	X86779	Homo sapiens FAST kinase	159	28.319
3118	X86779	Homo sapiens FAST kinase	90	28.125
3119	X86779	Homo sapiens FAST kinase	177	28.743
3120	X86779	Homo sapiens FAST kinase	325	28.852
3121	X86779	Homo sapiens FAST kinase	349	29.688
3123	AC007018	Arabidopsis thaliana unknown protein	152	28.395
3124	AC007018	Arabidopsis thaliana unknown protein	421	39.234
3125	AC007018	Arabidopsis thaliana unknown protein	331	50.000
3126	AC007018	Arabidopsis thaliana unknown protein	1209	33.877
3127	AC007018	Arabidopsis thaliana unknown protein	122	45.833
3128	AC007018	Arabidopsis thaliana unknown protein	76	24.359
3129	AC007018	Arabidopsis thaliana unknown protein	257	43.038
3130	AC007018	Arabidopsis thaliana unknown protein	58	57.143
3131	AC007018	Arabidopsis thaliana unknown protein	55	34.483
3132	AC007018	Arabidopsis thaliana unknown protein	1855	40.157
3133	L25899	Homo sapiens ribosomal protein L10	702	74.222
3134	M97796	Homo sapiens Id-2	553	93.407
3135	M97796	Homo sapiens Id-2	738	98.276
3136	M97796	Homo sapiens Id-2	293	64.626

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3137	U89439	Bos taurus ubiquitin-like protein	383	85.417
3138	X79536	Homo sapiens hnRNPcore protein A1	508	92.405
3139	X79536	Homo sapiens hnRNPcore protein A1	1725	96.498
3140	X79536	Homo sapiens hnRNPcore protein A1	851	56.727
3141	X79536	Homo sapiens hnRNPcore protein A1	874	47.515
3143	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	121	90.476
3144	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	110	31.532
3145	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	157	68.421
3146	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	116	86.364
3147	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	655	47.453
3148	AF021255	fowl adenovirus 8 unknown	142	33.929
3149	AF151885	Homo sapiens CGI-127 protein	666	100.000
3150	AF151885	Homo sapiens CGI-127 protein	517	82.540
3151	AF027140	Homo sapiens zinc finger protein	166	50.769
3152	AB014601	Homo sapiens KIAA0701 protein	48	36.667
3153	AB014601	Homo sapiens KIAA0701 protein	56	22.414
3154	AB014601	Homo sapiens KIAA0701 protein	45	22.222
3155	AB014601	Homo sapiens KIAA0701 protein	3242	94.671
3156	U58658	Homo sapiens unknown	231	60.274
3157	D14694	Homo sapiens Whole ORF continues from bp19 (right after 'tag') to bp1596 ('tga').; similar to chinese hamster phosphatidylserine synthase.	413	100.000
3158	D14694	Homo sapiens Whole ORF continues from bp19 (right after 'tag') to bp1596 ('tga').; similar to chinese hamster phosphatidylserine synthase.	2714	92.797
3160	X55683	Lycopersicon esculentum extensin (class I)	146	45.205
3161	AB018319	Homo sapiens KIAA0776 protein	1786	71.975
3162	AB018319	Homo sapiens KIAA0776 protein	4434	94.907
3163	AB021288	Homo sapiens beta 2-microglobulin	627	83.193
3164	AB021288	Homo sapiens beta 2-microglobulin	667	99.160
3165	U36764	Homo sapiens TGF-beta receptor interacting protein 1	433	98.551
3166	U36764	Homo sapiens TGF-beta receptor interacting protein 1	952	75.369
3168	U36764	Homo sapiens TGF-beta receptor interacting protein 1	51	23.256
3169	U36764	Homo sapiens TGF-beta receptor interacting protein 1	647	98.936
3170	U36764	Homo sapiens TGF-beta receptor interacting protein 1	50	25.455
3171	U36764	Homo sapiens TGF-beta receptor interacting protein 1	41	34.043
3172	U36764	Homo sapiens TGF-beta receptor interacting protein 1	993	72.754
3173	AF083115	Homo sapiens paraneoplastic cancer-testis-brain antigen	344	36.364

3174	L28918	Bos taurus cyanogen bromide	111	31.395
3175	AC004521	Arabidopsis thaliana hypothetical protein	97	28.421
3176	AC004521	Arabidopsis thaliana hypothetical protein	90	25.833
3177	AC004521	Arabidopsis thaliana hypothetical protein	396	31.313
3178	AF004715	Homo sapiens jerky gene product homolog	45	30.000
3179	AF004715	Homo sapiens jerky gene product homolog	636	33.249
3180	X55777	Homo sapiens put. ORF	311	63.291
3181	AJ388557	Canis familiaris zinc finger protein	1552	37.834
3182	M13100	Rattus norvegicus unknown protein	223	33.168
3184	M88365	Homo sapiens DNA-binding protein	106	43.182
3185	X55777	Homo sapiens put. ORF	253	47.253
3186	X51394	Xenopus laevis APEG precursor protein	179	27.946
3187	X99962	Homo sapiens rab-related GTP-binding protein	916	71.560
3188	U80929	Cloning vector pBACe3.6 levansucrase	2988	100.000
3194	U80929	Cloning vector pBACe3.6 levansucrase	1493	90.076
3199	U80929	Cloning vector pBACe3.6 levansucrase	871	98.519
3200	U80929	Cloning vector pBACe3.6 levansucrase	1939	72.747
3201	U80929	Cloning vector pBACe3.6 levansucrase	1508	98.712
3202	U80929	Cloning vector pBACe3.6 levansucrase	2641	92.222
3203	U80929	Cloning vector pBACe3.6 levansucrase	1499	96.250
3206	U80929	Cloning vector pBACe3.6 levansucrase	1244	100.000
3207	U80929	Cloning vector pBACe3.6 levansucrase	2974	99.778
3208	U80929	Cloning vector pBACe3.6 levansucrase	3105	100.000
3209	U80929	Cloning vector pBACe3.6 levansucrase	2778	100.000
3211	U80929	Cloning vector pBACe3.6 levansucrase	2622	98.010
3213	U80929	Cloning vector pBACe3.6 levansucrase	2110	84.461
3214	U80929	Cloning vector pBACe3.6 levansucrase	2040	90.368
3215	A78803	unidentified unnamed protein product	918	100.000
3216	A78803	unidentified unnamed protein product	543	78.295
3217	X59864	Rattus rattus ORF	390	50.968
3218	M19684	Homo sapiens alpha-1-antitrypsin-related protein	689	94.828
3219	M19684	Homo sapiens alpha-1-antitrypsin-related protein	2676	99.286
3220	U64033	Mus musculus Tera	1257	90.254
3221	D85818	Mus musculus RNA polymerase II subunit RPB14	409	70.476
3222	D85818	Mus musculus RNA polymerase II subunit RPB14	40	35.294
3223	D85818	Mus musculus RNA polymerase II subunit RPB14	35	30.435
3224	D85818	Mus musculus RNA polymerase II subunit RPB14	40	35.294
3225	D85818	Mus musculus RNA polymerase II subunit RPB14	240	83.673
3226	D85818	Mus musculus RNA polymerase II subunit RPB14	480	80.488
3227	L54057	Homo sapiens deduced protein product	41	35.714

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		shows significant homology to coactosin from Dictyostelium discoideum		
3228	L54057	Homo sapiens deduced protein product shows significant homology to coactosin from Dictyostelium discoideum	850	95.070
3249	V00488	Homo sapiens alpha globin	357	73.810
3250	J04599	Homo sapiens proteoglycan I precursor	1977	94.102
3251	AJ011863	Homo sapiens homeobox protein LSX	1799	76.010
3252	AJ011863	Homo sapiens homeobox protein LSX	4728	98.037
3254	AF044773	Homo sapiens breakpoint cluster region protein 1	51	53.846
3255	AF044773	Homo sapiens breakpoint cluster region protein 1	58	22.619
3256	AF044773	Homo sapiens breakpoint cluster region protein 1	574	100.000
3257	AF044773	Homo sapiens breakpoint cluster region protein 1	53	24.138
3258	AF044773	Homo sapiens breakpoint cluster region protein 1	497	71.622
3259	AJ238629	Chlorella protothecoides putative extensin-like protein	101	37.838
3260	AJ238629	Chlorella protothecoides putative extensin-like protein	81	38.776
3261	X67703	Drosophila melanogaster Mst84Dd	120	45.283
3262	AF083391	Homo sapiens putative WHSC1 protein	916	98.621
3263	AF083391	Homo sapiens putative WHSC1 protein	4107	100.000
3264	AF083391	Homo sapiens putative WHSC1 protein	73	19.167
3265	AF083391	Homo sapiens putative WHSC1 protein	4107	100.000
3266	AF083391	Homo sapiens putative WHSC1 protein	156	100.000
3267	AF083391	Homo sapiens putative WHSC1 protein	64	23.273
3268	AF083391	Homo sapiens putative WHSC1 protein	3205	91.439
3269	AF083391	Homo sapiens putative WHSC1 protein	3968	99.048
3270	AF063605	Homo sapiens brain my047 protein	152	76.667
3271	AF063605	Homo sapiens brain my047 protein	198	71.053
3272	AF063605	Homo sapiens brain my047 protein	152	76.667
3273	AF063605	Homo sapiens brain my047 protein	411	62.687
3274	X67247	Homo sapiens ribosomal protein S8	1160	90.865
3275	X67247	Homo sapiens ribosomal protein S8	402	60.965
3277	AJ133469	Equus caballus prostaglandin D2 synthase	301	70.312
3278	AJ133469	Equus caballus prostaglandin D2 synthase	680	69.744
3279	AF084445	synthetic construct calmodulin mutant SYNCAM17	243	71.429
3280	AF036145	Homo sapiens meningioma-expressed antigen 5	275	97.826
3281	AF036145	Homo sapiens meningioma-expressed antigen 5	4537	92.999
3282	AF036145	Homo sapiens meningioma-expressed antigen 5	1202	79.297
3284	AF036145	Homo sapiens meningioma-expressed antigen 5	4999	98.977

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3285	A78803	unidentified unnamed protein product	918	100.000
3286	A78803	unidentified unnamed protein product	391	71.654
3288	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	73	26.667
3289	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	129	33.684
3290	U66372	Bos taurus ribosomal protein S29	255	94.595
3291	U66372	Bos taurus ribosomal protein S29	412	98.214
3292	U66372	Bos taurus ribosomal protein S29	263	96.154
3293	K01899	Homo sapiens hbbm fused globin protein (beta chain sequence to base 268)	675	98.020
3294	K01899	Homo sapiens hbbm fused globin protein (beta chain sequence to base 268)	512	92.784
3295	AF117710	Homo sapiens hemoglobin beta chain	461	75.573
3296	AF062529	Homo sapiens diphosphoinositol polyphosphate phosphohydrolase	228	100.000
3297	AF062529	Homo sapiens diphosphoinositol polyphosphate phosphohydrolase	741	90.419
3298	U34343	Homo sapiens 13kD differentiation- associated protein	629	95.918
3299	U34343	Homo sapiens 13kD differentiation- associated protein	641	98.947
3300	U34343	Homo sapiens 13kD differentiation- associated protein	573	85.217
3301	M19434	Macaca mulatta gamma-globin	309	61.029
3302	M12429	Pongo pygmaeus alpha-2 globin	907	97.887
3303	M12429	Pongo pygmaeus alpha-2 globin	329	70.492
3304	M26650	Homo sapiens islet amyloid polypeptide (hIAPP)	530	97.753
3305	K02215	Homo sapiens preangiotensinogen	2352	91.718
3307	D26068	Homo sapiens KIAA0038	1255	96.983
3308	AF029893	Homo sapiens i-beta-1,3-N- acetylglucosaminyltransferase; poly-N- acetyllactosamine extension enzyme i- antigen; iGnT	627	100.000
3309	AF029893	Homo sapiens i-beta-1,3-N- acetylglucosaminyltransferase; poly-N- acetyllactosamine extension enzyme i- antigen; iGnT	2366	99.429
3310	AF029893	Homo sapiens i-beta-1,3-N- acetylglucosaminyltransferase; poly-N- acetyllactosamine extension enzyme i- antigen; iGnT	2294	94.498
3311	Z68179	Homo sapiens retinoic acid induced gene E	529	94.048
3312	Z68179	Homo sapiens retinoic acid induced gene E	374	76.978
3313	X75315	Homo sapiens SEB4B	144	100.000
3314	X75315	Homo sapiens SEB4B	1441	94.783
3315	AC006042	Homo sapiens supported by human ESTs AI681256.1 (NID:g4891438), N32168.1 (NID: g1152567), and genscan	57	27.273
3317	AC006042	Homo sapiens supported by human ESTs AI681256.1 (NID:g4891438), N32168.1 (NID: g1152567), and genscan	504	44.167

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3318	AC006042	Homo sapiens supported by human ESTs AI681256.1 (NID:g4891438), N32168.1 (NID:g1152567), and genscan	348	49.242
3319	AC005035	Homo sapiens nik-like; similar to U88984 (PID:g1872546)	663	61.780
3320	AC005035	Homo sapiens nik-like; similar to U88984 (PID:g1872546)	265	100.000
3321	AC005035	Homo sapiens nik-like; similar to U88984 (PID:g1872546)	772	91.912
3322	AC005035	Homo sapiens nik-like; similar to U88984 (PID:g1872546)	318	98.039
3323	AC005035	Homo sapiens nik-like; similar to U88984 (PID:g1872546)	7547	84.632
3324	M64716	Homo sapiens ribosomal protein	53	47.619
3325	M64716	Homo sapiens ribosomal protein	799	100.000
3326	M64716	Homo sapiens ribosomal protein	194	93.750
3327	M64716	Homo sapiens ribosomal protein	40	35.556
3328	M64716	Homo sapiens ribosomal protein	33	34.375
3329	M64716	Homo sapiens ribosomal protein	43	20.588
3330	M64716	Homo sapiens ribosomal protein	215	100.000
3331	M64716	Homo sapiens ribosomal protein	42	24.561
3332	M64716	Homo sapiens ribosomal protein	306	68.966
3333	X60730	Rattus norvegicus beta-globin chain	153	43.537
3334	M74493	Homo sapiens ADP-ribosylation factor 3	57	31.579
3335	M74493	Homo sapiens ADP-ribosylation factor 3	33	41.176
3336	M74493	Homo sapiens ADP-ribosylation factor 3	341	100.000
3337	M74493	Homo sapiens ADP-ribosylation factor 3	297	100.000
3338	M74493	Homo sapiens ADP-ribosylation factor 3	53	22.222
3339	M74493	Homo sapiens ADP-ribosylation factor 3	43	26.190
3340	M74493	Homo sapiens ADP-ribosylation factor 3	45	25.000
3341	M74493	Homo sapiens ADP-ribosylation factor 3	56	22.857
3342	M74493	Homo sapiens ADP-ribosylation factor 3	47	33.333
3343	M74493	Homo sapiens ADP-ribosylation factor 3	56	22.857
3344	M74493	Homo sapiens ADP-ribosylation factor 3	686	81.622
3345	X61046	Hydra sp. mini-collagen	150	39.706
3346	D45131	Homo sapiens basigin	116	52.174
3347	D45131	Homo sapiens basigin	1491	81.126
3348	D45131	Homo sapiens basigin	1373	95.556
3349	X15734	Rattus norvegicus s-adenosylmethionine synthetase	49	28.571
3350	X15734	Rattus norvegicus s-adenosylmethionine synthetase	44	31.250
3351	X15734	Rattus norvegicus s-adenosylmethionine synthetase	52	35.556
3352	X15734	Rattus norvegicus s-adenosylmethionine synthetase	2209	83.879
3353	AF132941	Homo sapiens CGI-07 protein	197	93.939
3354	AF132941	Homo sapiens CGI-07 protein	2917	92.157
3355	U53154	Caenorhabditis elegans No definition line found	40	71.429
3356	U53154	Caenorhabditis elegans No definition line found	301	28.326
3357	AC003083	Homo sapiens mitochondrial carrier protein-like; similar to Q09461	1862	97.727

		(PID:g2497990)		
3358	AE000757	Aquifex aeolicus hypothetical protein	320	42.953
3359	U64028	Homo sapiens NADPH:ubiquinone oxidoreductase subunit B13	426	65.487
3360	U64028	Homo sapiens NADPH:ubiquinone oxidoreductase subunit B13	401	96.522
3361	L76159	Homo sapiens FRG1 gene product	433	56.742
3362	L76159	Homo sapiens FRG1 gene product	391	73.469
3363	L76159	Homo sapiens FRG1 gene product	361	74.725
3364	L76159	Homo sapiens FRG1 gene product	538	73.228
3365	L76159	Homo sapiens FRG1 gene product	961	71.255
3366	L76159	Homo sapiens FRG1 gene product	1358	94.961
3367	M34059	Homo sapiens beta-globin	418	82.308
3368	AL117608	Homo sapiens hypothetical protein	800	100.000
3369	AL117608	Homo sapiens hypothetical protein	214	97.368
3370	M74019	Homo sapiens immunoglobulin light chain variable region	636	81.102
3371	D38305	Homo sapiens Tob	349	96.296
3372	D38305	Homo sapiens Tob	1773	95.652
3373	M69175	Homo sapiens H-protein	278	100.000
3374	M69175	Homo sapiens H-protein	735	88.571
3375	D23662	Homo sapiens ubiquitin-like protein	200	86.792
3376	Y00278	Homo sapiens CFAg (AA 1-94)	596	100.000
3377	Y00278	Homo sapiens CFAg (AA 1-94)	171	100.000
3378	Y00278	Homo sapiens CFAg (AA 1-94)	463	65.278
3379	Y00278	Homo sapiens CFAg (AA 1-94)	350	96.154
3380	L48220	Homo sapiens beta-globin	173	79.245
3381	M15386	Homo sapiens gamma-globin	897	93.421
3382	M15386	Homo sapiens gamma-globin	317	69.375
3383	AE000036	Mycoplasma pneumonia H08_orf157a Protein	106	38.095
3384	AF054181	Homo sapiens CI-MNLL homolog gene	323	97.917
3385	AF054181	Homo sapiens CI-MNLL homolog gene	336	93.548
3386	AF169481	Homo sapiens cytochrome b5 reductase 1	345	100.000
3387	AF169481	Homo sapiens cytochrome b5 reductase 1	344	60.000
3388	AF169481	Homo sapiens cytochrome b5 reductase 1	720	81.481
3389	AF169481	Homo sapiens cytochrome b5 reductase 1	1725	93.069
3390	M64247	Homo sapiens cardiac troponin I	218	72.059
3391	M64247	Homo sapiens cardiac troponin I	522	71.318
3392	M64247	Homo sapiens cardiac troponin I	642	87.603
3393	M64247	Homo sapiens cardiac troponin I	599	100.000
3394	M64247	Homo sapiens cardiac troponin I	1017	91.346
3395	J03910	Homo sapiens metallothionein-IG	169	77.778
3397	J03910	Homo sapiens metallothionein-IG	176	89.655
3398	U93162	Homo sapiens C4-sterol methyl oxidase homolog	674	83.088
3399	AC007633	Unknown similarity to several hypothetical proteins- Arabidopsis thaliana	523	45.217
3400	AJ223980	Homo sapiens BCL7C	305	70.588
3401	AJ223980	Homo sapiens BCL7C	983	85.202
3402	AJ225089	Homo sapiens 2'-5' oligoadenylate synthetase (p59OAS)	191	100.000
3404	AJ225089	Homo sapiens 2'-5' oligoadenylate	62	25.000

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		synthetase (p59OAS)		
3406	AJ225089	Homo sapiens 2'-5' oligoadenylate synthetase (p59OAS)	2969	98.586
3407	AJ006068	Homo sapiens dTDP-D-glucose 4,6-dehydratase	469	76.190
3408	AJ006068	Homo sapiens dTDP-D-glucose 4,6-dehydratase	2181	97.167
3409	X66285	Mus musculus HC1 ORF	152	41.176
3410	M29039	Homo sapiens transactivator	1667	84.507
3411	AB018257	Homo sapiens KIAA0714 protein	7252	99.820
3412	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	370	77.333
3413	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	2674	87.421
3414	Y14551	Homo sapiens DIF-2 protein	478	97.297
3415	Y14551	Homo sapiens DIF-2 protein	792	96.815
3416	Z14961	Homo sapiens codes for truncated alpha Ig chain of patient BEN	119	41.818
3417	Z14961	Homo sapiens codes for truncated alpha Ig chain of patient BEN	119	41.818
3418	Z14961	Homo sapiens codes for truncated alpha Ig chain of patient BEN	57	35.484
3419	AL050044	Homo sapiens hypothetical protein	572	100.000
3420	AL050044	Homo sapiens hypothetical protein	95	100.000
3421	AL050044	Homo sapiens hypothetical protein	466	89.516
3422	M93311	Homo sapiens metallothionein-III	147	59.091
3423	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	166	64.516
3424	AB014561	Homo sapiens KIAA0661 protein	3543	59.462
3425	AL050051	Homo sapiens hypothetical protein	48	33.333
3426	AL050051	Homo sapiens hypothetical protein	557	98.780
3427	AL050051	Homo sapiens hypothetical protein	43	33.333
3428	AL050051	Homo sapiens hypothetical protein	715	94.068
3429	M15530	Homo sapiens B-cell growth factor	172	75.610
3430	D87973	Mus musculus Impact	1611	76.582
3433	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	230	62.687
3434	AL032653	Caenorhabditis elegans similar to Ubiquitin-conjugating enzymes; cDNA EST EMBL:C08678 comes from this gene	499	56.463
3435	AC004255	Arabidopsis thaliana T1F9.23	221	39.683
3436	AC004255	Arabidopsis thaliana T1F9.23	76	39.286
3437	AC004255	Arabidopsis thaliana T1F9.23	235	33.621
3438	J01566	Plasmid ColE1 13.8 kd ORF	85	38.462
3439	J01566	Plasmid ColE1 13.8 kd ORF	212	36.975
3440	J01566	Plasmid ColE1 13.8 kd ORF	64	56.250
3441	J01566	Plasmid ColE1 13.8 kd ORF	58	32.727
3442	J01566	Plasmid ColE1 13.8 kd ORF	66	40.541
3443	J01566	Plasmid ColE1 13.8 kd ORF	184	35.965
3444	J01566	Plasmid ColE1 13.8 kd ORF	54	28.261
3445	J01566	Plasmid ColE1 13.8 kd ORF	181	37.273
3446	J01566	Plasmid ColE1 13.8 kd ORF	171	35.294
3447	J01566	Plasmid ColE1 13.8 kd ORF	204	36.975
3448	J01566	Plasmid ColE1 13.8 kd ORF	129	37.500

3449	J01566	Plasmid ColE1 13.8 kd ORF	165	36.937
3450	S76965	Homo sapiens protein kinase inhibitor, PKI	463	100.000
3451	S76965	Homo sapiens protein kinase inhibitor, PKI	32	31.579
3452	S76965	Homo sapiens protein kinase inhibitor, PKI	403	100.000
3453	AJ005565	Mus musculus SPR2G protein	164	41.270
3454	M15664	Oryza sativa histone 3	457	80.000
3455	AB030234	Canis familiaris D4 dopamine receptor	128	40.000
3456	U33837	Homo sapiens gp330 precursor	692	98.824
3457	U33837	Homo sapiens gp330 precursor	1458	100.000
3459	U33837	Homo sapiens gp330 precursor	1644	55.198
3461	U33837	Homo sapiens gp330 precursor	1598	32.513
3462	U33837	Homo sapiens gp330 precursor	24096	90.617
3463	U33837	Homo sapiens gp330 precursor	33391	99.399
3464	U67085	Homo sapiens Tcd37 homolog	184	45.349
3465	U67085	Homo sapiens Tcd37 homolog	817	72.864
3466	U67085	Homo sapiens Tcd37 homolog	587	90.566
3467	U67085	Homo sapiens Tcd37 homolog	478	94.118
3468	U67085	Homo sapiens Tcd37 homolog	2575	99.768
3469	J04513	Homo sapiens basic fibroblast growth factor (ctg start codon); putative	39	38.889
3470	J04513	Homo sapiens basic fibroblast growth factor (ctg start codon); putative	1370	98.558
3471	AF176514	Mus musculus E2F1-inducible protein	1337	90.955
3472	AF176514	Mus musculus E2F1-inducible protein	391	94.828
3473	AF002697	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3	317	98.039
3474	AF002697	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3	891	83.920
3475	AB033045	Homo sapiens KIAA1219 protein	2110	99.685
3476	AB033045	Homo sapiens KIAA1219 protein	3449	99.437
3477	AL110238	Homo sapiens hypothetical protein	53	32.558
3478	AL110238	Homo sapiens hypothetical protein	936	99.275
3479	U21049	Homo sapiens DD96	397	68.421
3480	U21049	Homo sapiens DD96	595	94.828
3481	AL031427	Homo sapiens dJ167A19.1 (novel protein)	610	77.612
3482	AL031427	Homo sapiens dJ167A19.1 (novel protein)	767	99.123
3483	AL031427	Homo sapiens dJ167A19.1 (novel protein)	51	30.233
3484	AL031427	Homo sapiens dJ167A19.1 (novel protein)	597	96.117
3485	AL031427	Homo sapiens dJ167A19.1 (novel protein)	1997	99.673
3486	AF042081	Homo sapiens SH3 domain binding glutamic acid-rich-like protein	450	81.356
3487	U79260	Homo sapiens unknown	51	25.000
3488	U79260	Homo sapiens unknown	175	51.000
3489	Y13141	Bromheadia finlaysoniana extensin	94	34.615
3490	Y13141	Bromheadia finlaysoniana extensin	73	27.273
3491	AF081258	Homo sapiens testis-specific	39	38.095

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		chromodomain Y-like protein		
3492	AF081258	Homo sapiens testis-specific chromodomain Y-like protein	1473	99.556
3493	AF081258	Homo sapiens testis-specific chromodomain Y-like protein	3478	93.613
3494	AC004770	Homo sapiens BC269730 1	888	80.571
3495	AC004770	Homo sapiens BC269730 1	50	32.258
3496	AC004770	Homo sapiens BC269730 1	608	98.095
3497	D13315	Homo sapiens lactoyl glutathione lyase	942	95.028
3498	AF009356	Homo sapiens regulator of G-protein signaling-16	488	83.516
3499	AF009356	Homo sapiens regulator of G-protein signaling-16	1027	94.608
3500	J03561	Homo sapiens gro protein	219	55.319
3501	J03561	Homo sapiens gro protein	444	77.670
3502	J03561	Homo sapiens gro protein	500	66.187
3503	J03561	Homo sapiens gro protein	596	91.667
3504	AF174592	Homo sapiens F-box protein Fbl6	897	95.000
3505	AF174592	Homo sapiens F-box protein Fbl6	457	74.257
3506	AF174592	Homo sapiens F-box protein Fbl6	1888	97.578
3507	D14696	Homo sapiens KIAA0108	1025	88.511
3508	U51205	Homo sapiens HCOP9	587	78.358
3509	U51205	Homo sapiens HCOP9	541	100.000
3510	U51205	Homo sapiens HCOP9	48	50.000
3511	U51205	Homo sapiens HCOP9	787	84.862
3512	AL031907	Schizosaccharomyces pombe hypothetical protein	138	25.373
3513	AL031907	Schizosaccharomyces pombe hypothetical protein	48	29.630
3514	AL031907	Schizosaccharomyces pombe hypothetical protein	96	26.761
3515	AL031907	Schizosaccharomyces pombe hypothetical protein	68	36.667
3516	AL031907	Schizosaccharomyces pombe hypothetical protein	235	33.333
3517	D89077	Homo sapiens Src-like adapter protein	45	62.500
3518	D89077	Homo sapiens Src-like adapter protein	603	90.196
3519	D89077	Homo sapiens Src-like adapter protein	1592	97.834
3520	L11566	Homo sapiens ribosomal protein L18	474	68.229
3521	AF011564	Oryctolagus cuniculus splicing factor SRp55 homolog	181	50.633
3522	X76105	Homo sapiens DAP-1	46	27.907
3523	X76105	Homo sapiens DAP-1	704	100.000
3524	X60673	Homo sapiens nucleoside-triphosphate--adenylate kinase	1076	94.643
3525	U64856	Caenorhabditis elegans weak similarity to TPR domains	314	47.664
3526	U64856	Caenorhabditis elegans weak similarity to TPR domains	547	42.640
3527	U64856	Caenorhabditis elegans weak similarity to TPR domains	701	34.550
3529	AL050197	Homo sapiens hypothetical protein	228	97.500
3530	AL050197	Homo sapiens hypothetical protein	1034	85.830
3531	AL023657	Homo sapiens SH2D1A	315	96.154

3532	AL023657	Homo sapiens SH2D1A	301	60.784
3533	AL023657	Homo sapiens SH2D1A	301	94.000
3534	AL023657	Homo sapiens SH2D1A	665	85.938
3535	AL023657	Homo sapiens SH2D1A	660	92.248
3536	S82297	Homo sapiens beta 2-microglobulin	227	82.692
3537	M85183	Rattus norvegicus vasopressin receptor	48	38.889
3538	M85183	Rattus norvegicus vasopressin receptor	48	38.462
3539	M85183	Rattus norvegicus vasopressin receptor	1721	59.091
3540	AL049667	Homo sapiens hypothetical protein	424	78.313
3541	AL049667	Homo sapiens hypothetical protein	713	84.615
3542	AL049667	Homo sapiens hypothetical protein	1194	73.868
3543	AL049667	Homo sapiens hypothetical protein	3455	99.058
3544	M12886	Homo sapiens T-cell receptor beta chain	232	100.000
3545	M12886	Homo sapiens T-cell receptor beta chain	250	89.362
3546	M12886	Homo sapiens T-cell receptor beta chain	1225	68.404
3547	M12886	Homo sapiens T-cell receptor beta chain	1457	79.934
3548	J05071	Bos taurus GTP-binding regulatory protein gamma-6 subunit	210	100.000
3549	J05071	Bos taurus GTP-binding regulatory protein gamma-6 subunit	227	100.000
3550	J05071	Bos taurus GTP-binding regulatory protein gamma-6 subunit	305	92.754
3552	AF092878	Homo sapiens zinc RING finger protein SAG	654	56.000
3553	AF092878	Homo sapiens zinc RING finger protein SAG	689	91.228
3554	X95073	Homo sapiens Translin associated protein X	1850	100.000
3555	AB007157	Homo sapiens ribosomal protein S21	276	100.000
3556	AB007157	Homo sapiens ribosomal protein S21	313	94.444
3557	AB007157	Homo sapiens ribosomal protein S21	269	100.000
3558	AC006585	Arabidopsis thaliana putative extragenic suppressor protein	196	33.333
3559	AC006585	Arabidopsis thaliana putative extragenic suppressor protein	1189	45.810
3560	J01175	Lytechinus pictus histone H3	289	75.207
3561	AL021106	Unknown /prediction=(method:"genscan", version:"1.0", score:"53.36"); /prediction=(method:"	299	58.824
3562	AL021106	Unknown /prediction=(method:"genscan", version:"1.0", score:"53.36"); /prediction=(method:"	225	60.294
3563	AL021106	Unknown /prediction=(method:"genscan", version:"1.0", score:"53.36"); /prediction=(method:"	618	54.124
3564	AB001022	Schizosaccharomyces pombe unnamed protein product	53	71.429

3565	AB001022	Schizosaccharomyces pombe unnamed protein product	147	48.780
3566	AL117419	Homo sapiens hypothetical protein	2356	91.484
3567	AL117419	Homo sapiens hypothetical protein	2490	97.922
3568	AF151820	Homo sapiens CGI-62 protein	183	100.000
3569	AF151820	Homo sapiens CGI-62 protein	1844	94.545
3570	AF047384	Rattus norvegicus postsynaptic protein CRIFT	500	98.020
3571	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	55	27.083
3572	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	61	26.923
3574	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	54	28.947
3575	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	68	26.437
3576	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	52	25.882
3578	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	55	33.333
3579	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	59	36.000
3580	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	50	40.000
3582	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	50	83.333
3583	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	54	28.000
3584	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	47	37.500
3585	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	3279	99.426
3586	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	2734	90.574
3587	U79745	Homo sapiens monocarboxylate transporter homologue MCT6	69	30.526
3588	X79238	Homo sapiens ribosomal protein L30	739	100.000
3589	X79238	Homo sapiens ribosomal protein L30	455	81.481
3590	X79238	Homo sapiens ribosomal protein L30	214	65.289
3591	AF064462	Gallus gallus transcription factor LEF-1	260	90.244
3592	AF064462	Gallus gallus transcription factor LEF-1	952	56.902
3593	AF064462	Gallus gallus transcription factor LEF-1	2120	84.962
3594	S58722	Homo sapiens X-linked retinopathy protein. {C-terminal, clone XEH.8c}	188	67.925
3595	AJ010973	Homo sapiens DEDD protein	72	39.286
3596	AJ010973	Homo sapiens DEDD protein	535	56.291
3597	AJ002308	Homo sapiens synaptogyrin 2	662	72.189
3598	AJ002308	Homo sapiens synaptogyrin 2	732	96.396
3599	AJ002308	Homo sapiens synaptogyrin 2	1361	98.206
3600	AF129534	Homo sapiens F-box protein Fbx4	192	46.903
3601	AF129534	Homo sapiens F-box protein Fbx4	2289	91.731

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3602	Y12711	Homo sapiens putative progesterone binding protein	212	48.148
3603	Y12711	Homo sapiens putative progesterone binding protein	421	92.500
3604	Y12711	Homo sapiens putative progesterone binding protein	939	92.929
3605	X56932	Homo sapiens 23 kD highly basic protein	545	80.660
3606	Y13736	Homo sapiens Protein Enriched in Diabetes	385	100.000
3607	Y13736	Homo sapiens Protein Enriched in Diabetes	464	100.000
3608	Y13736	Homo sapiens Protein Enriched in Diabetes	37	50.000
3609	Y13736	Homo sapiens Protein Enriched in Diabetes	35	100.000
3610	Y13736	Homo sapiens Protein Enriched in Diabetes	765	98.462
3611	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	117	38.824
3612	U39318	Homo sapiens Ubch5C	101	93.333
3613	U39318	Homo sapiens Ubch5C	43	42.105
3614	U39318	Homo sapiens Ubch5C	301	100.000
3615	U39318	Homo sapiens Ubch5C	666	92.617
3616	AL110265	Homo sapiens hypothetical protein	808	95.775
3617	U63131	Homo sapiens CDC37 homolog	46	32.000
3618	U63131	Homo sapiens CDC37 homolog	256	37.705
3619	U63131	Homo sapiens CDC37 homolog	730	40.938
3620	Z82285	Caenorhabditis elegans predicted using Genefinder	130	21.930
3621	Z82285	Caenorhabditis elegans predicted using Genefinder	134	27.119
3622	Z82285	Caenorhabditis elegans predicted using Genefinder	208	27.861
3623	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	773	100.000
3624	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	674	59.292
3625	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	667	85.075
3626	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	496	100.000
3627	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	57	27.273
3628	AF100754	Homo sapiens ancient ubiquitous protein AUP1 isoform	2492	81.784
3629	U22376	Homo sapiens alternatively spliced product using exon 13A	124	83.333
3630	U22376	Homo sapiens alternatively spliced product using exon 13A	407	78.571
3633	X52022	Homo sapiens collagen type VI, alpha 3 chain	20067	99.057
3634	AF156098	Homo sapiens RNA binding motif protein 7	131	55.000
3635	AF156098	Homo sapiens RNA binding motif protein	129	65.625

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3636	AF156098	Homo sapiens RNA binding motif protein 7	363	40.099
3637	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	119	42.857
3638	X64229	Homo sapiens putative oncogene	2231	97.600
3640	X07311	Drosophila melanogaster heat shock protein	161	38.028
3641	AC002301	Homo sapiens Homolog of rat Zymogen granule membrane protein	943	89.349
3642	AL080097	Homo sapiens hypothetical protein	212	100.000
3643	AL080097	Homo sapiens hypothetical protein	1303	88.519
3644	AF151887	Homo sapiens CGI-129 protein	148	100.000
3645	AF151887	Homo sapiens CGI-129 protein	281	75.000
3646	AJ237946	Homo sapiens DEAD Box Protein 5	302	100.000
3647	AJ237946	Homo sapiens DEAD Box Protein 5	637	86.154
3648	AJ237946	Homo sapiens DEAD Box Protein 5	126	87.500
3649	AJ237946	Homo sapiens DEAD Box Protein 5	290	75.000
3650	AJ237946	Homo sapiens DEAD Box Protein 5	452	94.444
3651	AJ237946	Homo sapiens DEAD Box Protein 5	466	96.429
3652	AJ237946	Homo sapiens DEAD Box Protein 5	2439	93.555
3653	U37283	Homo sapiens microfibril-associated glycoprotein-2 MAGP-2	808	88.652
3654	U37283	Homo sapiens microfibril-associated glycoprotein-2 MAGP-2	285	95.000
3655	U37283	Homo sapiens microfibril-associated glycoprotein-2 MAGP-2	591	81.868
3656	AC002528	Homo sapiens Genscan gene prediction; 90% similarity to AA023673 (NID:g1487590)	310	100.000
3657	AC002528	Homo sapiens Genscan gene prediction; 90% similarity to AA023673 (NID:g1487590)	780	81.366
3658	AF126743	Homo sapiens DNAJ domain-containing protein MCJ	509	88.742
3659	U62940	Rattus norvegicus mt-GrpE#1 precursor	495	65.714
3661	U96876	Homo sapiens insulin induced protein 1	473	100.000
3662	U96876	Homo sapiens insulin induced protein 1	535	95.294
3663	U96876	Homo sapiens insulin induced protein 1	1520	87.814
3664	AL050170	Homo sapiens hypothetical protein	367	54.887
3665	AL050170	Homo sapiens hypothetical protein	342	100.000
3666	AL050170	Homo sapiens hypothetical protein	681	93.284
3667	AB018292	Homo sapiens KIAA0749 protein	45	34.483
3668	AB018292	Homo sapiens KIAA0749 protein	4692	99.705
3669	Z97184	Homo sapiens HKE2	435	75.229
3670	Z97184	Homo sapiens HKE2	423	67.442
3671	Z97184	Homo sapiens HKE2	389	46.875
3672	Z97184	Homo sapiens HKE2	714	100.000
3673	D85758	Homo sapiens human protein homologous to DROER protein	35	71.429
3674	D85758	Homo sapiens human protein homologous to DROER protein	358	87.255
3675	AF151906	Homo sapiens CGI-148 protein	1067	92.090
3676	AF151906	Homo sapiens CGI-148 protein	40	24.194

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3677	AF151906	Homo sapiens CGI-148 protein	868	90.055
3678	Z26876	Homo sapiens ribosomal protein	279	100.000
3679	Z26876	Homo sapiens ribosomal protein	178	79.688
3680	X15001	Bacteriophage 186 computer protein 79	35	54.545
3681	X15001	Bacteriophage 186 computer protein 79	86	45.098
3682	X15954	Homo sapiens mannose binding protein	1514	98.387
3683	AE000775	Aquifex aeolicus hypothetical protein	260	48.101
3684	AE000775	Aquifex aeolicus hypothetical protein	221	32.571
3685	AE000775	Aquifex aeolicus hypothetical protein	74	25.490
3686	AE000775	Aquifex aeolicus hypothetical protein	1543	41.390
3687	AJ005569	Mus musculus SPR2K protein	29	100.000
3688	AJ005569	Mus musculus SPR2K protein	79	29.688
3691	AJ005569	Mus musculus SPR2K protein	32	33.333
3692	AJ005569	Mus musculus SPR2K protein	87	42.500
3693	U29380	Caenorhabditis elegans similar to adenylate cyclase	50	45.833
3694	U29380	Caenorhabditis elegans similar to adenylate cyclase	450	41.509
3695	AB024370	TT virus ORF1	128	54.545
3696	M21302	Homo sapiens small proline rich protein	94	41.304
3697	X02530	Homo sapiens early response precursor polypeptide (aa-21 to 77)	591	98.980
3698	Z35227	Homo sapiens small G protein	918	93.229
3700	AF004814	Mesocricetus auratus ubiquitin conjugating enzyme	989	89.873
3701	AF004814	Mesocricetus auratus ubiquitin conjugating enzyme	500	71.341
3703	AF143676	Homo sapiens multispansing nuclear envelope membrane protein nurim	1683	99.617
3704	AF036718	Homo sapiens FGFR signalling adaptor SNT-2	3403	99.187
3705	L29028	Unknown amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 ..	142	31.008
3707	AL050278	Homo sapiens hypothetical protein	346	57.983
3708	AL050278	Homo sapiens hypothetical protein	39	62.500
3709	AL050278	Homo sapiens hypothetical protein	571	88.430
3710	AB014543	Homo sapiens KIAA0643 protein	164	95.833
3711	AB014543	Homo sapiens KIAA0643 protein	390	100.000
3712	AB014543	Homo sapiens KIAA0643 protein	68	36.364
3713	AB014543	Homo sapiens KIAA0643 protein	2237	98.511
3714	AC004262	Homo sapiens R29368 2	1204	65.484
3715	AC004262	Homo sapiens R29368 2	1698	80.409
3716	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	325	59.690
3717	AF076974	Homo sapiens TRRAP protein	12447	92.864
3718	AF076974	Homo sapiens TRRAP protein	590	88.288
3719	AF076974	Homo sapiens TRRAP protein	10666	88.345
3720	AF076974	Homo sapiens TRRAP protein	24935	99.348
3721	AF076974	Homo sapiens TRRAP protein	25166	99.197
3722	AB000911	Sus scrofa ribosomal protein	242	61.151
3723	X52354	Homo sapiens KOX 23 protein (56 AA)	141	39.655
3724	M14300	Homo sapiens 2A9 peptide	342	100.000

3726	M14300	Homo sapiens 2A9 peptide	184	61.957
3727	D86984	Homo sapiens similar to yeast adenylate cyclase (S56776)	1516	53.092
3728	M36341	Homo sapiens ADP-ribosylation factor 4	830	90.608
3729	AF097994	Homo sapiens L-kynurenine/alpha-aminoadipate aminotransferase	2525	96.028
3730	AJ249731	Homo sapiens putative G8.1 protein	620	96.970
3732	AJ005567	Mus musculus SPR2I protein	102	41.463
3733	AF075587	Homo sapiens protein associated with Myc	1029	96.622
3734	AF075587	Homo sapiens protein associated with Myc	633	81.203
3735	AF075587	Homo sapiens protein associated with Myc	373	98.214
3736	AF075587	Homo sapiens protein associated with Myc	3777	92.718
3737	AF075587	Homo sapiens protein associated with Myc	30049	98.370
3738	AF106518	Homo sapiens sialomucin CD164	61	29.508
3739	AF106518	Homo sapiens sialomucin CD164	820	85.393
3740	AF132950	Homo sapiens CGI-16 protein	277	67.089
3741	AF132950	Homo sapiens CGI-16 protein	1883	87.470
3742	Z50194	Homo sapiens PQ-rich protein	2797	99.750
3743	AF148509	Homo sapiens alpha 1,2-mannosidase	579	90.291
3744	AF148509	Homo sapiens alpha 1,2-mannosidase	216	45.263
3745	AF148509	Homo sapiens alpha 1,2-mannosidase	289	60.976
3746	AF148509	Homo sapiens alpha 1,2-mannosidase	1562	99.142
3747	AF148509	Homo sapiens alpha 1,2-mannosidase	4566	98.426
3748	AF203978	Homo sapiens MAX-like bHLHZIP protein	172	96.154
3749	AF203978	Homo sapiens MAX-like bHLHZIP protein	1379	81.720
3750	AF203978	Homo sapiens MAX-like bHLHZIP protein	188	96.296
3751	AF203978	Homo sapiens MAX-like bHLHZIP protein	743	64.865
3752	AF203978	Homo sapiens MAX-like bHLHZIP protein	1376	93.117
3754	AB033117	Homo sapiens KIAA1291 protein	259	100.000
3755	AB033117	Homo sapiens KIAA1291 protein	264	75.000
3756	AB033117	Homo sapiens KIAA1291 protein	580	64.118
3757	AB033117	Homo sapiens KIAA1291 protein	412	95.455
3758	AB033117	Homo sapiens KIAA1291 protein	1719	73.902
3759	AB033117	Homo sapiens KIAA1291 protein	6696	96.917
3760	L48218	Homo sapiens beta-globin	111	77.273
3762	D14572	Mus musculus 'PEBP2b1 protein'	1121	98.780
3763	D14572	Mus musculus 'PEBP2b1 protein'	1133	96.471
3764	D14572	Mus musculus 'PEBP2b1 protein'	1139	88.325
3765	AJ001417	Homo sapiens extraneuronal monoamine transporter	192	90.909
3766	AJ001417	Homo sapiens extraneuronal monoamine transporter	3670	98.921
3767	AF148856	Homo sapiens unknown	43	31.111
3768	AF148856	Homo sapiens unknown	947	89.080
3769	U39317	Homo sapiens Ubch5B	101	93.333
3770	U39317	Homo sapiens Ubch5B	763	94.631
3771	U58658	Homo sapiens unknown	35	50.000
3772	U58658	Homo sapiens unknown	84	66.667
3773	U58658	Homo sapiens unknown	93	33.333

3774	U58658	Homo sapiens unknown	237	73.438
3775	X55777	Homo sapiens put. ORF	332	62.500
3776	AL049705	Homo sapiens hypothetical protein	36	18.919
3777	AL049705	Homo sapiens hypothetical protein	64	31.034
3778	AL049705	Homo sapiens hypothetical protein	702	100.000
3779	AL035494	Homo sapiens dJ635G19.2.2 (novel protein (PUTATIVE PARTIAL isoform 2))	308	60.638
3780	AL035494	Homo sapiens dJ635G19.2.2 (novel protein (PUTATIVE PARTIAL isoform 2))	143	55.128
3781	AJ002309	Homo sapiens synaptogyrin 3	1498	98.690
3782	X59727	Homo sapiens 63kDa protein kinase	339	38.189
3783	X59727	Homo sapiens 63kDa protein kinase	1070	94.767
3784	X59727	Homo sapiens 63kDa protein kinase	3483	97.853
3785	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	645	76.033
3786	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	1278	68.106
3787	Y15054	Rattus norvegicus 70 kD tumor-specific antigen	2410	83.790
3788	AB020715	Homo sapiens KIAA0908 protein	47	29.545
3789	AB020715	Homo sapiens KIAA0908 protein	2743	97.234
3791	Z36909	Acinetobacter calcoaceticus phenolhydroxylase component	182	27.826
3792	M26167	Homo sapiens platelet factor 4	350	62.832
3793	M26167	Homo sapiens platelet factor 4	288	66.667
3794	M57567	Homo sapiens ADP-ribosylation factor	28	27.778
3795	M57567	Homo sapiens ADP-ribosylation factor	812	92.308
3796	AF084256	Homo sapiens beta glucuronidase isoform d	175	69.231
3797	J04040	Homo sapiens preproglucagon	901	92.265
3799	Z38011	Mus musculus DMR-N9	371	91.935
3800	Z38011	Mus musculus DMR-N9	589	85.484
3801	Z38011	Mus musculus DMR-N9	4017	89.153
3802	Z11898	Homo sapiens octamer binding protein 3A	2082	88.116
3803	Z11898	Homo sapiens octamer binding protein 3A	2077	95.890
3804	AL050157	Homo sapiens hypothetical protein	379	98.718
3805	AL050157	Homo sapiens hypothetical protein	454	70.199
3806	U62039	Elephantulus edwardii reverse transcriptase	111	48.936
3807	M20189	synthetic construct tet protein	847	93.662
3809	M20189	synthetic construct tet protein	817	100.000
3810	M20189	synthetic construct tet protein	1795	99.281
3811	M20189	synthetic construct tet protein	1072	100.000
3812	M20189	synthetic construct tet protein	518	100.000
3813	M20189	synthetic construct tet protein	927	89.474
3815	M20189	synthetic construct tet protein	673	85.185
3816	M20189	synthetic construct tet protein	2507	100.000
3817	M20189	synthetic construct tet protein	1155	94.845
3818	M20189	synthetic construct tet protein	1150	99.438
3819	M20189	synthetic construct tet protein	2558	99.495
3820	M20189	synthetic construct tet protein	927	89.474
3821	M20189	synthetic construct tet protein	1293	100.000

3822	M20189	synthetic construct tet protein	1315	100.000
3823	M20189	synthetic construct tet protein	1150	91.220
3824	M20189	synthetic construct tet protein	1767	93.980
3827	M20189	synthetic construct tet protein	1147	100.000
3833	M20189	synthetic construct tet protein	1767	93.980
3834	M20189	synthetic construct tet protein	1150	91.220
3835	M20189	synthetic construct tet protein	540	100.000
3836	M20189	synthetic construct tet protein	930	88.439
3837	M20189	synthetic construct tet protein	1335	88.655
3839	M20189	synthetic construct tet protein	1672	93.310
3840	AF164680	Mus musculus precerebellin-1	907	76.166
3841	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	831	92.143
3843	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	2149	69.940
3844	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3177	83.128
3845	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3931	100.000
3846	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3676	90.429
3847	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3863	95.470
3848	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3602	86.246
3849	AF078832	Homo sapiens methyl-CpG binding protein splice variant 3	3271	88.225
3850	AL050405	Homo sapiens hypothetical protein	701	77.564
3851	AL050405	Homo sapiens hypothetical protein	161	78.125
3852	AL050405	Homo sapiens hypothetical protein	390	100.000
3853	AL050405	Homo sapiens hypothetical protein	1951	81.026
3854	AL050405	Homo sapiens hypothetical protein	1904	97.826
3855	AF119835	Homo sapiens stem cell factor precursor	81	100.000
3856	AF119835	Homo sapiens stem cell factor precursor	340	69.136
3857	AF119835	Homo sapiens stem cell factor precursor	1157	98.895
3858	AL050159	Homo sapiens hypothetical protein	925	57.269
3859	U97553	murine herpesvirus 68 unknown	107	32.394
3860	U97553	murine herpesvirus 68 unknown	123	35.714
3861	X74504	Mus musculus T10	191	80.000
3862	X74504	Mus musculus T10	741	61.905
3863	X74504	Mus musculus T10	44	41.176
3864	X74504	Mus musculus T10	378	85.135
3865	X74504	Mus musculus T10	1199	66.000
3866	AB006746	Homo sapiens hMmTRA1b	50	36.000
3867	AB006746	Homo sapiens hMmTRA1b	969	47.756
3868	AC008075	Arabidopsis thaliana F24J5.4	126	29.457
3869	U69161	Homo sapiens CC3	456	90.196
3870	U69161	Homo sapiens CC3	1283	96.667
3871	L31840	Rattus norvegicus nuclear pore complex protein NUP107	61	23.881
3872	L31840	Rattus norvegicus nuclear pore complex	55	21.379

		protein NUP107		
3873	L31840	Rattus norvegicus nuclear pore complex protein NUP107	57	24.675
3874	L31840	Rattus norvegicus nuclear pore complex protein NUP107	1415	50.732
3875	L31840	Rattus norvegicus nuclear pore complex protein NUP107	57	22.000
3876	AF060862	Homo sapiens unknown	240	100.000
3877	AF060862	Homo sapiens unknown	650	97.479
3878	U08018	Bos taurus cartilage leucine-rich protein	769	38.378
3879	U08018	Bos taurus cartilage leucine-rich protein	76	28.440
3880	AJ010103	Homo sapiens IRC1b	99	36.232
3881	AF094583	Homo sapiens putative HIV-1 infection related protein	589	98.851
3882	AF094583	Homo sapiens putative HIV-1 infection related protein	737	100.000
3884	U97006	Caenorhabditis elegans No definition line found	2203	41.540
3885	AL133045	Homo sapiens hypothetical protein	1147	91.045
3887	X67703	Drosophila melanogaster Mst84Dd	73	38.000
3888	AF151886	Homo sapiens CGI-128 protein	352	91.525
3889	AF151886	Homo sapiens CGI-128 protein	854	76.923
3890	AF151886	Homo sapiens CGI-128 protein	444	61.438
3891	AF151886	Homo sapiens CGI-128 protein	471	70.349
3892	AL033514	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D71127 comes from this gene; cDNA EST EMBL:D73731 comes from this gene; cDNA EST yk527c3.3 comes from this gene; cDNA EST yk645b5.3 comes from this gene	34	33.333
3893	AL033514	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:D71127 comes from this gene; cDNA EST EMBL:D73731 comes from this gene; cDNA EST yk527c3.3 comes from this gene; cDNA EST yk645b5.3 comes from this gene	635	47.037
3894	U01878	Saccharomyces cerevisiae unknown	93	46.875
3895	U01878	Saccharomyces cerevisiae unknown	190	40.650
3896	AL080058	Homo sapiens hypothetical protein	2140	91.008
3897	AL050008	Homo sapiens hypothetical protein	127	64.286
3898	AL050008	Homo sapiens hypothetical protein	163	42.353
3899	AL050008	Homo sapiens hypothetical protein	125	66.667
3900	AL050008	Homo sapiens hypothetical protein	709	57.436
3901	Z66521	Caenorhabditis elegans similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene	202	36.735
3902	Z66521	Caenorhabditis elegans similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene	313	65.217
3903	Z66521	Caenorhabditis elegans similar to mitochondrial RNA splicing MSR4 like	494	50.515

		protein; cDNA EST EMBL:C09217 comes from this gene		
3904	AF187305	Myxine glutinosa calmodulin	699	92.617
3905	AJ010103	Homo sapiens IRC1b	42	30.882
3906	AJ010103	Homo sapiens IRC1b	61	30.233
3907	AJ010103	Homo sapiens IRC1b	61	63.636
3908	AJ010103	Homo sapiens IRC1b	53	26.154
3909	AJ010103	Homo sapiens IRC1b	102	39.189
3910	AB032999	Homo sapiens KIAA1173 protein	433	100.000
3911	AB032999	Homo sapiens KIAA1173 protein	52	34.783
3912	AB032999	Homo sapiens KIAA1173 protein	458	97.333
3913	AB032999	Homo sapiens KIAA1173 protein	66	23.404
3914	AB032999	Homo sapiens KIAA1173 protein	142	100.000
3915	AB032999	Homo sapiens KIAA1173 protein	53	37.500
3916	AB032999	Homo sapiens KIAA1173 protein	53	30.769
3918	AB032999	Homo sapiens KIAA1173 protein	54	28.571
3919	AB032999	Homo sapiens KIAA1173 protein	1893	92.604
3921	D83146	Mus musculus Six5	3740	85.714
3922	U38544	Mus musculus alpha-1 type 1 collagen	47	41.667
3923	U38544	Mus musculus alpha-1 type 1 collagen	113	34.343
3924	AF037440	Edwardsiella ictaluri putative 26 kDa protein	66	24.000
3925	AF037440	Edwardsiella ictaluri putative 26 kDa protein	131	23.301
3926	AF176520	Mus musculus WD repeat-containing F-box protein FBW5	2857	85.442
3927	AF098066	Homo sapiens squamous cell carcinoma antigen recognized by T cell	2235	51.811
3928	AL031287	Homo sapiens match: ESTs: Em:N54388 Em:R14260 Em:H08089 Em:Z24943 Em:AA130053	575	96.739
3929	AL031287	Homo sapiens match: ESTs: Em:N54388 Em:R14260 Em:H08089 Em:Z24943 Em:AA130053	431	63.793
3930	AL031287	Homo sapiens match: ESTs: Em:N54388 Em:R14260 Em:H08089 Em:Z24943 Em:AA130053	2758	94.467
3931	D28877	Homo sapiens hnRNP B1 protein	2065	91.892
3932	D28877	Homo sapiens hnRNP B1 protein	488	100.000
3933	D28877	Homo sapiens hnRNP B1 protein	160	85.714
3934	D28877	Homo sapiens hnRNP B1 protein	59	24.000
3935	D28877	Homo sapiens hnRNP B1 protein	2314	96.893
3936	D28877	Homo sapiens hnRNP B1 protein	2168	95.882
3938	AF152497	Homo sapiens protocadherin beta 4	1212	75.397
3939	AF152497	Homo sapiens protocadherin beta 4	859	74.093
3940	AF152497	Homo sapiens protocadherin beta 4	1291	96.209
3941	AF152497	Homo sapiens protocadherin beta 4	4747	97.442
3942	D90870	Escherichia coli similar to	47	24.638
3943	D90870	Escherichia coli similar to	65	31.746
3944	D90870	Escherichia coli similar to	1618	99.618
3945	D90870	Escherichia coli similar to	1712	98.889
3946	AF133913	Mus musculus ARL-6 interacting protein-6	35	35.000
3947	AF133913	Mus musculus ARL-6 interacting	78	92.308

		protein-6		
3948	AF133913	Mus musculus ARL-6 interacting protein-6	78	92.308
3949	AF133913	Mus musculus ARL-6 interacting protein-6	455	66.087
3950	AB017800	Homo sapiens nolp	53	45.000
3951	AB017800	Homo sapiens nolp	291	67.213
3952	AB017800	Homo sapiens nolp	137	54.286
3953	AB017800	Homo sapiens nolp	233	44.037
3954	AB017800	Homo sapiens nolp	173	58.333
3955	AB017800	Homo sapiens nolp	1115	53.810
3956	AF059336	Plasmodium vivax circumsporozoite protein	132	27.317
3957	U89439	Bos taurus ubiquitin-like protein	398	79.381
3958	AL133078	Homo sapiens hypothetical protein	39	24.242
3959	AL133078	Homo sapiens hypothetical protein	63	30.508
3960	AL133078	Homo sapiens hypothetical protein	942	67.308
3961	Y18206	Homo sapiens serine-threonine specific protein phosphatase	352	36.420
3962	AF078164	Homo sapiens Ku70-binding protein	436	100.000
3963	AF078164	Homo sapiens Ku70-binding protein	1772	97.213
3965	U79260	Homo sapiens unknown	313	60.000
3967	AF039687	Homo sapiens antigen NY-CO-1	756	99.174
3968	AF039687	Homo sapiens antigen NY-CO-1	2067	96.739
3969	AF110532	Homo sapiens uncoupling protein UCP-4	1379	100.000
3970	AF110532	Homo sapiens uncoupling protein UCP-4	201	54.795
3971	X17098	Homo sapiens precursor (AA -34 to -390)	1582	59.449
3972	X17098	Homo sapiens precursor (AA -34 to -390)	1371	74.828
3973	X17098	Homo sapiens precursor (AA -34 to -390)	2387	87.198
3974	X17098	Homo sapiens precursor (AA -34 to -390)	1906	61.525
3975	X17098	Homo sapiens precursor (AA -34 to -390)	2402	87.440
3976	X17098	Homo sapiens precursor (AA -34 to -390)	2296	78.158
3977	X17098	Homo sapiens precursor (AA -34 to -390)	1856	53.695
3978	X17098	Homo sapiens precursor (AA -34 to -390)	1625	67.391
3979	X17098	Homo sapiens precursor (AA -34 to -390)	1436	61.667
3980	X17098	Homo sapiens precursor (AA -34 to -390)	2286	85.132
3981	X17098	Homo sapiens precursor (AA -34 to -390)	1955	78.788
3982	X17098	Homo sapiens precursor (AA -34 to -390)	2188	88.221
3984	AC004798	Homo sapiens R31546 1	4508	86.418
3985	AC004798	Homo sapiens R31546 1	4647	99.590
3986	AF110520	Mus musculus NG28	60	30.645
3987	AF110520	Mus musculus NG28	3317	72.453

3988	AB015343	Homo sapiens HRIHFB2122	41	50.000
3989	AB015343	Homo sapiens HRIHFB2122	1455	100.000
3990	X00824	Gallus gallus collagen	96	45.312
3993	AJ251595	Homo sapiens transmembrane glycoprotein	1039	99.367
3994	AJ251595	Homo sapiens transmembrane glycoprotein	536	100.000
3995	AJ251595	Homo sapiens transmembrane glycoprotein	156	90.909
3996	AJ251595	Homo sapiens transmembrane glycoprotein	5029	100.000
3997	AJ251595	Homo sapiens transmembrane glycoprotein	2743	66.173
3998	AJ251595	Homo sapiens transmembrane glycoprotein	1404	99.550
3999	X04601	Mus musculus short ORF (AA 1-62)	65	41.667
4000	L48220	Homo sapiens beta-globin	162	68.519
4001	X85545	Homo sapiens protein kinase	198	86.667
4002	X85545	Homo sapiens protein kinase	436	96.721
4003	X85545	Homo sapiens protein kinase	1261	97.382
4004	X85545	Homo sapiens protein kinase	716	67.027
4005	X85545	Homo sapiens protein kinase	2098	87.430
4006	X85545	Homo sapiens protein kinase	797	64.706
4007	X85545	Homo sapiens protein kinase	852	68.500
4008	X85545	Homo sapiens protein kinase	2315	99.721
4010	AF187987	Homo sapiens zinc finger protein ZNF221	2845	76.588
4011	AF187987	Homo sapiens zinc finger protein ZNF221	4111	96.812
4012	AF116909	Homo sapiens unknown	39	26.667
4013	AF116909	Homo sapiens unknown	838	93.985
4014	D49474	Mus musculus HMG-box transcription factor	2364	82.185
4015	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	55	22.581
4016	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	54	27.907
4017	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	911	71.569
4018	AF013969	Mus musculus antigen containing epitope to monoclonal antibody MMS-85/12	4894	57.293
4019	X88799	Oryza sativa DNA binding protein	138	38.667
4020	Z98602	Schizosaccharomyces pombe conserved uncharacterized protein domain-containing protein	306	33.146
4021	Z98602	Schizosaccharomyces pombe conserved uncharacterized protein domain-containing protein	687	43.443
4022	AC008015	Homo sapiens unknown	251	59.459
4023	AC008015	Homo sapiens unknown	337	100.000

4024	AC008015	Homo sapiens unknown	226	94.286
4025	AC008015	Homo sapiens unknown	296	53.488
4026	AC008015	Homo sapiens unknown	703	92.857
4027	U14969	Homo sapiens ribosomal protein L28	514	68.613
4028	U14969	Homo sapiens ribosomal protein L28	160	92.000
4029	U14969	Homo sapiens ribosomal protein L28	257	100.000
4031	U14969	Homo sapiens ribosomal protein L28	457	98.571
4032	U14969	Homo sapiens ribosomal protein L28	431	97.059
4033	U14969	Homo sapiens ribosomal protein L28	514	93.458
4034	U14969	Homo sapiens ribosomal protein L28	243	57.364
4035	L76159	Homo sapiens FRG1 gene product	36	25.806
4036	L76159	Homo sapiens FRG1 gene product	337	64.286
4037	L76159	Homo sapiens FRG1 gene product	1200	87.259
4038	L76159	Homo sapiens FRG1 gene product	873	70.485
4039	L76159	Homo sapiens FRG1 gene product	1046	78.298
4040	L76159	Homo sapiens FRG1 gene product	543	77.344
4041	L27065	Homo sapiens NF2	201	76.923
4042	AF092128	Homo sapiens putative transmembrane protein E3-16	1175	85.348
4043	AJ133104	Rattus norvegicus vesicle associated membrane protein 2B	601	96.396
4044	AF077204	Homo sapiens HSPC018	906	92.353
4045	U79260	Homo sapiens unknown	117	81.818
4046	U79260	Homo sapiens unknown	321	72.368
4047	U31382	Homo sapiens G protein gamma-4 subunit	438	97.333
4048	M11749	Homo sapiens Thy-1	592	96.875
4049	M11749	Homo sapiens Thy-1	965	98.052
4050	M11749	Homo sapiens Thy-1	44	26.923
4051	M11749	Homo sapiens Thy-1	805	95.062
4052	AF159055	Homo sapiens leucine zipper-like protein	88	59.375
4053	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	169	56.000
4054	AF084256	Homo sapiens beta glucuronidase isoform d	146	48.077
4056	AJ005559	Mus musculus SPR2A protein	95	36.735
4057	X62844	Pygmy chimpanzee papillomavirus type 1 E5	99	38.806
4058	U20897	Homo sapiens melanoma ubiquitous mutated protein	460	96.053
4059	U20897	Homo sapiens melanoma ubiquitous mutated protein	2900	99.542
4060	U20897	Homo sapiens melanoma ubiquitous mutated protein	2667	87.607
4061	X99404	Homo sapiens Berg36	40	71.429
4062	X99404	Homo sapiens Berg36	2161	99.375
4063	Y13141	Bromheadia finlaysoniana extensin	71	88.889
4064	Y13141	Bromheadia finlaysoniana extensin	114	33.871
4065	X52164	Mus musculus Q300 protein (AA 1-77)	122	50.000
4066	X74142	Homo sapiens transcription factor	3120	97.500
4067	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	48	32.500
4068	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	86	29.508

4069	AF155105	Homo sapiens putative zinc finger protein NY-REN-34 antigen	197	30.579
4070	AL079310	Homo sapiens hypothetical protein	804	72.775
4071	AL079310	Homo sapiens hypothetical protein	1588	95.667
4072	AL079310	Homo sapiens hypothetical protein	3096	98.381
4073	L05188	Homo sapiens small proline-rich protein 2	121	36.538
4074	D87470	Homo sapiens KIAA0280	802	92.593
4075	D87470	Homo sapiens KIAA0280	646	96.117
4077	D87470	Homo sapiens KIAA0280	49	29.630
4078	D87470	Homo sapiens KIAA0280	211	60.714
4079	D87470	Homo sapiens KIAA0280	1969	100.000
4080	AB018566	Homo sapiens Proline synthetase associated	590	96.296
4081	AB018566	Homo sapiens Proline synthetase associated	1279	90.311
4082	U69127	Homo sapiens FUSE binding protein 3	883	83.648
4083	U69127	Homo sapiens FUSE binding protein 3	2438	79.093
4084	U69127	Homo sapiens FUSE binding protein 3	237	100.000
4085	U69127	Homo sapiens FUSE binding protein 3	3830	97.655
4086	AF151883	Homo sapiens CGI-125 protein	481	72.500
4087	AF151883	Homo sapiens CGI-125 protein	642	100.000
4088	AF151883	Homo sapiens CGI-125 protein	560	82.222
4089	AF042713	Rattus norvegicus neurexophilin 3	1602	94.841
4090	X67507	Medicago sativa ENOD12B	57	32.558
4091	X67507	Medicago sativa ENOD12B	128	36.765
4092	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	58	29.730
4093	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	48	35.714
4094	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	52	50.000
4095	AL022238	Homo sapiens dJ1042K10.3 (novel protein)	1453	93.416
4096	AF191687	Homo sapiens alanine-glyoxylate aminotransferase homolog	83	39.286
4097	AF100772	Homo sapiens tenascin-M1	70	32.653
4098	AF100772	Homo sapiens tenascin-M1	2557	99.155
4099	AF100772	Homo sapiens tenascin-M1	8869	97.129
4100	AF100772	Homo sapiens tenascin-M1	18627	99.670
4101	L24521	Homo sapiens transformation-related protein	359	58.824
4102	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	939	87.356
4104	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	320	60.360
4105	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	146	100.000
4106	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	3147	96.903
4107	Y14391	Homo sapiens GTP-binding protein	395	71.717
4108	Y14391	Homo sapiens GTP-binding protein	62	43.243
4109	Y14391	Homo sapiens GTP-binding protein	2386	95.302
4111	U63542	Homo sapiens FAP protein	200	81.818

4112	U63542	Homo sapiens FAP protein	200	81.818
4113	U63542	Homo sapiens FAP protein	200	81.818
4114	U63542	Homo sapiens FAP protein	47	24.000
4115	U63542	Homo sapiens FAP protein	52	29.630
4116	U63542	Homo sapiens FAP protein	203	80.000
4117	U63542	Homo sapiens FAP protein	200	81.818
4118	U63542	Homo sapiens FAP protein	215	78.947
4119	A27282	Homo sapiens TGR-CL3C	98	39.394
4120	M64983	Homo sapiens fibrinogen beta chain	767	41.667
4121	M64983	Homo sapiens fibrinogen beta chain	46	33.333
4122	Z49825	Homo sapiens hepatocyte nuclear factor 4 alpha (HNF4alpha4)	3334	95.810
4123	Z49825	Homo sapiens hepatocyte nuclear factor 4 alpha (HNF4alpha4)	2940	91.633
4124	Z49825	Homo sapiens hepatocyte nuclear factor 4 alpha (HNF4alpha4)	2582	91.589
4125	Z49825	Homo sapiens hepatocyte nuclear factor 4 alpha (HNF4alpha4)	526	67.133
4126	Z49825	Homo sapiens hepatocyte nuclear factor 4 alpha (HNF4alpha4)	3079	93.849
4127	M15530	Homo sapiens B-cell growth factor	153	44.828
4128	X55687	Lycopersicon esculentum extensin (class II)	158	38.356
4129	X55687	Lycopersicon esculentum extensin (class II)	124	36.232
4131	L10908	Mus musculus Gcap1 gene product	87	30.357
4132	L10908	Mus musculus Gcap1 gene product	88	22.857
4134	U14913	Saccharomyces cerevisiae Ylr198cp	125	36.471
4136	X53581	Rattus norvegicus ORF4	248	51.389
4137	AF084256	Homo sapiens beta glucuronidase isoform d	35	60.000
4138	AF084256	Homo sapiens beta glucuronidase isoform d	191	57.143
4139	M69297	Homo sapiens ORF 3	149	62.500
4140	AF133849	Plasmodium falciparum DBL alpha protein	107	37.500
4141	AF076469	Canis familiaris cyclin-dependent kinase inhibitor	107	39.474
4142	A31038	Nicotiana glauca PRP3	145	36.620
4143	M60732	Hordeum vulgare cold-regulated	101	36.842
4144	M60732	Hordeum vulgare cold-regulated	142	33.696
4146	M15530	Homo sapiens B-cell growth factor	174	54.098
4148	D16632	Mus musculus A1	37	57.143
4149	D16632	Mus musculus A1	108	38.889
4150	M15530	Homo sapiens B-cell growth factor	167	63.158
4151	M15530	Homo sapiens B-cell growth factor	145	44.828
4152	M15530	Homo sapiens B-cell growth factor	148	50.000
4153	X55777	Homo sapiens put. ORF	243	53.012
4155	AF023530	Mus musculus RNA helicase A	371	72.152
4156	U01317	Homo sapiens beta-globin	636	75.385
4157	AF039853	Mus musculus anti-activating transcription factor 1 Ig variable heavy chain	46	32.432
4158	AF039853	Mus musculus anti-activating	42	36.364

		transcription factor 1 Ig variable heavy chain		
4159	AF039853	Mus musculus anti-activating transcription factor 1 Ig variable heavy chain	42	53.333
4160	AF039853	Mus musculus anti-activating transcription factor 1 Ig variable heavy chain	78	42.857
4161	AF039853	Mus musculus anti-activating transcription factor 1 Ig variable heavy chain	59	41.667
4162	AF039853	Mus musculus anti-activating transcription factor 1 Ig variable heavy chain	131	31.395
4163	Z73102	Caenorhabditis elegans Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene	225	33.898
4164	AJ005559	Mus musculus SPR2A protein	103	32.609
4165	AF107406	Homo sapiens GW128	129	50.000
4166	M36914	Zea mays cell wall protein (put.); putative	129	33.333
4167	AF034551	Zalophotrema atlanticum NADH dehydrogenase subunit 3	96	33.929
4168	X81900	Homo sapiens NADH oxidoreductase subunit MWFE	268	75.806
4169	K03208	Homo sapiens salivary proline-rich protein precursor	157	29.839
4170	A27282	Homo sapiens TGR-CL3C	61	37.500
4171	A27282	Homo sapiens TGR-CL3C	104	45.283
4172	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	130	47.500
4173	M15530	Homo sapiens B-cell growth factor	142	42.857
4174	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	45	29.787
4175	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	122	38.356
4176	L20934	Anopheles gambiae NADH dehydrogenase subunit 4L	110	31.343
4177	A31038	Nicotiana alata PRP3	136	36.486
4178	U03161	Pseudomonas aeruginosa predicted protein of 93 amino acids, MW of 9569	78	40.476
4180	AB030237	Canis familiaris D4 dopamine receptor	89	35.000
4181	AB030237	Canis familiaris D4 dopamine receptor	138	30.526
4182	D29833	Homo sapiens proline rich peptide P-B	117	39.394
4183	D29833	Homo sapiens proline rich peptide P-B	98	42.857
4184	M22332	Homo sapiens unknown protein	134	44.000
4185	U20239	Mus musculus fibrosin	97	35.938
4186	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ-HRGP	144	42.466
4187	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ-HRGP	448	34.855
4188	AF186275	Echinometra mathaei bindin precursor	111	40.000

4189	M15530	Homo sapiens B-cell growth factor	165	54.386
4190	AF022186	Cyanidium caldarium unknown	100	33.784
4191	AF070662	Homo sapiens HSPC006	527	83.654
4192	AF070662	Homo sapiens HSPC006	1023	89.005
4193	AF070662	Homo sapiens HSPC006	537	95.238
4194	U58658	Homo sapiens unknown	102	50.000
4195	U58658	Homo sapiens unknown	294	66.197
4196	AF008196	Homo sapiens bax epsilon	35	100.000
4197	AF008196	Homo sapiens bax epsilon	35	100.000
4199	AF008196	Homo sapiens bax epsilon	50	50.000
4200	AF008196	Homo sapiens bax epsilon	142	59.459
4202	U63332	Homo sapiens super cysteine rich protein; SCRP	128	35.556
4204	U89695	Rattus norvegicus non-histone chromosomal architectural protein HMGI-C	117	36.667
4205	AF019409	Homo sapiens uncoupling protein 2	443	88.608
4206	AF019409	Homo sapiens uncoupling protein 2	417	100.000
4207	AF019409	Homo sapiens uncoupling protein 2	601	66.092
4208	U05438	Human immunodeficiency virus type 1 envelope glycoprotein, v4v5 region	109	31.481
4209	AB016432	gallid herpesvirus 1 ORF 94	51	55.556
4210	AF092929	Mus musculus beta-defensin 3	88	35.484
4211	AP000060	Aeropyrum pernix 150aa long hypothetical protein	119	30.769
4212	M15530	Homo sapiens B-cell growth factor	176	53.448
4213	AB032918	Hylobates moloch dopamine receptor D4	95	34.211
4214	AB032918	Hylobates moloch dopamine receptor D4	78	24.561
4215	AB032918	Hylobates moloch dopamine receptor D4	89	29.630
4216	AF005370	Alcelaphine herpesvirus 1 capsid protein	87	26.549
4217	AF005370	Alcelaphine herpesvirus 1 capsid protein	170	33.071
4218	M19419	Mus musculus proline-rich salivary protein	195	33.333
4219	AP000061	Aeropyrum pernix 114aa long hypothetical protein	82	36.207
4220	AP000061	Aeropyrum pernix 114aa long hypothetical protein	118	30.769
4221	D16585	Homo sapiens T cell receptor alpha chain	107	31.148
4222	M15530	Homo sapiens B-cell growth factor	161	58.140
4223	AC011623	Arabidopsis thaliana unknown protein	124	61.538
4224	AC011623	Arabidopsis thaliana unknown protein	122	36.697
4225	X92485	Plasmodium vivax pval	77	31.373
4226	X92485	Plasmodium vivax pval	185	53.247
4229	U11682	Trypanoplasma borreli unassigned reading frame	68	27.273
4230	M15530	Homo sapiens B-cell growth factor	185	56.604
4231	AF159055	Homo sapiens leucine zipper-like protein	117	59.375
4232	AC003981	Arabidopsis thaliana F22013.17	47	38.889
4233	AF003534	Chilo iridescent virus hypothetical protein 030L	31	44.444

4234	AF003534	Chilo iridescent virus hypothetical protein 030L	35	42.857
4235	AF003534	Chilo iridescent virus hypothetical protein 030L	77	35.484
4236	AF003534	Chilo iridescent virus hypothetical protein 030L	38	35.294
4237	AF003534	Chilo iridescent virus hypothetical protein 030L	40	19.355
4238	AF003534	Chilo iridescent virus hypothetical protein 030L	40	70.000
4240	AF003534	Chilo iridescent virus hypothetical protein 030L	112	30.303
4241	X95276	Plasmodium falciparum rps8	97	31.776
4243	AJ005564	Mus musculus SPR2F protein	75	36.842
4245	AJ005564	Mus musculus SPR2F protein	89	33.333
4246	U28971	Caenorhabditis elegans similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	146	59.459
4247	L07809	Homo sapiens dynamin	138	41.667
4248	AF107406	Homo sapiens GW128	164	47.059
4250	L77967	Ovis aries small proline-rich protein with paired repeat	88	34.483
4251	AJ005564	Mus musculus SPR2F protein	102	41.860
4252	X90732	Brassica napus Biotin carboxyl carrier protein	133	25.342
4253	AF080560	beak and feather disease virus unknown	110	24.742
4254	AB032980	Homo sapiens KIAA1154 protein	1449	99.554
4255	M77663	Homo sapiens keratin 10	230	29.134
4256	U31928	Plasmodium vivax merozoite surface protein-1	104	25.954
4257	X98485	Plasmodium vivax putative	230	43.617
4258	M15530	Homo sapiens B-cell growth factor	162	72.222
4259	AF084256	Homo sapiens beta glucuronidase isoform d	113	36.145
4261	M88366	Homo sapiens DNA-binding protein	70	43.750
4262	M15530	Homo sapiens B-cell growth factor	168	42.222
4263	AJ005565	Mus musculus SPR2G protein	97	35.417
4264	AF007826	Homo sapiens bax epsilon	167	50.000
4265	M15530	Homo sapiens B-cell growth factor	155	68.571
4266	X55777	Homo sapiens put. ORF	240	54.286
4267	J02963	Homo sapiens platelet glycoprotein IIb precursor	168	75.000
4268	J02963	Homo sapiens platelet glycoprotein IIb precursor	164	58.537
4270	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	425	74.074
4271	X16827	Dictyostelium discoideum 2C gene product (AA 1-98)	110	33.846
4273	AL023781	Schizosaccharomyces pombe Caffeine-induced death protein Cid2p	120	21.875
4274	M15530	Homo sapiens B-cell growth factor	41	100.000
4275	M15530	Homo sapiens B-cell growth factor	120	67.857
4276	M15530	Homo sapiens B-cell growth factor	182	60.465
4277	S58431	Gallid herpesvirus 2 orf 24	118	45.283

4278	M14549	Drosophila melanogaster segmentation protein PRD 4	56	75.000
4279	M14549	Drosophila melanogaster segmentation protein PRD 4	100	52.381
4280	M15530	Homo sapiens B-cell growth factor	132	57.895
4281	AF058159	Human immunodeficiency virus type 1 envelope glycoprotein	72	46.667
4282	U58658	Homo sapiens unknown	67	80.000
4283	U58658	Homo sapiens unknown	72	90.000
4284	U58658	Homo sapiens unknown	157	46.774
4285	L10908	Mus musculus Gcap1 gene product	107	26.230
4286	M15530	Homo sapiens B-cell growth factor	187	71.053
4287	M15530	Homo sapiens B-cell growth factor	181	55.932
4288	AJ005559	Mus musculus SPR2A protein	107	33.824
4290	U05313	Trypanosoma brucei CR3	126	36.364
4291	X77858	Human papillomavirus type 59 ORF putative E5	87	66.667
4292	M15530	Homo sapiens B-cell growth factor	204	50.000
4293	U63542	Homo sapiens FAP protein	160	65.789
4294	L23927	Escherichia coli putative	39	41.667
4295	L23927	Escherichia coli putative	87	34.091
4296	Z22864	avian adenovirus ORF8	85	33.962
4297	Z22864	avian adenovirus ORF8	86	36.364
4319	AF126163	Homo sapiens HHLA3 protein	153	75.862
4322	AF126163	Homo sapiens HHLA3 protein	150	75.000
4323	D50915	Homo sapiens The KIAA0125 gene product is novel.	80	44.444
4325	M62415	Pseudopleuronectes americanus HPLC6	89	52.000
4327	X52164	Mus musculus Q300 protein (AA 1-77)	146	65.517
4328	M15530	Homo sapiens B-cell growth factor	136	59.459
4329	L10908	Mus musculus Gcap1 gene product	95	31.818
4330	X95276	Plasmodium falciparum rpl23	76	30.159
4331	AC004416	Homo sapiens WUGSC:H_RG013N12.gw.1335199.a gene product	30	38.462
4332	AC004416	Homo sapiens WUGSC:H_RG013N12.gw.1335199.a gene product	31	40.000
4335	L10908	Mus musculus Gcap1 gene product	84	38.462
4336	D87437	Homo sapiens KIAA0250	5405	99.751
4337	AF061244	Agrocybe aegerita unknown	117	30.667
4338	X66285	Mus musculus HC1 ORF	125	29.508
4339	X77816	Rattus norvegicus PR-Vbeta1	145	48.889
4340	U58658	Homo sapiens unknown	220	62.162
4341	U63542	Homo sapiens FAP protein	188	71.429
4343	S52457	Plasmodium falciparum, Malayan Camp isolate, Peptide Partial, 126 aa PfEMP2, MESA, PP330=large antigenic protein {repeating structure}	108	31.707
4345	AF004561	Homo sapiens p21-Arc	562	92.308
4346	AF004561	Homo sapiens p21-Arc	151	81.250
4347	AF004561	Homo sapiens p21-Arc	847	85.870
4348	M15530	Homo sapiens B-cell growth factor	142	49.057
4349	M15530	Homo sapiens B-cell growth factor	214	73.810

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4350	M15530	Homo sapiens B-cell growth factor	55	50.000
4351	AC004416	Homo sapiens WUGSC:H_RG013N12.gw.1335199.a gene product	153	58.333
4352	U58755	Caenorhabditis elegans C34D4.11 gene product	124	40.816
4353	U01849	Trypanosoma brucei ORF2	100	36.066
4354	M15530	Homo sapiens B-cell growth factor	167	71.795
4356	M69297	Homo sapiens ORF 2	367	73.810
4357	M69297	Homo sapiens ORF 2	440	78.261
4358	M69297	Homo sapiens ORF 2	425	81.176
4359	M69297	Homo sapiens ORF 2	407	77.647
4360	M15530	Homo sapiens B-cell growth factor	176	40.506
4361	AC007168	Arabidopsis thaliana hypothetical protein	85	57.895
4362	AC007168	Arabidopsis thaliana hypothetical protein	254	30.698
4363	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	108	33.088
4364	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	441	72.619
4365	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	152	34.940
4366	U97553	murine herpesvirus 68 unknown	121	36.082
4367	U97553	murine herpesvirus 68 unknown	145	36.264
4370	AF107406	Homo sapiens GW128	150	50.000
4372	X52164	Mus musculus Q300 protein (AA 1-77)	127	37.500
4373	D00570	Mus musculus open reading frame (251 AA)	119	23.506
4374	U16359	Rattus norvegicus nitric oxide synthase	42	35.294
4375	U16359	Rattus norvegicus nitric oxide synthase	112	100.000
4376	U16359	Rattus norvegicus nitric oxide synthase	112	71.429
4377	U96418	Dennys somadikartai cytochrome b	143	25.253
4378	X97667	Gallus gallus homologous to Drosophila homeobox gene tinman	47	26.829
4379	X97667	Gallus gallus homologous to Drosophila homeobox gene tinman	91	46.154
4380	X97667	Gallus gallus homologous to Drosophila homeobox gene tinman	149	42.857
4382	AF022985	Unknown Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA	102	34.711
4383	AF022985	Unknown Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA	125	32.609
4384	AF022985	Unknown Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA	157	33.636
4386	L23852	Homo sapiens Putative 3' end of coding region; putative	77	36.538
4387	L23852	Homo sapiens Putative 3' end of coding region; putative	77	36.538

4388	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	40.000
4389	X55777	Homo sapiens put. ORF	213	54.098
4390	X52164	Mus musculus Q300 protein (AA 1-77)	121	37.736
4391	M15530	Homo sapiens B-cell growth factor	174	68.421
4393	AF026689	Homo sapiens prostate-specific transglutaminase	131	62.791
4394	X92485	Plasmodium vivax pval	178	46.753
4395	M15386	Homo sapiens gamma-globin	897	93.421
4396	M15386	Homo sapiens gamma-globin	544	77.083
4398	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4399	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4400	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4401	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4402	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4403	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4404	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4405	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	219	87.879
4406	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	204	96.429
4407	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4408	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4410	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	212	85.294
4411	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	215	82.857
4413	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	187	39.831
4414	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	236	84.211
4415	AF014955	Homo sapiens TFAR19	436	74.590
4416	AF014955	Homo sapiens TFAR19	218	89.744
4418	U16359	Rattus norvegicus nitric oxide synthase	96	68.182
4419	X07858	Saccharomyces cerevisiae ORF (1 is 3rd base in codon) (266 is 1st base in codon)	107	30.488
4420	X92485	Plasmodium vivax pval	207	53.226
4421	X92485	Plasmodium vivax pval	55	53.846
4422	X79238	Homo sapiens ribosomal protein L30	739	100.000
4423	X79238	Homo sapiens ribosomal protein L30	291	94.231
4424	X79238	Homo sapiens ribosomal protein L30	397	78.814
4425	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	147	54.054

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4426	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	110	34.483
4427	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	142	52.273
4428	AF159055	Homo sapiens leucine zipper-like protein	147	80.000
4429	U34467	Fusarium sp. 'NRRL20459' beta-tubulin	110	36.170
4430	X63417	Homo sapiens IRLB	586	49.457
4431	X63417	Homo sapiens IRLB	142	36.066
4432	U18339	Variola virus D4L	125	53.846
4433	M12668	Measles virus unknown protein	124	35.526
4434	U16359	Rattus norvegicus nitric oxide synthase	109	68.000
4435	M55300	Rattus sp. synapsin I	106	35.385
4436	U23516	Caenorhabditis elegans No definition line found	57	25.000
4437	U23516	Caenorhabditis elegans No definition line found	70	32.609
4438	U23516	Caenorhabditis elegans No definition line found	1239	29.909
4439	V00488	Homo sapiens alpha globin	925	100.000
4440	V00488	Homo sapiens alpha globin	359	80.645
4441	A06407	synthetic construct tac-sod hybrid	288	64.286
4442	A06407	synthetic construct tac-sod hybrid	488	100.000
4443	A06407	synthetic construct tac-sod hybrid	286	69.565
4444	AF106329	Escherichia coli unknown; orf86	117	55.172
4445	M26730	Homo sapiens ubiquinone-binding protein (QP)	582	68.987
4446	M26730	Homo sapiens ubiquinone-binding protein (QP)	168	100.000
4447	M26730	Homo sapiens ubiquinone-binding protein (QP)	319	74.359
4448	X69962	Homo sapiens unnamed protein product	671	89.655
4449	X69962	Homo sapiens unnamed protein product	114	35.644
4450	X69962	Homo sapiens unnamed protein product	43	70.000
4451	X69962	Homo sapiens unnamed protein product	3819	93.513
4452	X69962	Homo sapiens unnamed protein product	4220	100.000
4453	V00489	Homo sapiens alpha globin	830	100.000
4454	V00489	Homo sapiens alpha globin	741	88.652
4455	V00489	Homo sapiens alpha globin	94	50.820
4460	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	53	23.256
4461	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	81	37.255
4465	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	57	53.333
4469	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	60	27.778
4478	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	68	27.778
4479	D90825	Escherichia coli Probable ATP-dependent helicase dinG homolog.	2727	99.523
4480	AB030483	Mus musculus B9	42	40.000
4481	AB030483	Mus musculus B9	78	25.253

4482	AB030483	Mus musculus B9	44	25.862
4483	AB030483	Mus musculus B9	163	26.543
4484	L26247	Homo sapiens isolog of yeast suil and rice gos2; putative	361	100.000
4485	X52164	Mus musculus Q300 protein (AA 1-77)	101	71.429
4486	A00279	synthetic construct Human serum albumin	548	39.286
4488	AL049685	Homo sapiens hypothetical protein	1193	100.000
4489	U18922	Saccharomyces cerevisiae Yer181cp	100	26.263
4490	S45142	Pisum sativum ENOD3=metal-binding protein	104	38.889
4491	L02426	Homo sapiens 26S protease (S4) regulatory subunit	1774	83.631
4492	L02426	Homo sapiens 26S protease (S4) regulatory subunit	371	89.394
4493	L02426	Homo sapiens 26S protease (S4) regulatory subunit	342	93.220
4494	L02426	Homo sapiens 26S protease (S4) regulatory subunit	2120	88.616
4495	M84237	Homo sapiens integrin beta-1 subunit	136	64.706
4496	M37679	Mus musculus Ig heavy chain precursor	75	60.000
4497	X15081	Crithidia fasciculata cytochrome c oxidase subunit I (2034 is 3rd base in codon)	68	62.500
4498	AP000062	Aeropyrum pernix 106aa long hypothetical protein	57	53.846
4499	AP000062	Aeropyrum pernix 106aa long hypothetical protein	58	38.710
4500	AP000062	Aeropyrum pernix 106aa long hypothetical protein	57	53.846
4501	AP000062	Aeropyrum pernix 106aa long hypothetical protein	111	32.432
4503	AP000062	Aeropyrum pernix 92aa long hypothetical protein	91	34.848
4504	X72879	Homo sapiens ORF	145	84.615
4505	AF107406	Homo sapiens GW128	46	36.000
4506	AF107406	Homo sapiens GW128	164	47.273
4507	X00822	Gallus gallus collagen type III	70	34.091
4509	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	136	79.167
4510	M93698	Oncorhynchus mykiss ependymin	185	25.490
4511	M93698	Oncorhynchus mykiss ependymin	249	24.752
4512	X55687	Lycopersicon esculentum extensin (class II)	43	46.154
4513	X55687	Lycopersicon esculentum extensin (class II)	82	32.432
4515	D38048	Homo sapiens proteasome subunit z	715	64.220
4516	D38048	Homo sapiens proteasome subunit z	319	100.000
4517	D38048	Homo sapiens proteasome subunit z	328	98.077
4518	D38048	Homo sapiens proteasome subunit z	1039	83.883
4519	AJ131555	Hepatitis B virus X protein	74	32.558
4521	AF095350	Homo sapiens RAB-like protein 2A	417	82.927
4522	AF095350	Homo sapiens RAB-like protein 2A	327	54.386
4523	AF095350	Homo sapiens RAB-like protein 2A	46	23.077

4524	AF095350	Homo sapiens RAB-like protein 2A	194	76.190
4525	AF095350	Homo sapiens RAB-like protein 2A	38	44.444
4526	AF095350	Homo sapiens RAB-like protein 2A	691	60.759
4527	AF095350	Homo sapiens RAB-like protein 2A	1418	93.724
4528	AF095350	Homo sapiens RAB-like protein 2A	1308	75.166
4530	AL021747	Schizosaccharomyces pombe hypothetical protein	152	33.721
4531	AL021747	Schizosaccharomyces pombe hypothetical protein	38	28.125
4532	AL021747	Schizosaccharomyces pombe hypothetical protein	127	36.364
4533	AL021747	Schizosaccharomyces pombe hypothetical protein	40	27.586
4534	AL021747	Schizosaccharomyces pombe hypothetical protein	42	21.429
4535	AL021747	Schizosaccharomyces pombe hypothetical protein	155	29.703
4536	AB013367	Bacillus halodurans unknown	152	43.103
4537	AB013367	Bacillus halodurans unknown	671	38.217
4538	X76288	Bacteriophage phi-C31 ORF 14	74	38.889
4539	Z14963	Homo sapiens codes for truncated alpha mRNA of alpha heavy chain disease patient LTE	80	51.613
4540	Z14963	Homo sapiens codes for truncated alpha mRNA of alpha heavy chain disease patient LTE	80	51.613
4541	Z14963	Homo sapiens codes for truncated alpha mRNA of alpha heavy chain disease patient LTE	86	30.556
4542	L10908	Mus musculus Gcpl gene product	115	40.541
4543	AJ242956	Homo sapiens E1 fusion protein	147	66.667
4544	L10908	Mus musculus Gcpl gene product	34	36.364
4545	L10908	Mus musculus Gcpl gene product	44	29.167
4546	L10908	Mus musculus Gcpl gene product	84	57.143
4547	Z66568	Schizosaccharomyces pombe hypothetical trp-asp repeats containing protein	59	33.333
4548	Z66568	Schizosaccharomyces pombe hypothetical trp-asp repeats containing protein	57	27.500
4549	Z66568	Schizosaccharomyces pombe hypothetical trp-asp repeats containing protein	938	54.741
4550	L10908	Mus musculus Gcpl gene product	240	50.000
4551	D26462	Nicotiana glauca X Nicotiana langsdorffii tumor-related protein	38	24.000
4552	D26462	Nicotiana glauca X Nicotiana langsdorffii tumor-related protein	84	37.143
4553	D16387	Asterina pectinifera cytochrome oxidase subunit III	75	38.462
4554	U16359	Rattus norvegicus nitric oxide synthase	70	44.444
4555	U16359	Rattus norvegicus nitric oxide synthase	123	63.333
4556	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	53	41.379
4557	S77099	Drosophila pseudoobscura, Peptide, 149	260	45.745

		aa Jan A		
4558	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	160	45.872
4559	AF001904	Homo sapiens 3-hydroxyacyl-CoA dehydrogenase isoform 2	104	47.727
4560	A50313	unidentified SEGMENT ALPHA OF HUMAN APOMYOglobin	294	100.000
4561	X52164	Mus musculus Q300 protein (AA 1-77)	131	38.000
4562	AL049638	Arabidopsis thaliana putative protein	388	41.011
4563	U16359	Rattus norvegicus nitric oxide synthase	52	30.303
4564	U16359	Rattus norvegicus nitric oxide synthase	106	47.500
4565	U31788	Human papillomavirus type 44 transforming protein E7	86	40.000
4566	M22659	Mus musculus TCR alpha-chain (Va8- Ja14T-C)	79	32.653
4567	U16359	Rattus norvegicus nitric oxide synthase	125	94.118
4568	U16359	Rattus norvegicus nitric oxide synthase	125	94.118
4569	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	211	56.757
4570	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	261	55.446
4571	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	518	100.000
4572	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	1200	99.451
4573	AF110315	Homo sapiens unknown	80	42.500
4582	AF110315	Homo sapiens unknown	85	31.132
4587	AF110315	Homo sapiens unknown	67	20.635
4592	AF110315	Homo sapiens unknown	81	25.466
4599	AF110315	Homo sapiens unknown	86	24.615
4601	AF110315	Homo sapiens unknown	2669	100.000
4603	U50403	Homo sapiens breast cancer suppressor element Ishmael Upper RP2	118	64.000
4604	X70050	Giardia intestinalis ubiquitin	156	32.857
4605	X66285	Mus musculus HC1 ORF	140	28.814
4606	L41675	Human T-cell lymphotropic virus type 2 protein 11 xV	84	39.286
4607	AB033064	Homo sapiens KIAA1238 protein	193	53.077
4608	AB033064	Homo sapiens KIAA1238 protein	2681	100.000
4609	Z83227	Caenorhabditis elegans predicted using Genefinder; Weak similarity to high- sulphur keratins.; cDNA EST yk663a1.3 comes from this gene	92	38.889
4610	K01664	Drosophila melanogaster Bkm-like protein	92	34.000
4611	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	143	79.167
4612	Y08982	Homo sapiens synaptonemal complex lateral element protein	9956	100.000
4613	AF030429	Canis familiaris dentatorubro-	129	29.032

		pallidolusian atrophy protein		
4614	AF043703	Caenorhabditis elegans No definition line found	104	38.636
4615	L10908	Mus musculus Gcap1 gene product	92	60.000
4617	AL117669	Streptomyces coelicolor A3(2) hypothetical protein	126	27.473
4620	Z70222	Homo sapiens ORF is homologous to hypothetical 9.8 kD protein ZK652.3 of Caenorhabditis elegans, spP34661	186	93.939
4621	AF159055	Homo sapiens leucine zipper-like protein	118	58.621
4622	AF068302	Homo sapiens choline/ethanolaminephosphotransferase	879	97.080
4623	X52560	Homo sapiens nuclear factor NF-IL6 (AA 1-345)	2385	99.420
4624	AB023483	Homo sapiens docking protein BRDG1	1927	99.661
4625	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	130	36.667
4626	AL121804	Drosophila melanogaster BACR7C10.z	45	30.303
4627	AL121804	Drosophila melanogaster BACR7C10.z	103	36.111
4628	D90764	Escherichia coli ORF_ID:o253#13; similar to	74	36.957
4629	AB032974	Homo sapiens KIAA1148 protein	53	29.787
4630	AB032974	Homo sapiens KIAA1148 protein	628	79.365
4631	AB032974	Homo sapiens KIAA1148 protein	49	29.825
4632	AB032974	Homo sapiens KIAA1148 protein	628	79.365
4633	AB032974	Homo sapiens KIAA1148 protein	40	45.455
4634	AB032974	Homo sapiens KIAA1148 protein	1032	100.000
4635	M11221	Daucus carota extensin	78	52.381
4636	AF066061	Mus musculus glucosidase II beta-subunit	46	21.212
4637	AF066061	Mus musculus glucosidase II beta-subunit	64	75.000
4638	AF066061	Mus musculus glucosidase II beta-subunit	106	69.565
4639	AF066061	Mus musculus glucosidase II beta-subunit	147	48.000
4640	U00039	Escherichia coli livF	224	96.970
4641	U00039	Escherichia coli livF	759	99.160
4642	U00039	Escherichia coli livF	1504	99.571
4643	U00039	Escherichia coli livF	1121	97.740
4644	U22229	Felis catus ribosomal protein L41	90	100.000
4645	U22229	Felis catus ribosomal protein L41	76	60.000
4646	AF159055	Homo sapiens leucine zipper-like protein	128	67.742
4647	X02375	Homo sapiens pro-alpha 1(II) collagen	69	46.429
4648	X77770	Homo sapiens ribosomal protein S26	37	36.364
4649	X77770	Homo sapiens ribosomal protein S26	785	98.261
4650	X77770	Homo sapiens ribosomal protein S26	647	87.387
4651	X77770	Homo sapiens ribosomal protein S26	392	98.333
4652	X77770	Homo sapiens ribosomal protein S26	314	65.079
4653	U18339	Variola virus D4L	97	40.000
4654	AE000659	Homo sapiens TCRAV10S1	620	84.211
4655	U16359	Rattus norvegicus nitric oxide	109	57.143

		synthase		
4656	AL022299	Schizosaccharomyces pombe hypothetical RNA-binding protein	144	29.885
4657	X80914	salmonid herpesvirus 2 orf	130	38.596
4658	M13941	Human herpesvirus 4 nuclear antigen 1	105	36.923
4659	A00142	Homo sapiens lympholine LAG-2	495	100.000
4660	A00142	Homo sapiens lympholine LAG-2	408	78.313
4661	M24743	Homo sapiens MHC heat shock protein HSP70-1	120	62.857
4665	Z68218	Caenorhabditis elegans K01H12.1	340	69.231
4666	X96401	Homo sapiens ROX protein	66	46.154
4667	X96401	Homo sapiens ROX protein	3808	100.000
4669	M37679	Mus musculus Ig heavy chain precursor	33	44.444
4670	M37679	Mus musculus Ig heavy chain precursor	102	53.333
4671	U11682	Trypanoplasma borreli unassigned reading frame	62	29.412
4673	AF149413	Arabidopsis thaliana contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1	1014	51.227
4674	Y11514	Homo sapiens transcription factor	912	94.937
4675	Z49966	Caenorhabditis elegans F35C11.4	176	23.792
4676	S65442	Homo sapiens furin	95	61.905
4677	AF159055	Homo sapiens leucine zipper-like protein	105	54.167
4678	U58755	Caenorhabditis elegans C34D4.11 gene product	123	47.826
4679	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	105	60.000
4680	AF084256	Homo sapiens beta glucuronidase isoform d	199	53.704
4681	X76717	Homo sapiens MT-11 protein	413	92.157
4682	X76717	Homo sapiens MT-11 protein	470	88.525
4685	D86422	Mus musculus glycine tyrosine-rich hair protein	31	50.000
4686	D86422	Mus musculus glycine tyrosine-rich hair protein	38	44.444
4687	D86422	Mus musculus glycine tyrosine-rich hair protein	73	41.935
4688	X02156	Saccharomyces cerevisiae URF 1	61	32.000
4689	X02156	Saccharomyces cerevisiae URF 1	58	21.053
4690	X02156	Saccharomyces cerevisiae URF 1	69	52.632
4691	U79260	Homo sapiens unknown	245	60.317
4692	X70050	Giardia intestinalis ubiquitin	156	32.857
4693	L77967	Ovis aries small proline-rich protein with paired repeat	103	32.609
4694	L77967	Ovis aries small proline-rich protein with paired repeat	103	32.609
4695	X66901	Mus musculus En-2/lacZ fusion protein	41	19.444
4696	X66901	Mus musculus En-2/lacZ fusion protein	307	90.196
4697	AJ010857	Homo sapiens MAFF protein	1055	100.000
4698	AF159055	Homo sapiens leucine zipper-like protein	132	64.516
4699	AF001160	Homo sapiens G-protein gamma subunit	448	100.000
4700	AJ005559	Mus musculus SPR2A protein	53	53.333

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4701	AJ005559	Mus musculus SPR2A protein	109	30.769
4702	AC004991	Homo sapiens match to spliced EST yc79ell.r1 (NID:674336); supported by Genscan	482	100.000
4703	S48406	Mus sp. alpha 1 (XII) collagen {triple-helical domain COL2}	109	43.478
4704	U50403	Homo sapiens breast cancer suppressor element Ishmael Upper RP2	143	68.966
4705	U34749	Bos taurus immunoglobulin heavy chain variable region	66	31.111
4706	X70070	Homo sapiens neurotensin receptor	990	100.000
4707	X70070	Homo sapiens neurotensin receptor	431	100.000
4708	X70070	Homo sapiens neurotensin receptor	46	50.000
4709	X70070	Homo sapiens neurotensin receptor	2743	100.000
4710	U18339	Variola virus D4L	92	66.667
4711	AF093098	Homo sapiens transcription factor TBLYM; T-box transcription factor family member	3821	100.000
4712	AF093098	Homo sapiens transcription factor TBLYM; T-box transcription factor family member	1357	99.465
4713	AF093098	Homo sapiens transcription factor TBLYM; T-box transcription factor family member	844	83.893
4714	AF093098	Homo sapiens transcription factor TBLYM; T-box transcription factor family member	3574	83.178
4715	M74421	human herpesvirus 1 ORF2	110	46.512
4716	Z71614	Saccharomyces cerevisiae ORF YNL338w	48	50.000
4717	Z71614	Saccharomyces cerevisiae ORF YNL338w	93	50.000
4718	U28944	Caenorhabditis elegans C18A3.7 gene product	92	27.536
4719	X92485	Plasmodium vivax pval	169	81.481
4720	U63332	Homo sapiens super cysteine rich protein; SCRP	168	62.963
4721	AF045940	Mus musculus nitric oxide synthase	49	58.333
4722	AF045940	Mus musculus nitric oxide synthase	44	36.842
4723	AF045940	Mus musculus nitric oxide synthase	72	55.000
4724	Y18423	Homo sapiens vasoactive intestinal polypeptide receptor 2	1630	100.000
4725	Y18423	Homo sapiens vasoactive intestinal polypeptide receptor 2	3008	100.000
4727	Y18423	Homo sapiens vasoactive intestinal polypeptide receptor 2	511	46.667
4728	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	60.000
4729	AE000848	Methanobacterium thermoautotrophicum ribosomal protein L37a	102	40.000
4731	AB001684	Chlorella vulgaris ORF54d	102	52.632
4733	L08193	Ricinus communis sugar carrier protein	94	36.957
4734	Z36002	Saccharomyces cerevisiae ORF YBR134w	105	37.931
4735	AC003058	Arabidopsis thaliana hypothetical protein	209	52.632
4736	U26748	Brassica napus protein kinase BNPK-4	129	43.860

4737	X77639	Sus scrofa cellular retinol binding protein II	569	59.398
4738	AB011528	Rattus norvegicus MEGF2	75	31.707
4739	AB011528	Rattus norvegicus MEGF2	62	33.898
4740	AB011528	Rattus norvegicus MEGF2	8832	93.353
4741	AB011528	Rattus norvegicus MEGF2	20430	90.994
4743	X63508	Mycobacterium tuberculosis predicted ORF	127	46.809
4744	X14776	Rattus norvegicus TP2	116	30.488
4746	Z71267	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene	77	45.833
4747	Z71267	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene	45	28.571
4748	Z71267	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene	79	45.833
4749	Z71267	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene	184	41.892
4750	AL034488	Unknown similar to DEAD/DEAH box helicase ; Helicases conserved C-terminal domain; cDNA EST yk313	1304	43.568
4751	U97553	murine herpesvirus 68 unknown	112	35.632
4752	Y10696	Homo sapiens INE1	381	100.000
4753	U28738	Caenorhabditis elegans T28D9.11 gene product	29	31.818
4754	U28738	Caenorhabditis elegans T28D9.11 gene product	48	56.522
4755	U28738	Caenorhabditis elegans T28D9.11 gene product	106	39.655
4756	AF084256	Homo sapiens beta glucuronidase isoform d	187	55.769
4757	M35611	Hordeum vulgare C-hordein storage protein	47	30.000
4758	M35611	Hordeum vulgare C-hordein storage protein	115	36.842
4759	AF159055	Homo sapiens leucine zipper-like protein	160	77.419
4760	X99226	Homo sapiens Fanconi anemia complementation group A protein	62	25.641
4761	X99226	Homo sapiens Fanconi anemia	56	53.846

		complementation group A protein		
4762	X99226	Homo sapiens Fanconi anemia complementation group A protein	9678	100.000
4763	L10908	Mus musculus Gcap1 gene product	77	45.833
4764	X52164	Mus musculus Q300 protein (AA 1-77)	115	46.667
4765	U93215	Arabidopsis thaliana glycine-rich protein isolog	98	51.724
4766	U93215	Arabidopsis thaliana glycine-rich protein isolog	88	56.522
4767	U93215	Arabidopsis thaliana glycine-rich protein isolog	162	37.778
4768	Z75532	Caenorhabditis elegans similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene	803	48.473
4769	Z75532	Caenorhabditis elegans similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene	804	44.898
4770	U57237	Human immunodeficiency virus type 1 Tat protein	106	36.667
4772	M11759	Lycopersicon esculentum cell wall hydroxyproline-rich glycoprotein	182	34.831
4773	AF083116	Homo sapiens paraneoplastic cancer- testis-brain antigen	671	31.579
4774	AC004381	Homo sapiens Unknown gene product	2866	100.000
4775	AL031910	Leishmania major hypothetical protein L2743.10	29	25.000
4776	AL031910	Leishmania major hypothetical protein L2743.10	80	73.333
4777	AF025642	Human immunodeficiency virus type 1 tat protein	74	64.706
4778	L77968	Ovis aries type II small proline-rich protein	83	37.838
4779	AB029612	Lactobacillus gasseri gassericin T1	98	53.333
4780	AF153830	Sus scrofa CD3 zeta chain	184	97.222
4781	AF153830	Sus scrofa CD3 zeta chain	146	100.000
4782	AF153830	Sus scrofa CD3 zeta chain	1062	98.171
4783	AC005328	Homo sapiens R26660 1, partial CDS	1514	92.975
4784	X71350	Xenopus laevis ribosomal protein S27 homologue	106	36.000
4785	Z48613	Saccharomyces cerevisiae unknown	100	35.000
4786	U59898	Cowpox virus unknown orf	51	30.233
4787	U59898	Cowpox virus unknown orf	100	38.298
4788	AJ388550	Canis familiaris hypothetical protein	62	45.283
4789	AJ388550	Canis familiaris hypothetical protein	102	37.097
4790	U58658	Homo sapiens unknown	238	60.938
4791	X53511	Chlamydia pneumoniae 9kDa CrP	60	34.091
4792	X53511	Chlamydia pneumoniae 9kDa CrP	104	40.426
4794	AP000061	Aeropyrum pernix 138aa long hypothetical protein	125	27.551
4795	Z67753	Odontella sinensis 50S ribosomal protein L23	106	29.310
4796	Y10148	Homo sapiens neurotensin receptor 2	1948	77.073
4799	Y10148	Homo sapiens neurotensin receptor 2	69	35.714
4801	Y10148	Homo sapiens neurotensin receptor 2	55	21.277

4802	Y10148	Homo sapiens neurotensin receptor 2	2733	100.000
4803	Y10148	Homo sapiens neurotensin receptor 2	50	39.130
4804	AL080235	Homo sapiens hypothetical protein	977	98.667
4805	U69537	Homo sapiens forkhead transcription factor HFH-4	2930	99.525
4806	D29833	Homo sapiens proline rich peptide P-B	89	30.556
4807	D29833	Homo sapiens proline rich peptide P-B	83	28.750
4808	D29833	Homo sapiens proline rich peptide P-B	68	38.235
4809	D29833	Homo sapiens proline rich peptide P-B	111	32.836
4810	X51987	Pisum sativum early nodule protein (ENOD2) C-terminal (112 AA)	114	28.814
4811	AF062529	Homo sapiens diphosphoinositol polyphosphate phosphohydrolase	738	76.871
4812	U18466	African swine fever virus pE66L	35	38.095
4813	U18466	African swine fever virus pE66L	44	23.077
4814	U18466	African swine fever virus pE66L	100	51.852
4815	U18466	African swine fever virus pE66L	51	25.714
4817	AF084256	Homo sapiens beta glucuronidase isoform d	121	59.375
4818	AC003058	Arabidopsis thaliana hypothetical protein	45	31.579
4819	AC003058	Arabidopsis thaliana hypothetical protein	37	20.000
4820	AC003058	Arabidopsis thaliana hypothetical protein	38	60.000
4821	AC003058	Arabidopsis thaliana hypothetical protein	121	76.000
4822	AF107406	Homo sapiens GW128	107	44.118
4823	M17375	Gallus gallus type XII collagen	34	71.429
4824	M17375	Gallus gallus type XII collagen	126	33.721
4825	AF027514	Homo sapiens zinc finger protein	3562	100.000
4826	X60435	Homo sapiens PACAP precursor	1176	100.000
4827	X92896	Homo sapiens ITBA2	124	32.000
4828	X66236	Mus musculus 185 kDa glycoprophosphoprotein	98	40.741
4829	U16359	Rattus norvegicus nitric oxide synthase	146	51.111
4830	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676	46	50.000
4831	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676	44	23.077
4832	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676	45	42.105
4833	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676	332	35.567
4834	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579-	57	24.138

		583; acidic transcr. activ. domain 620-640,,; homeobox motif 653-676		
4835	L02785	Homo sapiens Nuclear localization signal at AA 569-573, 576-580, 579- 583; acidic transcr. activ. domain 620-640,,; homeobox motif 653-676	648	30.853
4836	AC004416	Homo sapiens WUGSC:H_RG013N12.gw.1335199.a gene product	109	51.613
4837	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	43	23.913
4838	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	157	88.000
4839	AF146738	Rattus norvegicus testis specific protein	119	30.000
4840	U09366	Homo sapiens zinc finger protein ZNF133	1864	52.834
4841	X55683	Lycopersicon esculentum extensin (class I)	41	66.667
4842	X55683	Lycopersicon esculentum extensin (class I)	135	46.341
4843	AF018639	Dictyostelium discoideum PprA	135	34.091
4844	AF018639	Dictyostelium discoideum PprA	154	37.234
4845	V01532	Cercopithecidae gen. sp. metallothionein (2)	307	92.105
4846	V01532	Cercopithecidae gen. sp. metallothionein (2)	314	47.368
4847	AF174487	Homo sapiens BCL-2-related ovarian killer protein	1399	100.000
4848	U93023	Drosophila soonae hunchback protein	91	25.806
4849	U93023	Drosophila soonae hunchback protein	32	50.000
4850	U93023	Drosophila soonae hunchback protein	99	30.769
4851	AB000792	Sus scrofa metallothionein isoform	139	81.818
4852	AB000792	Sus scrofa metallothionein isoform	65	29.630
4853	AB000792	Sus scrofa metallothionein isoform	141	78.261
4855	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	59	31.818
4857	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	60	30.928
4859	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	49	50.000
4860	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	69	37.209
4861	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	64	26.415
4862	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	52	35.000
4863	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	58	52.632
4864	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	52	21.875
4866	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	62	31.325
4868	U82598	Escherichia coli 2,3- dihydroxybenzoate-AMP ligase	51	42.105

4869	U82598	Escherichia coli 2,3-dihydrosybenzoate-AMP ligase	52	38.462
4870	U82598	Escherichia coli 2,3-dihydrosybenzoate-AMP ligase	57	36.000
4872	U82598	Escherichia coli 2,3-dihydrosybenzoate-AMP ligase	2233	100.000
4873	AF017777	Drosophila melanogaster helicase	43	33.333
4874	AF017777	Drosophila melanogaster helicase	40	25.000
4875	AF017777	Drosophila melanogaster helicase	1448	49.012
4876	AF017777	Drosophila melanogaster helicase	1490	49.798
4877	M31607	Homo sapiens H-chain C-region MAL protein mRNA	87	58.333
4878	AF057285	Mus musculus intersectin-EH binding protein Ibp1	69	37.500
4879	Y10141	Homo sapiens variable number tandem repeat (VNTR)	100	31.579
4880	Y10141	Homo sapiens variable number tandem repeat (VNTR)	123	32.353
4881	AF159055	Homo sapiens leucine zipper-like protein	151	82.759
4882	U16359	Rattus norvegicus nitric oxide synthase	91	57.143
4883	X70811	Homo sapiens Beta 3 adrenergic receptor	2074	82.090
4884	X70811	Homo sapiens Beta 3 adrenergic receptor	2812	100.000
4885	U79260	Homo sapiens unknown	241	63.492
4886	D00596	Homo sapiens thymidylate synthase	651	81.250
4887	D00596	Homo sapiens thymidylate synthase	2110	98.408
4888	D00596	Homo sapiens thymidylate synthase	371	88.525
4889	Y08265	Homo sapiens DAN26	522	100.000
4890	AF008196	Homo sapiens bax epsilon	134	54.545
4891	L10908	Mus musculus Gcap1 gene product	96	30.263
4892	AF105371	Bos taurus neutrophil beta-defensin 12	54	34.211
4893	AF105371	Bos taurus neutrophil beta-defensin 12	67	35.000
4894	AF105371	Bos taurus neutrophil beta-defensin 12	70	33.333
4895	AF105371	Bos taurus neutrophil beta-defensin 12	46	45.833
4896	AF105371	Bos taurus neutrophil beta-defensin 12	48	33.333
4898	AF105371	Bos taurus neutrophil beta-defensin 12	110	39.216
4899	AB019241	Oryctolagus cuniculus c-myc	108	32.857
4900	AF159055	Homo sapiens leucine zipper-like protein	115	52.500
4901	M14170	Homo sapiens preplacental alkaline phosphatase (EC 3.1.3.1)	434	98.507
4902	M14170	Homo sapiens preplacental alkaline phosphatase (EC 3.1.3.1)	1125	77.682
4903	M14170	Homo sapiens preplacental alkaline phosphatase (EC 3.1.3.1)	3553	100.000
4904	U16359	Rattus norvegicus nitric oxide synthase	124	85.000
4905	S71386	Sus scrofa glucose transporter 4	82	51.852
4906	AE001111	Archaeoglobus fulgidus A. fulgidus predicted coding region AF2392	56	46.667
4907	S58722	Homo sapiens X-linked retinopathy	210	46.970

		protein {C-terminal, clone XEH.8c}		
4908	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	125	44.444
4909	Z81105	Caenorhabditis elegans R05D7.3	155	36.364
4910	AB016080	Mus musculus calcium binding protein Kip 2	40	33.333
4911	AB016080	Mus musculus calcium binding protein Kip 2	40	33.333
4912	AB016080	Mus musculus calcium binding protein Kip 2	36	33.333
4913	AB016080	Mus musculus calcium binding protein Kip 2	47	27.500
4914	AB016080	Mus musculus calcium binding protein Kip 2	40	33.333
4915	AB016080	Mus musculus calcium binding protein Kip 2	387	50.000
4916	AB016080	Mus musculus calcium binding protein Kip 2	44	46.667
4917	Y12670	Homo sapiens leptin receptor gene-related protein	196	100.000
4918	Y12670	Homo sapiens leptin receptor gene-related protein	657	87.857
4919	Y13141	Bromheadia finlaysoniana extensin	90	56.522
4920	X52164	Mus musculus Q300 protein (AA 1-77)	39	31.250
4921	X52164	Mus musculus Q300 protein (AA 1-77)	111	78.571
4922	S81809	Homo sapiens basic fibroblast growth factor, bFGF	104	39.706
4923	U16359	Rattus norvegicus nitric oxide synthase	96	80.000
4924	AL034567	Arabidopsis thaliana nodulin-like protein	134	40.000
4925	AB025355	Homo sapiens SOX20	71	50.000
4927	U31238	Hepatitis C virus core protein	111	33.962
4928	AF016446	Caenorhabditis elegans similar to C. elegans cuticlin 2 precursor CUT-2 (SP:P34682)	82	57.895
4929	AC004022	Homo sapiens Neurabin-like; similar to U72994 (PID:g2623757)	464	44.898
4930	Z28272	Saccharomyces cerevisiae ORF YKR047w	69	36.066
4931	Z28272	Saccharomyces cerevisiae ORF YKR047w	94	37.209
4932	AL035301	Homo sapiens hypothetical protein	31	22.727
4933	AL035301	Homo sapiens hypothetical protein	275	100.000
4935	X55686	Lycopersicon esculentum extensin (class II)	91	52.381
4936	M11325	Gallus gallus alpha-1 collagen type IX	107	36.364
4938	U60024	Ovis aries BIIIA3	41	66.667
4939	U60024	Ovis aries BIIIA3	72	37.143
4940	U78969	Streptococcus pyogenes unknown	96	37.879
4941	AL032637	Caenorhabditis elegans cDNA EST yk367g12.5 comes from this gene; cDNA EST yk367g12.3 comes from this gene	105	51.515
4942	U23523	Caenorhabditis elegans F53A9.1 gene product	96	71.429
4943	AL022729	Homo sapiens hypothetical protein	212	96.875

4944	D83735	Homo sapiens neutral calponin	1347	84.921
4945	D83735	Homo sapiens neutral calponin	314	71.429
4946	AJ005564	Mus musculus SPR2F protein	64	29.730
4947	AJ005564	Mus musculus SPR2F protein	141	39.394
4948	AJ005564	Mus musculus SPR2F protein	84	52.174
4949	Y00664	Homo sapiens open reading frame 1 (AA 1 - 86)	110	45.652
4950	AB033017	Homo sapiens KIAA1191 protein	44	66.667
4952	AB033017	Homo sapiens KIAA1191 protein	57	53.846
4953	AB033017	Homo sapiens KIAA1191 protein	623	94.118
4954	X97278	Danio rerio metallothionein	77	38.235
4955	U27113	Simulium nyssa NADH dehydrogenase subunit 4	65	47.059
4957	M21353	Homo sapiens alpha-2 type I collagen	44	37.500
4958	M21353	Homo sapiens alpha-2 type I collagen	82	58.333
4959	U63332	Homo sapiens super cysteine rich protein; SCRP	71	36.364
4960	D90857	Escherichia coli menD protein	34	30.000
4961	D90857	Escherichia coli menD protein	106	34.000
4962	AB028992	Homo sapiens KIAA1069 protein	68	28.333
4963	AB028992	Homo sapiens KIAA1069 protein	49	19.231
4964	AB028992	Homo sapiens KIAA1069 protein	57	39.130
4965	AB028992	Homo sapiens KIAA1069 protein	2525	94.595
4966	AB028992	Homo sapiens KIAA1069 protein	57	30.000
4967	AB028992	Homo sapiens KIAA1069 protein	5068	100.000
4968	Z97210	Schizosaccharomyces pombe hypothetical protein	75	22.222
4969	Z97210	Schizosaccharomyces pombe hypothetical protein	37	38.889
4970	Z97210	Schizosaccharomyces pombe hypothetical protein	201	40.196
4971	U80569	Human immunodeficiency virus type 1 tat protein	75	30.769
4972	M24900	Homo sapiens triiodothyronine receptor	29	16.000
4974	M24900	Homo sapiens triiodothyronine receptor	413	88.312
4975	M24900	Homo sapiens triiodothyronine receptor	585	96.774
4976	M24900	Homo sapiens triiodothyronine receptor	444	88.235
4978	L32783	Gallus gallus protein-tyrosine phosphatase	71	53.846
4979	AF110963	Human immunodeficiency virus type 1 Tat	120	32.000
4980	U42581	Rattus norvegicus p85	71	32.258
4983	Y14967	Mycobacterium leprae probable ESAT-6-like protein	102	38.298
4984	AB007861	Homo sapiens KIAA0401	63	43.333
4985	AB007861	Homo sapiens KIAA0401	2399	100.000
4986	X17622	Homo sapiens put. HBK2 protein (AA 1-529)	3570	100.000
4987	X17622	Homo sapiens put. HBK2 protein (AA 1-529)	3570	100.000
4988	A65268	unidentified unnamed protein product	69	48.000
4989	X79828	Mus musculus NK10	3084	80.855
4990	U79260	Homo sapiens unknown	285	50.806
4991	AB023188	Homo sapiens KIAA0971 protein	4094	99.692

4992	AB023188	Homo sapiens KIAA0971 protein	345	72.381
4993	X92485	Plasmodium vivax pval	46	22.222
4994	X92485	Plasmodium vivax pval	345	55.670
4996	X61046	Hydra sp. mini-collagen	68	37.037
4997	X61046	Hydra sp. mini-collagen	161	33.981
4998	X61046	Hydra sp. mini-collagen	154	36.264
5001	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	345	31.398
5002	Z46970	Leishmania mexicana secreted acid phosphatase 2 (SAP2)	93	23.103
5003	Z46970	Leishmania mexicana secreted acid phosphatase 2 (SAP2)	99	21.466
5004	Z46970	Leishmania mexicana secreted acid phosphatase 2 (SAP2)	773	38.202
5005	AF146793	Mus musculus PFT27	525	59.669
5006	AF146793	Mus musculus PFT27	324	76.119
5007	AF146793	Mus musculus PFT27	1357	85.449
5008	AF190797	Mus musculus actin-related protein 11	52	23.077
5009	AF190797	Mus musculus actin-related protein 11	258	50.000
5010	AF190797	Mus musculus actin-related protein 11	45	66.667
5012	AF190797	Mus musculus actin-related protein 11	493	59.355
5013	AJ225898	Oryctolagus cuniculus translationally controlled tumor protein	250	67.470
5014	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	316	59.813
5015	D86983	Homo sapiens similar to D.melanogaster peroxidase(U11052)	2781	60.089
5016	D86983	Homo sapiens similar to D.melanogaster peroxidase(U11052)	5275	93.510
5017	D86983	Homo sapiens similar to D.melanogaster peroxidase(U11052)	9621	98.663
5019	U44839	Homo sapiens UHX1 protein	311	96.154
5020	U44839	Homo sapiens UHX1 protein	698	59.746
5021	U44839	Homo sapiens UHX1 protein	3567	84.767
5022	X02761	Homo sapiens fibronectin precursor	3014	83.538
5023	X02761	Homo sapiens fibronectin precursor	6971	95.175
5024	X02761	Homo sapiens fibronectin precursor	574	100.000
5025	X02761	Homo sapiens fibronectin precursor	5136	96.091
5026	X02761	Homo sapiens fibronectin precursor	4869	87.068
5027	X02761	Homo sapiens fibronectin precursor	15815	96.238
5028	X02761	Homo sapiens fibronectin precursor	14788	97.469
5029	J04628	Rattus norvegicus 3-hydroxyisobutyrate dehydrogenase	456	97.143
5030	J04628	Rattus norvegicus 3-hydroxyisobutyrate dehydrogenase	805	83.226
5031	J04628	Rattus norvegicus 3-hydroxyisobutyrate dehydrogenase	1325	68.280
5033	X57958	Homo sapiens ribosomal protein L7	720	75.000
5034	X05006	Homo sapiens S-protein	302	100.000
5035	X05006	Homo sapiens S-protein	2003	84.940
5037	M19419	Mus musculus proline-rich salivary protein	66	38.462
5038	M19419	Mus musculus proline-rich salivary protein	176	40.741

5039	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	415	62.698
5040	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	54	28.000
5041	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	157	68.421
5042	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	580	56.650
5043	M11902	Mus musculus proline-rich salivary protein	51	40.000
5044	M11902	Mus musculus proline-rich salivary protein	117	35.000
5046	M11902	Mus musculus proline-rich salivary protein	198	32.353
5047	M11902	Mus musculus proline-rich salivary protein	121	36.082
5048	M11902	Mus musculus proline-rich salivary protein	184	39.130
5049	M11902	Mus musculus proline-rich salivary protein	140	31.250
5050	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	81	71.429
5051	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	108	55.882
5052	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	181	51.316
5053	U79260	Homo sapiens unknown	340	65.217
5054	U79260	Homo sapiens unknown	193	48.454
5055	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	395	69.149
5056	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	276	61.538
5057	U58652	Oryctolagus cuniculus ubiquitin-conjugating enzyme E2-32k	57	46.875
5058	U58652	Oryctolagus cuniculus ubiquitin-conjugating enzyme E2-32k	892	70.612
5059	U88968	Homo sapiens alpha enolase like 1	370	49.749
5060	AC003058	Arabidopsis thaliana unknown protein	255	34.932
5061	U22376	Homo sapiens alternatively spliced product using exon 13A	403	74.157
5062	D25215	Homo sapiens KIAA0032	435	40.110
5063	AB028954	Homo sapiens KIAA1031 protein	592	50.000
5064	AB028954	Homo sapiens KIAA1031 protein	556	46.544
5065	AB002348	Homo sapiens KIAA0350	50	30.864
5066	AB002348	Homo sapiens KIAA0350	164	96.552
5067	AB002348	Homo sapiens KIAA0350	175	100.000
5068	AB002348	Homo sapiens KIAA0350	324	92.453
5070	AB002348	Homo sapiens KIAA0350	1026	63.696
5071	AB002348	Homo sapiens KIAA0350	2554	69.711
5072	AB002348	Homo sapiens KIAA0350	5705	97.289
5073	AF086790	Homo sapiens aconitase precursor	4046	100.000
5074	AF086790	Homo sapiens aconitase precursor	246	69.444
5075	AF086790	Homo sapiens aconitase precursor	3541	91.405
5076	AL023854	Caenorhabditis elegans similar to	45	38.710

		Regulator of chromosome condensation (RCC1); cDNA EST yk246c2.5 comes from this gene		
5077	AL023854	Caenorhabditis elegans similar to Regulator of chromosome condensation (RCC1); cDNA EST yk246c2.5 comes from this gene	52	27.119
5079	AL023854	Caenorhabditis elegans similar to Regulator of chromosome condensation (RCC1); cDNA EST yk246c2.5 comes from this gene	312	37.104
5080	M15973	Human herpesvirus 4 unknown protein	91	28.302
5081	M15973	Human herpesvirus 4 unknown protein	127	26.891
5082	U22376	Homo sapiens alternatively spliced product using exon 13A	327	66.292
5083	U22376	Homo sapiens alternatively spliced product using exon 13A	401	66.000
5084	AB033033	Homo sapiens KIAA1207 protein	12333	100.000
5085	AB033033	Homo sapiens KIAA1207 protein	9434	96.230
5086	AB033033	Homo sapiens KIAA1207 protein	63	22.115
5087	AB033033	Homo sapiens KIAA1207 protein	57	28.125
5088	AB033033	Homo sapiens KIAA1207 protein	446	100.000
5089	AB033033	Homo sapiens KIAA1207 protein	54	21.978
5090	AB033033	Homo sapiens KIAA1207 protein	746	97.273
5091	AB033033	Homo sapiens KIAA1207 protein	55	20.213
5093	AB033033	Homo sapiens KIAA1207 protein	51	32.500
5094	AB033033	Homo sapiens KIAA1207 protein	47	25.287
5095	AB033033	Homo sapiens KIAA1207 protein	55	30.233
5096	AB033033	Homo sapiens KIAA1207 protein	60	31.034
5097	AB033033	Homo sapiens KIAA1207 protein	1632	89.103
5098	AF159297	Zea mays extensin-like protein	81	36.000
5099	AF159297	Zea mays extensin-like protein	109	35.294
5100	AF159297	Zea mays extensin-like protein	324	24.430
5101	X06323	Homo sapiens put. ribosomal protein L3 (AA 1 - 348)	590	67.232
5103	U22376	Homo sapiens alternatively spliced product using exon 13A	379	67.000
5104	U22376	Homo sapiens alternatively spliced product using exon 13A	407	70.103
5105	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	318	63.736
5106	U22376	Homo sapiens alternatively spliced product using exon 13A	390	72.527
5107	D87914	Homo sapiens ornithine decarboxylase antizyme	797	74.611
5108	D87914	Homo sapiens ornithine decarboxylase antizyme	494	65.333
5109	D87914	Homo sapiens ornithine decarboxylase antizyme	481	53.710
5110	U79260	Homo sapiens unknown	370	71.739
5111	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	308	70.588
5112	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	400	72.632

5113	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	481	54.419
5114	U79260	Homo sapiens unknown	383	68.817
5116	AC005532	Homo sapiens supported by GENSCAN prediction and spliced EST; similar to Z35641 (PID:g3874821) and AI059600 (NID:g3333377)	1657	93.455
5117	U22376	Homo sapiens alternatively spliced product using exon 13A	175	48.235
5118	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	91	26.087
5119	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	445	48.333
5120	U22376	Homo sapiens alternatively spliced product using exon 13A	344	58.416
5121	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	455	58.228
5122	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	195	60.000
5123	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	51	31.507
5124	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	340	44.937
5125	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	260	55.238
5126	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	112	37.647
5127	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	362	63.000
5128	X92485	Plasmodium vivax pval	283	45.775
5129	U22376	Homo sapiens alternatively spliced product using exon 13A	52	47.368
5131	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	193	47.674
5133	AL031349	Schizosaccharomyces pombe conserved hypothetical protein	560	51.337
5134	U58652	Oryctolagus cuniculus ubiquitin-conjugating enzyme E2-32k	947	75.502
5136	U22376	Homo sapiens alternatively spliced product using exon 13A	401	78.750
5137	U22376	Homo sapiens alternatively spliced product using exon 13A	271	64.557
5138	Z68302	Caenorhabditis elegans similar to Histidine acid phosphatases; cDNA EST yk432a1.3 comes from this gene; cDNA EST yk432a1.5 comes from this gene; cDNA EST yk504d7.3 comes from this gene; cDNA EST yk561d12.3 comes from this gene	202	25.466
5139	Z71316	Saccharomyces cerevisiae ORF YNL040w	80	31.579
5140	Z71316	Saccharomyces cerevisiae ORF YNL040w	398	28.256
5141	AF138957	Bos taurus type II collagen cyanogen bromide fragment CB8	107	36.782
5142	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	305	57.292

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5143	U22376	Homo sapiens alternatively spliced product using exon 13A	385	64.948
5144	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	203	62.500
5145	U79260	Homo sapiens unknown	142	62.500
5146	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	361	69.072
5147	U22376	Homo sapiens alternatively spliced product using exon 13A	374	71.429
5148	S60312	Mus sp. DMR-N9 {C-terminal}	688	52.913
5150	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	394	75.000
5151	AL109731	Schizosaccharomyces pombe putative ATP-dependent RNA helicase cdc28	132	31.313
5152	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	304	63.014
5154	L21990	Homo sapiens spliceosomal protein	262	30.385
5155	AF163772	Leishmania major 7138.2	403	39.698
5156	M11902	Mus musculus proline-rich salivary protein	236	31.731
5157	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	429	72.917
5158	U22376	Homo sapiens alternatively spliced product using exon 13A	396	66.000
5160	U79260	Homo sapiens unknown	327	64.894
5161	AF170303	Mus musculus nuclear body associated kinase 2a	2786	84.865
5162	M74495	Mus musculus adenylosuccinate synthetase	124	51.724
5163	M74495	Mus musculus adenylosuccinate synthetase	1780	85.965
5164	X92485	Plasmodium vivax pval	198	64.000
5166	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	667	60.847
5167	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	358	68.605
5168	AJ248288	Pyrococcus abyssi hypothetical protein	127	41.667
5169	AJ248288	Pyrococcus abyssi hypothetical protein	200	36.567
5170	AJ248288	Pyrococcus abyssi hypothetical protein	54	29.268
5171	AJ248288	Pyrococcus abyssi hypothetical protein	55	28.889
5172	AJ248288	Pyrococcus abyssi hypothetical protein	207	35.971
5173	AJ248288	Pyrococcus abyssi hypothetical protein	238	34.884
5174	U90908	Homo sapiens unknown	83	37.500
5175	U90908	Homo sapiens unknown	265	59.091
5176	U90908	Homo sapiens unknown	382	31.429
5177	AL049929	Homo sapiens hypothetical protein	765	64.384
5178	AL049929	Homo sapiens hypothetical protein	865	78.947
5179	AL049929	Homo sapiens hypothetical protein	1098	79.056
5180	U41557	Caenorhabditis elegans proline and glycine-rich	141	27.976
5181	U41557	Caenorhabditis elegans proline and glycine-rich	73	29.592
5182	U41557	Caenorhabditis elegans proline and glycine-rich	179	31.765

5183	U41557	Caenorhabditis elegans proline and glycine-rich	310	30.263
5184	U97191	Caenorhabditis elegans similar to nucleoporins	266	29.515
5185	AJ011812	Homo sapiens transcription factor NRF	287	28.470
5187	AJ003087	Homo sapiens liver glycogen synthase	4341	95.352
5188	AJ003087	Homo sapiens liver glycogen synthase	1283	77.778
5189	AJ003087	Homo sapiens liver glycogen synthase	285	79.032
5190	Z83227	Caenorhabditis elegans predicted using Genefinder; Weak similarity to high-sulphur keratins.; cDNA EST yk663a1.3 comes from this gene	205	32.026
5191	U56964	Caenorhabditis elegans weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386)	192	50.820
5192	U56964	Caenorhabditis elegans weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386)	760	36.034
5193	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	403	68.421
5194	U22376	Homo sapiens alternatively spliced product using exon 13A	356	73.864
5195	U93564	Homo sapiens p40	749	94.531
5196	U09874	Mus musculus SKD3	1223	97.884
5197	U09874	Mus musculus SKD3	1052	97.531
5198	U09874	Mus musculus SKD3	49	45.833
5199	U09874	Mus musculus SKD3	1183	89.069
5200	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	276	42.328
5201	U22376	Homo sapiens alternatively spliced product using exon 13A	357	64.948
5202	AF092449	Heterodera glycines mucin-like protein	152	31.250
5205	U02020	Homo sapiens pre-B cell enhancing factor	437	93.902
5206	AL080220	Homo sapiens hypothetical protein	313	100.000
5207	AL080220	Homo sapiens hypothetical protein	2197	96.089
5208	M15888	Bos taurus endozepine-related protein precursor	1906	76.804
5210	AF104413	Homo sapiens large tumor suppressor 1	44	62.500
5211	AF104413	Homo sapiens large tumor suppressor 1	3434	52.845
5212	AF104413	Homo sapiens large tumor suppressor 1	84	29.412
5213	L26290	Caenorhabditis elegans clathrin-associated protein homologue	237	70.513
5214	M27826	Homo sapiens neutral protease large subunit	244	57.333
5215	M27826	Homo sapiens neutral protease large subunit	646	71.523
5216	U67734	Homo sapiens cPLA2 interacting protein	861	99.270
5217	U67734	Homo sapiens cPLA2 interacting protein	47	33.333
5218	U67734	Homo sapiens cPLA2 interacting protein	3125	99.783
5219	U67734	Homo sapiens cPLA2 interacting protein	2748	87.084
5220	U67734	Homo sapiens cPLA2 interacting protein	616	62.000
5221	X92485	Plasmodium vivax pval	270	57.955
5222	S58722	Homo sapiens X-linked retinopathy	269	67.164

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		protein {C-terminal, clone XEH.8c}		
5223	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	280	76.119
5224	AF098504	Caenorhabditis elegans contains similarity to protein kinases (Pfam:kinase.hmm, score: 149.36)	391	32.484
5226	J05031	Rattus norvegicus isovaleryl-CoA dehydrogenase precursor (EC 1.3.99.10)	2238	87.793
5227	J05031	Rattus norvegicus isovaleryl-CoA dehydrogenase precursor (EC 1.3.99.10)	954	70.035
5228	AF002281	Rattus norvegicus alpha-actinin-2 associated LIM protein	283	40.132
5229	AF026689	Homo sapiens prostate-specific transglutaminase	101	49.020
5232	X92485	Plasmodium vivax pval	231	54.545
5233	AF132150	Drosophila melanogaster unknown	351	44.615
5234	AF132150	Drosophila melanogaster unknown	586	41.126
5235	AF132150	Drosophila melanogaster unknown	352	44.604
5236	Y10372	Bos taurus actin-binding protein CP3	755	93.388
5237	Y10372	Bos taurus actin-binding protein CP3	604	94.949
5238	Y10372	Bos taurus actin-binding protein CP3	326	100.000
5240	Y10372	Bos taurus actin-binding protein CP3	1217	78.641
5241	U46751	Homo sapiens phosphotyrosine independent ligand for the Lck SH2 domain p62	318	67.857
5242	U46751	Homo sapiens phosphotyrosine independent ligand for the Lck SH2 domain p62	620	54.753
5243	U46751	Homo sapiens phosphotyrosine independent ligand for the Lck SH2 domain p62	2391	90.625
5244	AF057019	Dictyostelium discoideum interaptin	74	21.569
5245	AF057019	Dictyostelium discoideum interaptin	275	19.666
5249	X92485	Plasmodium vivax pval	345	60.825
5250	X71442	Rattus norvegicus ORF 1; putative	38	40.000
5251	X71442	Rattus norvegicus ORF 1; putative	49	26.471
5252	X71442	Rattus norvegicus ORF 1; putative	38	20.000
5253	X71442	Rattus norvegicus ORF 1; putative	34	62.500
5254	X71442	Rattus norvegicus ORF 1; putative	192	46.154
5255	U22376	Homo sapiens alternatively spliced product using exon 13A	422	45.856
5258	AB020656	Homo sapiens KIAA0849 protein	867	86.228
5259	AB020656	Homo sapiens KIAA0849 protein	672	100.000
5260	AB020656	Homo sapiens KIAA0849 protein	320	100.000
5262	AB020656	Homo sapiens KIAA0849 protein	2987	92.969
5264	U22376	Homo sapiens alternatively spliced product using exon 13A	257	64.045
5265	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	180	76.923
5266	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	180	76.923
5267	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	199	56.897
5269	AL030996	Homo sapiens dJ1189B24.4 (novel	190	60.784

		PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)		
5270	AL030996	Homo sapiens dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)	75	60.000
5271	AL030996	Homo sapiens dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)	1097	55.501
5272	AL030996	Homo sapiens dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)	6855	96.619
5273	M87306	Tetrahymena thermophila micronuclear linker histone polyprotein	143	23.154
5274	X78327	Rattus norvegicus ribosomal protein L13	229	61.957
5276	U34958	Rattus norvegicus G protein beta 1 subunit	495	100.000
5277	U34958	Rattus norvegicus G protein beta 1 subunit	951	85.311
5278	U34958	Rattus norvegicus G protein beta 1 subunit	570	84.354
5279	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	230	58.120
5280	U14971	Homo sapiens ribosomal protein S9	885	77.202
5282	U14971	Homo sapiens ribosomal protein S9	511	71.154
5283	U22376	Homo sapiens alternatively spliced product using exon 13A	281	55.682
5284	D89052	Homo sapiens proton-ATPase-like protein	437	55.689
5285	D89052	Homo sapiens proton-ATPase-like protein	549	59.836
5286	AL117626	Homo sapiens hypothetical protein	491	73.684
5287	AL117626	Homo sapiens hypothetical protein	879	51.176
5288	U22376	Homo sapiens alternatively spliced product using exon 13A	348	67.816
5289	U55366	Caenorhabditis elegans Similar to cuticle collagen	150	31.250
5290	AF061938	Homo sapiens staufer protein	92	40.541
5291	AF061938	Homo sapiens staufer protein	49	27.273
5292	AF061938	Homo sapiens staufer protein	971	48.526
5293	X53581	Rattus norvegicus ORF4	140	32.867
5294	Y00638	Homo sapiens LCA (AA -23 to 1281)	1932	81.934
5295	U87607	Rattus norvegicus putative RNA binding protein 1	420	40.000
5296	M23236	Mus musculus proline-rich protein	268	32.877
5297	AB011532	Rattus norvegicus MEGF6	2066	74.143
5298	U09411	Homo sapiens zinc finger protein ZNF132	266	34.066
5301	X92485	Plasmodium vivax pval	280	52.727
5302	AL032637	Caenorhabditis elegans cDNA EST EMBL:D66101 comes from this gene; cDNA	134	32.558

		EST EMBL:D69769 comes from this gene		
5303	AL032637	Caenorhabditis elegans cDNA EST EMBL:D66101 comes from this gene; cDNA EST EMBL:D69769 comes from this gene	47	25.641
5304	AL032637	Caenorhabditis elegans cDNA EST EMBL:D66101 comes from this gene; cDNA EST EMBL:D69769 comes from this gene	59	40.000
5305	AL032637	Caenorhabditis elegans cDNA EST EMBL:D66101 comes from this gene; cDNA EST EMBL:D69769 comes from this gene	135	30.709
5306	L11231	Xenopus laevis myosin heavy chain B	305	38.863
5307	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	365	65.979
5308	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	53	25.397
5309	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	466	58.940
5310	U22376	Homo sapiens alternatively spliced product using exon 13A	193	50.000
5311	X92485	Plasmodium vivax pval	198	49.524
5312	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	226	63.855
5313	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	168	62.791
5314	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	497	49.153
5315	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	230	61.644
5316	U79260	Homo sapiens unknown	165	50.633
5317	M26361	Mus musculus LINE/Ig H-chain fusion protein	144	50.000
5318	AF055985	Onchocerca volvulus pyrrolidone-rich antigen	169	36.082
5319	U22376	Homo sapiens alternatively spliced product using exon 13A	290	71.212
5320	U22376	Homo sapiens alternatively spliced product using exon 13A	251	55.789
5321	AF045253	Mus musculus tousled-like kinase	462	76.842
5322	AF045253	Mus musculus tousled-like kinase	623	100.000
5323	U97553	murine herpesvirus 68 unknown	182	30.976
5324	X92485	Plasmodium vivax pval	48	46.667
5325	X92485	Plasmodium vivax pval	312	65.432
5326	AF029061	Homo sapiens BAT1	37	46.154
5327	AF029061	Homo sapiens BAT1	54	30.435
5328	AF029061	Homo sapiens BAT1	38	71.429
5329	AF029061	Homo sapiens BAT1	173	43.956
5330	AF029061	Homo sapiens BAT1	49	25.806
5331	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	106	26.733
5332	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	605	52.823
5335	X66285	Mus musculus HC1 ORF	120	37.500
5336	AB028981	Homo sapiens KIAA1058 protein	623	38.674
5337	AF149422	Homo sapiens unknown	872	52.537

5340	Z67990	Caenorhabditis elegans similar to cuticle collagen	154	37.288
5341	U22376	Homo sapiens alternatively spliced product using exon 13A	163	45.570
5342	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	330	67.532
5343	U12822	Peromyscus maniculatus major histocompatibility complex class I antigen	1171	62.147
5344	U79260	Homo sapiens unknown	171	50.000
5345	AF041054	Mus musculus E1B 19K/Bcl-2-binding protein homolog	282	61.364
5347	X92485	Plasmodium vivax pval	150	43.590
5348	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	219	39.048
5350	U79260	Homo sapiens unknown	343	70.000
5351	U48852	Cricetulus griseus HT protein	1397	69.725
5352	AB007862	Homo sapiens KIAA0402	60	50.000
5353	AB007862	Homo sapiens KIAA0402	9971	88.382
5354	AB007862	Homo sapiens KIAA0402	10962	95.259
5355	AB007862	Homo sapiens KIAA0402	10930	98.906
5357	AF049588	Canis familiaris synapsin I	109	29.310
5358	AF049588	Canis familiaris synapsin I	137	31.132
5359	M17463	Human papillomavirus type 5 ORF E4 from bp 3285 to 4022; putative	131	28.502
5360	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	354	68.750
5361	AL132862	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	353	28.772
5362	AL132862	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	1129	26.759
5363	AF101074	Homo sapiens step II splicing factor SLU7	1730	84.881
5364	D87515	Rattus norvegicus aminopeptidase-B	1657	48.362
5365	AL133084	Homo sapiens hypothetical protein	792	92.701
5366	U49973	Homo sapiens ORF2: function unknown	237	67.742
5369	U37143	Homo sapiens cytochrome P450 monooxygenase CYP2J2	212	47.059
5370	U37143	Homo sapiens cytochrome P450 monooxygenase CYP2J2	207	44.286
5371	U37143	Homo sapiens cytochrome P450 monooxygenase CYP2J2	637	35.811
5372	AC006233	Arabidopsis thaliana hypothetical protein	94	68.182
5373	AC006233	Arabidopsis thaliana hypothetical protein	104	30.435
5374	AF047002	Homo sapiens transcriptional coactivator ALY	1090	92.373
5376	U22376	Homo sapiens alternatively spliced product using exon 13A	392	61.321
5377	U79260	Homo sapiens unknown	278	56.383
5378	X56015	Crithidia oncopelti NADH dehydrogenase subunit 5	152	30.370
5379	AF010144	Homo sapiens neuronal thread protein	163	35.938

		AD7c-NTP		
5380	U22376	Homo sapiens alternatively spliced product using exon 13A	330	76.812
5381	U22376	Homo sapiens alternatively spliced product using exon 13A	312	59.140
5382	U22376	Homo sapiens alternatively spliced product using exon 13A	411	74.444
5383	U22376	Homo sapiens alternatively spliced product using exon 13A	407	64.000
5386	L11672	Homo sapiens zinc finger protein	187	48.611
5388	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	248	62.025
5389	Z99709	Caenorhabditis elegans cDNA EST EMBL:D73217 comes from this gene; cDNA EST yk478c5.3 comes from this gene; cDNA EST EMBL:M89187 comes from this gene	210	27.941
5390	U79260	Homo sapiens unknown	192	46.154
5391	U79260	Homo sapiens unknown	175	40.171
5392	U27196	Gallus gallus zinc finger protein	484	64.567
5393	AF133124	Homo sapiens transcription factor IIIC63	366	89.394
5394	AF133124	Homo sapiens transcription factor IIIC63	305	100.000
5395	AF133124	Homo sapiens transcription factor IIIC63	1499	79.211
5399	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	133	37.895
5400	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	363	68.000
5401	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	298	50.000
5402	U22376	Homo sapiens alternatively spliced product using exon 13A	52	25.000
5403	U22376	Homo sapiens alternatively spliced product using exon 13A	337	59.783
5404	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	400	53.020
5405	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	337	66.279
5406	X92485	Plasmodium vivax pval	46	23.256
5407	X92485	Plasmodium vivax pval	48	28.571
5408	X92485	Plasmodium vivax pval	265	58.140
5409	U22376	Homo sapiens alternatively spliced product using exon 13A	340	68.000
5410	U22376	Homo sapiens alternatively spliced product using exon 13A	328	60.000
5411	M94043	Rattus norvegicus rab-related GTP-binding protein	395	57.627
5412	X66285	Mus musculus HCl ORF	121	32.787
5413	AF116463	Streptomyces lincolnensis unknown	103	29.060
5414	AF116463	Streptomyces lincolnensis unknown	185	28.213
5415	X55777	Homo sapiens put. ORF	222	44.444
5416	U40420	Caenorhabditis elegans weak similarity to procollagen alpha chain 1(V) chain	359	41.317

5418	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	108	27.660
5419	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	56	24.419
5420	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	370	22.662
5421	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	315	65.060
5422	U79260	Homo sapiens unknown	291	58.511
5423	U93569	Homo sapiens p40	566	50.838
5424	M69297	Homo sapiens ORF 3	242	41.221
5425	M77349	Homo sapiens transforming growth factor induced protein	376	98.333
5426	M77349	Homo sapiens transforming growth factor induced protein	3242	90.691
5427	U22376	Homo sapiens alternatively spliced product using exon 13A	197	40.594
5428	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	243	51.402
5429	X92485	Plasmodium vivax pval	259	61.039
5430	U22376	Homo sapiens alternatively spliced product using exon 13A	362	77.778
5432	L07925	Rattus rattus guanine nucleotide dissociation stimulator	318	70.833
5433	L07925	Rattus rattus guanine nucleotide dissociation stimulator	402	79.747
5434	L07925	Rattus rattus guanine nucleotide dissociation stimulator	3898	69.353
5435	AF180350	Rattus norvegicus protein phosphatase 2A B regulatory subunit delta isoform	862	85.366
5436	AF180350	Rattus norvegicus protein phosphatase 2A B regulatory subunit delta isoform	283	92.063
5437	AF180350	Rattus norvegicus protein phosphatase 2A B regulatory subunit delta isoform	1769	79.830
5438	M19419	Mus musculus proline-rich salivary protein	85	25.664
5439	M19419	Mus musculus proline-rich salivary protein	44	27.027
5440	M19419	Mus musculus proline-rich salivary protein	191	33.121
5442	U79260	Homo sapiens unknown	360	69.474
5443	U73199	Mus musculus Rho-guanine nucleotide exchange factor	126	47.826
5444	U73199	Mus musculus Rho-guanine nucleotide exchange factor	125	48.980
5445	U73199	Mus musculus Rho-guanine nucleotide exchange factor	838	55.212
5446	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	116	86.364
5448	AC005306	Homo sapiens R27216_1	41	40.000
5449	AC005306	Homo sapiens R27216_1	270	52.439
5450	AC005306	Homo sapiens R27216_1	69	27.273

5451	AC005306	Homo sapiens R27216 1	1169	78.138
5452	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	326	53.043
5454	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	54	27.500
5455	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	1223	86.726
5457	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	625	85.047
5458	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	1740	92.642
5459	AF132984	Homo sapiens nuclear pore complex interacting protein NPIP	756	95.161
5461	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	229	35.795
5463	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	367	67.089
5464	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	339	67.816
5465	D32202	Homo sapiens alpha 1C adrenergic receptor isoform 2	252	63.095
5466	AL023893	Drosophila melanogaster /prediction=(method:"genefinder", version:"084", score:"111.64"); /prediction=(method:"genscan", version:"1.0")	500	32.530
5467	Z47357	Caenorhabditis elegans ZK1128.2	517	34.129
5468	Z81479	Unknown predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65495 comes from this gene;	158	28.230
5469	AJ000506	Mus musculus Homeodomain protein Meis2c	54	33.333
5470	AJ000506	Mus musculus Homeodomain protein Meis2c	181	92.857
5471	AJ000506	Mus musculus Homeodomain protein Meis2c	2481	84.449
5472	U76638	Homo sapiens BRCA1-associated RING domain protein	252	29.811
5473	X55777	Homo sapiens put. ORF	167	37.857
5474	U22376	Homo sapiens alternatively spliced product using exon 13A	396	73.563
5475	D13748	Homo sapiens eukaryotic initiation factor 4AI	612	75.676
5476	D13748	Homo sapiens eukaryotic initiation factor 4AI	360	69.811
5477	D13748	Homo sapiens eukaryotic initiation factor 4AI	806	65.126
5478	D13748	Homo sapiens eukaryotic initiation factor 4AI	1591	79.524
5480	U78597	Plectonema boryanum kinesin light chain	552	35.759
5481	U78597	Plectonema boryanum kinesin light chain	61	34.694
5482	U78597	Plectonema boryanum kinesin light chain	447	40.359

5483	X55777	Homo sapiens put. ORF	265	58.442
5485	X89858	Drosophila melanogaster actin binding protein	240	76.316
5486	X89858	Drosophila melanogaster actin binding protein	61	28.261
5487	X89858	Drosophila melanogaster actin binding protein	466	49.324
5488	X89858	Drosophila melanogaster actin binding protein	763	31.546
5490	AB020684	Homo sapiens KIAA0877 protein	274	48.819
5491	AB020684	Homo sapiens KIAA0877 protein	429	54.730
5492	AF077032	Homo sapiens sec61 homolog	451	94.521
5493	AF077032	Homo sapiens sec61 homolog	1306	93.519
5494	AB003102	Homo sapiens 26S proteasome subunit p44.5	255	41.830
5495	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	256	29.703
5496	U22376	Homo sapiens alternatively spliced product using exon 13A	353	71.264
5497	U79260	Homo sapiens unknown	158	42.308
5500	L11672	Homo sapiens zinc finger protein	2471	57.288
5501	L11672	Homo sapiens zinc finger protein	2827	55.116
5503	L32372	Mus musculus AMPA selective glutamate receptor	232	80.392
5505	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	272	39.614
5506	AL117428	Homo sapiens hypothetical protein	445	39.070
5508	AF131207	Mus musculus G21 protein	1837	70.044
5509	AF131207	Mus musculus G21 protein	884	67.797
5510	AF131207	Mus musculus G21 protein	859	65.789
5511	AF131207	Mus musculus G21 protein	241	53.097
5512	AF131207	Mus musculus G21 protein	2136	96.588
5513	U22376	Homo sapiens alternatively spliced product using exon 13A	386	75.000
5514	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	272	52.727
5515	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	381	68.571
5516	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	54	29.268
5517	AL008726	Homo sapiens dJ337018.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C))	264	49.265
5518	AL008726	Homo sapiens dJ337018.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C))	1492	97.211
5519	X92485	Plasmodium vivax pval	194	48.913
5520	M12100	Mus musculus proline-rich protein MP-3	411	38.535
5521	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	50	31.429
5522	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	276	57.317

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5523	X65165	Volvox carteri extensin	219	32.474
5526	AF182645	Homo sapiens chondrosarcoma-associated protein 2	2980	86.535
5527	AF182645	Homo sapiens chondrosarcoma-associated protein 2	1541	82.392
5528	AF182645	Homo sapiens chondrosarcoma-associated protein 2	214	100.000
5529	AF182645	Homo sapiens chondrosarcoma-associated protein 2	2597	78.956
5530	M12100	Mus musculus proline-rich protein MP-3	55	39.130
5531	M12100	Mus musculus proline-rich protein MP-3	43	30.000
5532	M12100	Mus musculus proline-rich protein MP-3	66	27.536
5533	M12100	Mus musculus proline-rich protein MP-3	55	53.333
5534	M12100	Mus musculus proline-rich protein MP-3	62	27.907
5536	M12100	Mus musculus proline-rich protein MP-3	65	35.714
5537	M12100	Mus musculus proline-rich protein MP-3	212	32.450
5538	M12100	Mus musculus proline-rich protein MP-3	50	41.176
5539	M12100	Mus musculus proline-rich protein MP-3	63	24.658
5541	M12100	Mus musculus proline-rich protein MP-3	44	54.545
5542	M12100	Mus musculus proline-rich protein MP-3	46	83.333
5543	M12100	Mus musculus proline-rich protein MP-3	155	31.356
5544	M12100	Mus musculus proline-rich protein MP-3	352	38.860
5546	U49973	Homo sapiens ORF2: function unknown	252	78.846
5547	AE001799	Thermotoga maritima translation elongation factor G	42	31.579
5550	AE001799	Thermotoga maritima translation elongation factor G	588	42.857
5551	AE001799	Thermotoga maritima translation elongation factor G	53	31.818
5552	AE001799	Thermotoga maritima translation elongation factor G	656	33.333
5553	AL031027	Unknown /prediction=(method:"genefinder", version:"084", score:"67.72"); /prediction=(metho	285	35.404
5554	D00632	Homo sapiens glutathione peroxidase	37	28.125
5557	D00632	Homo sapiens glutathione peroxidase	1379	92.035
5558	D00632	Homo sapiens glutathione peroxidase	1057	86.580
5560	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ- HRGP	397	32.203
5561	M35297	Rattus norvegicus G-protein coupled receptor	401	82.143
5562	U22376	Homo sapiens alternatively spliced product using exon 13A	292	57.609
5563	U22376	Homo sapiens alternatively spliced product using exon 13A	435	43.500
5564	U22376	Homo sapiens alternatively spliced product using exon 13A	275	64.103
5565	U12141	Saccharomyces cerevisiae Ynl2430p	43	100.000
5566	U12141	Saccharomyces cerevisiae Ynl2430p	279	29.936
5567	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	91	84.615
5569	D87459	Homo sapiens Similar to Volvox carteri	153	33.083

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		extensin (S22697)		
5570	AF095737	Homo sapiens unknown	195	48.421
5572	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	274	60.811
5573	D88440	Gallus gallus high molecular mass nuclear antigen	158	24.219
5574	D88440	Gallus gallus high molecular mass nuclear antigen	82	26.733
5575	D88440	Gallus gallus high molecular mass nuclear antigen	74	24.242
5577	D88440	Gallus gallus high molecular mass nuclear antigen	236	27.211
5578	D88440	Gallus gallus high molecular mass nuclear antigen	114	25.260
5579	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	200	43.243
5580	U37429	Caenorhabditis elegans similar to M. musculus MER5 and other AHPC/TSA proteins	1005	45.052
5581	U37429	Caenorhabditis elegans similar to M. musculus MER5 and other AHPC/TSA proteins	349	42.484
5582	U79260	Homo sapiens unknown	285	63.953
5583	U79260	Homo sapiens unknown	46	25.000
5584	U79260	Homo sapiens unknown	225	54.444
5585	AB018338	Homo sapiens KIAA0795 protein	208	25.000
5586	U79260	Homo sapiens unknown	190	82.353
5587	U79260	Homo sapiens unknown	190	82.353
5588	X92485	Plasmodium vivax pval	239	52.688
5589	X92485	Plasmodium vivax pval	302	58.621
5590	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	113	35.185
5591	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	88	75.000
5592	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	413	69.903
5593	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV233 hypothetical protein	117	29.114
5594	U79260	Homo sapiens unknown	339	62.637
5595	U22376	Homo sapiens alternatively spliced product using exon 13A	401	75.281
5596	AJ243459	Leishmania major proteophosphoglycan	178	24.658
5597	D45913	Mus musculus leucine-rich-repeat protein	4285	93.733
5598	L11672	Homo sapiens zinc finger protein	442	36.466
5599	U22376	Homo sapiens alternatively spliced product using exon 13A	100	65.385
5600	U22376	Homo sapiens alternatively spliced product using exon 13A	333	68.750
5601	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	362	51.572
5602	X92485	Plasmodium vivax pval	352	59.596
5603	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	307	61.905

5605	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	180	76.923
5606	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	180	76.923
5607	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	201	57.143
5608	X92485	Plasmodium vivax pval	155	44.444
5609	X52574	Mus musculus GTP binding protein	542	56.696
5611	U22376	Homo sapiens alternatively spliced product using exon 13A	234	68.852
5612	AL049628	Streptomyces coelicolor hypothetical proline-rich protein	67	35.849
5613	AL049628	Streptomyces coelicolor hypothetical proline-rich protein	179	36.190
5615	AB032904	Hylobates syndactylus dopamine receptor D4	128	29.630
5616	U77415	Mus musculus Bop1	626	69.178
5617	U77415	Mus musculus Bop1	3572	82.749
5618	AF131833	Homo sapiens Unknown	187	63.333
5620	Z35597	Caenorhabditis elegans C36E8.4	219	24.675
5622	AF070572	Homo sapiens unknown	1052	39.841
5623	M15530	Homo sapiens B-cell growth factor	128	51.852
5624	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	53	41.379
5625	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	260	45.745
5626	S77099	Drosophila pseudoobscura, Peptide, 149 aa Jan A	164	39.450
5628	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	278	67.568
5629	U22376	Homo sapiens alternatively spliced product using exon 13A	352	68.605
5630	U79260	Homo sapiens unknown	325	66.667
5631	AJ388521	Canis familiaris Ribosomal protein	146	50.413
5632	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	269	71.014
5633	M13100	Rattus norvegicus unknown protein	223	41.481
5634	AF159297	Zea mays extensin-like protein	383	23.791
5635	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	301	67.568
5636	U79260	Homo sapiens unknown	99	82.353
5637	U79260	Homo sapiens unknown	280	63.218
5638	U79260	Homo sapiens unknown	346	69.388
5640	AL035064	Schizosaccharomyces pombe queuine trna-ribosyltransferase	1036	61.847
5641	AL035064	Schizosaccharomyces pombe queuine trna-ribosyltransferase	513	47.345
5642	U22376	Homo sapiens alternatively spliced product using exon 13A	330	63.366
5643	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	274	41.830
5644	AL117513	Homo sapiens hypothetical protein	2392	100.000
5645	AL117513	Homo sapiens hypothetical protein	210	78.571
5646	AF010144	Homo sapiens neuronal thread protein	164	73.171

		AD7c-NTP		
5647	U22376	Homo sapiens alternatively spliced product using exon 13A	457	72.165
5648	AF049588	Canis familiaris synapsin I	70	27.143
5649	AF049588	Canis familiaris synapsin I	232	30.085
5651	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	216	52.174
5652	U55366	Caenorhabditis elegans Similar to cuticle collagen	179	29.911
5653	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	94	72.727
5654	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	160	61.905
5655	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	624	58.421
5656	X92485	Plasmodium vivax pval	217	49.451
5657	U22376	Homo sapiens alternatively spliced product using exon 13A	400	77.647
5658	M20471	Homo sapiens clathrin light-chain a	644	83.465
5659	M20471	Homo sapiens clathrin light-chain a	1169	98.889
5660	S70011	Rattus sp. tricarboxylate carrier	378	78.571
5661	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	316	46.763
5662	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	124	65.714
5663	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	415	44.490
5664	X15014	Homo sapiens RAL A polypeptide (AA 1-206)	638	80.303
5666	X15014	Homo sapiens RAL A polypeptide (AA 1-206)	1216	85.062
5667	X15014	Homo sapiens RAL A polypeptide (AA 1-206)	939	88.942
5668	X92485	Plasmodium vivax pval	128	72.414
5669	X92485	Plasmodium vivax pval	80	37.931
5670	X92485	Plasmodium vivax pval	375	64.444
5671	X78933	Homo sapiens zinc finger protein	759	58.911
5672	U22376	Homo sapiens alternatively spliced product using exon 13A	257	52.000
5673	M58378	Homo sapiens synapsin Ib	187	27.863
5674	U79260	Homo sapiens unknown	71	64.706
5675	U79260	Homo sapiens unknown	99	82.353
5676	U79260	Homo sapiens unknown	360	64.356
5677	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	368	70.238
5678	AL132862	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	53	24.138
5679	AL132862	Caenorhabditis elegans predicted using Genefinder; preliminary prediction	876	27.368
5680	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	124	73.333
5681	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	65	26.562
5682	AF000996	Homo sapiens ubiquitous TPR motif, Y	310	63.529

		isoform		
5683	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	185	50.549
5684	U22376	Homo sapiens alternatively spliced product using exon 13A	298	56.522
5685	X92485	Plasmodium vivax pval	208	49.515
5686	AC002074	Homo sapiens collagen I alpha-2 prepropeptide	126	34.884
5687	AF067728	Rattus norvegicus transactivating protein BRIDGE	157	88.462
5688	AF067728	Rattus norvegicus transactivating protein BRIDGE	355	79.452
5689	AF067728	Rattus norvegicus transactivating protein BRIDGE	986	76.829
5690	AF067728	Rattus norvegicus transactivating protein BRIDGE	265	66.957
5691	AF085809	Mus musculus synapsin Ib	195	29.555
5692	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	327	62.376
5693	D86978	Homo sapiens similar to a C.elegans protein encoded in cosmid K12D12(249069)	705	63.200
5694	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	83	36.232
5695	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	244	28.986
5696	X83413	Human herpesvirus 6 U88	241	31.731
5697	AF126867	Mus musculus calpain-like protease	906	60.223
5698	S64860	Mus sp. NonO=non-POU domain-containing octamer-binding protein	92	36.735
5699	S64860	Mus sp. NonO=non-POU domain-containing octamer-binding protein	343	78.788
5700	S64860	Mus sp. NonO=non-POU domain-containing octamer-binding protein	354	61.111
5701	S64860	Mus sp. NonO=non-POU domain-containing octamer-binding protein	1135	50.909
5702	M69297	Homo sapiens ORF 3	162	39.024
5704	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	242	69.091
5705	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	59	26.957
5706	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	50	32.609
5707	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	167	47.761
5708	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	72	25.510
5709	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	142	48.980
5710	L77968	Ovis aries type II small proline-rich protein	90	38.182
5711	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	448	72.449
5712	U22376	Homo sapiens alternatively spliced product using exon 13A	244	64.179

5713	U22376	Homo sapiens alternatively spliced product using exon 13A	392	77.108
5714	AF134726	Homo sapiens NG22	813	62.963
5717	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	371	66.019
5718	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	321	42.857
5719	AF187072	Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	438	98.529
5720	AF187072	Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	3438	97.683
5721	AB011094	Homo sapiens KIAA0522 protein	96	26.966
5722	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	340	54.088
5723	Z11583	Homo sapiens NuMA protein	8771	94.095
5725	Z11583	Homo sapiens NuMA protein	493	70.677
5727	Z11583	Homo sapiens NuMA protein	542	75.833
5728	Z11583	Homo sapiens NuMA protein	696	100.000
5729	Z11583	Homo sapiens NuMA protein	9382	93.337
5730	X92485	Plasmodium vivax pval	273	47.368
5731	AF121893	Rattus norvegicus sequence-specific single-stranded-DNA-binding protein	955	65.816
5735	AF121893	Rattus norvegicus sequence-specific single-stranded-DNA-binding protein	1176	52.401
5737	AB020686	Homo sapiens KIAA0879 protein	41	31.250
5738	AB020686	Homo sapiens KIAA0879 protein	321	29.876
5739	AB020686	Homo sapiens KIAA0879 protein	45	28.571
5740	AB020686	Homo sapiens KIAA0879 protein	213	31.111
5741	AB020686	Homo sapiens KIAA0879 protein	38	40.000
5742	AB020686	Homo sapiens KIAA0879 protein	272	27.700
5743	AB020686	Homo sapiens KIAA0879 protein	49	29.167
5744	AJ005071	Gallus gallus Tapasin	48	30.526
5745	AJ005071	Gallus gallus Tapasin	207	34.848
5746	Z46787	Caenorhabditis elegans similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	572	50.581
5747	Z46787	Caenorhabditis elegans similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	1186	51.266
5749	U48251	Homo sapiens protein kinase C-binding protein RACK7	1037	70.115
5750	U48251	Homo sapiens protein kinase C-binding protein RACK7	1726	84.638
5751	U48251	Homo sapiens protein kinase C-binding protein RACK7	615	68.156
5752	U48251	Homo sapiens protein kinase C-binding protein RACK7	3245	90.150
5753	U48251	Homo sapiens protein kinase C-binding protein RACK7	2985	92.844
5754	AF110103	Tupaia belangeri beta-actin	347	87.302
5755	AF110103	Tupaia belangeri beta-actin	865	100.000
5756	AF110103	Tupaia belangeri beta-actin	312	64.286

5757	L24775	Rattus norvegicus tropomyosin	912	90.541
5758	L24775	Rattus norvegicus tropomyosin	1160	95.673
5759	AF021873	Canis familiaris beta-actin	369	76.316
5760	AF021873	Canis familiaris beta-actin	1991	88.451
5761	D37984	Homo sapiens DNA helicase Q1	42	46.667
5762	D37984	Homo sapiens DNA helicase Q1	827	100.000
5763	D37984	Homo sapiens DNA helicase Q1	219	89.130
5764	AF184157	Macaca mulatta demidefensin 2	281	86.207
5765	AF016270	Homo sapiens thyroid hormone receptor coactivating protein	5462	93.696
5766	AF016270	Homo sapiens thyroid hormone receptor coactivating protein	471	75.497
5767	AF016270	Homo sapiens thyroid hormone receptor coactivating protein	193	97.143
5768	AF016270	Homo sapiens thyroid hormone receptor coactivating protein	5776	98.914
5769	Z22658	Homo sapiens thrombin inhibitor	612	72.000
5770	AL034433	Schizosaccharomyces pombe ptr3 or ubiquitin-activating enzyme e1	390	45.989
5771	X52851	Homo sapiens peptidylprolyl isomerase	292	97.917
5772	X52851	Homo sapiens peptidylprolyl isomerase	357	56.383
5774	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ-HRGP	264	38.168
5775	U22376	Homo sapiens alternatively spliced product using exon 13A	285	71.014
5776	X70223	Rattus norvegicus peroxisomal membrane protein	584	65.896
5777	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	311	64.634
5778	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	203	53.704
5779	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	236	56.098
5781	X89633	Saccharomyces cerevisiae hypothetical protein	71	52.632
5782	X89633	Saccharomyces cerevisiae hypothetical protein	229	30.058
5783	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	55	50.000
5784	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	46	35.088
5785	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	66	34.884
5786	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	51	19.149
5787	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	47	42.857
5788	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of	50	28.125

		the SNF2 family		
5789	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	64	37.500
5790	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	60	27.027
5791	AC005724	Arabidopsis thaliana putative DNA repair and recombination protein of the SNF2 family	1010	31.870
5794	M90657	Homo sapiens L6	166	74.194
5795	M90657	Homo sapiens L6	734	78.199
5796	M90657	Homo sapiens L6	342	84.848
5797	U22376	Homo sapiens alternatively spliced product using exon 13A	395	69.697
5798	AB014596	Homo sapiens KIAA0696 protein	956	83.060
5799	AB014596	Homo sapiens KIAA0696 protein	1300	85.597
5800	AB014596	Homo sapiens KIAA0696 protein	2780	80.622
5801	AB014596	Homo sapiens KIAA0696 protein	268	86.000
5802	AB014596	Homo sapiens KIAA0696 protein	265	83.019
5803	AB014596	Homo sapiens KIAA0696 protein	191	42.017
5804	AB014596	Homo sapiens KIAA0696 protein	725	50.000
5805	AB014596	Homo sapiens KIAA0696 protein	3690	99.636
5807	U82163	Oryctolagus cuniculus No definition line found	201	39.216
5808	U82163	Oryctolagus cuniculus No definition line found	289	51.327
5809	AB023175	Homo sapiens KIAA0958 protein	763	100.000
5810	AB023175	Homo sapiens KIAA0958 protein	251	100.000
5811	AB023175	Homo sapiens KIAA0958 protein	2644	96.020
5812	AB023175	Homo sapiens KIAA0958 protein	49	46.154
5813	AB023175	Homo sapiens KIAA0958 protein	1812	57.233
5814	AB023175	Homo sapiens KIAA0958 protein	2943	100.000
5817	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	334	67.089
5818	AF004107	Mus musculus unknown	215	64.286
5819	AF004107	Mus musculus unknown	1298	69.333
5820	AF004107	Mus musculus unknown	405	50.920
5821	AF004107	Mus musculus unknown	646	70.000
5822	AF055085	Mus musculus erythroid differentiation-related factor	300	48.544
5823	Z93244	Homo sapiens bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	135	54.348
5824	Z93244	Homo sapiens bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	140	54.717
5825	AL117482	Homo sapiens hypothetical protein	71	36.000
5826	AL117482	Homo sapiens hypothetical protein	55	30.233
5827	AL117482	Homo sapiens hypothetical protein	533	100.000
5828	AL117482	Homo sapiens hypothetical protein	1901	100.000
5829	L18865	Homo sapiens , gene product	41	71.429
5830	L18865	Homo sapiens , gene product	45	43.750
5831	L18865	Homo sapiens , gene product	45	43.750

5832	L18865	Homo sapiens , gene product	494	97.403
5833	L18865	Homo sapiens , gene product	1261	100.000
5834	L18865	Homo sapiens , gene product	1256	100.000
5835	AC004668	Homo sapiens similar to murine cell cycle regulator MIDA1; similar to A57591 (PID:g2137417)	391	71.579
5836	AC004668	Homo sapiens similar to murine cell cycle regulator MIDA1; similar to A57591 (PID:g2137417)	537	73.846
5837	AC004668	Homo sapiens similar to murine cell cycle regulator MIDA1; similar to A57591 (PID:g2137417)	3664	90.866
5838	AC004668	Homo sapiens similar to murine cell cycle regulator MIDA1; similar to A57591 (PID:g2137417)	4150	100.000
5839	AF149414	Arabidopsis thaliana contains similarity to Pfam family PF00145 (C-5 cytosine-specific DNA methylase); score=10.4. E=0.051, N=1	584	59.333
5840	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	316	77.419
5841	U22376	Homo sapiens alternatively spliced product using exon 13A	326	63.158
5842	U79260	Homo sapiens unknown	38	71.429
5843	U79260	Homo sapiens unknown	250	63.514
5844	X92485	Plasmodium vivax pval	149	68.293
5846	AB014513	Homo sapiens KIAA0613 protein	55	22.222
5847	AB014513	Homo sapiens KIAA0613 protein	4900	99.591
5848	L16547	Bos taurus chloride channel protein	860	87.571
5849	AF041206	Homo sapiens midline 1 cerebellar isoform 1	199	23.469
5850	AF106062	Homo sapiens Wiskott-Aldrich syndrome protein interacting protein	277	45.385
5852	Y08134	Homo sapiens acid sphingomyelinase-like phosphodiesterase	2747	95.494
5853	L38941	Homo sapiens ribosomal protein L34	199	85.366
5855	L38941	Homo sapiens ribosomal protein L34	344	71.311
5856	AF086624	Rattus norvegicus serine threonine kinase	55	70.000
5857	AF086624	Rattus norvegicus serine threonine kinase	39	27.778
5862	AF086624	Rattus norvegicus serine threonine kinase	51	39.130
5863	AF086624	Rattus norvegicus serine threonine kinase	1486	92.116
5864	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	567	62.308
5865	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	568	49.083
5866	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	428	36.735
5867	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	563	66.142
5868	U04301	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1,2-mannosidase	1334	63.352

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5869	U21324	Caenorhabditis elegans similar to entire S. cerevisiae ABC1 protein (Swiss-Prot Acc: P27697)	1144	45.985
5870	U59299	Homo sapiens MCT	3185	96.654
5871	U59299	Homo sapiens MCT	250	62.025
5872	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	268	75.862
5873	Z28201	Saccharomyces cerevisiae ORF YKL201c	271	40.288
5874	J04204	Bos taurus 32 kd accessory protein	867	66.995
5875	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	52	30.303
5876	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	43	42.857
5877	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	43	43.750
5878	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	46	53.333
5879	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	53	35.714
5880	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	46	31.579
5881	AL023553	Homo sapiens dJ347H13.5 (novel protein similar to yeast DNA-directed RNA Polymerase III 25 kd Polypeptide)	262	84.906
5882	M15182	Homo sapiens beta-glucuronidase precursor (EC 3.2.1.31)	367	83.333
5883	M15182	Homo sapiens beta-glucuronidase precursor (EC 3.2.1.31)	1030	70.079
5884	M15182	Homo sapiens beta-glucuronidase precursor (EC 3.2.1.31)	533	68.531
5885	M15182	Homo sapiens beta-glucuronidase precursor (EC 3.2.1.31)	480	39.840
5886	AC004382	Homo sapiens Unknown gene product	1214	66.987
5887	AC004382	Homo sapiens Unknown gene product	864	91.758
5888	AC004382	Homo sapiens Unknown gene product	1443	73.902
5889	AC004382	Homo sapiens Unknown gene product	1097	95.745
5891	AF017369	Mus musculus facio-genital dysplasia protein 3	824	61.275
5892	AL110151	Homo sapiens hypothetical protein	1889	98.294
5893	AL110151	Homo sapiens hypothetical protein	2327	99.164
5894	AJ388545	Canis familiaris hypothetical protein	94	41.935
5895	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	236	52.830
5896	AC005594	Homo sapiens R26984 1	382	47.619
5897	AC005594	Homo sapiens R26984 1	952	70.899
5898	AC005594	Homo sapiens R26984 1	819	67.358
5899	AF042838	Homo sapiens MEK kinase 1	235	88.636
5900	AF042838	Homo sapiens MEK kinase 1	267	73.077
5901	AF042838	Homo sapiens MEK kinase 1	352	56.522

5902	AF042838	Homo sapiens MEK kinase 1	2753	61.538
5903	AF042838	Homo sapiens MEK kinase 1	9906	99.599
5904	M22332	Homo sapiens unknown protein	181	93.333
5905	M22332	Homo sapiens unknown protein	186	93.548
5906	M22332	Homo sapiens unknown protein	1107	96.815
5907	M22332	Homo sapiens unknown protein	1101	96.178
5908	M22332	Homo sapiens unknown protein	1034	92.308
5909	M22332	Homo sapiens unknown protein	1097	94.904
5910	M22332	Homo sapiens unknown protein	1050	92.903
5911	M22332	Homo sapiens unknown protein	1063	92.994
5912	M22332	Homo sapiens unknown protein	1101	98.052
5913	M22332	Homo sapiens unknown protein	1040	92.357
5914	M22332	Homo sapiens unknown protein	1072	92.994
5915	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	281	80.000
5916	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	1331	99.524
5917	M14676	Homo sapiens src-like tyrosine kinase (put.); putative	512	59.146
5918	Z36948	Caenorhabditis elegans contains 3 cysteine rich repeats	113	27.559
5919	Z36948	Caenorhabditis elegans contains 3 cysteine rich repeats	156	36.283
5920	AL050150	Homo sapiens hypothetical protein	257	60.135
5921	AL050150	Homo sapiens hypothetical protein	1937	94.385
5922	AF153879	Fugu rubripes BAW	92	60.000
5923	AF153879	Fugu rubripes BAW	325	72.414
5924	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	348	67.500
5925	M13751	Escherichia coli branching enzyme (EC 2.4.1.18)	56	29.032
5926	M13751	Escherichia coli branching enzyme (EC 2.4.1.18)	61	35.484
5927	M13751	Escherichia coli branching enzyme (EC 2.4.1.18)	1202	96.571
5928	M13751	Escherichia coli branching enzyme (EC 2.4.1.18)	1826	94.139
5930	M13751	Escherichia coli branching enzyme (EC 2.4.1.18)	1744	91.727
5931	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	385	49.645
5932	AF179286	Homo sapiens death effector domain-associated factor	380	88.235
5933	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1298	55.844
5934	U09823	Oryctolagus cuniculus elongation factor 1 alpha	871	48.866
5935	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1313	95.814
5936	U09823	Oryctolagus cuniculus elongation factor 1 alpha	752	71.304
5937	U79260	Homo sapiens unknown	103	75.000
5938	U79260	Homo sapiens unknown	313	68.182
5939	AL049628	Streptomyces coelicolor hypothetical	156	51.220

10905

		proline-rich protein		
5940	AB012726	Mus musculus C184M protein	238	59.459
5941	AB012726	Mus musculus C184M protein	880	94.366
5942	L11015	Homo sapiens lymphotoxin-beta	1468	93.852
5943	L11015	Homo sapiens lymphotoxin-beta	1359	95.902
5944	AF145688	Drosophila melanogaster BcDNA.LD26050	212	31.967
5945	AF124394	Mus musculus fragile-X-related protein 1 isoform f	685	55.556
5946	AF124394	Mus musculus fragile-X-related protein 1 isoform f	3775	86.733
5947	AF124394	Mus musculus fragile-X-related protein 1 isoform f	3665	92.769
5948	AF124394	Mus musculus fragile-X-related protein 1 isoform f	702	95.161
5949	AL133105	Homo sapiens hypothetical protein	890	59.447
5950	AB020682	Homo sapiens KIAA0875 protein	137	100.000
5952	AB020682	Homo sapiens KIAA0875 protein	3405	93.701
5953	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	228	65.000
5954	X92485	Plasmodium vivax pval	151	68.421
5955	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	139	69.767
5956	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	46	46.154
5957	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
5958	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
5959	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	373	46.897
5960	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	466	53.005
5963	M36654	Mus musculus homeo box 2.6 (Hox-2.6) gene product	1614	86.447
5964	AB014570	Homo sapiens KIAA0670 protein	926	97.973
5965	AB014570	Homo sapiens KIAA0670 protein	8208	99.532
5966	AB014570	Homo sapiens KIAA0670 protein	7017	92.869
5967	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	145	75.000
5968	AF126780	Homo sapiens retinal short-chain dehydrogenase/reductase retSDR2	1763	95.440
5969	X78926	Homo sapiens zinc finger protein	2804	98.500
5970	AB012726	Mus musculus C184M protein	170	42.857
5972	X51755	Homo sapiens open reading frame (458 AA)	360	63.441
5973	X51755	Homo sapiens open reading frame (458 AA)	461	93.333
5974	X51755	Homo sapiens open reading frame (458 AA)	634	78.125
5975	X51755	Homo sapiens open reading frame (458 AA)	522	56.886
5976	X51755	Homo sapiens open reading frame (458 AA)	124	34.021
5978	X51755	Homo sapiens open reading frame (458 AA)	433	61.538

10906

		AA)		
5979	X51755	Homo sapiens open reading frame (458 AA)	387	75.862
5980	X51755	Homo sapiens open reading frame (458 AA)	1915	94.792
5983	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	262	53.448
5984	AF155115	Homo sapiens NY-REN-58 antigen	605	86.726
5985	AF155115	Homo sapiens NY-REN-58 antigen	2766	97.660
5986	AB020643	Homo sapiens KIAA0836 protein	4040	99.836
5987	U79260	Homo sapiens unknown	260	60.000
5988	AF129756	Homo sapiens BAT5	651	73.077
5989	AF129756	Homo sapiens BAT5	731	87.603
5990	AF129756	Homo sapiens BAT5	1395	92.827
5991	AF129756	Homo sapiens BAT5	54	47.826
5992	AF129756	Homo sapiens BAT5	2368	90.200
5993	AF145634	Drosophila melanogaster BcDNA.GH06193	120	60.000
5994	AF145634	Drosophila melanogaster BcDNA.GH06193	335	54.237
5995	AF014955	Homo sapiens TFAR19	436	74.590
5996	AF014955	Homo sapiens TFAR19	133	82.857
5997	AF073771	Homo sapiens RNA polymerase II termination factor	393	80.723
5998	AL031775	Homo sapiens dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	886	95.425
6000	J03191	Homo sapiens profilin	341	71.831
6001	X92485	Plasmodium vivax pval	50	28.571
6002	X92485	Plasmodium vivax pval	270	75.410
6003	AJ011916	Homo sapiens hypothetical protein	1170	79.098
6004	AJ011916	Homo sapiens hypothetical protein	856	97.872
6005	AJ011916	Homo sapiens hypothetical protein	1191	90.119
6006	U79260	Homo sapiens unknown	208	54.651
6007	U79260	Homo sapiens unknown	379	67.347
6008	AL031115	Homo sapiens ZXDA, ZXDB (zinc finger X-linked protein)	1202	60.571
6009	D17554	Homo sapiens TAXREB107	37	38.462
6010	D17554	Homo sapiens TAXREB107	193	75.000
6012	U79260	Homo sapiens unknown	226	47.692
6013	AJ002424	Rattus norvegicus p65 protein	422	62.585
6014	S58544	Homo sapiens 75 kda infertility-related sperm protein	786	98.374
6015	S58544	Homo sapiens 75 kda infertility-related sperm protein	3379	98.866
6016	A00328	synthetic construct beta-endothelial cell growth factor	888	95.484
6017	A00328	synthetic construct beta-endothelial cell growth factor	287	62.195
6018	A00328	synthetic construct beta-endothelial cell growth factor	390	93.548
6019	A00328	synthetic construct beta-endothelial cell growth factor	723	76.433
6020	A00328	synthetic construct beta-endothelial cell growth factor	668	56.716
6021	AF053003	Homo sapiens diphthamide biosynthesis protein-2; DPH2	3222	96.933

6023	X58826	Drosophila melanogaster RNA polymerase III second-largest subunit	1190	73.593
6024	X58826	Drosophila melanogaster RNA polymerase III second-largest subunit	405	67.045
6025	AB000216	Rattus norvegicus CCA3	184	80.556
6026	AB000216	Rattus norvegicus CCA3	3458	86.834
6027	S58722	Homo sapiens X-linked retinopathy protein (C-terminal, clone XEH.8c)	170	68.421
6028	AL049783	Homo sapiens hypothetical protein	671	100.000
6029	AL049783	Homo sapiens hypothetical protein	3259	100.000
6030	AL049783	Homo sapiens hypothetical protein	4111	100.000
6031	AL049783	Homo sapiens hypothetical protein	289	95.455
6032	U79260	Homo sapiens unknown	295	61.364
6033	U22376	Homo sapiens alternatively spliced product using exon 13A	374	68.132
6037	U79260	Homo sapiens unknown	203	58.462
6038	AL117662	Homo sapiens hypothetical protein	56	22.222
6039	AL117662	Homo sapiens hypothetical protein	207	96.970
6040	AL117662	Homo sapiens hypothetical protein	718	65.641
6041	AL117662	Homo sapiens hypothetical protein	1318	97.573
6042	AL117662	Homo sapiens hypothetical protein	1384	100.000
6043	AF155117	Homo sapiens NY-REN-62 antigen	3962	100.000
6044	AF125176	Mus musculus angiopoietin-related protein-2	364	56.122
6045	AF125176	Mus musculus angiopoietin-related protein-2	962	54.874
6046	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	298	68.571
6047	AL050285	Homo sapiens hypothetical protein	621	95.876
6048	AC002400	Homo sapiens Gene product with similarity to Ubiquitin binding enzyme	458	96.000
6049	AC002400	Homo sapiens Gene product with similarity to Ubiquitin binding enzyme	341	90.741
6050	AC002400	Homo sapiens Gene product with similarity to Ubiquitin binding enzyme	3312	95.741
6053	AP000559	Oryza sativa ESTs AU078277(S1084), AU078273(S13585), D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965)	97	44.444
6054	AP000559	Oryza sativa ESTs AU078277(S1084), AU078273(S13585), D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965)	381	52.525
6055	AP000559	Oryza sativa ESTs AU078277(S1084), AU078273(S13585), D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965)	486	36.905
6056	AP000559	Oryza sativa ESTs AU078277(S1084), AU078273(S13585),	445	47.059

		D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965)		
6057	M22414	Homo sapiens ribonuclease inhibitor precursor	375	87.324
6058	AL031187	Arabidopsis thaliana kinesin-related protein kata (fragment)	78	34.545
6059	AL031187	Arabidopsis thaliana kinesin-related protein kata (fragment)	88	32.039
6060	AL031187	Arabidopsis thaliana kinesin-related protein kata (fragment)	175	24.324
6061	U79260	Homo sapiens unknown	373	73.034
6062	AL110147	Homo sapiens hypothetical protein	797	97.500
6063	U79260	Homo sapiens unknown	71	64.706
6064	U79260	Homo sapiens unknown	266	58.947
6065	D17629	Homo sapiens GALNS	778	98.165
6066	D17629	Homo sapiens GALNS	60	100.000
6067	D17629	Homo sapiens GALNS	530	92.308
6068	D17629	Homo sapiens GALNS	3560	99.808
6069	AB001914	Homo sapiens PACE4C	4294	99.679
6070	AB001914	Homo sapiens PACE4C	4294	99.679
6071	AB001914	Homo sapiens PACE4C	4152	97.753
6072	AB001914	Homo sapiens PACE4C	4294	99.679
6073	AB001914	Homo sapiens PACE4C	730	84.444
6074	AJ225124	Mus musculus hyperpolarization-activated cation channel, HAC3	151	31.754
6075	AF180728	Drosophila melanogaster sulfate transporter	484	36.237
6077	AC004794	Homo sapiens F02569_2	2936	73.025
6078	U22376	Homo sapiens alternatively spliced product using exon 13A	142	79.167
6079	U22376	Homo sapiens alternatively spliced product using exon 13A	415	66.667
6080	AF091047	Mus musculus KH domain RNA binding protein QKI-7B	1415	100.000
6081	AF091047	Mus musculus KH domain RNA binding protein QKI-7B	441	100.000
6082	AF127765	Homo sapiens calpain 3; calcium activated neutral protease; CAPN3; CL1	725	92.366
6083	AF127765	Homo sapiens calpain 3; calcium activated neutral protease; CAPN3; CL1	508	80.357
6084	AB020720	Homo sapiens KIAA0913 protein	8478	99.216
6085	AF036549	Homo sapiens RGC32	129	76.667
6086	AF036549	Homo sapiens RGC32	641	100.000
6087	AL050018	Homo sapiens hypothetical protein	36	40.000
6088	AL050018	Homo sapiens hypothetical protein	490	77.119
6089	AL050018	Homo sapiens hypothetical protein	370	96.721
6090	AL050018	Homo sapiens hypothetical protein	2294	94.256
6093	L25125	Mus musculus RNA helicase	61	38.462
6094	L25125	Mus musculus RNA helicase	58	26.316
6095	L25125	Mus musculus RNA helicase	69	26.786
6096	L25125	Mus musculus RNA helicase	65	21.854
6098	L25125	Mus musculus RNA helicase	330	63.636

6100	L25125	Mus musculus RNA helicase	48	29.630
6104	L25125	Mus musculus RNA helicase	61	38.462
6105	L25125	Mus musculus RNA helicase	56	23.077
6110	L25125	Mus musculus RNA helicase	70	23.871
6111	L25125	Mus musculus RNA helicase	821	63.547
6112	Z92832	Caenorhabditis elegans F31D4.2	324	35.862
6113	Z92832	Caenorhabditis elegans F31D4.2	556	45.455
6115	AC005594	Homo sapiens R26984_1	910	67.876
6116	AC005594	Homo sapiens R26984_1	808	66.321
6117	Z75526	Caenorhabditis elegans Weak similarity to Staphylococcus autolysin gene (TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene	290	50.588
6118	Z75526	Caenorhabditis elegans Weak similarity to Staphylococcus autolysin gene (TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene	672	48.485
6119	AB010959	Cyprinus carpio natural killer cell enhancing factor	376	51.034
6120	AB010959	Cyprinus carpio natural killer cell enhancing factor	325	48.858
6122	Z11115	Caenorhabditis elegans predicted using Genefinder; cDNA EST yk281d4.5 comes from this gene; cDNA EST yk288c12.5 comes from this gene; cDNA EST yk406g11.5 comes from this gene	194	40.909
6123	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	453	47.291
6124	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	48	32.258
6125	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	308	50.450
6126	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	1266	63.969
6127	AF144757	Homo sapiens PR-domain zinc-finger protein PFM1	5078	98.500
6128	U08819	Mus musculus microtubule-associated protein 4	1606	47.013
6129	U08819	Mus musculus microtubule-associated protein 4	2261	44.151
6130	U08819	Mus musculus microtubule-associated protein 4	1840	51.398
6131	U22376	Homo sapiens alternatively spliced product using exon 13A	396	69.000
6132	U79260	Homo sapiens unknown	343	64.894
6133	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	1753	50.903
6134	AF036705	Unknown Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. el	361	56.122
6136	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	204	59.615

6137	U22376	Homo sapiens alternatively spliced product using exon 13A	134	76.667
6138	U22376	Homo sapiens alternatively spliced product using exon 13A	320	74.648
6140	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	112	64.000
6141	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	553	60.000
6142	AF060228	Homo sapiens retinoic acid receptor responder 3	200	71.154
6143	AJ243136	Trachemys scripta elegans putative pyruvate kinase	269	60.227
6144	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ-HRGP	203	54.386
6146	U22376	Homo sapiens alternatively spliced product using exon 13A	431	73.469
6147	U79260	Homo sapiens unknown	344	64.835
6149	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	357	70.115
6151	U22376	Homo sapiens alternatively spliced product using exon 13A	58	72.727
6152	U22376	Homo sapiens alternatively spliced product using exon 13A	54	26.316
6153	U22376	Homo sapiens alternatively spliced product using exon 13A	58	72.727
6154	U22376	Homo sapiens alternatively spliced product using exon 13A	191	44.000
6155	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	181	64.000
6156	U22376	Homo sapiens alternatively spliced product using exon 13A	427	70.103
6157	AF169301	Homo sapiens Na+/sulfate cotransporter SUT-1	168	78.125
6158	AF169301	Homo sapiens Na+/sulfate cotransporter SUT-1	4047	100.000
6159	U49973	Homo sapiens ORF1; MER37; putative transposase similar to pogo element	210	34.167
6160	AB033021	Homo sapiens KIAA1195 protein	294	43.269
6161	U49954	Caenorhabditis elegans coded for by C. elegans cDNA CEESG19F; short region of weak similarity to Thermomonospora protein kinase (GB:U23820)	54	29.730
6162	U49954	Caenorhabditis elegans coded for by C. elegans cDNA CEESG19F; short region of weak similarity to Thermomonospora protein kinase (GB:U23820)	46	29.412
6163	U49954	Caenorhabditis elegans coded for by C. elegans cDNA CEESG19F; short region of weak similarity to Thermomonospora protein kinase (GB:U23820)	256	43.750
6164	U49954	Caenorhabditis elegans coded for by C. elegans cDNA CEESG19F; short region of weak similarity to Thermomonospora protein kinase (GB:U23820)	211	40.323

6165	U37376	Xenopus laevis MAM domain protein	443	53.125
6166	U37376	Xenopus laevis MAM domain protein	173	58.000
6167	U37376	Xenopus laevis MAM domain protein	347	46.970
6168	U37376	Xenopus laevis MAM domain protein	574	42.400
6169	U37376	Xenopus laevis MAM domain protein	1645	63.243
6170	AL078630	Mus musculus 573K1.5 (novel protein similar to worm, yeast and plant proteins)	375	51.639
6171	AL078630	Mus musculus 573K1.5 (novel protein similar to worm, yeast and plant proteins)	558	66.667
6172	Z81561	Caenorhabditis elegans cDNA EST yk338f6.5 comes from this gene; cDNA EST EMBL:D75296 comes from this gene	50	38.095
6173	Z81561	Caenorhabditis elegans cDNA EST yk338f6.5 comes from this gene; cDNA EST EMBL:D75296 comes from this gene	250	35.537
6174	Z14020	Nicotiana tabacum Pistil extensin like protein, partial CDS only	82	33.333
6175	Z14020	Nicotiana tabacum Pistil extensin like protein, partial CDS only	205	42.045
6176	Z14020	Nicotiana tabacum Pistil extensin like protein, partial CDS only	197	42.683
6177	U79260	Homo sapiens unknown	376	71.591
6178	U22376	Homo sapiens alternatively spliced product using exon 13A	362	62.376
6179	Y08715	Mus musculus vascular cadherin-2	283	26.439
6180	AF000152	Homo sapiens OS-4 protein	288	88.235
6181	AF000152	Homo sapiens OS-4 protein	934	95.333
6182	AF171938	Homo sapiens NUMB isoform 1	4408	100.000
6183	AF171938	Homo sapiens NUMB isoform 1	406	95.161
6184	AF171938	Homo sapiens NUMB isoform 1	424	67.961
6186	AF171938	Homo sapiens NUMB isoform 1	564	34.568
6187	AF171938	Homo sapiens NUMB isoform 1	3014	82.753
6189	AF171938	Homo sapiens NUMB isoform 1	4274	98.310
6190	AF171938	Homo sapiens NUMB isoform 1	3529	87.023
6191	AF171938	Homo sapiens NUMB isoform 1	3666	90.505
6192	X53581	Rattus norvegicus ORF4	40	26.923
6193	X53581	Rattus norvegicus ORF4	47	27.273
6194	X53581	Rattus norvegicus ORF4	180	52.239
6195	X16623	Rattus sp. neuraxin (AA 1-863)	512	34.286
6196	S63758	Mus sp. metallothionein-I gene transcription activator	250	93.103
6197	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	511	38.579
6198	X86779	Homo sapiens FAST kinase	620	60.476
6199	AB032983	Homo sapiens KIAA1157 protein	355	57.609
6200	L12147	Mus musculus early B-cell factor	207	91.176
6201	L12147	Mus musculus early B-cell factor	214	100.000
6202	L12147	Mus musculus early B-cell factor	1646	99.219
6203	U22376	Homo sapiens alternatively spliced product using exon 13A	283	58.763
6204	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	1066	51.422

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6205	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	181	36.943
6206	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	481	35.984
6207	AF055666	Mus musculus kinesin light chain 2	224	70.690
6208	D45371	Homo sapiens a novel adipose specific collagen-like factor, apM1 (adipose most abundant gene transcript 1)	241	42.537
6209	X70476	Homo sapiens subunit of coatomer complex	66	30.000
6210	X70476	Homo sapiens subunit of coatomer complex	335	78.824
6211	Z86109	Saccharomyces pastorianus unknown	123	35.227
6216	U79260	Homo sapiens unknown	58	44.444
6217	U79260	Homo sapiens unknown	308	58.889
6218	M25113	Homo sapiens sickle beta-hemoglobin	720	89.600
6221	AJ223814	Homo sapiens striatin	5149	100.000
6222	AJ223814	Homo sapiens striatin	3862	96.753
6223	AJ223814	Homo sapiens striatin	402	82.432
6229	X92485	Plasmodium vivax pval	242	50.000
6230	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	343	62.376
6231	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	338	61.321
6233	Z93244	Homo sapiens bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	132	58.824
6234	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	152	26.255
6235	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	187	41.176
6236	AB032907	Hylobates lar dopamine receptor D4	78	26.027
6237	AB032907	Hylobates lar dopamine receptor D4	73	29.032
6238	AB032907	Hylobates lar dopamine receptor D4	57	54.545
6239	AB032907	Hylobates lar dopamine receptor D4	89	35.000
6240	AB032907	Hylobates lar dopamine receptor D4	87	29.333
6241	AB032907	Hylobates lar dopamine receptor D4	137	32.632
6242	U22376	Homo sapiens alternatively spliced product using exon 13A	336	56.522
6243	U53153	Caenorhabditis elegans one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922)	185	29.457
6244	M15530	Homo sapiens B-cell growth factor	149	62.791
6245	AB033034	Homo sapiens KIAA1208 protein	171	73.529
6246	X92485	Plasmodium vivax pval	154	70.968
6247	U58658	Homo sapiens unknown	188	48.052
6248	U22376	Homo sapiens alternatively spliced product using exon 13A	424	68.000
6249	U32462	Ithomia sp. NADH dehydrogenase subunit 1	104	26.829

6250	AF095737	Homo sapiens unknown	256	54.945
6252	AF159055	Homo sapiens leucine zipper-like protein	144	70.000
6253	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	259	51.163
6254	U09823	Oryctolagus cuniculus elongation factor 1 alpha	619	77.600
6255	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1307	94.628
6256	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	346	65.432
6257	AC002451	Homo sapiens pyruvate dehydrogenase kinase isoform 4	2405	87.302
6258	AC002451	Homo sapiens pyruvate dehydrogenase kinase isoform 4	182	45.714
6259	AC002451	Homo sapiens pyruvate dehydrogenase kinase isoform 4	2722	100.000
6261	AC004473	Arabidopsis thaliana T13D8.31	519	33.163
6262	AC004473	Arabidopsis thaliana T13D8.31	494	46.471
6265	AF033339	Caenorhabditis briggsae UNC-45	149	23.077
6266	X67863	Mus musculus T2	252	49.398
6267	AE001875	Deinococcus radiodurans hypothetical protein	141	22.609
6268	AL034556	Plasmodium falciparum predicted using hexExon; MAL3P5.9 (PFC0615w), Hypothetical protein, len: 332 aa	127	41.304
6270	X92485	Plasmodium vivax pval	218	59.322
6272	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	346	64.935
6274	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	425	68.317
6276	AF116553	Drosophila melanogaster antennal-specific short-chain dehydrogenase/reductase	226	30.216
6277	AF116553	Drosophila melanogaster antennal-specific short-chain dehydrogenase/reductase	44	22.857
6278	AF116553	Drosophila melanogaster antennal-specific short-chain dehydrogenase/reductase	358	28.339
6279	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	307	58.333
6280	U73522	Homo sapiens AMSH	690	98.990
6281	U73522	Homo sapiens AMSH	266	69.231
6282	L26953	Homo sapiens chromosomal protein	124	54.717
6283	L26953	Homo sapiens chromosomal protein	44	30.000
6284	L26953	Homo sapiens chromosomal protein	165	45.283
6285	U22376	Homo sapiens alternatively spliced product using exon 13A	200	46.988
6286	U16359	Rattus norvegicus nitric oxide synthase	121	53.333
6287	X92485	Plasmodium vivax pval	178	45.455
6289	X92485	Plasmodium vivax pval	329	44.872
6291	AF013213	Bos taurus elongation factor 1 alpha	132	95.833

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6292	AF013213	Bos taurus elongation factor 1 alpha	732	100.000
6293	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	271	53.165
6294	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	148	35.955
6295	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	197	53.333
6296	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	333	66.234
6297	X16064	Homo sapiens tumor protein (AA 1 - 172)	230	100.000
6298	X16064	Homo sapiens tumor protein (AA 1 - 172)	603	75.138
6299	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	310	56.322
6300	X92485	Plasmodium vivax pva1	192	74.286
6301	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	261	72.727
6302	U22376	Homo sapiens alternatively spliced product using exon 13A	359	71.605
6303	L24804	Homo sapiens p23	969	98.551
6304	L24804	Homo sapiens p23	161	82.759
6305	L40357	Homo sapiens thyroid receptor interactor	467	91.250
6306	L40357	Homo sapiens thyroid receptor interactor	109	65.517
6307	L40357	Homo sapiens thyroid receptor interactor	625	90.625
6308	U39208	Rattus norvegicus cytochrome P450 4F6	130	34.568
6309	AF182070	Bdelloura candida calcium channel alpha-1 subunit	71	20.168
6310	AF182070	Bdelloura candida calcium channel alpha-1 subunit	49	26.531
6311	AF182070	Bdelloura candida calcium channel alpha-1 subunit	43	27.273
6312	Z30425	Homo sapiens orphan nuclear hormone receptor	43	40.000
6313	Z30425	Homo sapiens orphan nuclear hormone receptor	873	79.348
6314	Z30425	Homo sapiens orphan nuclear hormone receptor	2295	97.734
6315	Z30425	Homo sapiens orphan nuclear hormone receptor	246	93.023
6316	U18997	Escherichia coli ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	65	28.261
6317	U18997	Escherichia coli ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	64	37.500
6318	U18997	Escherichia coli ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	60	16.667

6320	U18997	Escherichia coli ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	59	26.667
6321	U18997	Escherichia coli ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	691	38.992
6323	AF047441	Homo sapiens RNA polymerase I 40kD subunit	170	35.417
6324	AF149809	Oryza sativa circumsporozoite protein precursor homolog	116	30.851
6325	X92485	Plasmodium vivax pval	235	59.701
6326	AF117831	Mus musculus putative protein phosphatase type 2C	40	35.000
6327	AF117831	Mus musculus putative protein phosphatase type 2C	285	65.753
6328	AF117831	Mus musculus putative protein phosphatase type 2C	49	25.806
6329	AF117831	Mus musculus putative protein phosphatase type 2C	37	38.889
6330	AF117831	Mus musculus putative protein phosphatase type 2C	34	63.636
6331	AF117831	Mus musculus putative protein phosphatase type 2C	44	21.154
6332	AF117831	Mus musculus putative protein phosphatase type 2C	48	31.579
6333	AF117831	Mus musculus putative protein phosphatase type 2C	53	42.857
6334	AL049730	Arabidopsis thaliana PEARLI 1-like protein	143	36.765
6335	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	399	73.333
6336	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	346	73.529
6337	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	160	67.568
6338	U23515	Caenorhabditis elegans weak similarity to adenylyl cyclase-associated protein (CAP) and to P. chabaudi adami major merozoite surface antigen protein (PIR:A32555). Final exon overlaps gene predicted on other strand.	76	31.081
6339	U23515	Caenorhabditis elegans weak similarity to adenylyl cyclase-associated protein (CAP) and to P. chabaudi adami major merozoite surface antigen protein (PIR:A32555). Final exon overlaps gene predicted on other strand.	121	51.351
6340	Z81113	Unknown similar to WD domain, G-beta repeats (4 domains); cDNA EST EMBL:D75228 comes from this gene	153	46.296
6341	Z81113	Unknown similar to WD domain, G-beta repeats (4 domains); cDNA EST EMBL:D75228 comes from this gene	151	23.118

6342	X61048	Hydra sp. mini-collagen	147	38.272
6343	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV249 hypotehtical protein	48	22.581
6344	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV249 hypotehtical protein	41	25.000
6345	AF063866	Melanoplus sanguinipes entomopoxvirus ORF MSV249 hypotehtical protein	67	22.581
6346	M15530	Homo sapiens B-cell growth factor	114	60.526
6347	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	218	50.000
6348	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	434	77.333
6349	AF067216	Caenorhabditis elegans No definition line found	223	44.248
6350	AL121745	Schizosaccharomyces pombe hypothetical zinc finger protein	187	38.202
6351	U22376	Homo sapiens alternatively spliced product using exon 13A	382	58.407
6352	U22376	Homo sapiens alternatively spliced product using exon 13A	73	23.810
6353	D83516	Homo sapiens HLA-A9HH antigen	630	84.404
6354	D83516	Homo sapiens HLA-A9HH antigen	290	58.947
6356	AF027144	Homo sapiens zinc finger protein	270	51.471
6357	AF027144	Homo sapiens zinc finger protein	139	45.283
6358	AF027144	Homo sapiens zinc finger protein	225	44.595
6359	AF080217	Sinorhizobium meliloti acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme	95	32.203
6360	AF080217	Sinorhizobium meliloti acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme	772	47.699
6361	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	112	37.647
6362	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	379	63.366
6364	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	296	63.514
6365	AF030357	Arabidopsis thaliana C-8,7 sterol isomerase; aSI1	136	50.000
6366	AF030357	Arabidopsis thaliana C-8,7 sterol isomerase; aSI1	194	38.462
6367	X66171	Homo sapiens CMRF-35 antigen	179	43.023
6368	X66171	Homo sapiens CMRF-35 antigen	800	62.212
6369	AJ000644	Homo sapiens SPOP	163	89.286
6370	AJ000644	Homo sapiens SPOP	2290	95.225
6371	AF199413	Pseudorabies virus thymidine kinase	72	33.010
6372	AF199413	Pseudorabies virus thymidine kinase	140	28.571
6373	X51605	Xenopus laevis nuclear actin-binding protein chain a	35	37.500
6374	X51605	Xenopus laevis nuclear actin-binding protein chain a	40	44.444
6375	X51605	Xenopus laevis nuclear actin-binding protein chain a	33	29.412
6376	X51605	Xenopus laevis nuclear actin-binding	43	26.667

		protein chain a		
6377	X51605	Xenopus laevis nuclear actin-binding protein chain a	236	97.368
6378	D87969	Homo sapiens CMP-sialic acid transporter	264	66.176
6380	U22376	Homo sapiens alternatively spliced product using exon 13A	322	75.000
6381	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	268	51.111
6383	M82829	Homo sapiens fusion protein	1828	83.143
6384	M82829	Homo sapiens fusion protein	4517	76.618
6385	K00557	Homo sapiens alpha-tubulin	775	83.333
6387	K00557	Homo sapiens alpha-tubulin	1328	94.660
6388	K00557	Homo sapiens alpha-tubulin	1755	89.174
6389	X92485	Plasmodium vivax pval	226	46.667
6390	U22376	Homo sapiens alternatively spliced product using exon 13A	212	67.308
6392	AE001910	Deinococcus radiodurans hypothetical protein	42	28.571
6393	AE001910	Deinococcus radiodurans hypothetical protein	101	36.667
6394	AE001910	Deinococcus radiodurans hypothetical protein	106	36.923
6395	X78928	Homo sapiens zinc finger protein	183	34.694
6396	AF083132	Porcine adenovirus 3 putative 13.1 kDa E3 protein	128	30.120
6398	L04673	Saccharomyces cerevisiae phosphatase	206	30.178
6399	AF095737	Homo sapiens unknown	201	50.000
6400	X12701	Homo sapiens PAI precursor polypeptide	954	98.039
6401	X12701	Homo sapiens PAI precursor polypeptide	367	88.235
6402	Z48955	Didelphis virginiana ORF-2, putative RT	145	41.509
6403	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	383	72.603
6404	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	416	75.610
6406	L26953	Homo sapiens chromosomal protein	120	71.429
6407	U47856	Araneus diadematus fibroin-4	45	50.000
6409	U47856	Araneus diadematus fibroin-4	30	41.667
6411	U47856	Araneus diadematus fibroin-4	172	35.385
6412	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	313	60.274
6413	X92485	Plasmodium vivax pval	131	51.282
6414	X80035	Oryctolagus cuniculus cysteine rich hair keratin associated protein	156	41.176
6416	X80035	Oryctolagus cuniculus cysteine rich hair keratin associated protein	187	36.000
6417	X80035	Oryctolagus cuniculus cysteine rich hair keratin associated protein	151	37.143
6419	L35013	Homo sapiens spliceosomal protein	206	32.934
6420	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	278	58.571
6421	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	54	25.806

6423	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	229	76.190
6424	AJ243459	Leishmania major proteophosphoglycan	102	29.565
6425	AJ243459	Leishmania major proteophosphoglycan	164	24.424
6426	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	347	67.442
6431	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	273	50.495
6432	U41007	Caenorhabditis elegans similar to mitochondrial precursor proteins import receptors	78	57.895
6434	U41007	Caenorhabditis elegans similar to mitochondrial precursor proteins import receptors	142	32.381
6435	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
6436	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
6437	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	157	68.421
6438	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	408	52.899
6440	U01849	Trypanosoma brucei ORF2	143	39.286
6443	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	56	35.000
6444	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	354	69.333
6445	U41557	Caenorhabditis elegans histidine-rich	137	31.783
6446	AF051098	Mus musculus seven transmembrane domain orphan receptor	137	28.736
6447	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	371	69.512
6448	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	251	64.407
6451	X92485	Plasmodium vivax pval	195	57.143
6452	AB001684	Chlorella vulgaris ORF49b	41	28.571
6453	AB001684	Chlorella vulgaris ORF49b	68	47.368
6455	AF151843	Homo sapiens CGI-85 protein	190	83.784
6456	X79417	Sus scrofa 40S ribosomal protein S12	340	100.000
6457	X79417	Sus scrofa 40S ribosomal protein S12	471	66.187
6458	X79417	Sus scrofa 40S ribosomal protein S12	240	97.222
6459	X79417	Sus scrofa 40S ribosomal protein S12	847	98.485
6460	AF153208	Homo sapiens GC-rich sequence DNA-binding factor candidate	175	43.056
6461	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	234	56.923
6462	Z14014	Nicotiana tabacum Pistil extensin like protein, partial CDS only	111	41.463
6463	M69297	Homo sapiens ORF 3	159	44.231
6464	X16064	Homo sapiens tumor protein (AA 1 - 172)	776	100.000
6465	X16064	Homo sapiens tumor protein (AA 1 - 172)	230	100.000
6466	X16064	Homo sapiens tumor protein (AA 1 -	1080	98.837

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6467	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	23.932
6468	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	62	34.694
6469	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	36.000
6470	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	108	33.088
6471	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	366	65.854
6472	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	61	29.412
6474	U22376	Homo sapiens alternatively spliced product using exon 13A	307	59.259
6475	AF189307	Homo sapiens unknown	143	39.535
6476	AF051850	Homo sapiens supervillin	6925	92.048
6477	AF051850	Homo sapiens supervillin	11827	100.000
6478	AF051850	Homo sapiens supervillin	10929	80.759
6479	AF051850	Homo sapiens supervillin	366	61.616
6481	X66285	Mus musculus HC1 ORF	134	34.884
6483	AF009829	Mycobacterium bovis unknown	160	27.074
6484	AF009829	Mycobacterium bovis unknown	203	28.205
6485	AL031133	Homo sapiens dJ281H8.3 (PUTATIVE novel protein)	260	43.137
6486	D64154	Homo sapiens Mr 110,000 antigen	347	85.484
6487	D64154	Homo sapiens Mr 110,000 antigen	306	52.985
6488	D64154	Homo sapiens Mr 110,000 antigen	568	91.667
6489	AB010430	Aspergillus oryzae HAPB	163	30.435
6490	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	289	58.228
6491	U63542	Homo sapiens FAP protein	178	72.727
6492	U63542	Homo sapiens FAP protein	200	81.818
6493	U63542	Homo sapiens FAP protein	200	81.818
6494	U63542	Homo sapiens FAP protein	200	81.818
6495	U63542	Homo sapiens FAP protein	200	81.818
6496	U63542	Homo sapiens FAP protein	200	81.818
6497	U63542	Homo sapiens FAP protein	190	76.471
6498	U63542	Homo sapiens FAP protein	209	80.000
6499	U63542	Homo sapiens FAP protein	200	81.818
6502	D87831	Mus musculus myocyte enhancer factor 2B type B-1	130	33.846
6503	D87831	Mus musculus myocyte enhancer factor 2B type B-1	127	29.258
6504	D87831	Mus musculus myocyte enhancer factor 2B type B-1	89	26.496
6506	U22376	Homo sapiens alternatively spliced product using exon 13A	247	63.014
6508	L17308	Gossypium hirsutum proline-rich cell wall protein	58	37.037
6509	L17308	Gossypium hirsutum proline-rich cell wall protein	170	30.000
6511	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	122	56.250

6512	U39318	Homo sapiens Ubch5C	101	93.333
6513	U39318	Homo sapiens Ubch5C	425	93.939
6514	AF095737	Homo sapiens unknown	298	57.609
6515	X72963	Nicotiana tabacum pAP8 product	115	29.412
6516	U22376	Homo sapiens alternatively spliced product using exon 13A	354	63.529
6517	U22376	Homo sapiens alternatively spliced product using exon 13A	114	83.333
6518	U22376	Homo sapiens alternatively spliced product using exon 13A	182	62.500
6521	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	262	60.294
6523	U22376	Homo sapiens alternatively spliced product using exon 13A	205	53.968
6524	M15530	Homo sapiens B-cell growth factor	143	62.857
6526	Z98980	Schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog 1	215	28.571
6527	A46482	unidentified TAX	134	33.750
6529	X02954	Escherichia coli parA (aa 1-398)	1611	87.582
6530	X02954	Escherichia coli parA (aa 1-398)	1031	87.234
6531	X02954	Escherichia coli parA (aa 1-398)	236	25.769
6532	X02954	Escherichia coli parA (aa 1-398)	61	34.545
6533	X02954	Escherichia coli parA (aa 1-398)	1797	80.577
6534	X02954	Escherichia coli parA (aa 1-398)	758	94.309
6535	X02954	Escherichia coli parA (aa 1-398)	989	54.286
6536	X02954	Escherichia coli parA (aa 1-398)	1775	90.968
6537	X02954	Escherichia coli parA (aa 1-398)	756	99.138
6542	X02954	Escherichia coli parA (aa 1-398)	2281	100.000
6543	X02954	Escherichia coli parA (aa 1-398)	1782	99.640
6544	X02954	Escherichia coli parA (aa 1-398)	2406	98.681
6545	X02954	Escherichia coli parA (aa 1-398)	62	26.190
6546	X02954	Escherichia coli parA (aa 1-398)	2406	98.681
6548	AE001863	Deinococcus radiodurans hypothetical protein	55	38.095
6549	AE001863	Deinococcus radiodurans hypothetical protein	126	35.616
6550	U22376	Homo sapiens alternatively spliced product using exon 13A	130	73.913
6551	U22376	Homo sapiens alternatively spliced product using exon 13A	488	69.725
6552	U16368	Sus scrofa skeletal alpha actin	492	98.667
6553	U16368	Sus scrofa skeletal alpha actin	372	96.429
6555	D83485	Homo sapiens ER-60 protease	363	64.706
6556	D83485	Homo sapiens ER-60 protease	885	85.326
6557	U19247	Homo sapiens interferon-gamma receptor alpha chain	185	96.429
6558	U19247	Homo sapiens interferon-gamma receptor alpha chain	35	23.077
6559	U19247	Homo sapiens interferon-gamma receptor alpha chain	2985	97.741
6560	X94438	Homo sapiens transcription factor	57	32.407
6561	X94438	Homo sapiens transcription factor	2807	98.595
6562	X94438	Homo sapiens transcription factor	1459	91.429
6563	AF009668	multiple sclerosis associated	670	70.803

		retrovirus polyprotein		
6564	AF009668	multiple sclerosis associated retrovirus polyprotein	326	56.989
6566	AF009668	multiple sclerosis associated retrovirus polyprotein	379	67.368
6567	AF009668	multiple sclerosis associated retrovirus polyprotein	282	62.121
6569	AF009668	multiple sclerosis associated retrovirus polyprotein	432	68.041
6573	AF009668	multiple sclerosis associated retrovirus polyprotein	1231	74.059
6577	AF009668	multiple sclerosis associated retrovirus polyprotein	276	61.905
6579	AF009668	multiple sclerosis associated retrovirus polyprotein	1299	75.100
6580	AF009668	multiple sclerosis associated retrovirus polyprotein	995	53.529
6581	AF009668	multiple sclerosis associated retrovirus polyprotein	2849	61.178
6582	AF009668	multiple sclerosis associated retrovirus polyprotein	1299	75.100
6583	AF117897	Bos taurus rab11 binding protein	278	88.000
6584	AB033040	Homo sapiens KIAA1214 protein	349	46.457
6585	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	312	66.667
6586	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	658	100.000
6587	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	3098	96.894
6588	X52604	Artemia sp. actin (329 AA)	692	82.812
6589	X52604	Artemia sp. actin (329 AA)	360	75.000
6590	X52604	Artemia sp. actin (329 AA)	1172	70.213
6591	X52604	Artemia sp. actin (329 AA)	1172	70.213
6592	X52604	Artemia sp. actin (329 AA)	1981	89.602
6593	X52604	Artemia sp. actin (329 AA)	2013	95.719
6595	X52604	Artemia sp. actin (329 AA)	1648	85.976
6596	U22376	Homo sapiens alternatively spliced product using exon 13A	421	68.421
6597	U22376	Homo sapiens alternatively spliced product using exon 13A	366	55.932
6598	U73819	Mus musculus polypeptide GalNAc transferase-T4	1772	67.102
6599	U73819	Mus musculus polypeptide GalNAc transferase-T4	1690	48.947
6600	AF061025	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1	60	21.649
6601	AF061025	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1	4759	99.729
6602	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	258	56.338
6603	M76595	Homo sapiens erythropoietin receptor	34	44.444
6604	M76595	Homo sapiens erythropoietin receptor	64	35.294
6605	M76595	Homo sapiens erythropoietin receptor	688	100.000
6606	M76595	Homo sapiens erythropoietin receptor	173	78.947

6607	X92963	Homo sapiens ubiquitin-conjugating enzyme UbcH6	153	75.862
6608	M27364	Homo sapiens elongation factor 1 alpha	132	95.833
6609	M27364	Homo sapiens elongation factor 1 alpha	125	87.500
6610	M27364	Homo sapiens elongation factor 1 alpha	1041	88.718
6611	AF191020	Homo sapiens E2IG5	130	100.000
6612	AF191020	Homo sapiens E2IG5	303	59.873
6613	S39127	human, testis, Peptide, 331 aa cathepsin S-cysteine proteinase	467	100.000
6614	S39127	human, testis, Peptide, 331 aa cathepsin S-cysteine proteinase	2005	96.096
6615	S39127	human, testis, Peptide, 331 aa cathepsin S-cysteine proteinase	598	90.526
6617	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	56.667
6618	AF207550	Homo sapiens unknown	163	26.271
6619	AB007185	Homo sapiens ribosomal protein L38	215	100.000
6620	AB007185	Homo sapiens ribosomal protein L38	220	97.222
6622	AB007185	Homo sapiens ribosomal protein L38	214	100.000
6623	AB007185	Homo sapiens ribosomal protein L38	215	100.000
6624	AB007185	Homo sapiens ribosomal protein L38	220	97.222
6626	AB007185	Homo sapiens ribosomal protein L38	214	100.000
6627	A62731	unidentified unnamed protein product	202	94.118
6628	A62731	unidentified unnamed protein product	153	72.727
6629	M62387	Oryctolagus cuniculus ubiquitin conjugating-protein	862	92.466
6630	M62387	Oryctolagus cuniculus ubiquitin conjugating-protein	622	73.649
6631	M62387	Oryctolagus cuniculus ubiquitin conjugating-protein	626	83.186
6632	M62387	Oryctolagus cuniculus ubiquitin conjugating-protein	199	100.000
6633	M62387	Oryctolagus cuniculus ubiquitin conjugating-protein	538	79.747
6634	X91656	Mus musculus alternatively spliced; truncated	325	65.060
6635	X91656	Mus musculus alternatively spliced; truncated	280	86.667
6636	X91656	Mus musculus alternatively spliced; truncated	701	92.381
6637	X91656	Mus musculus alternatively spliced; truncated	641	100.000
6638	X91656	Mus musculus alternatively spliced; truncated	405	73.109
6639	AB002330	Homo sapiens KIAA0332	49	38.462
6640	AB002330	Homo sapiens KIAA0332	60	24.468
6641	AB002330	Homo sapiens KIAA0332	51	47.619
6642	AB002330	Homo sapiens KIAA0332	355	81.690
6643	U22376	Homo sapiens alternatively spliced product using exon 13A	124	83.333
6644	U22376	Homo sapiens alternatively spliced product using exon 13A	175	44.681
6645	U79260	Homo sapiens unknown	137	68.750
6646	AE000710	Aquifex aeolicus hypothetical protein	65	24.561

6647	AE000710	Aquifex aeolicus hypothetical protein	59	39.286
6649	AE000710	Aquifex aeolicus hypothetical protein	262	26.695
6652	X72963	Nicotiana tabacum pAP8 product	115	40.816
6653	Y10487	Homo sapiens stress-activated protein kinase-3	47	40.741
6654	Y10487	Homo sapiens stress-activated protein kinase-3	978	55.840
6655	Y10487	Homo sapiens stress-activated protein kinase-3	308	76.471
6656	Y10487	Homo sapiens stress-activated protein kinase-3	145	91.667
6657	Y10487	Homo sapiens stress-activated protein kinase-3	43	83.333
6658	Y10487	Homo sapiens stress-activated protein kinase-3	43	46.154
6659	Y10487	Homo sapiens stress-activated protein kinase-3	2413	99.728
6660	Y10487	Homo sapiens stress-activated protein kinase-3	585	61.326
6661	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	217	60.714
6662	AF007826	Homo sapiens bax epsilon	206	55.769
6663	M90054	Homo sapiens ribosomal protein L3	1209	80.972
6664	M90054	Homo sapiens ribosomal protein L3	1918	84.223
6665	M12759	Homo sapiens Ig J-chain	359	100.000
6666	M12759	Homo sapiens Ig J-chain	30	36.364
6667	M12759	Homo sapiens Ig J-chain	681	91.367
6668	M12759	Homo sapiens Ig J-chain	179	100.000
6669	U22376	Homo sapiens alternatively spliced product using exon 13A	177	66.667
6670	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
6671	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	189	78.947
6672	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	77	29.730
6673	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	122	90.909
6674	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	125	90.909
6675	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	123	57.576
6676	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	373	44.286
6678	X92485	Plasmodium vivax pval	136	70.000
6679	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	217	64.407
6682	D90901	Synechocystis sp. hypothetical protein	75	34.921
6683	D90901	Synechocystis sp. hypothetical protein	117	31.111
6684	U22376	Homo sapiens alternatively spliced product using exon 13A	190	63.830
6685	U22376	Homo sapiens alternatively spliced product using exon 13A	124	83.333
6686	M60119	Homo sapiens HIV-EP2/Schnurri-2	12463	99.945

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6687	M60119	Homo sapiens HIV-EP2/Schnurri-2	12288	95.568
6688	Z82062	Caenorhabditis elegans cDNA EST yk415c12.5 comes from this gene; cDNA EST yk526h3.3 comes from this gene; cDNA EST yk599b1.3 comes from this gene	484	43.094
6689	Z82062	Caenorhabditis elegans cDNA EST yk415c12.5 comes from this gene; cDNA EST yk526h3.3 comes from this gene; cDNA EST yk599b1.3 comes from this gene	139	39.130
6690	AB002375	Homo sapiens KIAA0377	169	82.353
6691	AF070968	Caenorhabditis elegans PAR-6	135	35.938
6695	M33519	Homo sapiens HLA-B-associated transcript 3 (BAT3)	185	83.784
6696	M33519	Homo sapiens HLA-B-associated transcript 3 (BAT3)	7379	99.029
6697	AF015043	Homo sapiens EH-binding protein	240	97.368
6698	AF090326	Mus musculus AE-1 binding protein AEBP2	298	100.000
6699	AF008442	Homo sapiens RNA polymerase I subunit hRPA39	204	53.571
6700	AF008442	Homo sapiens RNA polymerase I subunit hRPA39	2152	98.559
6701	AF121860	Homo sapiens sorting nexin 10	40	40.000
6702	AF121860	Homo sapiens sorting nexin 10	127	85.714
6703	D84342	Homo sapiens SM22 alpha	736	99.099
6704	D84342	Homo sapiens SM22 alpha	644	65.854
6705	AB011109	Homo sapiens KIAA0537 protein	495	42.157
6706	AJ005458	Bos taurus protein Phosphatase 2C beta	903	94.964
6707	AJ005458	Bos taurus protein Phosphatase 2C beta	2525	96.364
6708	AJ005458	Bos taurus protein Phosphatase 2C beta	609	94.681
6709	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	41	31.579
6710	Z34286	Oryctolagus cuniculus ORF might extend further in 5'-direction	416	39.535
6711	AJ005560	Mus musculus SPR2B protein	129	42.000
6712	X92968	Streptococcus pyogenes protein SIC	172	40.845
6715	U93197	Rattus norvegicus RN protein	215	87.179
6716	U93197	Rattus norvegicus RN protein	2011	97.476
6717	X68392	Borna disease virus p38 /39	142	34.021
6718	AB033007	Homo sapiens KIAA1181 protein	57	37.838
6719	AB033007	Homo sapiens KIAA1181 protein	2282	100.000
6720	AB033007	Homo sapiens KIAA1181 protein	57	37.838
6721	AB033007	Homo sapiens KIAA1181 protein	1364	69.643
6723	M15530	Homo sapiens B-cell growth factor	115	55.000
6724	AB007925	Homo sapiens KIAA0456 protein	955	98.592
6725	AB007925	Homo sapiens KIAA0456 protein	319	98.000
6726	U22376	Homo sapiens alternatively spliced product using exon 13A	202	69.231
6727	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	39	52.941
6728	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	299	52.577

6729	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	304	69.231
6731	U58658	Homo sapiens unknown	166	65.789
6732	U29154	Caenorhabditis elegans T07F12.1 gene product	426	33.617
6733	X76116	Caenorhabditis elegans carrier protein (c2)	190	56.364
6734	AF095737	Homo sapiens unknown	69	55.556
6735	AF095737	Homo sapiens unknown	336	60.440
6739	AC006323	Homo sapiens cullin 1	209	97.059
6740	AC006323	Homo sapiens cullin 1	3283	100.000
6741	AC006323	Homo sapiens cullin 1	3223	100.000
6742	X85019	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase	592	95.652
6743	D37991	Homo sapiens beta-signal sequence receptor	310	100.000
6744	D37991	Homo sapiens beta-signal sequence receptor	1001	94.565
6745	AF029061	Homo sapiens BAT1	782	82.803
6746	AF029061	Homo sapiens BAT1	1643	100.000
6747	Y07569	Homo sapiens PHAPI2a protein	90	45.455
6748	Y07569	Homo sapiens PHAPI2a protein	206	46.429
6749	AL133161	Homo sapiens hypothetical protein	146	49.254
6750	X92485	Plasmodium vivax pval	181	46.739
6751	X58099	Saccharomyces cerevisiae eIF4a	384	74.667
6753	X58099	Saccharomyces cerevisiae eIF4a	455	76.136
6754	X58099	Saccharomyces cerevisiae eIF4a	455	76.136
6755	X58099	Saccharomyces cerevisiae eIF4a	203	91.176
6756	X58099	Saccharomyces cerevisiae eIF4a	167	60.563
6757	J00194	Homo sapiens hla-dr antigen alpha chain	1475	89.764
6758	J00194	Homo sapiens hla-dr antigen alpha chain	1498	97.244
6759	D86980	Homo sapiens KIAA0227	117	33.333
6760	D86980	Homo sapiens KIAA0227	568	98.864
6761	D86980	Homo sapiens KIAA0227	2275	100.000
6762	L46722	Homo sapiens BTG1 binding factor 1	306	93.878
6763	L46722	Homo sapiens BTG1 binding factor 1	1366	96.186
6764	AB001684	Chlorella vulgaris ORF63	50	33.333
6765	AB001684	Chlorella vulgaris ORF63	72	83.333
6766	U12404	Homo sapiens Csa-19	594	68.310
6767	U12404	Homo sapiens Csa-19	696	83.111
6768	Z22181	Caenorhabditis elegans cDNA EST yk253b12.3 comes from this gene; cDNA EST yk253b12.5 comes from this gene	47	25.676
6769	Z22181	Caenorhabditis elegans cDNA EST yk253b12.3 comes from this gene; cDNA EST yk253b12.5 comes from this gene	118	28.947
6771	AB001684	Chlorella vulgaris ORF49b	32	66.667
6773	AB001684	Chlorella vulgaris ORF49b	62	42.308
6774	AB001684	Chlorella vulgaris ORF49b	45	38.095
6775	AB001684	Chlorella vulgaris ORF49b	67	66.667
6776	A58791	unidentified unnamed protein product	273	93.182
6777	A58791	unidentified unnamed protein product	2829	100.000

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6778	A58791	unidentified unnamed protein product	353	97.917
6779	A58791	unidentified unnamed protein product	2446	88.262
6780	AB001684	Chlorella vulgaris ORF54d	108	66.667
6781	X92485	Plasmodium vivax pval	259	55.056
6782	AF160864	Tetrahymena pyriformis orf98	66	50.000
6783	AF160864	Tetrahymena pyriformis orf98	74	52.941
6784	AB002371	Homo sapiens KIAA0373	3704	94.896
6785	Z77666	Unknown cDNA EST EMBL:T01059 comes from this gene; cDNA EST EMBL:D71534 comes from this gene; cDNA	502	37.500
6786	AL033502	Candida albicans hypothetical protein	74	22.162
6787	AL033502	Candida albicans hypothetical protein	61	24.590
6788	AL033502	Candida albicans hypothetical protein	63	21.951
6789	AL033502	Candida albicans hypothetical protein	54	43.750
6791	AL033502	Candida albicans hypothetical protein	50	38.889
6792	AL033502	Candida albicans hypothetical protein	49	21.429
6793	AL033502	Candida albicans hypothetical protein	60	22.131
6794	AL033502	Candida albicans hypothetical protein	54	18.919
6795	AL033502	Candida albicans hypothetical protein	57	22.404
6797	AL033502	Candida albicans hypothetical protein	270	27.451
6799	X07507	Xenopus borealis actin	717	86.719
6800	X07507	Xenopus borealis actin	355	73.684
6801	X07507	Xenopus borealis actin	715	77.848
6802	X07507	Xenopus borealis actin	396	95.161
6803	X07507	Xenopus borealis actin	944	97.945
6804	X07507	Xenopus borealis actin	2182	98.663
6805	U39621	Gallus gallus type V collagen	84	34.848
6806	U39621	Gallus gallus type V collagen	67	32.530
6807	U39621	Gallus gallus type V collagen	419	34.583
6808	Z12840	Oryctolagus cuniculus protein of unknown function	308	29.834
6809	Z12840	Oryctolagus cuniculus protein of unknown function	377	32.955
6810	AF047826	Homo sapiens cadherin-7	2059	100.000
6811	U92545	Gallus gallus tubby	45	41.667
6812	U92545	Gallus gallus tubby	202	87.500
6813	AF139166	Cavia porcellus prion protein	129	31.818
6814	X04201	Homo sapiens skeletal muscle tropomyosin (AA 1-285)	1012	77.778
6815	X04201	Homo sapiens skeletal muscle tropomyosin (AA 1-285)	320	98.148
6816	X04201	Homo sapiens skeletal muscle tropomyosin (AA 1-285)	1550	99.298
6817	M12140	Homo sapiens envelope protein	420	37.037
6818	M12140	Homo sapiens envelope protein	186	30.435
6819	M12140	Homo sapiens envelope protein	323	42.029
6820	M12140	Homo sapiens envelope protein	47	36.538
6821	M12140	Homo sapiens envelope protein	1433	47.863
6822	M15841	Homo sapiens U2 small nuclear ribonucleoprotein B''	129	86.364
6823	AF152996	Mus musculus peroxisomal assembly protein PEX3	212	100.000
6825	X02585	Xenopus laevis unidentified open reading frame 1 (166 aa)	199	76.316

6826	X02585	Xenopus laevis unidentified open reading frame 1 (166 aa)	201	53.448
6827	X02585	Xenopus laevis unidentified open reading frame 1 (166 aa)	233	41.129
6828	AF098788	Gallus gallus nuclear calmodulin-binding protein	346	52.893
6829	AF098788	Gallus gallus nuclear calmodulin-binding protein	64	29.167
6830	AF098788	Gallus gallus nuclear calmodulin-binding protein	752	76.923
6831	AF098788	Gallus gallus nuclear calmodulin-binding protein	65	35.185
6832	AF098788	Gallus gallus nuclear calmodulin-binding protein	808	62.255
6833	U22376	Homo sapiens alternatively spliced product using exon 13A	211	63.830
6834	U22376	Homo sapiens alternatively spliced product using exon 13A	211	63.830
6835	U22376	Homo sapiens alternatively spliced product using exon 13A	428	61.765
6836	AF155832	Homo sapiens adenosine 5'-diphosphosugar pyrophosphatase	89	83.333
6837	AF155832	Homo sapiens adenosine 5'-diphosphosugar pyrophosphatase	341	100.000
6838	AF155832	Homo sapiens adenosine 5'-diphosphosugar pyrophosphatase	970	87.611
6839	M76744	Homo sapiens BGP	113	62.500
6840	U77494	Homo sapiens RANBP8	357	100.000
6841	AF070663	Homo sapiens HSPC007	223	100.000
6843	X92485	Plasmodium vivax pval	145	60.606
6844	X92485	Plasmodium vivax pval	348	56.667
6845	Y10389	Xenopus laevis nuclear protein	134	24.561
6846	U44083	Human immunodeficiency virus type 1 rev gene product	42	34.483
6847	U44083	Human immunodeficiency virus type 1 rev gene product	50	39.130
6848	U44083	Human immunodeficiency virus type 1 rev gene product	91	55.000
6849	X55777	Homo sapiens put. ORF	181	49.153
6850	AE001111	Archaeoglobus fulgidus conserved hypothetical transmembrane protein	42	25.000
6851	AE001111	Archaeoglobus fulgidus conserved hypothetical transmembrane protein	53	34.211
6852	AE001111	Archaeoglobus fulgidus conserved hypothetical transmembrane protein	138	24.603
6853	U12204	Mus musculus phosphoprotein phosphatase	158	36.667
6854	U12204	Mus musculus phosphoprotein phosphatase	251	36.429
6855	AF103540	Homo sapiens immunoglobulin kappa light chain variable region	528	82.653
6856	AF103540	Homo sapiens immunoglobulin kappa light chain variable region	627	94.000
6858	A44601	Bos taurus unnamed protein product	266	88.636
6859	AF139768	Homo sapiens type II transmembrane	252	87.805

		protein MDL-1		
6860	AL031290	Homo sapiens dJ774I24.1 (similar to PREGNANCY-ASSOCIATED PLASMA PROTEIN A PRECURSOR)	308	93.182
6861	M76744	Homo sapiens BGP	101	68.000
6862	AL021748	Schizosaccharomyces pombe similar to dna-damage-inducible protein	206	40.541
6863	U39648	Caenorhabditis elegans T13C5.6 gene product	52	36.364
6864	U39648	Caenorhabditis elegans T13C5.6 gene product	121	52.632
6865	U39648	Caenorhabditis elegans T13C5.6 gene product	413	56.198
6866	U39648	Caenorhabditis elegans T13C5.6 gene product	309	53.922
6867	U39648	Caenorhabditis elegans T13C5.6 gene product	208	39.370
6868	AF067219	Caenorhabditis elegans contains similarity to human homeobox protein CDX-1 (SW: CDX1 HUMAN)	109	35.484
6869	M22332	Homo sapiens unknown protein	146	46.341
6870	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	198	46.250
6871	AB014537	Homo sapiens KIAA0637 protein	147	33.784
6872	Z72499	Homo sapiens herpesvirus associated ubiquitin-specific protease (HAUSP)	598	78.740
6873	Z72499	Homo sapiens herpesvirus associated ubiquitin-specific protease (HAUSP)	262	100.000
6875	AF162472	Mus musculus inducible protein	199	80.000
6876	AF038535	Homo sapiens synaptotagmin VII	239	24.254
6877	AF112476	Chlamydomonas reinhardtii outer arm dynein light chain 1	120	36.508
6879	AB002349	Homo sapiens KIAA0351	56	29.032
6880	AB002349	Homo sapiens KIAA0351	229	100.000
6881	U93567	Homo sapiens p40	454	50.735
6882	AL021747	Schizosaccharomyces pombe hypothetical protein	162	36.842
6883	Z47087	Homo sapiens RNA polymerase II elongation factor-like protein	214	100.000
6885	M25246	Homo sapiens vimentin	266	100.000
6886	M25246	Homo sapiens vimentin	927	72.318
6887	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	319	67.606
6888	AF153208	Homo sapiens GC-rich sequence DNA-binding factor candidate	295	92.857
6889	AF153208	Homo sapiens GC-rich sequence DNA-binding factor candidate	159	95.833
6890	U77948	Homo sapiens Bruton's tyrosine kinase-associated protein-135; BAP-135	6189	95.491
6891	U77948	Homo sapiens Bruton's tyrosine kinase-associated protein-135; BAP-135	355	73.077
6892	U77948	Homo sapiens Bruton's tyrosine kinase-associated protein-135; BAP-135	6242	97.444
6893	U77948	Homo sapiens Bruton's tyrosine kinase-associated protein-135; BAP-135	133	100.000

6894	U77948	Homo sapiens Bruton's tyrosine kinase-associated protein-135; BAP-135	6209	99.791
6896	AB015630	Homo sapiens type II membrane protein	388	48.819
6897	D26076	Oryctolagus cuniculus chloride channel	384	89.394
6898	D26076	Oryctolagus cuniculus chloride channel	1235	90.377
6900	X76538	Homo sapiens hMpv17	130	100.000
6901	J03756	Homo sapiens hGH-V2	373	62.393
6903	J03756	Homo sapiens hGH-V2	508	60.927
6904	J03756	Homo sapiens hGH-V2	961	79.670
6905	J03756	Homo sapiens hGH-V2	886	87.117
6906	J03756	Homo sapiens hGH-V2	361	62.821
6907	AJ004832	Homo sapiens neuropathy target esterase	183	59.524
6908	AJ004832	Homo sapiens neuropathy target esterase	1635	63.683
6909	AF032666	Rattus norvegicus rsec5	507	90.805
6912	AB002368	Homo sapiens KIAA0370	56	41.667
6913	AB002368	Homo sapiens KIAA0370	300	74.324
6914	AB002368	Homo sapiens KIAA0370	429	100.000
6915	AB002368	Homo sapiens KIAA0370	4330	96.076
6916	X91242	Xenopus laevis XrpFIbetal	38	38.889
6917	X91242	Xenopus laevis XrpFIbetal	134	42.424
6919	AL050018	Homo sapiens hypothetical protein	2504	100.000
6920	U57317	Homo sapiens p300/CBP-associated factor	5276	97.962
6921	U57317	Homo sapiens p300/CBP-associated factor	371	100.000
6922	Z74990	Saccharomyces cerevisiae ORF YOR082c	115	52.632
6923	AL049925	Homo sapiens hypothetical protein	407	68.354
6924	AL049925	Homo sapiens hypothetical protein	199	56.000
6925	AC007182	Homo sapiens unknown	415	100.000
6926	AF003535	Homo sapiens ORF2-like protein	200	60.417
6927	AF007826	Homo sapiens bax epsilon	186	70.588
6928	AF007826	Homo sapiens bax epsilon	186	70.588
6929	AF007826	Homo sapiens bax epsilon	205	42.308
6930	AF007826	Homo sapiens bax epsilon	127	77.273
6931	AF007826	Homo sapiens bax epsilon	192	63.043
6932	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	43	26.733
6934	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	238	70.213
6935	L08483	Drosophila melanogaster ring canal protein	869	31.327
6936	AB032984	Homo sapiens KIAA1158 protein	334	100.000
6937	AL022018	Unknown /prediction=(method:"genscan", version:"1.0", score:"294.38"); /match=(desc:"THIAZ	338	27.273
6938	AF045646	Caenorhabditis elegans contains similarity to collagens	125	38.889
6940	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	310	61.957
6941	U76759	Mus musculus nuclear protein NIP45	295	65.823
6942	U76759	Mus musculus nuclear protein NIP45	1199	80.702

6943	U88964	Homo sapiens HEM45	232	51.136
6944	AB028994	Homo sapiens KIAA1071 protein	2729	95.043
6945	AB028994	Homo sapiens KIAA1071 protein	3001	100.000
6946	AF055634	Homo sapiens transmembrane receptor UNC5C	54	21.875
6947	AF055634	Homo sapiens transmembrane receptor UNC5C	6322	100.000
6948	AF055634	Homo sapiens transmembrane receptor UNC5C	524	76.636
6949	AB018324	Homo sapiens KIAA0781 protein	4316	100.000
6950	X00824	Gallus gallus collagen	83	43.333
6951	U22376	Homo sapiens alternatively spliced product using exon 13A	417	71.264
6952	AF061022	Homo sapiens CTH	859	96.350
6953	S79410	Mus sp. nuclear localization signals (NLS)-binding protein=spot-1	118	35.593
6954	L26953	Homo sapiens chromosomal protein	43	30.233
6955	L26953	Homo sapiens chromosomal protein	123	55.172
6957	AB033034	Homo sapiens KIAA1208 protein	140	71.429
6958	J05016	Homo sapiens protein disulfide isomerase-related protein	306	100.000
6959	J05016	Homo sapiens protein disulfide isomerase-related protein	3798	96.918
6961	Z49199	Homo sapiens RNA polymerase II subunit hRPB17	774	97.333
6962	M32305	Human papillomavirus type 47 E1/E4 fusion protein	174	54.000
6965	U22376	Homo sapiens alternatively spliced product using exon 13A	66	27.586
6966	U22376	Homo sapiens alternatively spliced product using exon 13A	431	71.579
6967	X03145	Homo sapiens pot. ORF VI	48	32.258
6968	X03145	Homo sapiens pot. ORF VI	380	68.235
6969	X03145	Homo sapiens pot. ORF VI	367	69.620
6970	U22376	Homo sapiens alternatively spliced product using exon 13A	54	24.000
6971	U22376	Homo sapiens alternatively spliced product using exon 13A	56	24.324
6972	U22376	Homo sapiens alternatively spliced product using exon 13A	80	27.273
6973	U22376	Homo sapiens alternatively spliced product using exon 13A	70	24.286
6974	U22376	Homo sapiens alternatively spliced product using exon 13A	68	32.558
6976	U22376	Homo sapiens alternatively spliced product using exon 13A	226	72.549
6977	U22376	Homo sapiens alternatively spliced product using exon 13A	100	65.385
6978	U22376	Homo sapiens alternatively spliced product using exon 13A	269	79.630
6979	AF109906	Mus musculus NG22	302	34.351
6981	AF109906	Mus musculus NG22	402	29.524
6982	AF109906	Mus musculus NG22	285	37.226
6984	X86031	Sus scrofa homologue of	132	37.209

		proline/arginine-rich antibacterial protein		
6987	AF011373	Bos taurus chitinase-like protein 1	1930	83.735
6988	AF011373	Bos taurus chitinase-like protein 1	1943	84.940
6989	AF011373	Bos taurus chitinase-like protein 1	246	78.261
6991	AF008196	Homo sapiens bax epsilon	110	54.167
6992	AF008196	Homo sapiens bax epsilon	43	40.000
6993	U79260	Homo sapiens unknown	140	73.077
6994	U79260	Homo sapiens unknown	338	66.667
6997	X58197	Zea mays 27kDa storage protein, zein	105	32.222
6998	X58197	Zea mays 27kDa storage protein, zein	128	34.884
6999	M35258	Rattus norvegicus malic enzyme (EC 1.1.1.40)	77	63.158
7000	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	283	26.718
7001	AF125176	Mus musculus angiopoietin-related protein-2	61	53.333
7002	AF125176	Mus musculus angiopoietin-related protein-2	430	58.763
7003	AB032956	Homo sapiens KIAA1130 protein	3936	100.000
7004	AB032956	Homo sapiens KIAA1130 protein	1868	85.758
7005	AF139923	Mus musculus receptor-activated calcium channel	576	76.119
7006	AF139923	Mus musculus receptor-activated calcium channel	1560	97.166
7007	M38435	Brugia malayi collagen-like antigen	111	33.981
7008	L05090	Homo sapiens ribosomal protein S13	103	100.000
7010	U09608	Homo sapiens cell surface protein	774	100.000
7011	U09608	Homo sapiens cell surface protein	870	91.018
7012	D50372	Homo sapiens myosin regulatory light chain	879	85.549
7013	D50372	Homo sapiens myosin regulatory light chain	549	73.913
7014	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	41	54.545
7015	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	55	34.783
7016	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	55	34.783
7017	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	55	34.783
7018	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	55	34.783
7019	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	55	34.783
7020	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	610	69.784
7021	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	49	27.778
7022	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	45	66.667
7023	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	46	27.027
7024	U19940	Fragaria x ananassa putative 40S	58	38.095

		ribosomal protein s12		
7025	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	232	81.818
7026	U19940	Fragaria x ananassa putative 40S ribosomal protein s12	57	40.741
7028	U09116	Homo sapiens ORF1, encodes a 40 kDa product	122	66.667
7029	D80009	Homo sapiens KIAA0187	385	60.284
7030	D80009	Homo sapiens KIAA0187	743	66.176
7031	D80009	Homo sapiens KIAA0187	663	98.131
7032	D80009	Homo sapiens KIAA0187	8360	99.766
7033	D80009	Homo sapiens KIAA0187	257	100.000
7034	M22332	Homo sapiens unknown protein	238	67.308
7035	AF095737	Homo sapiens unknown	300	56.322
7036	U22376	Homo sapiens alternatively spliced product using exon 13A	182	77.500
7037	X92485	Plasmodium vivax pval	154	67.568
7038	U22376	Homo sapiens alternatively spliced product using exon 13A	99	50.000
7039	U22376	Homo sapiens alternatively spliced product using exon 13A	61	42.222
7040	U22376	Homo sapiens alternatively spliced product using exon 13A	357	73.034
7041	D82361	Homo sapiens MSSP-2	1734	92.708
7042	D82361	Homo sapiens MSSP-2	1856	98.264
7043	U22376	Homo sapiens alternatively spliced product using exon 13A	183	71.429
7045	AL117646	Homo sapiens hypothetical protein	570	69.828
7046	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	244	31.624
7047	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	107	42.000
7048	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	658	28.656
7049	AF103939	Homo sapiens echinoderm microtubule-associated protein-like EMAP2	813	32.037
7050	AF085357	Homo sapiens flotillin	456	64.130
7051	AF085357	Homo sapiens flotillin	2649	99.766
7052	AF085357	Homo sapiens flotillin	335	100.000
7053	AF085357	Homo sapiens flotillin	2067	89.838
7054	U22376	Homo sapiens alternatively spliced product using exon 13A	362	61.856
7055	AP000060	Aeropyrum pernix 100aa long hypothetical protein	102	47.500
7056	Z99753	Schizosaccharomyces pombe putative beta-mannosyltransferase	282	46.875
7057	Z99753	Schizosaccharomyces pombe putative beta-mannosyltransferase	45	30.000
7058	Z99753	Schizosaccharomyces pombe putative beta-mannosyltransferase	232	38.136
7059	Z99753	Schizosaccharomyces pombe putative beta-mannosyltransferase	319	36.123
7060	AB007888	Homo sapiens KIAA0428	1674	69.415
7061	AB007888	Homo sapiens KIAA0428	204	65.909

7062	AB007888	Homo sapiens KIAA0428	217	47.761
7063	AF004327	Homo sapiens angiopoietin-2	465	100.000
7064	AF004327	Homo sapiens angiopoietin-2	52	38.095
7065	AF004327	Homo sapiens angiopoietin-2	449	89.189
7066	AF004327	Homo sapiens angiopoietin-2	3294	100.000
7067	AF004327	Homo sapiens angiopoietin-2	1240	68.354
7068	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	601	94.565
7069	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	530	100.000
7070	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	980	75.234
7071	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	1101	81.308
7072	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	853	56.727
7073	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	125	77.778
7074	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	1595	59.881
7075	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	535	86.957
7076	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	2496	90.338
7077	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	926	52.890
7078	M33666	Homo sapiens pregnancy-specific beta-1-glycoprotein 6	1344	71.667
7079	U22376	Homo sapiens alternatively spliced product using exon 13A	374	70.330
7080	AB028972	Homo sapiens KIAA1049 protein	847	76.966
7081	AB028972	Homo sapiens KIAA1049 protein	368	96.296
7082	AB028972	Homo sapiens KIAA1049 protein	3481	99.093
7083	X17652	Homo sapiens IgG Fc receptor	359	82.812
7084	AF170726	Myxoma virus m147R	217	34.167
7085	AF170726	Myxoma virus m147R	399	31.905
7086	AJ010063	Homo sapiens telethonin	225	86.842
7087	AJ010063	Homo sapiens telethonin	59	30.667
7088	AL117579	Homo sapiens hypothetical protein	61	34.783
7089	AL117579	Homo sapiens hypothetical protein	877	70.536
7090	AL117579	Homo sapiens hypothetical protein	1729	100.000
7091	Z81490	Unknown similar to WD domain; G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene	134	47.059
7092	S77772	Homo sapiens aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	135	81.818
7093	AC004392	Arabidopsis thaliana Similar to gb AF072908 calcium-dependent protein kinase from Nicotiana tabacum.	59	32.500
7094	AC004392	Arabidopsis thaliana Similar to gb AF072908 calcium-dependent protein kinase from Nicotiana tabacum.	116	27.049
7095	AC004392	Arabidopsis thaliana Similar to	299	40.351

		gb AF072908 calcium-dependent protein kinase from <i>Nicotiana tabacum</i> .		
7096	AC004392	<i>Arabidopsis thaliana</i> Similar to gb AF072908 calcium-dependent protein kinase from <i>Nicotiana tabacum</i> .	71	28.846
7097	L31920	<i>Mus spretus</i> recognized by HS-63 monoclonal antibody	161	27.368
7099	D30648	<i>Homo sapiens</i> flavoprotein subunit of complex II	43	32.353
7100	D30648	<i>Homo sapiens</i> flavoprotein subunit of complex II	43	34.483
7101	D30648	<i>Homo sapiens</i> flavoprotein subunit of complex II	178	89.655
7102	D30648	<i>Homo sapiens</i> flavoprotein subunit of complex II	290	65.672
7103	U22376	<i>Homo sapiens</i> alternatively spliced product using exon 13A	133	74.194
7105	X13338	<i>Homo sapiens</i> plasminogen activator inhibitor 1	270	100.000
7106	X13338	<i>Homo sapiens</i> plasminogen activator inhibitor 1	529	91.111
7107	AF010144	<i>Homo sapiens</i> neuronal thread protein AD7c-NTP	361	68.919
7108	M76744	<i>Homo sapiens</i> BGP	34	22.500
7110	M76744	<i>Homo sapiens</i> BGP	99	61.538
7112	AL031447	<i>Homo sapiens</i> dJ126A5.2.1 (novel protein) (isoform 1)	236	23.506
7114	K02569	<i>Homo sapiens</i> gamma fibrinogen type A (AA at 202)	213	100.000
7115	K02569	<i>Homo sapiens</i> gamma fibrinogen type A (AA at 202)	924	96.078
7116	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	266	62.651
7118	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	288	63.095
7119	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	251	67.123
7121	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	192	52.564
7122	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	328	70.130
7123	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	290	52.427
7124	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	336	68.675
7125	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	287	63.855
7126	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	265	65.278
7127	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	279	65.060
7128	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	273	65.789
7129	S58722	<i>Homo sapiens</i> X-linked retinopathy protein {C-terminal, clone XEH.8c}	282	64.286

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7130	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	68.000
7132	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	302	62.791
7135	U46859	Yersinia enterocolitica (type 0:8) WbcI	138	29.348
7137	L07810	Homo sapiens dynamin	319	95.556
7138	L07810	Homo sapiens dynamin	866	100.000
7139	D83206	Mus musculus P24 protein	220	91.667
7140	U10485	Homo sapiens lymphoid-restricted membrane protein	57	40.625
7141	U10485	Homo sapiens lymphoid-restricted membrane protein	3535	98.746
7142	U10485	Homo sapiens lymphoid-restricted membrane protein	311	94.231
7143	AF163302	Homo sapiens somatostatin receptor interacting protein splice variant a	6066	97.773
7144	X16576	Homo sapiens KUP protein	461	32.493
7145	AL031431	Homo sapiens dJ462023.1 (novel protein)	751	75.145
7146	AL031431	Homo sapiens dJ462023.1 (novel protein)	1767	77.528
7147	L27428	Homo sapiens reverse transcriptase	167	62.500
7148	X58338	Arabidopsis thaliana glycine rich protein	440	58.559
7149	X58338	Arabidopsis thaliana glycine rich protein	438	58.716
7150	AF021351	Homo sapiens RNA polymerase III largest subunit	441	100.000
7151	S67247	Homo sapiens smooth muscle myosin heavy chain isoform SMemb	159	88.889
7152	Z85981	Brugia malayi actin	225	94.118
7153	Z85981	Brugia malayi actin	2197	95.467
7154	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	60.714
7155	AF072508	Homo sapiens envelope protein	36	38.462
7156	AF072508	Homo sapiens envelope protein	47	60.000
7157	AF072508	Homo sapiens envelope protein	146	46.667
7158	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	363	71.233
7160	U20106	Rattus norvegicus synaptotagmin VII	460	83.908
7161	X52164	Mus musculus Q300 protein (AA 1-77)	130	76.190
7162	U79278	Homo sapiens protein disulfide isomerase-related protein 5	149	96.000
7163	U79278	Homo sapiens protein disulfide isomerase-related protein 5	2767	99.525
7164	U79278	Homo sapiens protein disulfide isomerase-related protein 5	250	87.500
7165	U79278	Homo sapiens protein disulfide isomerase-related protein 5	2414	94.588
7166	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	40	23.077
7167	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	326	51.695

7168	X62839	Rattus rattus voltage-gated potassium channel	142	75.000
7169	U22376	Homo sapiens alternatively spliced product using exon 13A	142	79.167
7170	U22376	Homo sapiens alternatively spliced product using exon 13A	502	86.905
7173	AF048977	Homo sapiens Ser/Arg-related nuclear matrix protein	216	36.250
7174	U23502	Plasmodium chabaudi chabaudi POM1	679	46.383
7175	U23502	Plasmodium chabaudi chabaudi POM1	329	41.071
7176	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	184	67.857
7177	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	110	31.532
7178	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	402	71.154
7179	U58736	Caenorhabditis elegans Similar to cuticular collagen	141	37.681
7180	U58736	Caenorhabditis elegans Similar to cuticular collagen	85	31.034
7181	X12883	Homo sapiens cytokeratin 18 (424 AA)	1197	81.181
7182	X12883	Homo sapiens cytokeratin 18 (424 AA)	1197	81.181
7183	X12883	Homo sapiens cytokeratin 18 (424 AA)	43	23.256
7184	X12883	Homo sapiens cytokeratin 18 (424 AA)	2237	97.362
7185	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	302	59.596
7186	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	200	73.333
7187	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	321	62.651
7188	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	101	33.333
7189	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	62	35.714
7190	X14420	Homo sapiens prepro-alpha-1 type 3 collagen	238	32.153
7191	AF071081	Mycobacterium tuberculosis proline-rich mucin homolog	202	27.188
7192	Z46913	Streptomyces ambofaciens polyketide synthase	165	36.301
7193	Z46913	Streptomyces ambofaciens polyketide synthase	144	34.307
7197	U97553	murine herpesvirus 68 unknown	221	33.898
7199	X60382	Homo sapiens collagen subunit (alpha-1 (X)) 3	165	29.123
7202	X55777	Homo sapiens put. ORF	234	55.263
7205	K02212	Homo sapiens alpha-1-antitrypsin	168	96.296
7206	K02212	Homo sapiens alpha-1-antitrypsin	1540	84.706
7208	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	330	63.830
7211	AF163302	Homo sapiens somatostatin receptor interacting protein splice variant a	156	33.884
7213	AF079967	Phytomonas serpens MURF1	154	24.691
7219	U22376	Homo sapiens alternatively spliced	309	56.190

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		product using exon 13A		
7222	AF003535	Homo sapiens ORF2-like protein	168	33.333
7223	AJ245453	Mus musculus putative protein kinase	321	35.909
7225	U22376	Homo sapiens alternatively spliced product using exon 13A	149	40.541
7228	M13002	Mus musculus 2855 is the position of the first start codon in ORF 2; putative	171	60.784
7230	AB018705	Mus musculus ORF2	208	34.862
7231	D38595	Homo sapiens inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP)	5175	89.032
7232	D38595	Homo sapiens inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP)	333	57.692
7233	D38595	Homo sapiens inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP)	5875	98.498
7237	X61048	Hydra sp. mini-collagen	153	33.750
7238	AF028832	Homo sapiens Hsp89-alpha-delta-N	665	89.076
7239	AF028832	Homo sapiens Hsp89-alpha-delta-N	600	54.086
7240	AF028832	Homo sapiens Hsp89-alpha-delta-N	2535	92.650
7242	AF145679	Drosophila melanogaster BcDNA.LD22726	219	37.363
7248	AF042800	Homo sapiens suppressor of white apricot homolog 2	83	32.308
7249	AF042800	Homo sapiens suppressor of white apricot homolog 2	201	30.579
7251	AF058807	Bos taurus GTP-binding protein rah	649	72.121
7252	AF058807	Bos taurus GTP-binding protein rah	221	54.762
7253	AF058807	Bos taurus GTP-binding protein rah	645	65.104
7254	AF058807	Bos taurus GTP-binding protein rah	652	69.500
7255	S63654	Mus sp. type VII collagen	61	37.500
7256	S63654	Mus sp. type VII collagen	92	30.275
7260	AF053091	Drosophila melanogaster eyelid	259	30.000
7261	D50857	Homo sapiens DOCK180 protein	881	72.959
7262	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	115	90.000
7263	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	387	62.264
7266	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	382	57.391
7267	U61538	Homo sapiens calcium-binding protein chp	133	31.579
7269	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	388	60.377
7273	AF003535	Homo sapiens ORF2-like protein	151	59.322
7274	X89267	Homo sapiens uroporphyrinogen decarboxylase	661	100.000
7275	X89267	Homo sapiens uroporphyrinogen decarboxylase	1416	95.720
7276	K03332	Human herpesvirus 4 nuclear antigen 2	104	31.333
7277	K03332	Human herpesvirus 4 nuclear antigen 2	152	31.707
7279	M22334	Homo sapiens unknown protein	153	40.000
7280	M22334	Homo sapiens unknown protein	261	28.280

7281	M14144	Homo sapiens vimentin	552	72.932
7282	M14144	Homo sapiens vimentin	2018	85.895
7283	U93572	Homo sapiens putative p150	173	28.829
7284	U93572	Homo sapiens putative p150	1247	48.430
7285	AB012223	Canis familiaris ORF2	321	42.775
7287	AL033534	Schizosaccharomyces pombe serine-rich protein	237	29.492
7288	AB033031	Homo sapiens KIAA1205 protein	103	33.613
7289	AB033031	Homo sapiens KIAA1205 protein	87	28.571
7292	X55777	Homo sapiens put. ORF	234	55.263
7297	AC004665	Arabidopsis thaliana unknown protein	186	31.818
7302	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	314	61.165
7303	AC002291	Arabidopsis thaliana Similar ATP-dependent RNA Helicase	197	26.887
7304	AC002291	Arabidopsis thaliana Similar ATP-dependent RNA Helicase	674	39.634
7305	U07932	Homo sapiens AF-17	118	24.573
7307	Z95976	Homo sapiens RNA editing deaminase 1	174	67.442
7308	Z78542	Unknown cDNA EST EMBL:D72182 comes from this gene; cDNA EST EMBL:D72353 comes from this gene; cDNA	57	32.075
7309	Z78542	Unknown cDNA EST EMBL:D72182 comes from this gene; cDNA EST EMBL:D72353 comes from this gene; cDNA	201	31.788
7310	U85494	Zea mays LON1 protease	1519	55.625
7315	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	182	42.400
7316	L24521	Homo sapiens transformation-related protein	291	68.182
7321	X03484	Homo sapiens raf protein (aa 1-648)	3688	95.699
7327	AL079308	Streptomyces coelicolor putative serine/threonine protein kinase	95	29.375
7328	AF051944	Gallus gallus Xin	346	25.000
7330	L20249	Streptomyces coriofaciens homologous to Saccharopolyspora erythraea beta-ketoacyl synthase	150	32.812
7332	J03770	Mus musculus homeobox protein	150	36.782
7334	AF000996	Homo sapiens ubiquitous TPR motif, Y isoform	250	62.319
7335	U07224	Brugia malayi a2 (IV) basement membrane collagen	191	31.667
7338	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	314	45.699
7342	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	297	58.163
7343	U25281	Rattus norvegicus SH3 domain binding protein	203	27.706
7344	AB001971	Deinococcus radiodurans hypothetical protein	172	27.551
7345	AL133220	Streptomyces coelicolor A3(2) putative multi-domain regulatory protein.	170	28.814
7346	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	171	24.046

7347	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	99	30.303
7349	X72579	Homo sapiens collagen X	89	33.333
7350	X72579	Homo sapiens collagen X	223	32.121
7351	X83413	Human herpesvirus 6 U88	175	38.971
7352	M22334	Homo sapiens unknown protein	401	44.444
7353	M13002	Mus musculus 2855 is the position of the first start codon in ORF 2; putative	321	57.522
7355	AF183139	Cercopithecine herpesvirus 15 truncated type 2 EBNA2	155	28.458
7356	AF183139	Cercopithecine herpesvirus 15 truncated type 2 EBNA2	205	30.742
7358	X13885	Nicotiana tabacum extensin (AA 1-620)	243	35.745
7359	X13885	Nicotiana tabacum extensin (AA 1-620)	156	32.389
7363	U93567	Homo sapiens putative p150	316	50.388
7364	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	344	65.217
7366	U67557	Methanococcus jannaschii cell division control protein 48 (cdc48), AAA family	146	36.190
7367	U67557	Methanococcus jannaschii cell division control protein 48 (cdc48), AAA family	690	40.237
7368	D80009	Homo sapiens KIAA0187	971	57.525
7369	D80009	Homo sapiens KIAA0187	7181	91.510
7370	D80009	Homo sapiens KIAA0187	1086	78.970
7372	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	289	52.381
7373	AB032965	Homo sapiens KIAA1139 protein	168	33.987
7375	X15332	Homo sapiens alpha-1 (III) collagen	425	31.818
7377	AB007923	Homo sapiens KIAA0454 protein	82	22.605
7378	AB007923	Homo sapiens KIAA0454 protein	490	54.237
7379	AB007923	Homo sapiens KIAA0454 protein	226	41.129
7380	AB007923	Homo sapiens KIAA0454 protein	12006	100.000
7381	AB007923	Homo sapiens KIAA0454 protein	71	25.676
7382	AB007923	Homo sapiens KIAA0454 protein	62	28.000
7383	AB007923	Homo sapiens KIAA0454 protein	266	26.829
7384	AB007923	Homo sapiens KIAA0454 protein	532	67.123
7385	AF003535	Homo sapiens ORF2-like protein	200	51.515
7386	AF003535	Homo sapiens ORF2-like protein	200	51.515
7387	AB011164	Homo sapiens KIAA0592 protein	1275	93.213
7388	AB011164	Homo sapiens KIAA0592 protein	931	51.020
7389	AB011164	Homo sapiens KIAA0592 protein	499	79.798
7390	AB011164	Homo sapiens KIAA0592 protein	1496	78.370
7392	U76112	Mus musculus translation repressor NAT1	457	48.707
7393	U76112	Mus musculus translation repressor NAT1	5385	93.668
7394	AF062655	Mus musculus plenty-of-prolines-101; POP101; SH3-philo-protein	219	26.415
7395	X61295	Rattus norvegicus L1 retroposon, a portion of its ORF2 sequence	392	50.340
7396	U07973	Gallus gallus alpha-1 collagen type III	148	33.824
7398	X13783	Homo sapiens alpha-1 type 2 collagen	209	27.660

		(714 AA)		
7399	Z29560	Caenorhabditis elegans similar to Transmembrane and sushi domain; cDNA EST EMBL:D67777 comes from this gene; cDNA EST EMBL:D64676 comes from this gene	133	28.571
7400	Z29560	Caenorhabditis elegans similar to Transmembrane and sushi domain; cDNA EST EMBL:D67777 comes from this gene; cDNA EST EMBL:D64676 comes from this gene	291	29.412
7402	X57527	Homo sapiens alpha 1(VIII) collagen	148	33.884
7403	X57527	Homo sapiens alpha 1(VIII) collagen	159	28.571
7404	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform	183	28.796
7405	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	329	46.632
7408	J02009	Abelson murine leukemia virus p120-gag-abl polyprotein	174	25.773
7410	X03145	Homo sapiens pot. ORF I	209	38.806
7412	AF017369	Mus musculus facio-genital dysplasia protein 3	500	77.876
7413	AF017369	Mus musculus facio-genital dysplasia protein 3	603	77.953
7414	AF017369	Mus musculus facio-genital dysplasia protein 3	2521	73.779
7415	X97675	Homo sapiens plakophilin 2b	179	67.442
7416	U41557	Caenorhabditis elegans proline and glycine-rich	96	33.735
7417	U41557	Caenorhabditis elegans proline and glycine-rich	282	30.932
7420	AF038600	Sus scrofa pol protein	310	32.218
7421	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	411	43.701
7422	Z72875	Saccharomyces cerevisiae ORF YGR090w	212	33.708
7423	M80341	Homo sapiens ORF2 contains a reverse transcriptase domain.; ORF2	655	61.350
7425	AF169388	Mus musculus alpha 4 collagen IV	292	28.049
7426	AB027251	Homo sapiens zinc finger protein (ZFD25)	356	39.691
7427	U83303	Homo sapiens line-1 reverse transcriptase	216	42.105
7428	AJ001701	Homo sapiens deoxyhypusine synthase	358	66.038
7429	AJ001701	Homo sapiens deoxyhypusine synthase	875	77.928
7432	AL021086	Unknown /prediction=(method:"genefinder", version:"084", score:"147.90"); /match=(desc:"LI	213	54.667
7433	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	353	65.957
7435	U93563	Homo sapiens putative p150	163	33.628
7437	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	332	52.903
7439	AF169387	Mus musculus alpha 3 collagen IV	169	32.258
7440	AF106929	Medicago truncatula putative cell wall	78	28.000

		protein		
7443	X15081	Crithidia fasciculata MURF2 protein (AA 1-348)	192	25.446
7444	AF000298	Caenorhabditis elegans weak similarity to collagens; glycine- and proline-rich	94	30.723
7445	AF000298	Caenorhabditis elegans weak similarity to collagens; glycine- and proline-rich	185	31.818
7446	AB028236	Tricholoma nauseosum Pol (reverse transcriptase-RNase H-integrase)	162	29.299
7448	AF160864	Tetrahymena pyriformis orf443	143	28.125
7450	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	210	52.041
7451	X83413	Human herpesvirus 6 U87	84	23.789
7454	X83413	Human herpesvirus 6 U87	138	30.000
7456	X17403	human herpesvirus 5 HCMVUL61	145	29.545
7458	L27841	Homo sapiens pericentriol material 1	1707	96.503
7459	L27841	Homo sapiens pericentriol material 1	1096	84.685
7461	AB011167	Homo sapiens KIAA0595 protein	266	25.575
7462	M13100	Rattus norvegicus unknown protein	144	58.824
7464	Y17794	Gallus gallus winged-helix transcription factor	158	30.317
7465	AB002362	Homo sapiens KIAA0364	68	25.000
7466	AB002362	Homo sapiens KIAA0364	55	34.783
7468	AB002362	Homo sapiens KIAA0364	438	32.536
7469	AF043944	Mytilus edulis nongradient byssal precursor	353	29.279
7470	X52046	Mus musculus type III collagen	265	28.036
7474	D87744	Mus musculus DRPLA protein	181	24.409
7480	Y17397	Homo sapiens collagen alpha 4 type IV	170	26.546
7483	AB033026	Homo sapiens KIAA1200 protein	1037	57.934
7484	U79260	Homo sapiens unknown	176	54.930
7485	X13885	Nicotiana tabacum extensin (AA 1-620)	135	27.429
7489	X69838	Homo sapiens G9a	487	52.349
7490	AF039052	Caenorhabditis elegans No definition line found	205	39.394
7491	AF039052	Caenorhabditis elegans No definition line found	201	31.203
7492	AF039052	Caenorhabditis elegans No definition line found	217	38.356
7493	L24521	Homo sapiens transformation-related protein	234	45.000
7494	AB035541	Homo sapiens pancreatic zymogen granule membrane associated protein GP2 alpha form	342	45.968
7496	AB017337	Mus musculus sterol regulatory element-binding protein-1 (SREBP-1)	150	26.577
7498	U56862	Rattus norvegicus pancreas only zinc finger protein	770	50.973
7500	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	341	49.359
7503	AL021813	Schizosaccharomyces pombe hypothetical protein	53	37.500

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7504	AL021813	Schizosaccharomyces pombe hypothetical protein	169	22.342
7505	X59244	Homo sapiens ZNF43	871	61.017
7506	M14123	Homo sapiens gag 2 protein	603	42.920
7509	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	158	27.320
7510	Z82268	Unknown cDNA EST yk338g10.5 comes from this gene; cDNA EST EMBL:D27934 comes from this gene; cDNA E	208	33.333
7511	S80119	Rattus sp. reverse transcriptase homolog	188	49.206
7512	S80119	Rattus sp. reverse transcriptase homolog	299	39.394
7513	S80119	Rattus sp. reverse transcriptase homolog	188	49.206
7514	S80119	Rattus sp. reverse transcriptase homolog	299	39.394
7515	Y18890	Human endogenous retrovirus K env protein	292	37.121
7521	X15332	Homo sapiens alpha-1 (III) collagen	421	30.191
7522	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	73	40.000
7523	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	64	33.333
7524	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	129	29.560
7525	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	180	29.348
7526	AF053538	Alvinella pompejana fibrillar collagen chain FAp1 alpha	312	29.661
7528	X04758	Homo sapiens pro- alpha (V) collagen (AA 1099)	90	32.941
7529	X04758	Homo sapiens pro- alpha (V) collagen (AA 1099)	93	34.746
7530	X04758	Homo sapiens pro- alpha (V) collagen (AA 1099)	83	32.624
7531	X04758	Homo sapiens pro- alpha (V) collagen (AA 1099)	186	30.061
7532	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	64	26.250
7535	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	71	25.217
7536	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	60	39.130
7537	AF140675	Homo sapiens zinc metalloprotease ADAMTS7	334	46.154
7539	AF071172	Homo sapiens HERC2	1208	95.604
7540	AF071172	Homo sapiens HERC2	53	28.571
7542	AF071172	Homo sapiens HERC2	60	34.375
7543	AF071172	Homo sapiens HERC2	55	25.758
7544	AF071172	Homo sapiens HERC2	1516	98.291
7545	AF071172	Homo sapiens HERC2	68	25.984
7546	AF071172	Homo sapiens HERC2	66	30.108
7547	AF071172	Homo sapiens HERC2	66	27.273

7548	AF071172	Homo sapiens HERC2	2680	85.328
7549	AF071172	Homo sapiens HERC2	3574	66.077
7550	U67056	Acanthamoeba castellanii myosin I heavy chain kinase	191	36.842
7552	M87306	Tetrahymena thermophila micronuclear linker histone polyprotein	193	26.768
7553	M87306	Tetrahymena thermophila micronuclear linker histone polyprotein	61	18.557
7554	M87306	Tetrahymena thermophila micronuclear linker histone polyprotein	244	27.236
7555	M22334	Homo sapiens unknown protein	513	49.761
7556	AB021641	Homo sapiens gonadotropin inducible transcription repressor-1	635	48.691
7561	AF181631	Drosophila melanogaster BcDNA.GH04929	202	29.012
7562	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	112	37.647
7563	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	126	74.074
7564	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	350	53.595
7566	S64572	Strongylocentrotus purpuratus=sea urchin, Peptide Partial, 907 aa nonfibrillar collagen	164	29.956
7567	AB012223	Canis familiaris ORF2	286	42.975
7570	AB023143	Homo sapiens KIAA0926 protein	165	27.500
7571	AB023143	Homo sapiens KIAA0926 protein	94	31.522
7572	AB023143	Homo sapiens KIAA0926 protein	314	26.025
7573	AB023143	Homo sapiens KIAA0926 protein	331	26.409
7575	L26953	Homo sapiens chromosomal protein	164	57.143
7577	L26953	Homo sapiens chromosomal protein	102	32.927
7578	L26953	Homo sapiens chromosomal protein	295	50.000
7579	X83413	Human herpesvirus 6 U88	202	60.000
7581	L26953	Homo sapiens chromosomal protein	132	39.706
7583	AB014607	Homo sapiens KIAA0707 protein	414	38.462
7585	AB023167	Homo sapiens KIAA0950 protein	637	79.508
7586	AB023167	Homo sapiens KIAA0950 protein	1004	99.346
7587	AF053091	Drosophila melanogaster eyelid	104	35.000
7588	AF053091	Drosophila melanogaster eyelid	79	30.556
7589	AF053091	Drosophila melanogaster eyelid	216	27.985
7593	L20216	Cercopithecus aethiops UV-damaged DNA-binding protein	7425	99.649
7594	L20216	Cercopithecus aethiops UV-damaged DNA-binding protein	456	90.244
7596	X16468	Homo sapiens prepropeptide (AA 1-1418)	424	27.953
7597	U15647	Mus musculus reverse transcriptase	802	43.956
7598	AB007407	Mus musculus myeloid zinc finger protein-2	139	45.000
7599	AB008683	Bos taurus alpha2(I) collagen	112	37.313
7600	AB008683	Bos taurus alpha2(I) collagen	114	27.711
7601	Z72496	Homo sapiens mucin MUC5B	157	23.907
7603	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	342	32.734
7604	U93572	Homo sapiens putative p150	466	56.934
7605	U93572	Homo sapiens putative p150	480	56.391

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7606	U93572	Homo sapiens putative p150	513	66.418
7609	X14254	Rattus rattus invariant chain (AA 1-280)	659	69.767
7610	X14254	Rattus rattus invariant chain (AA 1-280)	459	44.891
7611	X14254	Rattus rattus invariant chain (AA 1-280)	1000	69.930
7613	AB018333	Homo sapiens KIAA0790 protein	428	52.083
7614	AB018333	Homo sapiens KIAA0790 protein	788	40.618
7615	U62315	Rattus norvegicus alpha globin	724	74.648
7616	U62315	Rattus norvegicus alpha globin	286	57.600
7617	AC004990	Homo sapiens atrophin-1 interacting protein 1	95	34.211
7618	AC004990	Homo sapiens atrophin-1 interacting protein 1	138	33.577
7621	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	158	55.556
7622	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	235	68.966
7624	L24521	Homo sapiens transformation-related protein	246	62.195
7626	X13885	Nicotiana tabacum extensin (AA 1-620)	125	29.452
7627	X13885	Nicotiana tabacum extensin (AA 1-620)	52	26.786
7628	X13885	Nicotiana tabacum extensin (AA 1-620)	125	26.357
7630	X15334	Homo sapiens creatine kinase B	763	74.033
7631	X15334	Homo sapiens creatine kinase B	320	94.444
7632	X15334	Homo sapiens creatine kinase B	800	86.131
7633	X15334	Homo sapiens creatine kinase B	1762	87.532
7634	AL117466	Homo sapiens hypothetical protein	273	82.143
7635	AL117466	Homo sapiens hypothetical protein	151	88.889
7636	AL117466	Homo sapiens hypothetical protein	4080	100.000
7637	AJ242540	Volvox carteri f. nagariensis hydroxyproline-rich glycoprotein DZ-HRGP	183	37.895
7638	U66619	Homo sapiens SWI/SNF complex 60 KDa subunit	366	56.115
7639	U66619	Homo sapiens SWI/SNF complex 60 KDa subunit	2486	93.450
7640	AF061742	Bos taurus retinal short-chain dehydrogenase/reductase retSDR1	277	92.000
7641	AF061742	Bos taurus retinal short-chain dehydrogenase/reductase retSDR1	1167	82.609
7643	L11672	Homo sapiens zinc finger protein	3305	51.579
7646	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	268	66.667
7649	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	132	41.250
7650	U00049	Caenorhabditis elegans weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein	268	62.500
7651	M20681	Homo sapiens glucose transporter-like protein	1735	95.053
7652	M20681	Homo sapiens glucose transporter-like protein	258	74.667

7654	Y07632	Zea mays potassium channel	59	34.483
7655	Y07632	Zea mays potassium channel	169	35.052
7658	AF167295	Gallus gallus reversion-induced LIM protein	215	46.429
7661	U22376	Homo sapiens alternatively spliced product using exon 13A	346	66.292
7663	AF155110	Homo sapiens NY-REN-45 antigen	86	31.111
7665	AF155110	Homo sapiens NY-REN-45 antigen	239	40.972
7666	AF155110	Homo sapiens NY-REN-45 antigen	2082	73.821
7667	AF068625	Mus musculus DNA cytosine-5 methyltransferase 3A	92	30.864
7668	AF068625	Mus musculus DNA cytosine-5 methyltransferase 3A	209	39.604
7669	AF172288	Mus musculus hairy-related transcription factor 3	311	50.000
7673	S72008	Homo sapiens CDC10 homolog=hCDC10	440	66.667
7674	S72008	Homo sapiens CDC10 homolog=hCDC10	453	81.319
7675	S72008	Homo sapiens CDC10 homolog=hCDC10	1099	97.884
7676	AB002388	Homo sapiens KIAA0390	359	42.742
7677	AB002388	Homo sapiens KIAA0390	622	39.697
7678	Z68108	Caenorhabditis elegans similar to phosphoinositide-specific phospholipase C; cDNA EST EMBL:D28105 comes from this gene; cDNA EST EMBL:D28104 comes from this gene	205	29.333
7680	AB002584	Rattus norvegicus beta-alanine-pyruvate aminotransferase	326	58.252
7681	AB002584	Rattus norvegicus beta-alanine-pyruvate aminotransferase	146	59.459
7683	AB002584	Rattus norvegicus beta-alanine-pyruvate aminotransferase	262	76.812
7684	U79260	Homo sapiens unknown	156	56.667
7686	Z49909	Caenorhabditis elegans C14A4.14	232	35.652
7687	Z49909	Caenorhabditis elegans C14A4.14	402	32.468
7689	AF159356	Rattus norvegicus Munc13-4 protein	4440	85.888
7693	D80009	Homo sapiens KIAA0187	593	60.513
7694	D80009	Homo sapiens KIAA0187	760	83.571
7695	D80009	Homo sapiens KIAA0187	1166	75.676
7696	D80009	Homo sapiens KIAA0187	2029	94.813
7698	L28808	Oryctolagus cuniculus manganese superoxide dismutase	886	48.294
7699	L28808	Oryctolagus cuniculus manganese superoxide dismutase	246	90.000
7700	L28808	Oryctolagus cuniculus manganese superoxide dismutase	1109	91.584
7703	AF030131	Mus musculus Plenty of SH3s; POSH	291	28.904
7704	U79260	Homo sapiens unknown	156	56.667
7705	U79260	Homo sapiens unknown	156	56.667
7706	AB005549	Rattus norvegicus atypical PKC specific binding protein	838	80.702
7710	U49385	Mus musculus CTP synthetase homolog	780	86.765
7711	AF103801	Homo sapiens unknown	292	97.727
7713	X97675	Homo sapiens plakophilin 2b	173	74.286
7715	AF030131	Mus musculus Plenty of SH3s; POSH	811	93.548

7716	AB027520	Mus musculus TAP-like ABC transporter	810	91.367
7717	AB002306	Homo sapiens KIAA0308	349	35.565
7718	U22376	Homo sapiens alternatively spliced product using exon 13A	285	65.385
7720	AF053356	Homo sapiens leucin rich neuronal protein	5713	99.880
7721	AF053356	Homo sapiens leucin rich neuronal protein	570	78.906
7723	AL035656	Arabidopsis thaliana putative protein	498	63.303
7724	AL035656	Arabidopsis thaliana putative protein	426	41.579
7725	AL035656	Arabidopsis thaliana putative protein	143	41.176
7726	AL035656	Arabidopsis thaliana putative protein	686	46.617
7727	AL035656	Arabidopsis thaliana putative protein	833	52.795
7729	X56203	Plasmodium falciparum liver stage antigen	204	24.375
7730	L26953	Homo sapiens chromosomal protein	148	73.333
7732	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	677	69.006
7733	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	646	91.346
7734	D16226	Oryctolagus cuniculus one of the members of sodium-glucose cotransporter family	1310	90.367
7735	M76670	Lycopersicon esculentum extensin (class I)	129	24.510
7737	M76670	Lycopersicon esculentum extensin (class I)	170	31.250
7739	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	211	73.333
7740	AF000298	Caenorhabditis elegans weak similarity to collagens; glycine- and proline-rich	144	38.043
7741	X64712	Gallus gallus collagen-alpha-3 type IX	149	37.113
7742	AB032961	Homo sapiens KIAA1135 protein	375	52.448
7743	AL022373	Arabidopsis thaliana putative protein	201	28.622
7745	Z50142	Schizosaccharomyces pombe hypothetical PHD-finger protein	164	33.036
7746	AB020642	Homo sapiens KIAA0835 protein	210	84.091
7747	X97675	Homo sapiens plakophilin 2b	159	86.207
7748	AF030131	Mus musculus Plenty of SH3s; POSH	2613	87.879
7749	Z11584	Homo sapiens NuMA protein	13102	99.054
7750	Z11584	Homo sapiens NuMA protein	10652	98.907
7751	Z11584	Homo sapiens NuMA protein	13010	99.810
7752	Z11584	Homo sapiens NuMA protein	520	86.408
7753	X16318	Canis familiaris 54k protein (AA 1-504)	367	100.000
7754	X16318	Canis familiaris 54k protein (AA 1-504)	3085	97.222
7755	AF083501	Macaca mulatta rhadinovirus 17577 latent nuclear antigen	186	30.075
7757	AF181250	Homo sapiens Ras guanine nucleotide exchange factor 2	951	51.196

7758	AF181250	Homo sapiens Ras guanine nucleotide exchange factor 2	942	98.611
7759	AF181250	Homo sapiens Ras guanine nucleotide exchange factor 2	8176	99.919
7760	AF181250	Homo sapiens Ras guanine nucleotide exchange factor 2	271	88.679
7761	AF026205	Caenorhabditis elegans No definition line found	162	25.589
7764	AJ006278	Mus musculus acetylglucosaminyltransferase-like protein	916	58.498
7765	AJ006278	Mus musculus acetylglucosaminyltransferase-like protein	1768	67.574
7766	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	56	42.857
7769	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	161	56.604
7770	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	46	23.529
7771	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	46	35.294
7772	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	235	68.966
7773	AF099989	Homo sapiens Ste-20 related kinase SPAK	547	94.565
7774	AF099989	Homo sapiens Ste-20 related kinase SPAK	274	69.136
7775	AJ005162	Homo sapiens UDP-glucuronosyltransferase	3531	98.864
7776	AJ005162	Homo sapiens UDP-glucuronosyltransferase	677	69.512
7777	AJ005162	Homo sapiens UDP-glucuronosyltransferase	3531	98.864
7778	AJ005162	Homo sapiens UDP-glucuronosyltransferase	3502	99.432
7779	U79260	Homo sapiens unknown	239	66.102
7782	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1038	93.443
7785	U09823	Oryctolagus cuniculus elongation factor 1 alpha	684	95.146
7786	U09823	Oryctolagus cuniculus elongation factor 1 alpha	746	94.118
7787	U09823	Oryctolagus cuniculus elongation factor 1 alpha	741	97.458
7788	U09823	Oryctolagus cuniculus elongation factor 1 alpha	625	49.853
7789	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2307	97.734
7790	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2228	96.335
7794	D64009	Mus musculus seizure-related gene product 6 type 2 precursor	551	94.186
7795	D64009	Mus musculus seizure-related gene product 6 type 2 precursor	67	31.250

7796	D64009	Mus musculus seizure-related gene product 6 type 2 precursor	2259	83.582
7799	AF047383	Homo sapiens uroporphyrinogen decarboxylase	661	100.000
7800	AF047383	Homo sapiens uroporphyrinogen decarboxylase	1046	88.701
7803	X07273	Mesocricetus auratus beta-myosin heavy chain (974 AA); S2 fragment and LMM region	245	70.270
7804	X07273	Mesocricetus auratus beta-myosin heavy chain (974 AA); S2 fragment and LMM region	561	83.803
7805	X70944	Homo sapiens PTB-associated splicing factor	206	40.230
7806	L20321	Homo sapiens protein serine/threonine kinase	146	57.895
7807	U79260	Homo sapiens unknown	382	71.910
7808	U79260	Homo sapiens unknown	267	61.290
7809	AF174427	Arabidopsis thaliana formin-like protein AHF1	107	39.024
7811	U38847	Homo sapiens TAR RNA loop binding protein	395	59.756
7812	U38847	Homo sapiens TAR RNA loop binding protein	2005	100.000
7814	U93568	Homo sapiens putative p150	250	73.585
7819	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	123	41.667
7821	M22334	Homo sapiens unknown protein	284	62.500
7823	U10281	Sus scrofa gastric mucin	146	33.071
7825	X97675	Homo sapiens plakophilin 2b	201	50.000
7839	AB033011	Homo sapiens KIAA1185 protein	249	97.297
7840	AB033011	Homo sapiens KIAA1185 protein	179	96.774
7841	AB033011	Homo sapiens KIAA1185 protein	1010	100.000
7843	M27878	Homo sapiens DNA binding protein	1209	53.074
7847	J01415	Homo sapiens cytochrome oxidase subunit 3	369	68.269
7848	J01415	Homo sapiens cytochrome oxidase subunit 3	191	90.625
7850	M87583	Equine infectious anemia virus deoxyuridine triphosphatase	118	23.770
7853	Y15918	Homo sapiens COL1A1 and PDGFB fusion transcript	126	36.364
7854	Y15918	Homo sapiens COL1A1 and PDGFB fusion transcript	89	27.215
7857	AL096723	Homo sapiens hypothetical protein	5411	100.000
7858	AL096723	Homo sapiens hypothetical protein	5205	94.667
7860	AF070561	Homo sapiens beta-tubulin	1756	79.657
7865	U66469	Homo sapiens cell growth regulator CGR19	289	95.652
7866	U66469	Homo sapiens cell growth regulator CGR19	1600	69.727
7867	X53795	Homo sapiens inducible membrane protein	463	100.000
7868	X53795	Homo sapiens inducible membrane	1265	100.000

		protein		
7869	M21332	Mus musculus 42 kd polypeptide (RD), (first expressed exon)	133	31.868
7870	D13748	Homo sapiens eukaryotic initiation factor 4AI	558	43.068
7871	D13748	Homo sapiens eukaryotic initiation factor 4AI	612	75.676
7872	D13748	Homo sapiens eukaryotic initiation factor 4AI	410	62.698
7873	D13748	Homo sapiens eukaryotic initiation factor 4AI	554	97.727
7874	D13748	Homo sapiens eukaryotic initiation factor 4AI	528	91.209
7875	D13748	Homo sapiens eukaryotic initiation factor 4AI	1732	85.817
7876	U86602	Homo sapiens nucleolar protein p40	593	74.400
7881	Z49127	Unknown Serine/proline rich protein; cDNA EST EMBL:D69024 comes from this gene; cDNA EST EMBL:D6989	146	33.333
7882	AL034559	Plasmodium falciparum predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa	78	46.154
7884	AF013213	Bos taurus elongation factor 1 alpha	213	97.500
7885	AF013213	Bos taurus elongation factor 1 alpha	582	79.661
7889	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	213	53.731
7890	AF058290	Homo sapiens imidazoline receptor antisera-selected protein	3988	100.000
7891	AF058290	Homo sapiens imidazoline receptor antisera-selected protein	148	44.595
7893	X55777	Homo sapiens put. ORF	243	64.407
7894	L24521	Homo sapiens transformation-related protein	286	60.759
7895	L24521	Homo sapiens transformation-related protein	178	60.000
7900	U22376	Homo sapiens alternatively spliced product using exon 13A	335	74.627
7903	S63654	Mus sp. type VII collagen	163	32.051
7904	S78454	Mus musculus metal response element DNA-binding protein M96	1243	96.985
7905	S78454	Mus musculus metal response element DNA-binding protein M96	154	58.696
7906	M10126	Leishmania tarentolae NH2 terminus uncertain	169	24.201
7907	AF176688	Rattus norvegicus sodium/calcium/potassium exchanger NCKX1	193	33.333
7914	Z70690	Schizosaccharomyces pombe hypothetical coiled-coil protein	102	29.060
7915	Z70690	Schizosaccharomyces pombe hypothetical coiled-coil protein	149	23.009
7916	AL049487	Arabidopsis thaliana putative protein	173	30.769
7920	X70944	Homo sapiens PTB-associated splicing factor	195	39.744
7921	S58722	Homo sapiens X-linked retinopathy	66	47.826

		protein {C-terminal, clone XEH.8c}		
7922	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	258	67.692
7924	AB020656	Homo sapiens KIAA0849 protein	867	86.228
7925	AB020656	Homo sapiens KIAA0849 protein	998	98.052
7927	D28818	Mus musculus NBL4	456	45.238
7945	X67863	Mus musculus T2	177	52.000
7946	AE002089	Deinococcus radiodurans hypothetical protein	138	30.208
7949	V00503	Homo sapiens procollagen (1 is 3rd base in codon)	142	37.736
7950	V00503	Homo sapiens procollagen (1 is 3rd base in codon)	100	36.458
7951	V00503	Homo sapiens procollagen (1 is 3rd base in codon)	191	28.000
7953	AJ010063	Homo sapiens telethonin	742	100.000
7954	AJ010063	Homo sapiens telethonin	1016	95.833
7955	M29863	Homo sapiens farnesyl pyrophosphate synthetase	771	89.552
7956	M29863	Homo sapiens farnesyl pyrophosphate synthetase	214	48.315
7957	M29863	Homo sapiens farnesyl pyrophosphate synthetase	1930	96.275
7958	AF046873	Homo sapiens synapsin IIIa	144	27.068
7960	X92485	Plasmodium vivax pval	126	73.913
7962	U22376	Homo sapiens alternatively spliced product using exon 13A	258	49.020
7963	U81031	Homo sapiens KIAA0167	5287	95.607
7964	U81031	Homo sapiens KIAA0167	359	55.970
7968	AF038599	Sus scrofa env protein	226	24.521
7970	Z86099	human herpesvirus 2 UL26.5	80	47.059
7971	Z86099	human herpesvirus 2 UL26.5	161	30.682
7972	Z36715	Homo sapiens Net	2500	98.775
7973	Z36715	Homo sapiens Net	2129	98.503
7977	D88461	Rattus rattus N-WASP	246	36.601
7979	Y14690	Homo sapiens procollagen alpha 2(V)	169	32.919
7980	M36676	Homo sapiens apolipoprotein B100	2164	99.710
7981	M36676	Homo sapiens apolipoprotein B100	2104	99.710
7982	AF078866	Homo sapiens SURF-4	685	84.397
7983	AF078866	Homo sapiens SURF-4	1557	97.778
7989	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	236	61.667
7992	U22376	Homo sapiens alternatively spliced product using exon 13A	243	53.165
7996	D50086	Mus musculus neuropilin	49	23.077
7998	AB001563	Homo sapiens RES4-22D	842	61.044
7999	AB001563	Homo sapiens RES4-22D	4596	100.000
8000	AB001563	Homo sapiens RES4-22D	4411	99.533
8001	AB001563	Homo sapiens RES4-22D	1759	100.000
8002	AB001563	Homo sapiens RES4-22D	4493	98.943
8003	D87744	Mus musculus DRPLA protein	154	36.667
8005	AF046873	Homo sapiens synapsin IIIa	152	27.976
8008	L07597	Homo sapiens ribosomal protein S6 kinase 1	4756	97.690

8009	L07597	Homo sapiens ribosomal protein S6 kinase 1	2480	86.313
8014	U79260	Homo sapiens unknown	382	71.910
8015	U79260	Homo sapiens unknown	267	61.290
8021	M25282	Paracentrotus lividus alpha collagen type 1 precursor	220	30.342
8023	AF036699	Caenorhabditis elegans Similar to cuticular collagen; F58F6.2	161	33.529
8024	AF036699	Caenorhabditis elegans Similar to cuticular collagen; F58F6.2	182	34.783
8027	A78803	unidentified unnamed protein product	769	90.071
8028	A78803	unidentified unnamed protein product	865	98.582
8029	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	199	56.250
8031	U09823	Oryctolagus cuniculus elongation factor 1 alpha	816	70.531
8033	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2333	90.578
8035	AF190797	Mus musculus actin-related protein 11	258	50.000
8037	X92485	Plasmodium vivax pval	134	67.742
8039	Z81592	Caenorhabditis elegans predicted using Genefinder; cDNA EST EMBL:M89005 comes from this gene	128	25.967
8042	U49974	Homo sapiens mariner transposase	491	70.690
8046	AB032905	Hylobates concolor dopamine receptor D4	68	30.952
8047	AB032905	Hylobates concolor dopamine receptor D4	155	38.462
8048	AB032905	Hylobates concolor dopamine receptor D4	139	35.714
8050	X55777	Homo sapiens put. ORF	165	48.333
8052	U79260	Homo sapiens unknown	194	43.678
8053	U79260	Homo sapiens unknown	282	57.692
8054	U79260	Homo sapiens unknown	141	42.857
8055	U79260	Homo sapiens unknown	138	48.889
8056	U79260	Homo sapiens unknown	351	70.213
8057	U79260	Homo sapiens unknown	263	60.241
8060	X92485	Plasmodium vivax pval	61	25.532
8061	X92485	Plasmodium vivax pval	146	86.364
8062	L15189	Homo sapiens MTHSP75	316	98.000
8063	L15189	Homo sapiens MTHSP75	4014	97.496
8064	U22376	Homo sapiens alternatively spliced product using exon 13A	377	78.082
8066	A61971	unidentified MCSP	76	29.167
8067	A61971	unidentified MCSP	56	33.333
8068	A61971	unidentified MCSP	66	37.209
8069	A61971	unidentified MCSP	1433	93.478
8070	X79440	Homo sapiens NADP+-dependent malic enzyme	865	77.320
8071	X79440	Homo sapiens NADP+-dependent malic enzyme	318	94.231
8072	X79440	Homo sapiens NADP+-dependent malic enzyme	3477	93.290
8073	L20321	Homo sapiens protein serine/threonine	160	58.696

		kinase		
8074	D25220	Bos taurus selenoprotein P like protein	130	35.849
8075	X55656	Homo sapiens gamma-G globin	958	97.333
8076	X55656	Homo sapiens gamma-G globin	435	87.261
8080	X97675	Homo sapiens plakophilin 2b	151	77.778
8081	X97675	Homo sapiens plakophilin 2b	198	84.375
8082	X97675	Homo sapiens plakophilin 2b	213	62.222
8083	X97675	Homo sapiens plakophilin 2b	166	66.667
8086	AF135789	Mus musculus m6a methyltransferase	1201	99.419
8087	AF135789	Mus musculus m6a methyltransferase	942	62.724
8092	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	1359	90.837
8093	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	162	92.593
8094	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase	1501	98.805
8096	AL050297	Homo sapiens hypothetical protein	117	30.233
8097	U88170	Caenorhabditis elegans No definition line found	401	44.156
8098	U88170	Caenorhabditis elegans No definition line found	375	32.258
8099	AF132941	Homo sapiens CGI-07 protein	197	93.939
8100	AF132941	Homo sapiens CGI-07 protein	3349	99.008
8102	X51755	Homo sapiens open reading frame (458 AA)	461	93.333
8103	X51755	Homo sapiens open reading frame (458 AA)	564	65.823
8104	X51755	Homo sapiens open reading frame (458 AA)	503	70.866
8105	X51755	Homo sapiens open reading frame (458 AA)	479	71.053
8106	X51755	Homo sapiens open reading frame (458 AA)	421	83.951
8108	X51755	Homo sapiens open reading frame (458 AA)	750	75.625
8111	X97675	Homo sapiens plakophilin 2b	46	23.913
8112	X97675	Homo sapiens plakophilin 2b	177	87.879
8113	X97675	Homo sapiens plakophilin 2b	186	76.316
8115	X80169	Mus musculus tsg24	607	80.374
8116	X80169	Mus musculus tsg24	76	25.974
8121	AJ006295	Rattus norvegicus AF-9	601	80.702
8122	AJ006295	Rattus norvegicus AF-9	1941	88.830
8126	AB002342	Homo sapiens KIAA0344	7872	99.838
8127	AB002342	Homo sapiens KIAA0344	7947	100.000
8129	AF182215	Tilapia mossambica chloride channel CLC-3	154	66.667
8130	AL096723	Homo sapiens hypothetical protein	5411	100.000
8131	AL096723	Homo sapiens hypothetical protein	835	80.899
8132	AL096723	Homo sapiens hypothetical protein	5103	93.826
8133	M22333	Homo sapiens unknown protein	42	50.000
8134	M22333	Homo sapiens unknown protein	1442	83.271
8135	M22333	Homo sapiens unknown protein	609	79.310
8136	Z66511	Unknown similar to ribokinase; cDNA	140	32.632

		EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 come		
8142	A00279	synthetic construct Human serum albumin	864	97.674
8143	A00279	synthetic construct Human serum albumin	548	39.286
8144	AF003540	Homo sapiens Krueppel family zinc finger protein	120	59.459
8150	AL035064	Schizosaccharomyces pombe queuine trna-ribosyltransferase	601	56.000
8152	AF007170	Homo sapiens unknown	1781	58.176
8158	U79260	Homo sapiens unknown	397	63.636
8159	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	122	28.378
8160	AC005396	Arabidopsis thaliana putative proline-rich cell wall protein	202	34.234
8163	Z66496	Unknown cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA	144	33.708
8164	Z66496	Unknown cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA	97	23.596
8165	Z66496	Unknown cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA	47	58.333
8167	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	158	64.706
8169	U64856	Caenorhabditis elegans weak similarity to TPR domains	219	41.346
8170	U64856	Caenorhabditis elegans weak similarity to TPR domains	705	43.089
8171	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	278	71.212
8172	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	297	54.808
8175	X97675	Homo sapiens plakophilin 2b	194	62.500
8177	Y09085	Mus musculus hypoxia-inducible factor one alpha	505	60.355
8178	Y09085	Mus musculus hypoxia-inducible factor one alpha	1122	80.000
8182	AL032653	Caenorhabditis elegans similar to Ubiquitin-conjugating enzymes; cDNA EST EMBL:C08678 comes from this gene	442	74.684
8183	AL032653	Caenorhabditis elegans similar to Ubiquitin-conjugating enzymes; cDNA EST EMBL:C08678 comes from this gene	499	56.463
8184	L20321	Homo sapiens protein serine/threonine kinase	186	66.667
8187	K02212	Homo sapiens alpha-1-antitrypsin	605	90.179
8188	K02212	Homo sapiens alpha-1-antitrypsin	1278	78.214
8192	U66469	Homo sapiens cell growth regulator CGR19	289	95.652
8193	U66469	Homo sapiens cell growth regulator CGR19	1340	66.484
8194	D00654	Homo sapiens enteric smooth muscle	1047	94.545

		gamma-actin		
8195	D00654	Homo sapiens enteric smooth muscle gamma-actin	1012	93.750
8196	D00654	Homo sapiens enteric smooth muscle gamma-actin	1808	84.319
8200	AB028980	Homo sapiens KIAA1057 protein	253	32.787
8202	Z46267	Caenorhabditis elegans cDNA EST yk251d5.5 comes from this gene; cDNA EST yk356d9.5 comes from this gene; cDNA EST yk377h11.5 comes from this gene	133	25.410
8203	M60626	Homo sapiens N-formylpeptide receptor fMLP-R98	686	74.627
8204	M60626	Homo sapiens N-formylpeptide receptor fMLP-R98	1753	86.908
8207	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	242	70.909
8208	AB028997	Homo sapiens KIAA1074 protein	713	38.202
8212	AL117448	Homo sapiens hypothetical protein	177	86.667
8213	L40157	Homo sapiens endosome-associated protein	168	27.053
8214	L40157	Homo sapiens endosome-associated protein	159	29.310
8215	Z48166	Schizosaccharomyces pombe gar2	113	26.471
8217	U78524	Homo sapiens Gu binding protein	1339	98.522
8218	U78524	Homo sapiens Gu binding protein	300	100.000
8219	D29677	Homo sapiens KIAA0054	4168	68.302
8220	D29677	Homo sapiens KIAA0054	13192	100.000
8221	AC006963	Homo sapiens similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	1563	92.800
8224	AF198532	Homo sapiens lymphoid enhancer binding factor-1	193	100.000
8225	AE000528	Helicobacter pylori 26695 H. pylori predicted coding region HP0059	107	24.359
8227	L22453	Homo sapiens TARBP-b gene product	946	74.091
8228	L22453	Homo sapiens TARBP-b gene product	420	95.890
8229	L22453	Homo sapiens TARBP-b gene product	758	70.934
8232	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	278	71.212
8233	S58722	Homo sapiens X-linked retinopathy protein {C-terminal, clone XEH.8c}	297	54.808
8234	S66385	Mus sp. CREB-binding protein, CBP	58	35.294
8235	S66385	Mus sp. CREB-binding protein, CBP	272	33.742
8239	Z79754	Caenorhabditis elegans Similarity to some phosphatases and kinases; cDNA EST EMBL:Z14643 comes from this gene; cDNA EST yk531b4.3 comes from this gene; cDNA EST yk642e5.3 comes from this gene	354	41.935
8240	Z79754	Caenorhabditis elegans Similarity to some phosphatases and kinases; cDNA EST EMBL:Z14643 comes from this gene; cDNA EST yk531b4.3 comes from this gene; cDNA EST yk642e5.3 comes from	913	60.748

		this gene		
8241	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	265	70.370
8242	M84911	Pseudomonas aeruginosa ORF located downstream of mmsAB operon, has sequence similarity to an acetyl-CoA synthetase; ORF1; putative	662	58.385
8243	M84911	Pseudomonas aeruginosa ORF located downstream of mmsAB operon, has sequence similarity to an acetyl-CoA synthetase; ORF1; putative	679	53.297
8247	L16547	Bos taurus chloride channel protein	55	36.364
8248	L16547	Bos taurus chloride channel protein	521	80.612
8250	U08813	Oryctolagus cuniculus 597 aa protein related to Na/glucose cotransporters	1509	75.490
8251	U08813	Oryctolagus cuniculus 597 aa protein related to Na/glucose cotransporters	1401	69.486
8252	D78348	Canis familiaris zymogen granule membrane associated protein	344	48.039
8253	AF115480	Mus musculus cAMP-dependent Rap1 guanine-nucleotide exchange factor	226	35.849
8257	U70063	Homo sapiens acid ceramidase	431	95.588
8258	U70063	Homo sapiens acid ceramidase	2293	95.214
8259	X54422	Mytilus edulis polyphenolic adhesive protein	85	20.202
8260	X54422	Mytilus edulis polyphenolic adhesive protein	143	29.070
8261	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	186	38.144
8262	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	119	37.255
8263	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	183	95.833
8264	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	188	56.818
8267	M81483	Mus musculus calmodulin dependent phosphatase catalytic subunit	822	89.189
8268	M81483	Mus musculus calmodulin dependent phosphatase catalytic subunit	869	97.183
8269	M81483	Mus musculus calmodulin dependent phosphatase catalytic subunit	172	100.000
8270	AB033026	Homo sapiens KIAA1200 protein	213	89.189
8271	AJ249706	Mus musculus myosin X	318	87.931
8272	X97675	Homo sapiens plakophilin 2b	172	78.125
8274	AF126867	Mus musculus calpain-like protease	558	70.000
8275	AF126867	Mus musculus calpain-like protease	66	30.000
8277	AF131820	Homo sapiens Unknown	453	90.909
8278	AF131820	Homo sapiens Unknown	407	100.000
8279	AF131820	Homo sapiens Unknown	1134	76.022
8280	AL117452	Homo sapiens hypothetical protein	136	72.727
8281	AL117452	Homo sapiens hypothetical protein	398	75.862
8282	U34932	Rattus norvegicus Fos-related antigen	301	68.421
8283	D88026	Mus musculus DhM2 protein	219	84.848
8286	AF017306	Homo sapiens UnpES	560	75.591

8287	AF017306	Homo sapiens UnpES	343	98.077
8288	AF017306	Homo sapiens UnpES	1415	100.000
8289	U54638	Mus musculus rhotekin	149	38.983
8291	L05424	Homo sapiens cell surface glycoprotein CD44	4568	99.555
8292	L05424	Homo sapiens cell surface glycoprotein CD44	449	87.671
8296	U23147	Caenorhabditis elegans No definition line found	323	31.282
8298	AB018335	Homo sapiens KIAA0792 protein	777	67.456
8299	AB018335	Homo sapiens KIAA0792 protein	47	37.500
8300	X91879	Homo sapiens sperm specific protein	190	86.111
8302	X90858	Homo sapiens uridine phosphorylase	481	85.882
8303	X90858	Homo sapiens uridine phosphorylase	209	91.667
8304	X90858	Homo sapiens uridine phosphorylase	939	94.611
8306	U51576	Felis catus MHC class II antigen	1332	79.921
8307	U51576	Felis catus MHC class II antigen	139	95.238
8308	U51576	Felis catus MHC class II antigen	1269	84.375
8309	AB013384	Homo sapiens HIP1R	47	36.364
8310	AB013384	Homo sapiens HIP1R	2810	56.262
8311	AB013384	Homo sapiens HIP1R	5628	100.000
8312	AB013384	Homo sapiens HIP1R	207	100.000
8315	AF118125	Homo sapiens polycystin-2-like protein	190	21.456
8316	Z77660	Homo sapiens Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from th	270	44.898
8319	AF078777	Homo sapiens ABC transporter	199	100.000
8325	X51829	Mus musculus MyD116 protein (AA 1-657)	147	37.143
8329	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	48	40.000
8330	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	48	40.000
8331	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	57	36.842
8332	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683)	159	70.000
8333	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	141	42.857
8335	U61262	Homo sapiens neogenin	352	82.609
8338	AB007897	Homo sapiens KIAA0437	335	56.701
8340	AB023224	Homo sapiens KIAA1007 protein	307	97.674
8341	AB023224	Homo sapiens KIAA1007 protein	6808	96.621
8342	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1051	88.830
8343	U09823	Oryctolagus cuniculus elongation factor 1 alpha	948	91.304
8344	U09823	Oryctolagus cuniculus elongation factor 1 alpha	807	97.541
8345	U09823	Oryctolagus cuniculus elongation factor 1 alpha	612	78.195
8346	U09823	Oryctolagus cuniculus elongation factor 1 alpha	764	63.404
8347	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1441	94.805

8396	X99211	Drosophila melanogaster ubiquitin-specific protease	281	55.000
8397	X53778	Homo sapiens uracil DNA glycosylase	622	87.903
8398	X53778	Homo sapiens uracil DNA glycosylase	1251	83.673
8400	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	134	29.870
8401	X13482	Homo sapiens U2 snRNP-specific A' protein (AA 1-255)	167	26.712
8403	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	133	25.610
8404	X90568	Homo sapiens Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	10724	87.211
8406	AF191018	Homo sapiens E2IG3	3666	100.000
8407	AF191018	Homo sapiens E2IG3	1772	85.445
8411	U00968	Homo sapiens SREBP-1	532	100.000
8412	U00968	Homo sapiens SREBP-1	380	69.792
8413	AF181856	Rattus norvegicus tRNA selenocysteine associated protein	380	93.333
8414	AF165163	Mus musculus growth suppressor 1L	461	52.893
8415	AF165163	Mus musculus growth suppressor 1L	49	26.744
8416	AF165163	Mus musculus growth suppressor 1L	916	40.097
8418	AB020706	Homo sapiens KIAA0899 protein	287	97.619
8419	AB020706	Homo sapiens KIAA0899 protein	5715	98.499
8428	AF039698	Homo sapiens antigen NY-CO-33	393	47.619
8431	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2684	90.217
8432	U09823	Oryctolagus cuniculus elongation factor 1 alpha	1960	85.124
8433	AB018566	Homo sapiens Proline synthetase associated	468	100.000
8434	AB018566	Homo sapiens Proline synthetase associated	500	93.827
8435	AB018566	Homo sapiens Proline synthetase associated	1261	88.542
8436	Z83864	Mycobacterium tuberculosis hypothetical protein Rv3835	117	53.846
8437	M22334	Homo sapiens unknown protein	126	70.833
8439	U97079	Mus musculus U5-116kD	239	92.500
8440	U97079	Mus musculus U5-116kD	6344	98.561
8444	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2253	87.898
8445	AL031032	Arabidopsis thaliana extensin-like protein	323	40.157
8446	AF086702	Pseudorabies virus glycoprotein gD precursor	42	28.571
8447	AF086702	Pseudorabies virus glycoprotein gD precursor	158	47.692
8452	X04655	Rattus norvegicus synapsin I (AA 1-691)	50	47.826
8453	X04655	Rattus norvegicus synapsin I (AA 1-	58	70.000

8348	U09823	Oryctolagus cuniculus elongation factor 1 alpha	838	72.081
8349	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2307	79.874
8350	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2658	90.043
8351	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2575	97.985
8352	U09823	Oryctolagus cuniculus elongation factor 1 alpha	2735	94.635
8353	U29244	Caenorhabditis elegans No definition line found	319	36.806
8354	U29244	Caenorhabditis elegans No definition line found	254	43.956
8355	AF006621	Homo sapiens embryonic lung protein	373	65.049
8356	AF006621	Homo sapiens embryonic lung protein	1042	100.000
8357	AB029040	Homo sapiens KIAA1117 protein	468	98.701
8358	AB029040	Homo sapiens KIAA1117 protein	8967	100.000
8363	M76546	Helianthus annuus hydroxyproline-rich protein	129	33.898
8366	X80397	Streptococcus pyogenes orf1	131	29.814
8367	AF061258	Homo sapiens LIM protein	1304	95.238
8372	AF069602	Homo sapiens myosin light chain kinase isoform 3A	74	27.083
8373	AF069602	Homo sapiens myosin light chain kinase isoform 3A	68	30.986
8374	AF069602	Homo sapiens myosin light chain kinase isoform 3A	61	24.167
8375	AF069602	Homo sapiens myosin light chain kinase isoform 3A	75	57.692
8377	AF069602	Homo sapiens myosin light chain kinase isoform 3A	74	34.177
8378	AF069602	Homo sapiens myosin light chain kinase isoform 3A	68	35.556
8379	AF069602	Homo sapiens myosin light chain kinase isoform 3A	65	29.825
8380	AF069602	Homo sapiens myosin light chain kinase isoform 3A	103	27.933
8381	AF069602	Homo sapiens myosin light chain kinase isoform 3A	330	57.944
8382	AF069602	Homo sapiens myosin light chain kinase isoform 3A	61	20.213
8383	U82535	Homo sapiens fatty acid amide hydrolase	817	88.435
8384	U82535	Homo sapiens fatty acid amide hydrolase	3884	99.827
8385	U82535	Homo sapiens fatty acid amide hydrolase	163	96.000
8387	AB011157	Homo sapiens KIAA0585 protein	131	100.000
8390	U64601	Caenorhabditis elegans Gene probably begins in the next cosmid	547	63.025
8391	Y19188	Homo sapiens aczonin	148	33.333
8394	X90858	Homo sapiens uridine phosphorylase	381	87.671
8395	X90858	Homo sapiens uridine phosphorylase	1551	93.269

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		691)		
8454	X04655	Rattus norvegicus synapsin I (AA 1-691)	98	24.561
8455	X75947	Mus musculus mCBP	488	83.654
8456	X75947	Mus musculus mCBP	1071	82.807
8457	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	796	96.094
8458	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	4177	96.997
8459	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	194	60.345
8460	Z28407	Homo sapiens ribosomal protein L8	846	79.121
8461	Z28407	Homo sapiens ribosomal protein L8	1379	91.603
8463	AF109906	Mus musculus NG22	69	31.667
8464	AF109906	Mus musculus NG22	138	28.767
8469	A03758	Homo sapiens serum albumin	996	87.912
8470	A03758	Homo sapiens serum albumin	705	55.039
8473	A03758	Homo sapiens serum albumin	1099	65.033
8474	A03758	Homo sapiens serum albumin	1334	68.293
8475	A03758	Homo sapiens serum albumin	2767	77.094
8476	A03758	Homo sapiens serum albumin	1566	87.279
8477	A03758	Homo sapiens serum albumin	1083	99.387
8478	A03758	Homo sapiens serum albumin	3469	74.031
8481	AB002375	Homo sapiens KIAA0377	143	67.647
8482	X99711	Spodoptera littoralis nuclear polyhedrosis virus orf 1035	140	32.692
8485	X97675	Homo sapiens plakophilin 2b	191	70.270
8488	AF096709	Drosophila virilis failed axon connections protein	237	35.971
8489	AF096709	Drosophila virilis failed axon connections protein	235	40.952
8490	L23113	Homo sapiens binding protein	598	95.876
8491	L23113	Homo sapiens binding protein	2918	89.101
8492	L23113	Homo sapiens binding protein	2881	87.103
8493	L23113	Homo sapiens binding protein	371	98.438
8494	L23113	Homo sapiens binding protein	3158	98.476
8497	AF106685	Homo sapiens myelin gene expression factor 2	1442	99.107
8499	AF034580	Mus musculus TSG118.1	270	43.796
8500	AF034580	Mus musculus TSG118.1	1622	58.378
8501	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	66	21.505
8502	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	400	36.723

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		691)		
8454	X04655	Rattus norvegicus synapsin I (AA 1-691)	98	24.561
8455	X75947	Mus musculus mCBP	488	83.654
8456	X75947	Mus musculus mCBP	1071	82.807
8457	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	796	96.094
8458	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	4177	96.997
8459	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	194	60.345
8460	Z28407	Homo sapiens ribosomal protein L8	846	79.121
8461	Z28407	Homo sapiens ribosomal protein L8	1379	91.603
8463	AF109906	Mus musculus NG22	69	31.667
8464	AF109906	Mus musculus NG22	138	28.767
8469	A03758	Homo sapiens serum albumin	996	87.912
8470	A03758	Homo sapiens serum albumin	705	55.039
8473	A03758	Homo sapiens serum albumin	1099	65.033
8474	A03758	Homo sapiens serum albumin	1334	68.293
8475	A03758	Homo sapiens serum albumin	2767	77.094
8476	A03758	Homo sapiens serum albumin	1566	87.279
8477	A03758	Homo sapiens serum albumin	1083	99.387
8478	A03758	Homo sapiens serum albumin	3469	74.031
8481	AB002375	Homo sapiens KIAA0377	143	67.647
8482	X99711	Spodoptera littoralis nuclear polyhedrosis virus orf 1035	140	32.692
8485	X97675	Homo sapiens plakophilin 2b	191	70.270
8488	AF096709	Drosophila virilis failed axon connections protein	237	35.971
8489	AF096709	Drosophila virilis failed axon connections protein	235	40.952
8490	L23113	Homo sapiens binding protein	598	95.876
8491	L23113	Homo sapiens binding protein	2918	89.101
8492	L23113	Homo sapiens binding protein	2881	87.103
8493	L23113	Homo sapiens binding protein	371	98.438
8494	L23113	Homo sapiens binding protein	3158	98.476
8497	AF106685	Homo sapiens myelin gene expression factor 2	1442	99.107
8499	AF034580	Mus musculus TSG118.1	270	43.796
8500	AF034580	Mus musculus TSG118.1	1622	58.378
8501	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	66	21.505
8502	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	400	36.723

		691)		
8454	X04655	Rattus norvegicus synapsin I (AA 1-691)	98	24.561
8455	X75947	Mus musculus mCBP	488	83.654
8456	X75947	Mus musculus mCBP	1071	82.807
8457	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	796	96.094
8458	AL049709	Homo sapiens dJ18C9.2 (novel gene (locus D20S101) similar to Gamma-glutamyltranspeptidase, contains CCA trinucleotide repeat, based on Genscan and Fgenesh predictions.)	4177	96.997
8459	AF010144	Homo sapiens neuronal thread protein AD7c-NTP	194	60.345
8460	Z28407	Homo sapiens ribosomal protein L8	846	79.121
8461	Z28407	Homo sapiens ribosomal protein L8	1379	91.603
8463	AF109906	Mus musculus NG22	69	31.667
8464	AF109906	Mus musculus NG22	138	28.767
8469	A03758	Homo sapiens serum albumin	996	87.912
8470	A03758	Homo sapiens serum albumin	705	55.039
8473	A03758	Homo sapiens serum albumin	1099	65.033
8474	A03758	Homo sapiens serum albumin	1334	68.293
8475	A03758	Homo sapiens serum albumin	2767	77.094
8476	A03758	Homo sapiens serum albumin	1566	87.279
8477	A03758	Homo sapiens serum albumin	1083	99.387
8478	A03758	Homo sapiens serum albumin	3469	74.031
8481	AB002375	Homo sapiens KIAA0377	143	67.647
8482	X99711	Spodoptera littoralis nuclear polyhedrosis virus orf 1035	140	32.692
8485	X97675	Homo sapiens plakophilin 2b	191	70.270
8488	AF096709	Drosophila virilis failed axon connections protein	237	35.971
8489	AF096709	Drosophila virilis failed axon connections protein	235	40.952
8490	L23113	Homo sapiens binding protein	598	95.876
8491	L23113	Homo sapiens binding protein	2918	89.101
8492	L23113	Homo sapiens binding protein	2881	87.103
8493	L23113	Homo sapiens binding protein	371	98.438
8494	L23113	Homo sapiens binding protein	3158	98.476
8497	AF106685	Homo sapiens myelin gene expression factor 2	1442	99.107
8499	AF034580	Mus musculus TSG118.1	270	43.796
8500	AF034580	Mus musculus TSG118.1	1622	58.378
8501	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	66	21.505
8502	Y12713	Mus musculus Pro-Pol-dUTPase polyprotein	400	36.723

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